

	Report	
	Bacillus_subtilis-8_fa	Bacillus_subtilis-8_fa_broken
# contigs (>= 0 bp)	192	-
# contigs (>= 1000 bp)	82	85
Total length (>= 0 bp)	4166779	-
Total length (>= 1000 bp)	4145005	4143314
# contigs	85	89
Largest contig	286084	245642
Total length	4146817	4145994
Reference length	4299632	4299632
GC (%)	43.27	43.27
Reference GC (%)	43.35	43.35
N50	93665	93665
NG50	89587	89587
N90	30816	30816
NG90	23003	19092
auN	112356.0	103457.6
auNG	108362.7	99760.8
L50	14	15
LG50	15	16
L90	44	45
LG90	49	51
# misassemblies	58	58
# misassembled contigs	29	30
Misassembled contigs length	2285594	2284626
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	3
# unaligned contigs	20 + 53 part	22 + 54 part
Unaligned length	573878	573878
Genome fraction (%)	83.519	83.445
Duplication ratio	1.001	1.001
# N's per 100 kbp	7.23	0.00
# mismatches per 100 kbp	1244.25	1244.53
# indels per 100 kbp	43.83	43.22
# genomic features	7374 + 239 part	7361 + 241 part
# predicted rRNA genes	5 + 3 part	4 + 4 part
Largest alignment	241424	241424
Total aligned length	3568655	3567932
NA50	44292	43313
NGA50	43313	42941
NA90	-	-
NGA90	-	-
auNA	65047.4	63098.6
auNGA	62735.6	60843.9
LA50	25	26
LGA50	26	27
LA90	-	-
LGA90	-	-

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

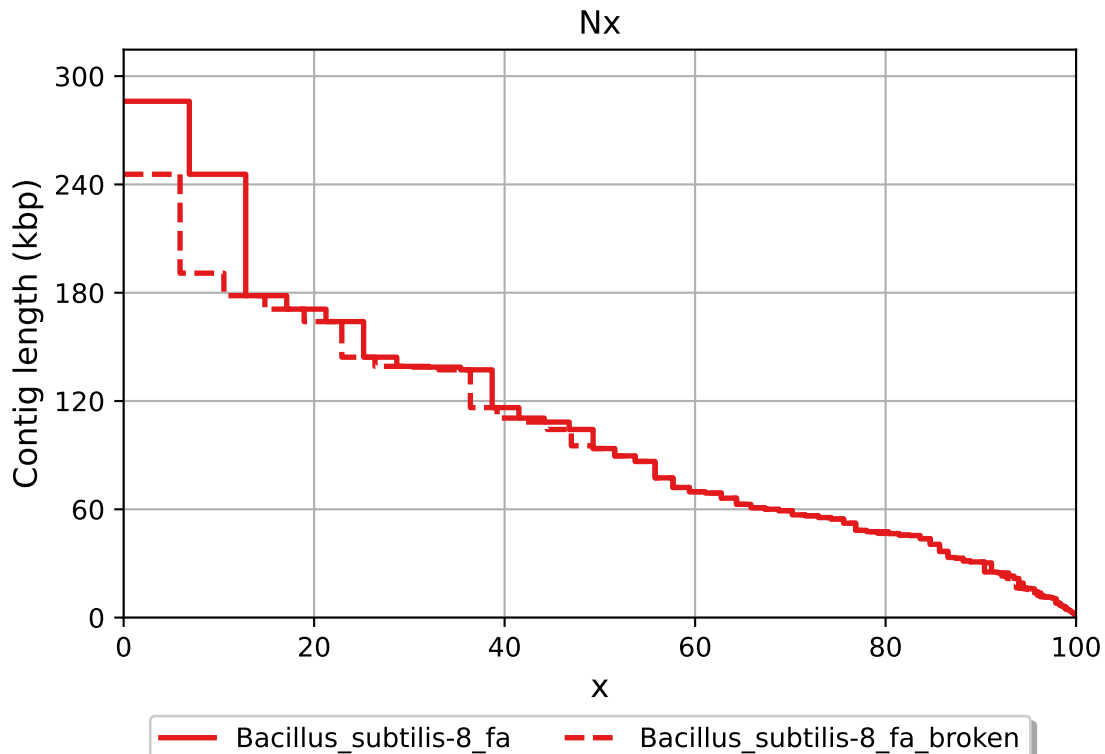
	Bacillus_subtilis-8_fa	Bacillus_subtilis-8_fa_broken
# misassemblies	58	58
# contig misassemblies	58	58
# c. relocations	56	56
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	29	30
Misassembled contigs length	2285594	2284626
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	3
# mismatches	44403	44404
# indels	1564	1542
# indels (<= 5 bp)	1376	1366
# indels (> 5 bp)	188	176
Indels length	7905	7241

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).

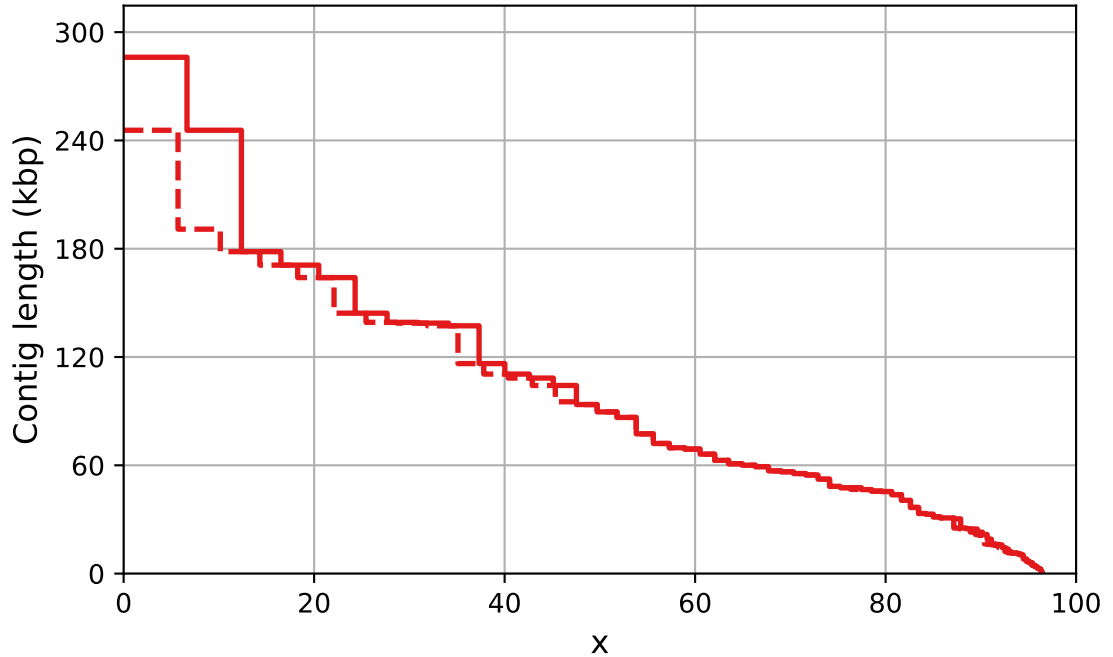
Unaligned report

	Bacillus_subtilis-8_fa	Bacillus_subtilis-8_fa_broken
# fully unaligned contigs	20	22
Fully unaligned length	187440	187440
# partially unaligned contigs	53	54
Partially unaligned length	386438	386438
# N's	300	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).

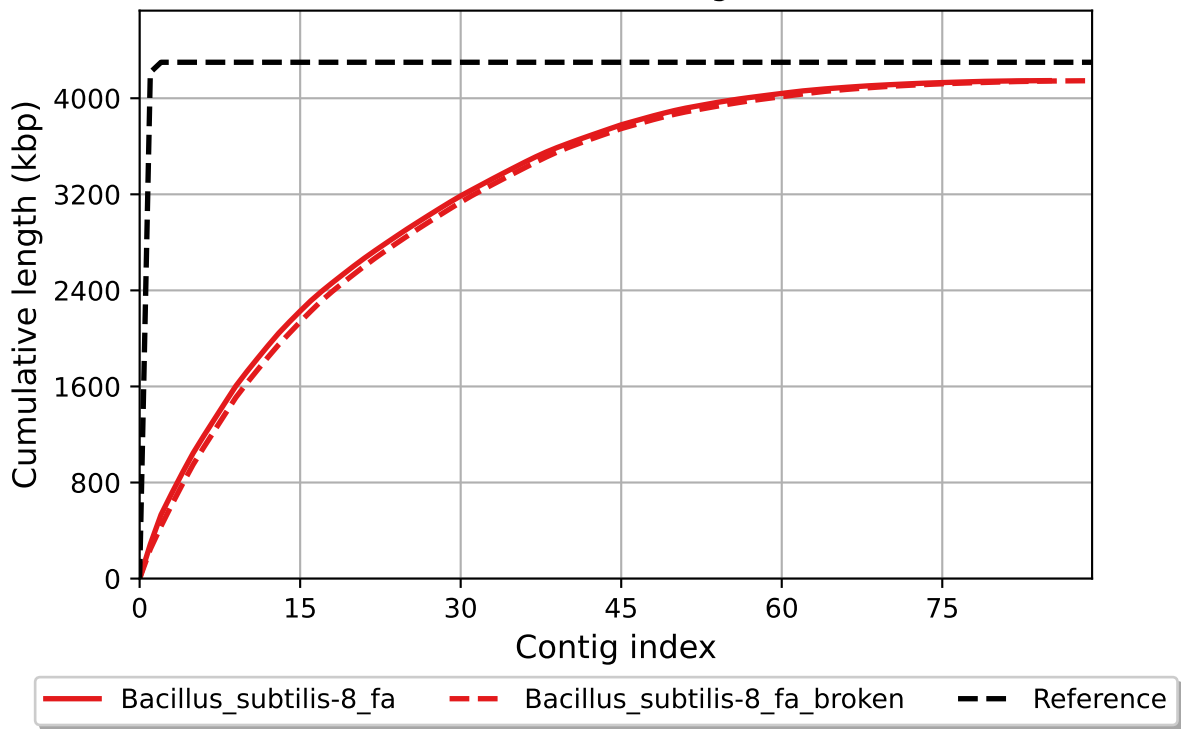


NGx

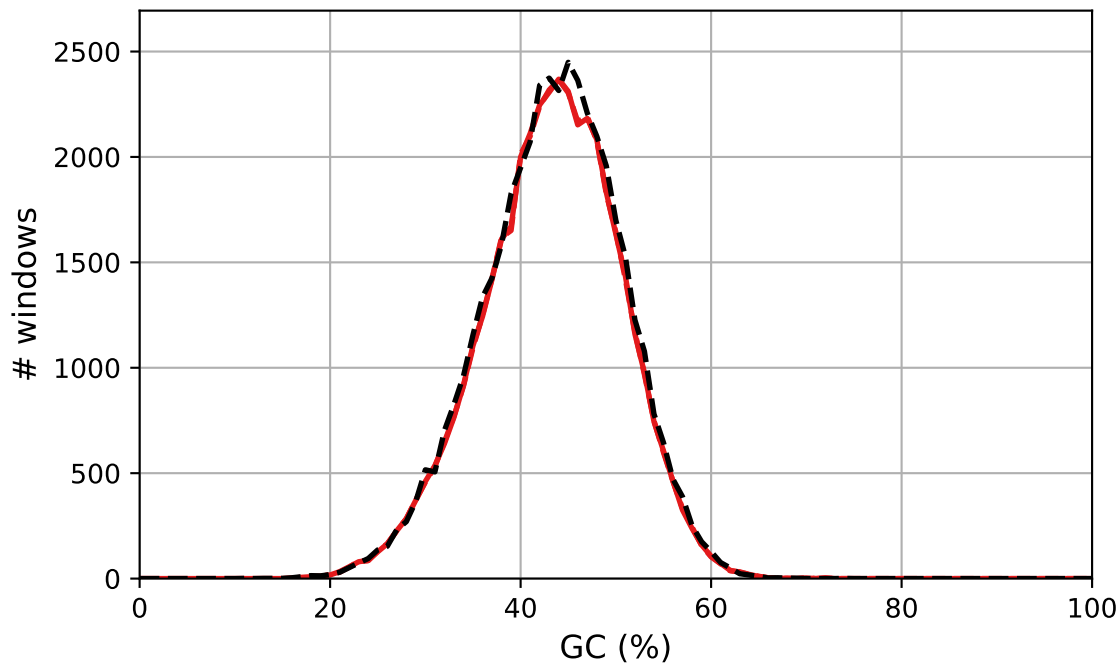


— Bacillus_subtilis-8_fa - - - Bacillus_subtilis-8_fa_broken

Cumulative length

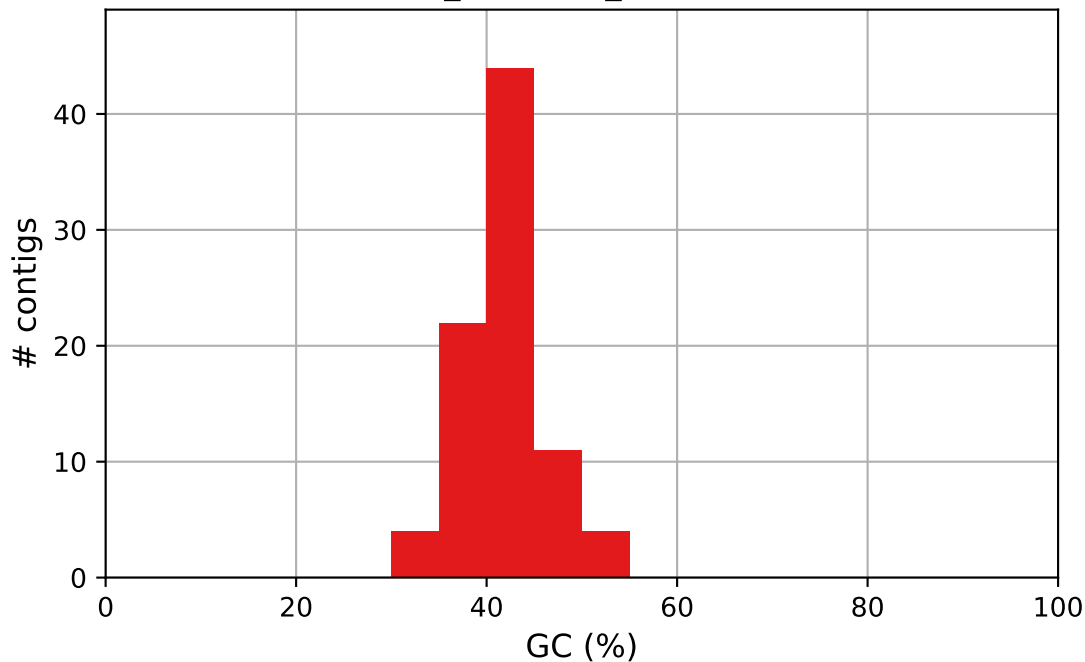


GC content



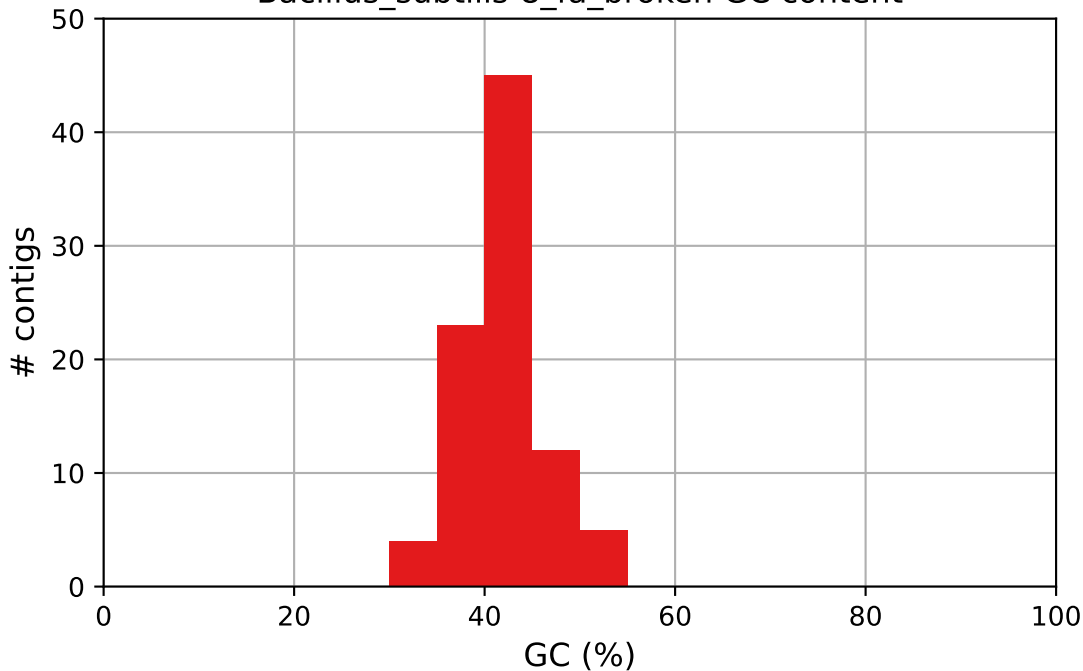
— Bacillus_subtilis-8_fa - - Bacillus_subtilis-8_fa_broken - - Reference

Bacillus_subtilis-8_fa GC content



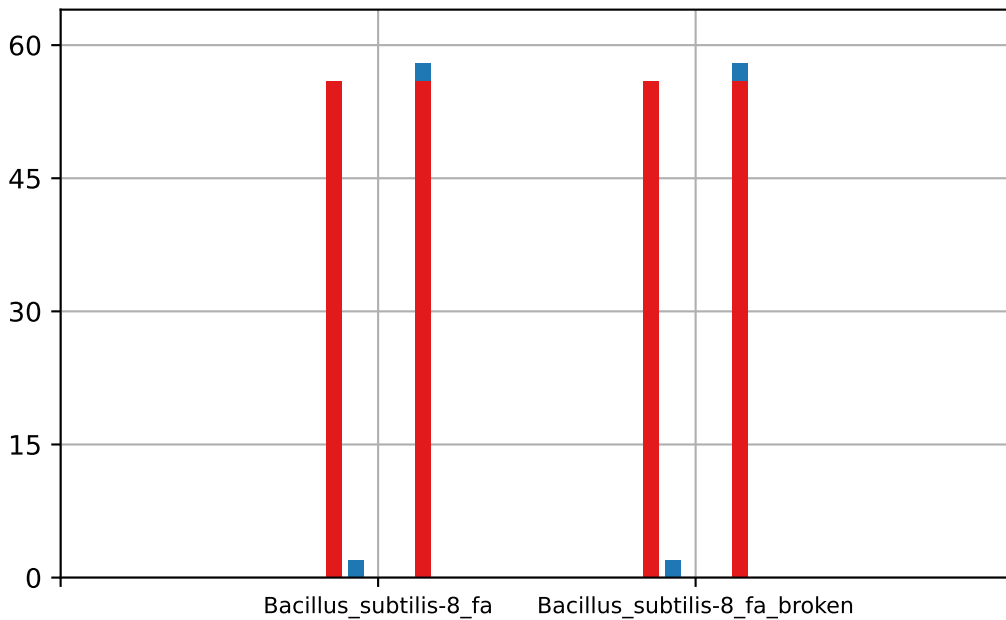
Bacillus_subtilis-8_fa

Bacillus_subtilis-8_fa_broken GC content



Bacillus_subtilis-8_fa_broken

Misassemblies

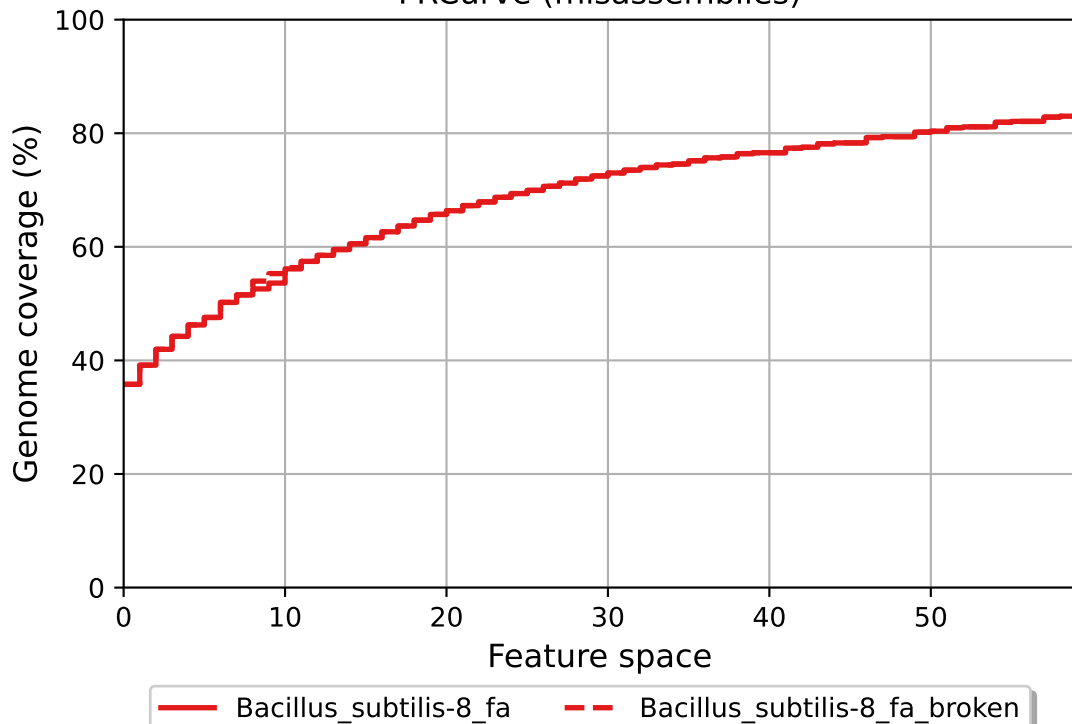


relocations

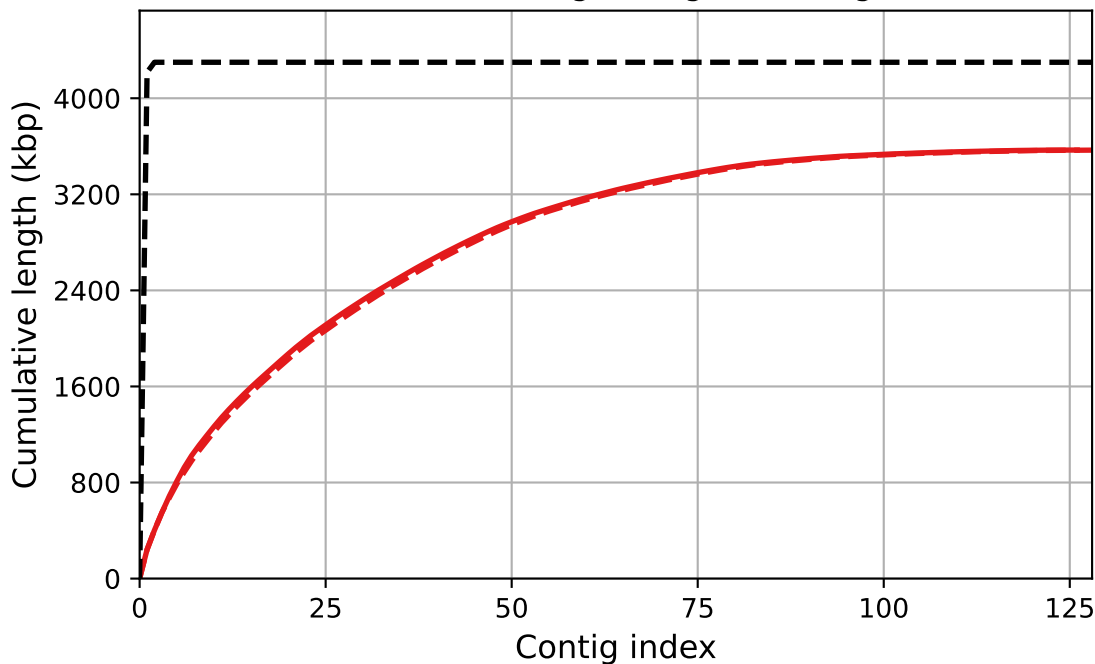


translocations

FRCurve (misassemblies)

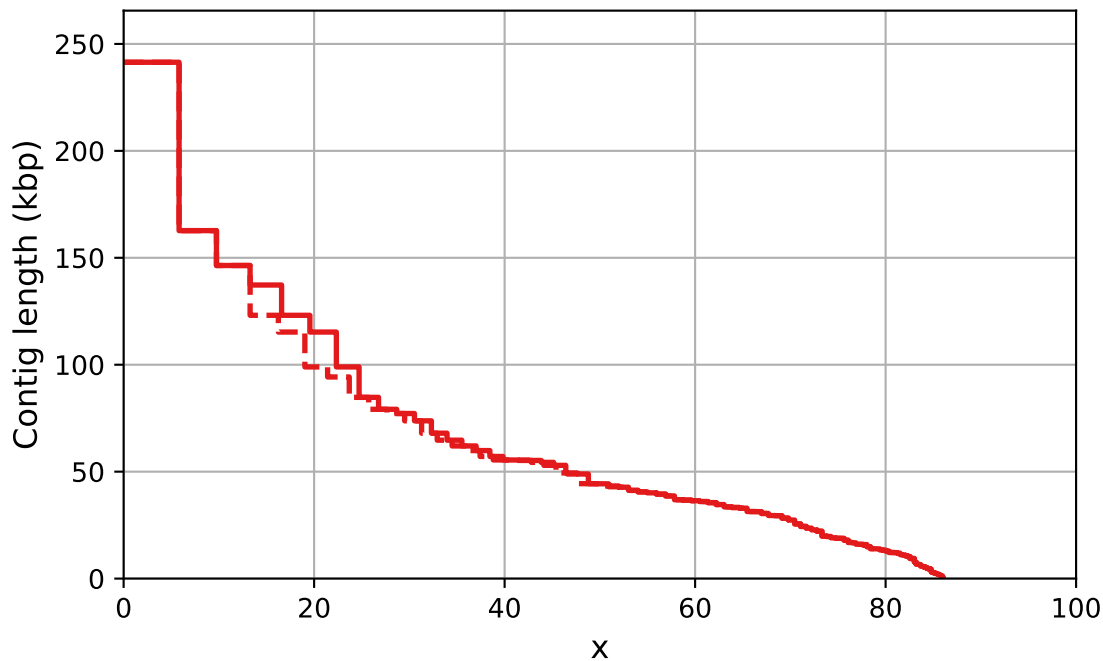


Cumulative length (aligned contigs)



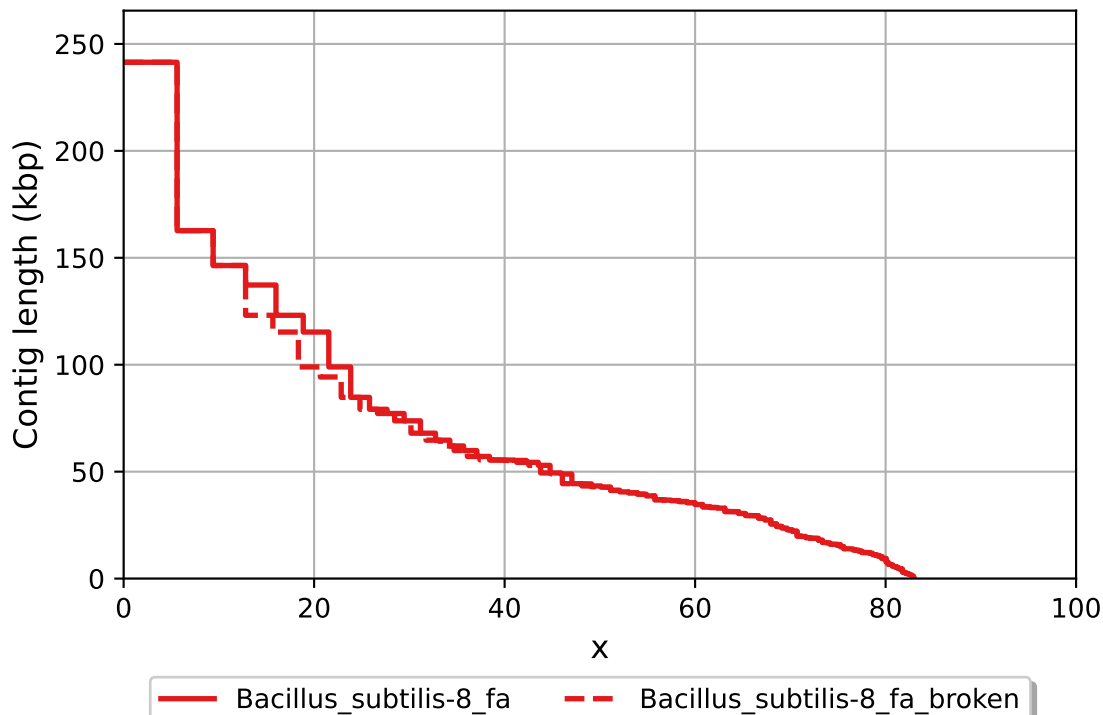
— Bacillus_subtilis-8_fa - - Bacillus_subtilis-8_fa_broken - - Reference

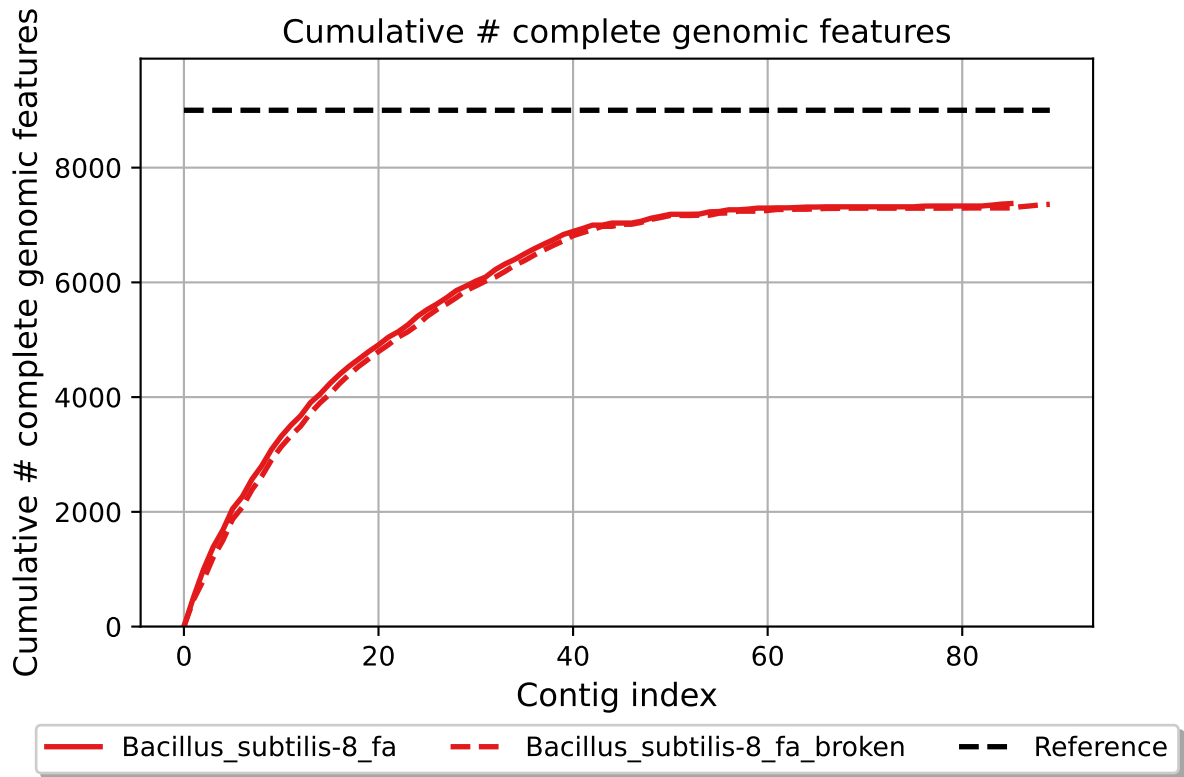
NAx



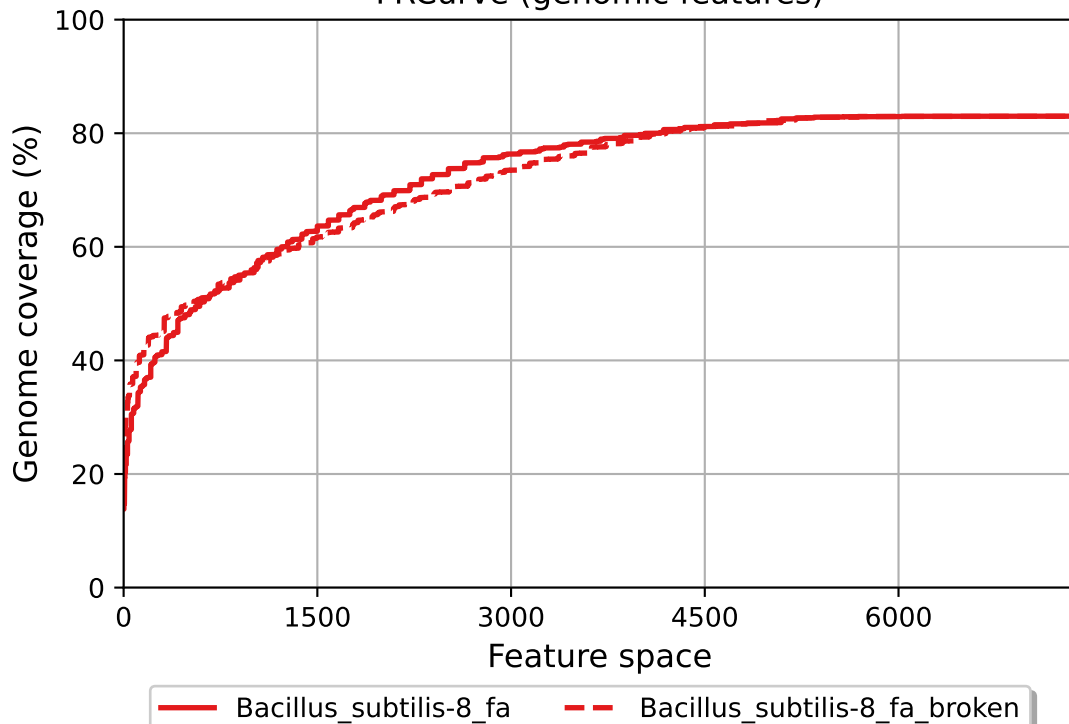
— Bacillus_subtilis-8_fa - - - Bacillus_subtilis-8_fa_broken

NGAx

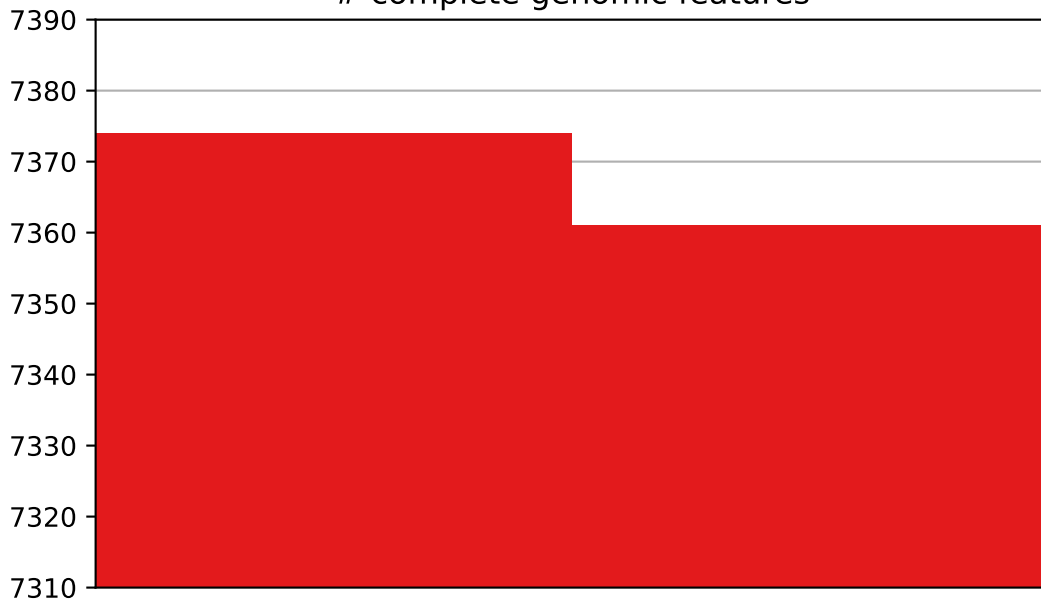




FRCurve (genomic features)



complete genomic features



Bacillus_subtilis-8_fa



Bacillus_subtilis-8_fa_broken

Genome fraction, %



Bacillus_subtilis-8_fa



Bacillus_subtilis-8_fa_broken