

Report

	ypestis-8_fa	ypestis-8_fa_broken
# contigs (>= 0 bp)	1114	-
# contigs (>= 1000 bp)	397	397
Total length (>= 0 bp)	4669048	-
Total length (>= 1000 bp)	4518129	4515405
# contigs	449	453
Largest contig	56670	56670
Total length	4552839	4552639
Reference length	4658411	4658411
GC (%)	47.58	47.58
Reference GC (%)	47.63	47.63
N50	17523	17523
NG50	16980	16980
N90	5751	5751
NG90	4849	4849
auN	19845.1	19843.0
auNG	19395.4	19392.5
L50	84	84
LG50	87	87
L90	256	256
LG90	275	275
# misassemblies	29	29
# misassembled contigs	27	27
Misassembled contigs length	473856	473856
# local misassemblies	13	13
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	12 + 16 part	13 + 15 part
Unaligned length	137929	137891
Genome fraction (%)	95.635	95.629
Duplication ratio	1.009	1.009
# N's per 100 kbp	4.39	0.00
# mismatches per 100 kbp	9.36	9.36
# indels per 100 kbp	4.92	4.74
# genomic features	7775 + 521 part	7773 + 521 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 1 part	2 + 2 part
Largest alignment	55685	55685
Total aligned length	4411191	4411043
NA50	16553	16553
NGA50	16189	16189
NA90	4282	4282
NGA90	3375	3375
auNA	18519.8	18519.1
auNGA	18100.1	18098.6
LA50	89	89
LGA50	93	93
LA90	284	284
LGA90	308	308

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

	ypestis-8_fa	ypestis-8_fa_broken
# misassemblies	29	29
# contig misassemblies	29	29
# c. relocations	28	28
# c. translocations	0	0
# c. inversions	1	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	27	27
Misassembled contigs length	473856	473856
# local misassemblies	13	13
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	413	413
# indels	217	209
# indels (<= 5 bp)	92	86
# indels (> 5 bp)	125	123
Indels length	4567	4466

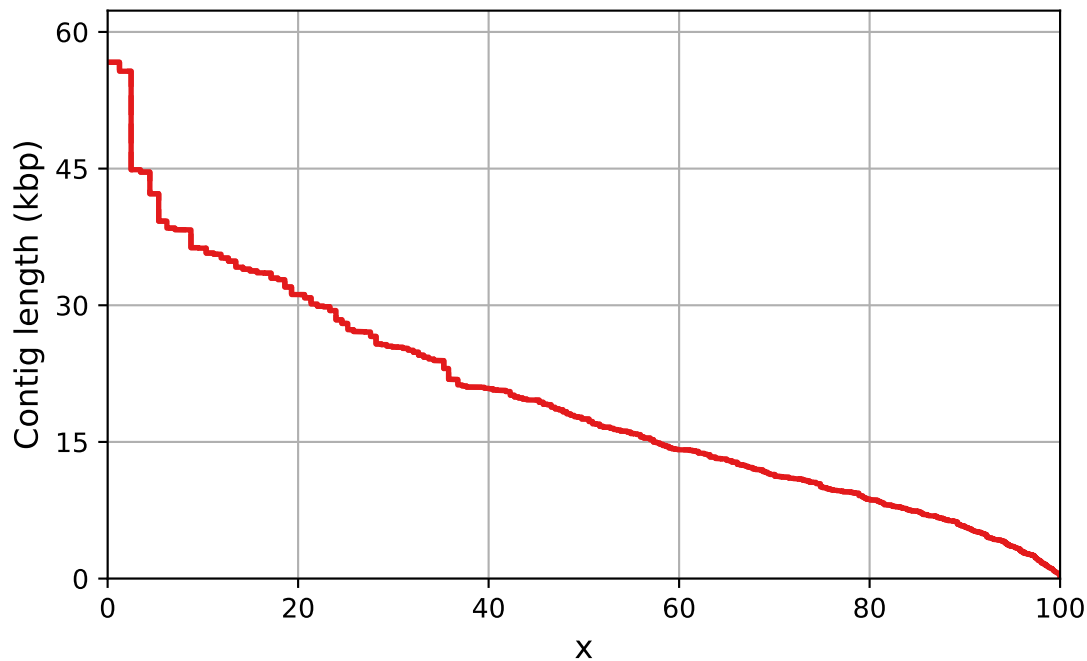
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ypestis-8_fa	ypestis-8_fa_broken
# fully unaligned contigs	12	13
Fully unaligned length	31748	32709
# partially unaligned contigs	16	15
Partially unaligned length	106181	105182
# N's	200	0

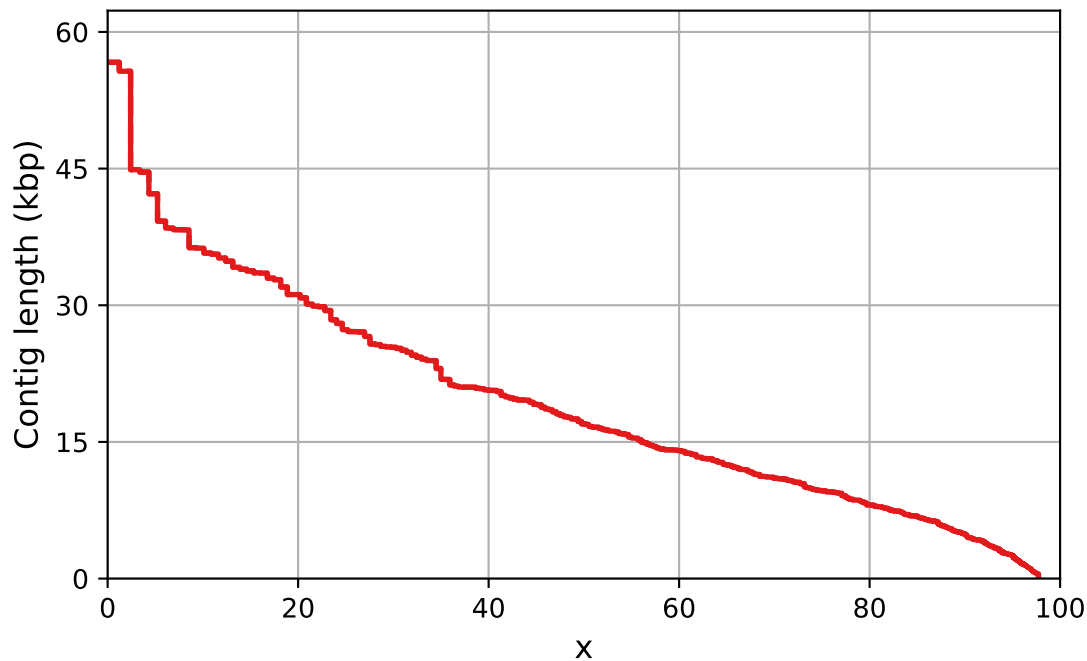
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

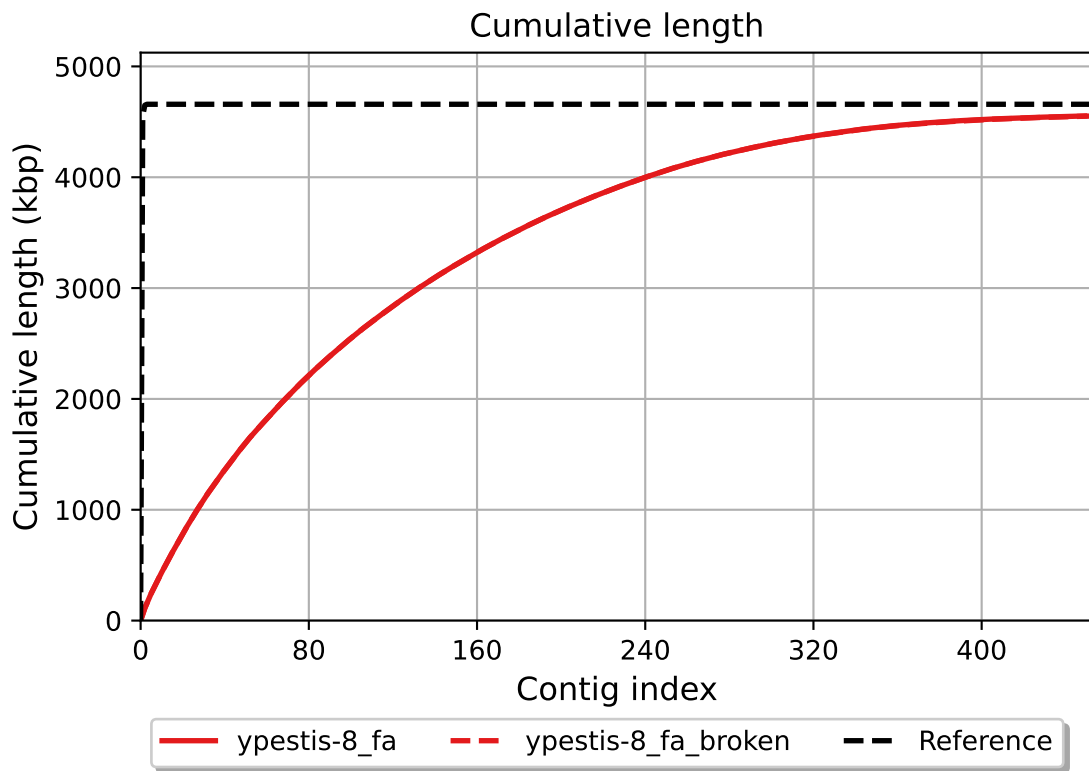


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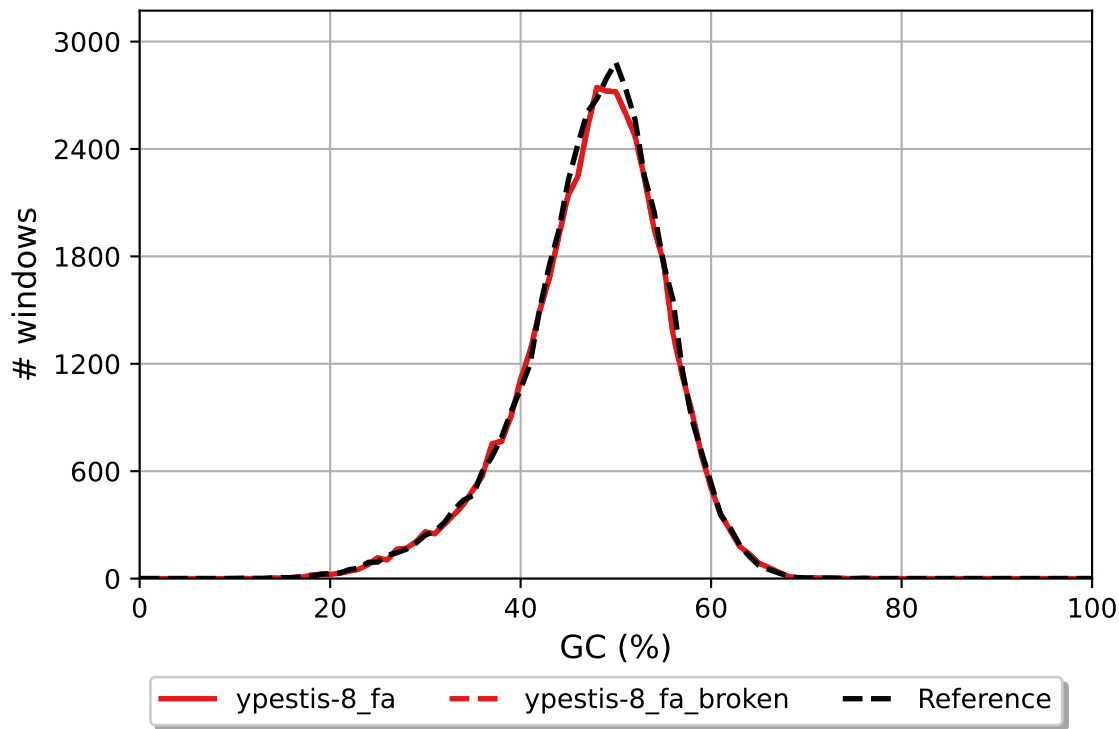
NGx



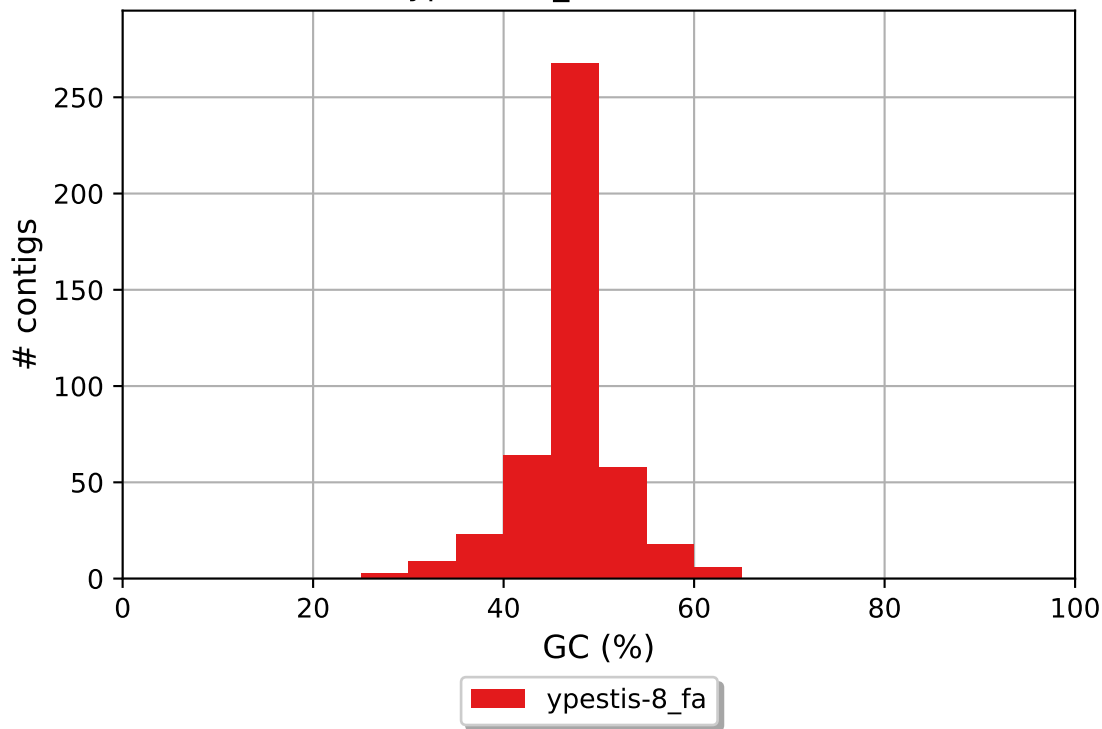
ypestis-8_fa ypestis-8_fa_broken



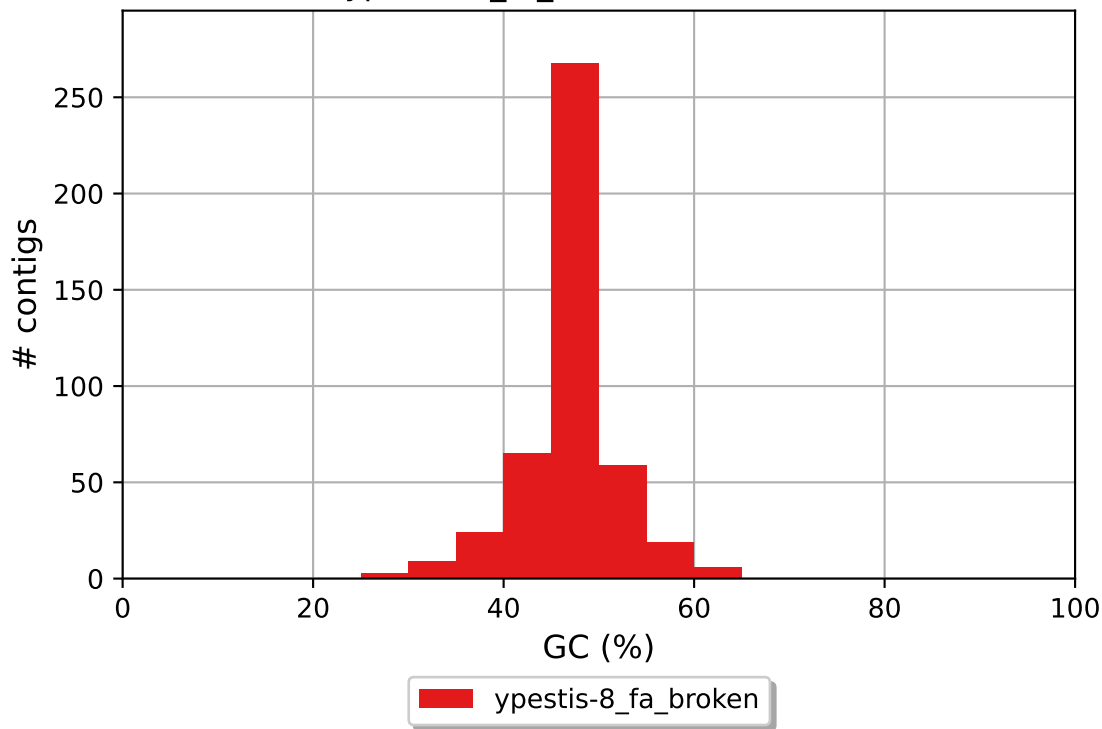
GC content



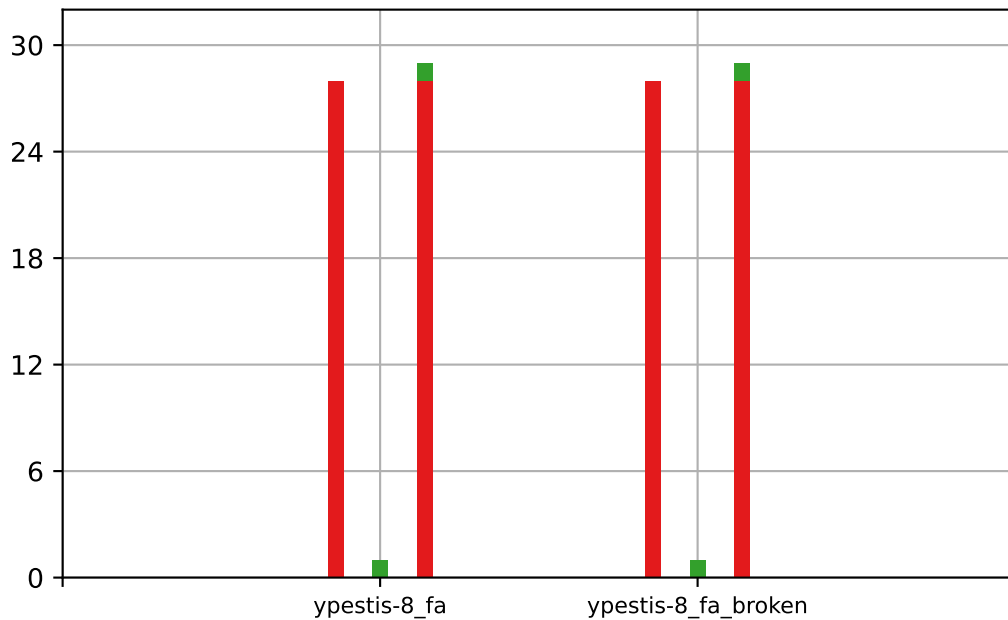
ypestis-8_fa GC content



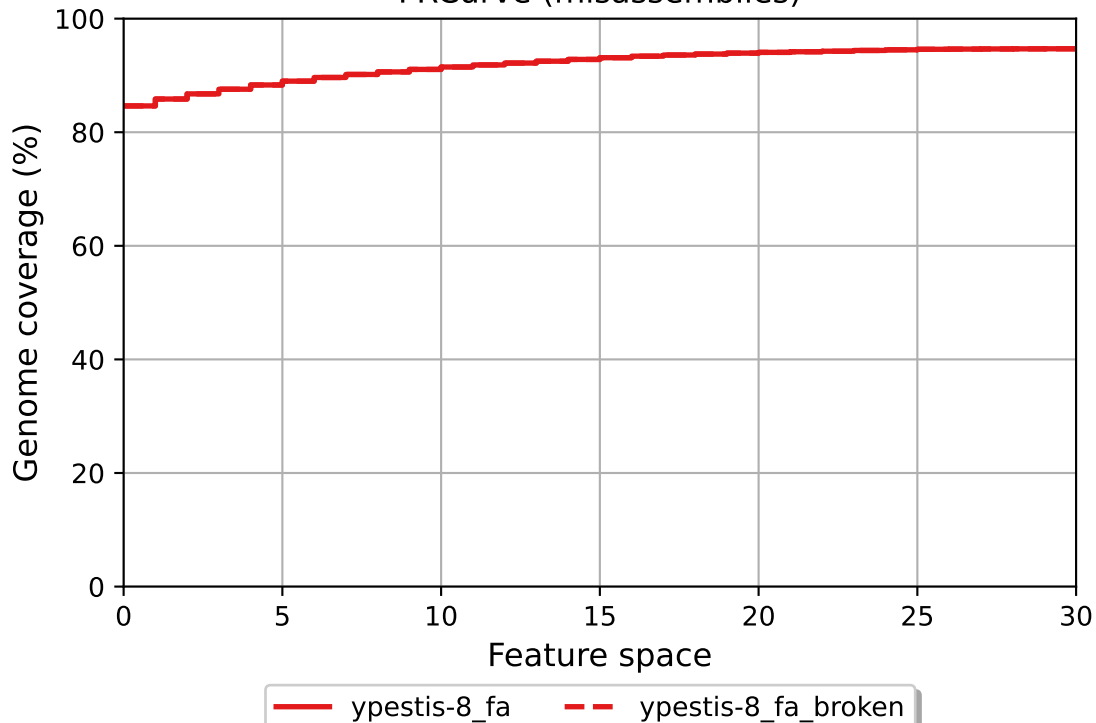
ypestis-8_fa_broken GC content



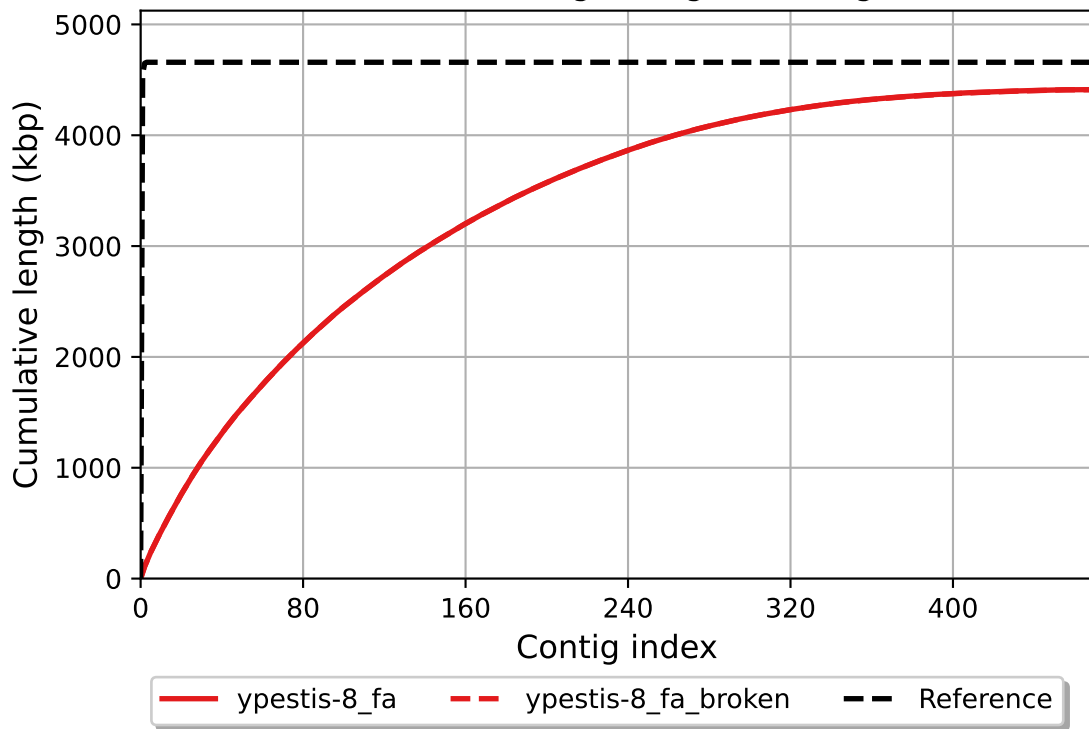
Misassemblies



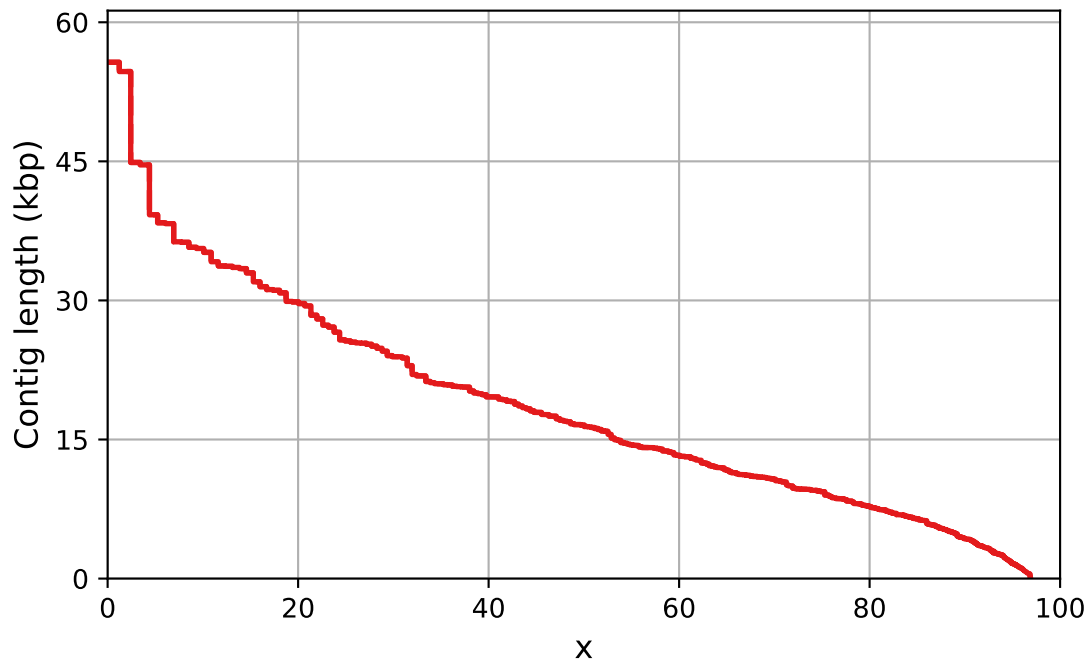
FRCurve (misassemblies)



Cumulative length (aligned contigs)

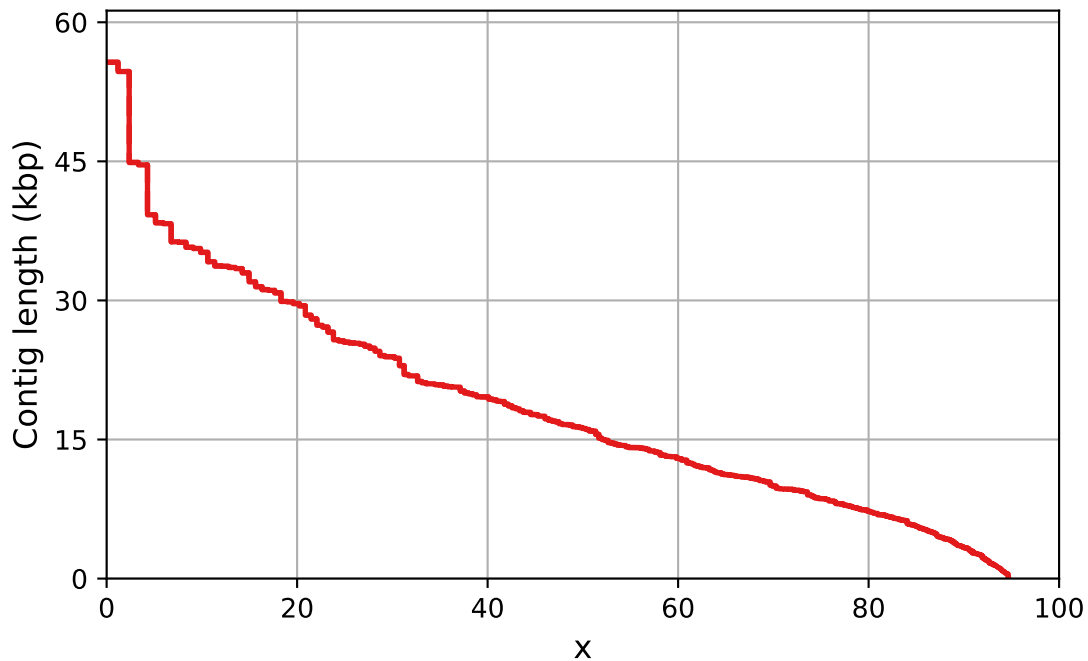


NAx



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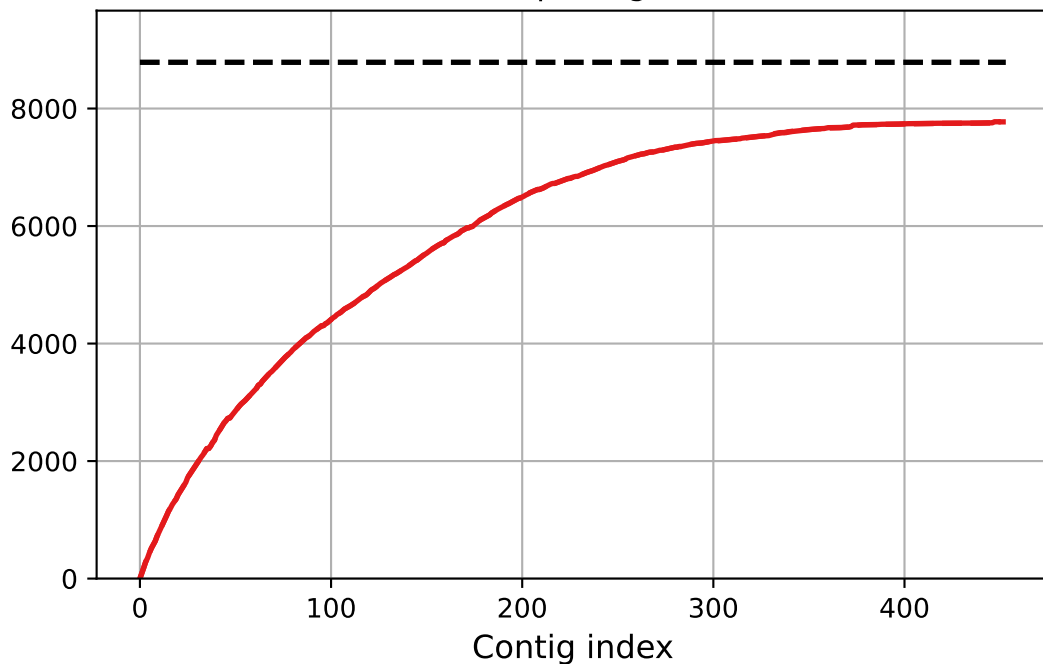
NGAx



ypestis-8_fa ypestis-8_fa_broken

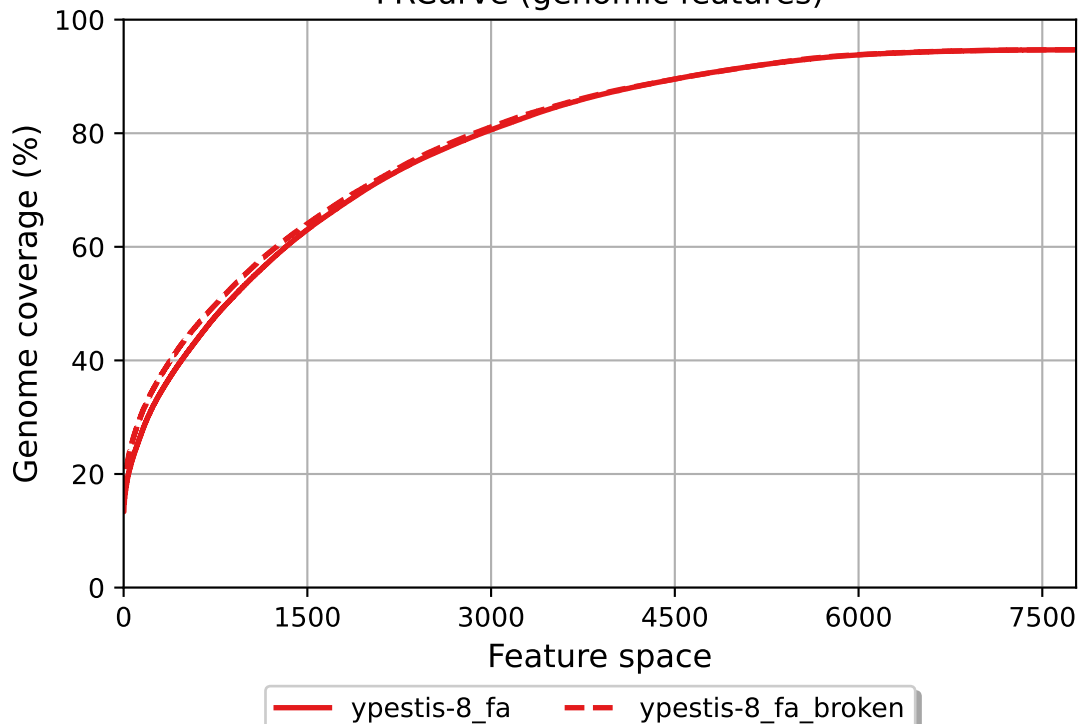
Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)



complete genomic features



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Genome fraction, %



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