

Report

	KlebsiellaAbyssAssembly-8_fa	KlebsiellaAbyssAssembly-8_fa_broken
# contigs (>= 0 bp)	233	-
# contigs (>= 1000 bp)	114	126
Total length (>= 0 bp)	5617775	-
Total length (>= 1000 bp)	5583469	5580090
# contigs	128	145
Largest contig	312358	290168
Total length	5594192	5593341
Reference length	5682322	5682322
GC (%)	57.17	57.17
Reference GC (%)	57.12	57.12
N50	99911	94728
NG50	94728	94728
N90	24478	22077
NG90	22711	19566
auN	128611.0	116006.8
auNG	126616.3	114190.2
L50	16	18
LG50	17	18
L90	60	66
LG90	63	69
# misassemblies	70	71
# misassembled contigs	39	44
Misassembled contigs length	3590696	3397484
# local misassemblies	26	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	5	4
# unaligned contigs	20 + 56 part	22 + 61 part
Unaligned length	747121	746809
Genome fraction (%)	84.860	85.227
Duplication ratio	1.013	1.013
# N's per 100 kbp	16.55	1.34
# mismatches per 100 kbp	684.94	685.67
# indels per 100 kbp	20.14	20.02
# genomic features	9591 + 282 part	9578 + 310 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 3 part	4 + 3 part
Largest alignment	205242	205242
Total aligned length	4845401	4844305
NA50	45003	42571
NGA50	42571	42390
NA90	-	-
NGA90	-	-
auNA	64170.0	62930.1
auNGA	63174.7	61944.7
LA50	31	32
LGA50	32	33
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

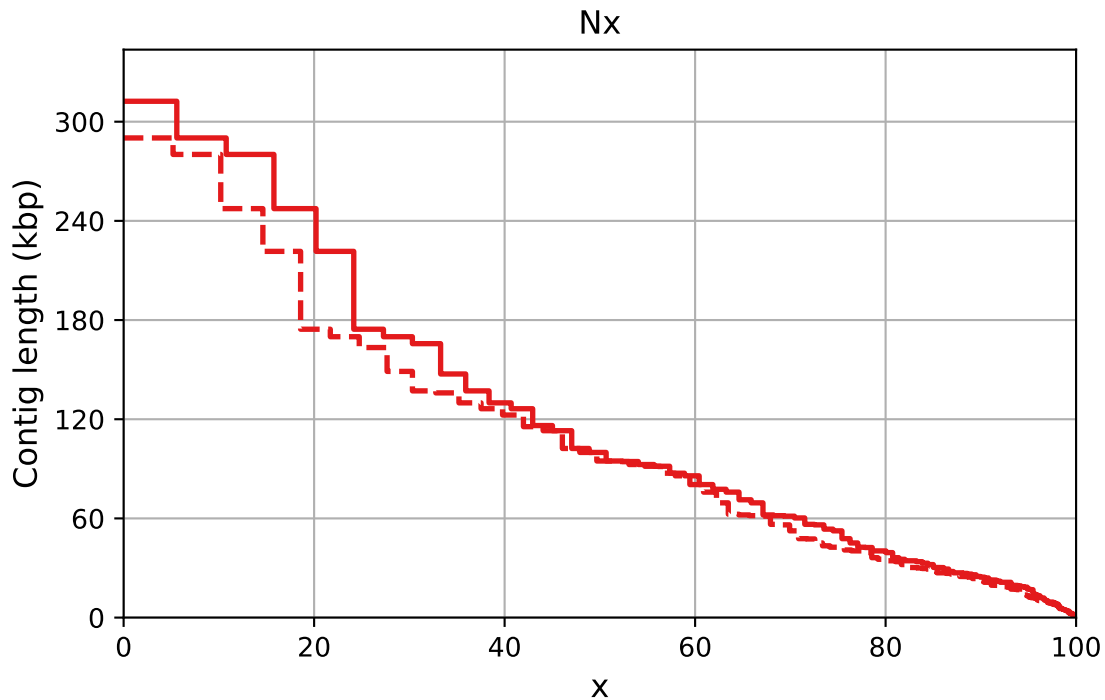
	KlebsiellaAbyssAssembly-8_fa	KlebsiellaAbyssAssembly-8_fa_broken
# misassemblies	70	71
# contig misassemblies	70	71
# c. relocations	68	69
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	39	44
Misassembled contigs length	3590696	3397484
# local misassemblies	26	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	5	4
# mismatches	33188	33216
# indels	976	970
# indels (<= 5 bp)	832	837
# indels (> 5 bp)	144	133
Indels length	10604	10011

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Unaligned report

	KlebsiellaAbyssAssembly-8_fa	KlebsiellaAbyssAssembly-8_fa_broken
# fully unaligned contigs	20	22
Fully unaligned length	67976	79872
# partially unaligned contigs	56	61
Partially unaligned length	679145	666937
# N's	926	75

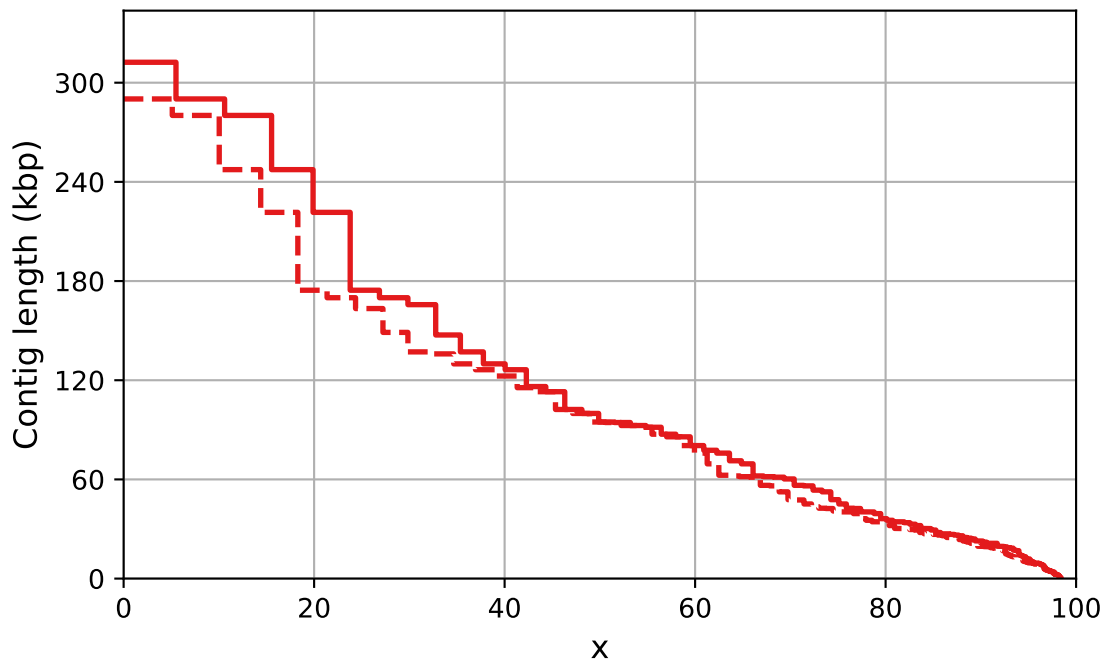
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— KlebsiellaAbyssAssembly-8_fa

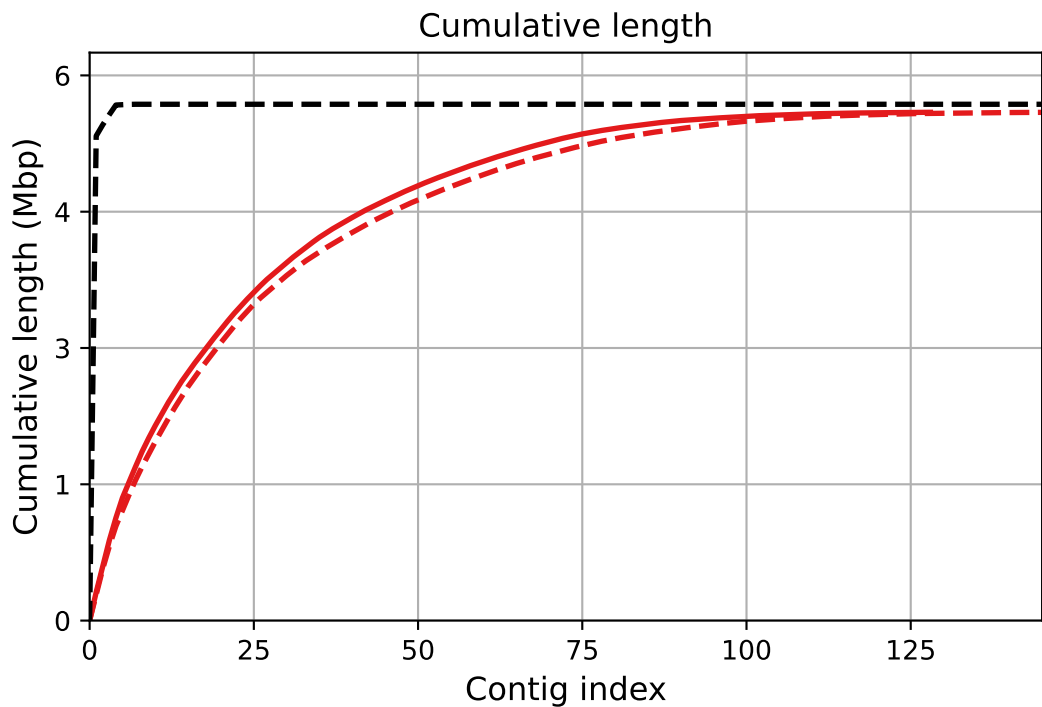
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NGx



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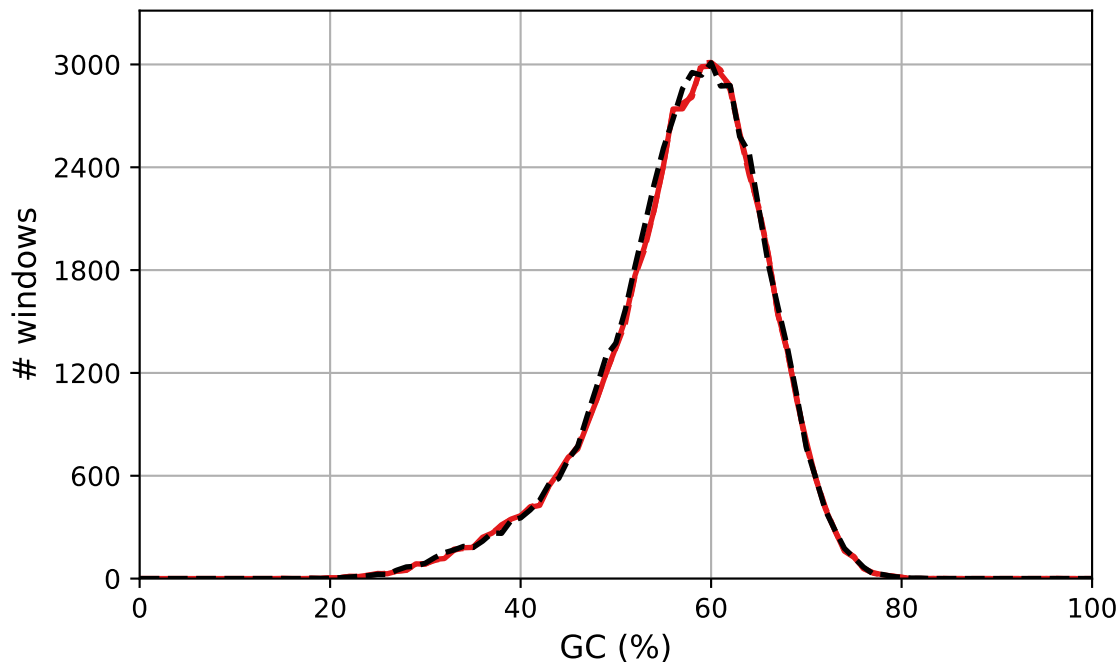


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--- Reference

GC content

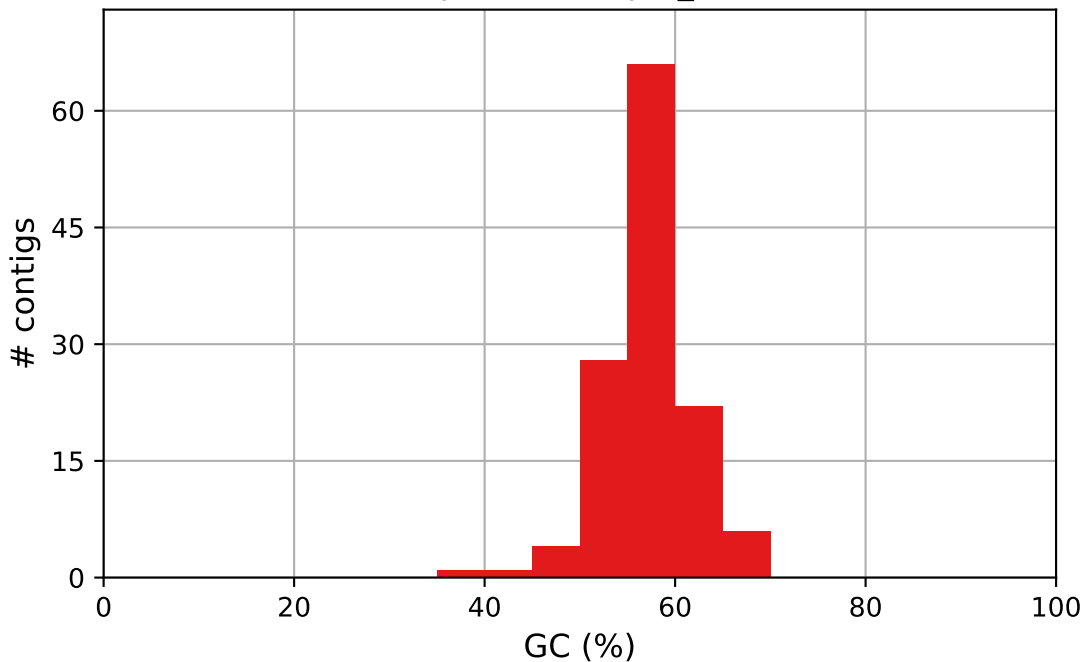


KlebsiellaAbyssAssembly-8_fa

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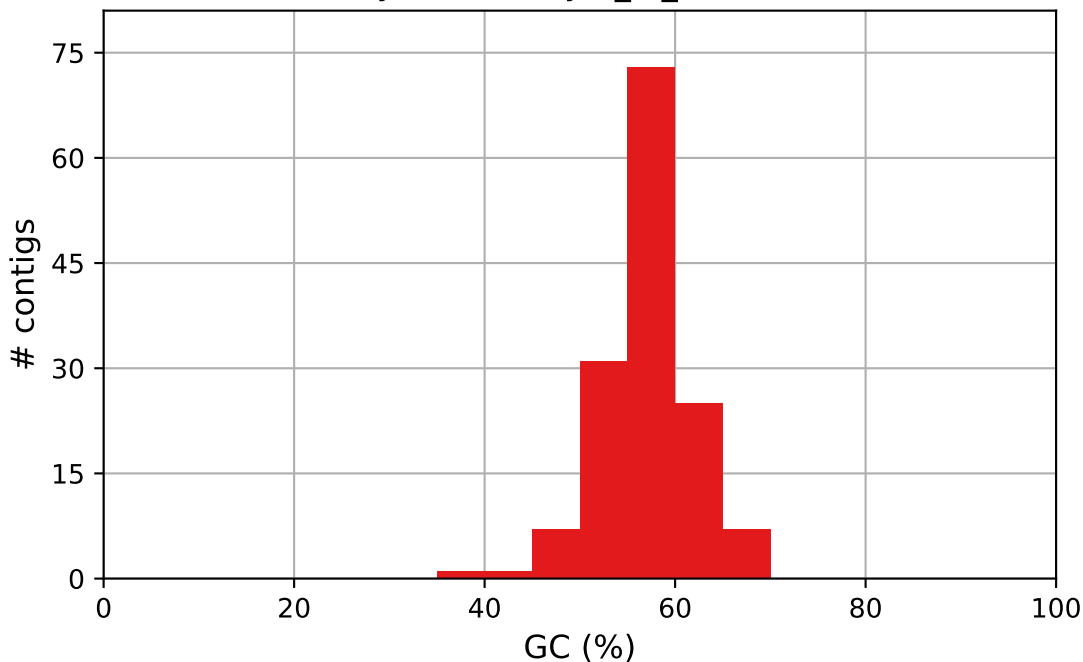
--- Refe

KlebsiellaAbyssAssembly-8_fa GC content



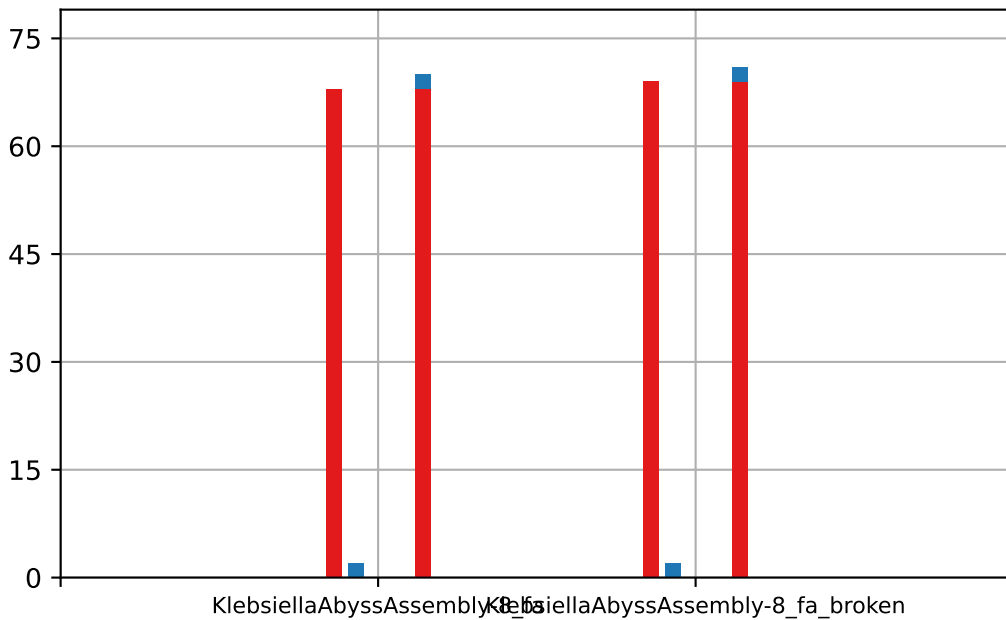
KlebsiellaAbyssAssembly-8_fa

KlebsiellaAbyssAssembly-8_fa_broken GC content



KlebsiellaAbyssAssembly-8_fa_broken

Misassemblies

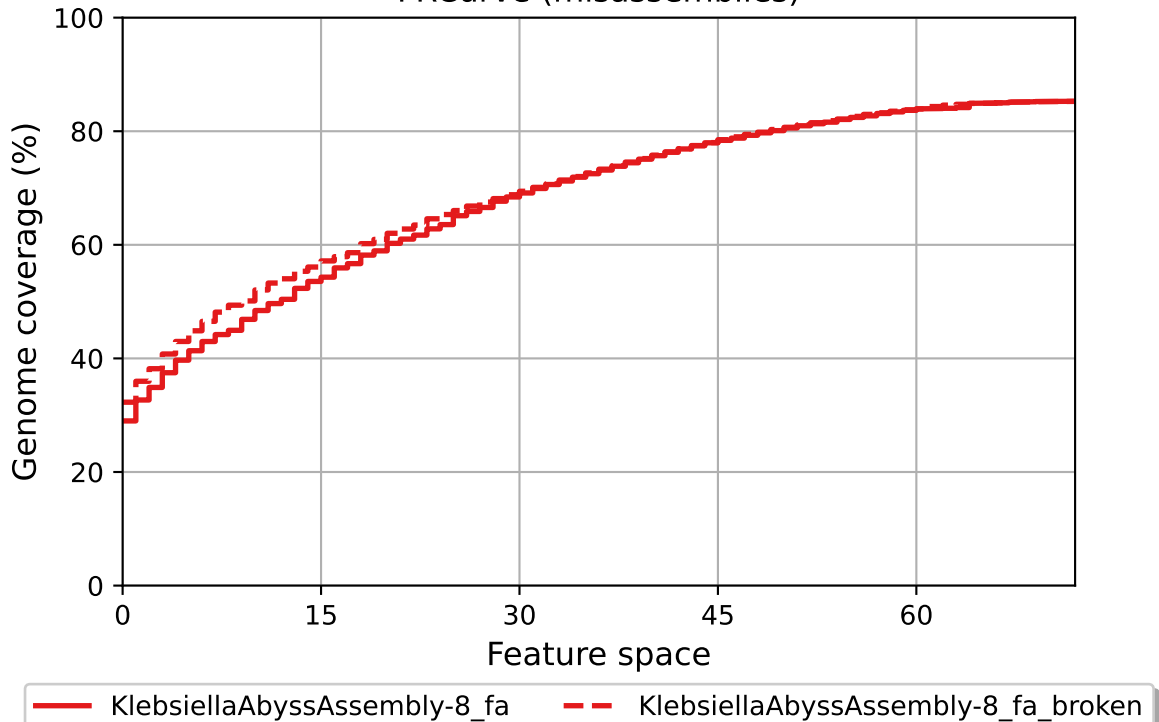


relocations

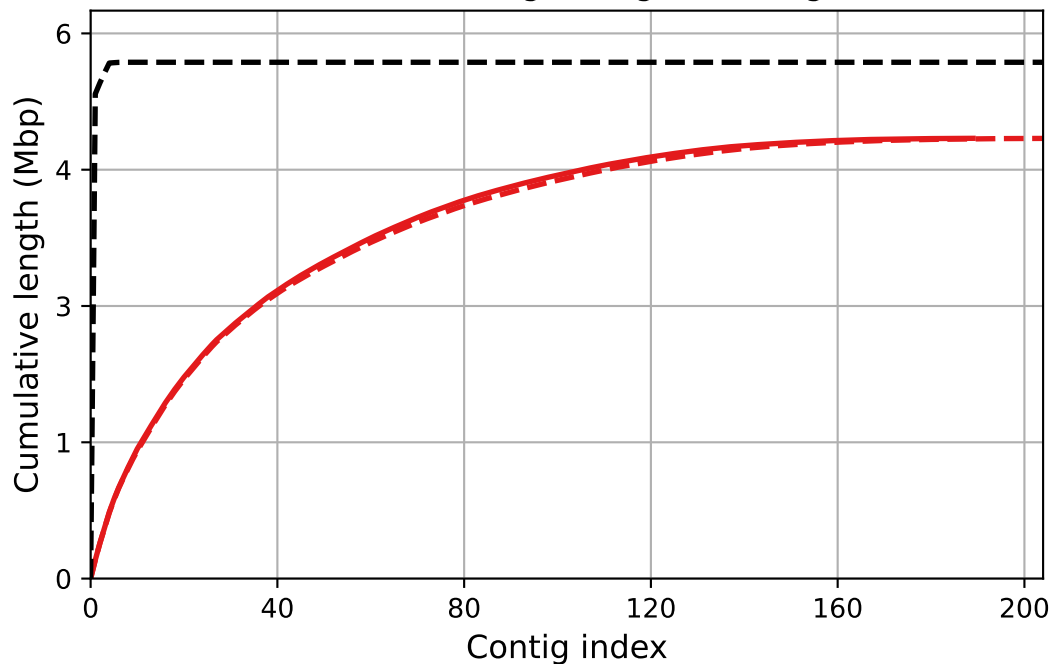


translocations

FRCurve (misassemblies)



Cumulative length (aligned contigs)

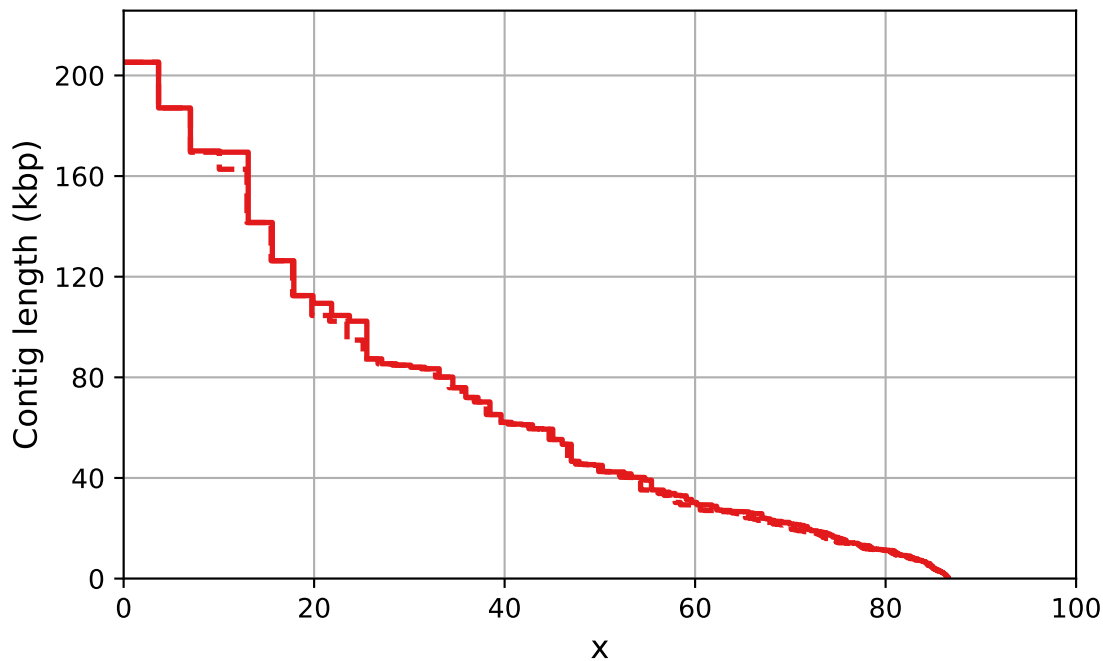


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--- Reference

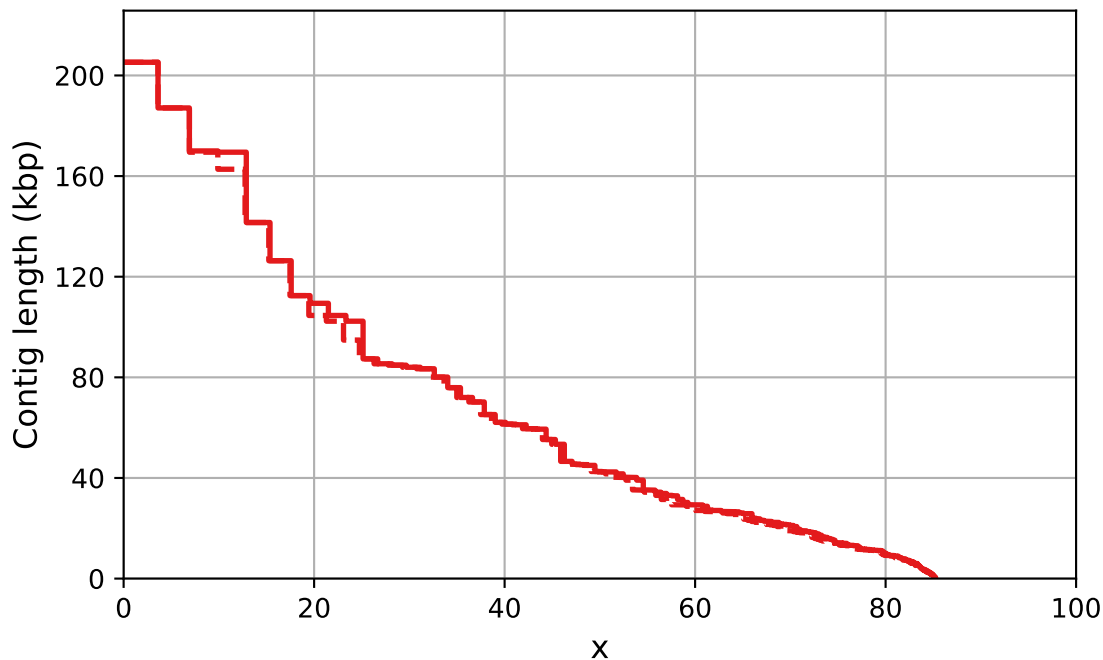
NAx



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NGAx

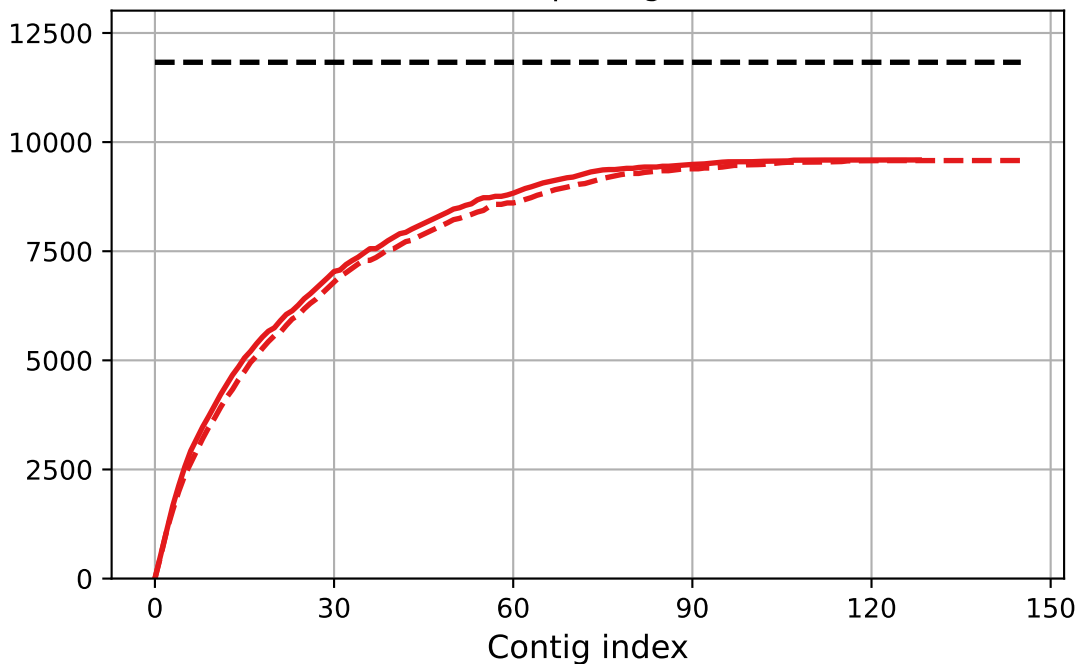


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Cumulative # complete genomic features

Cumulative # complete genomic features

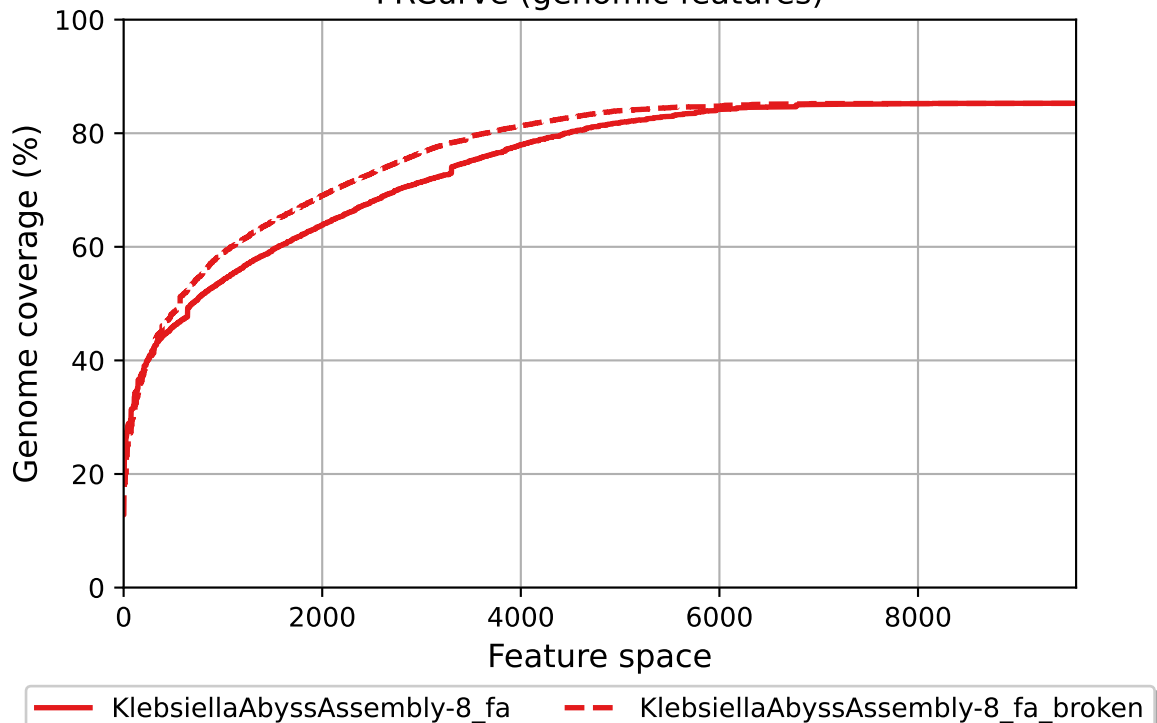


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--- Ref

FRCurve (genomic features)



complete genomic features



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Genome fraction, %



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