

Report

	GCF_040819585.1_PFhe_I_PB_III_cons_genomic
# contigs (>= 0 bp)	15
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1341511
Total length (>= 1000 bp)	1341511
Total length (>= 5000 bp)	1341511
Total length (>= 10000 bp)	1341511
Total length (>= 25000 bp)	1284530
Total length (>= 50000 bp)	964042
# contigs	15
Largest contig	910259
Total length	1341511
Reference length	1521208
GC (%)	28.43
Reference GC (%)	28.18
N50	910259
NG50	910259
N90	28903
NG90	-
auN	628530.9
auNG	554283.9
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	4
# misassembled contigs	2
Misassembled contigs length	46260
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	3 + 5 part
Unaligned length	140728
Genome fraction (%)	78.539
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	525.65
# indels per 100 kbp	34.93
# genomic features	1255 + 25 part
Largest alignment	910146
Total aligned length	1199459
NA50	910146
NGA50	910146
NA90	-
NGA90	-
auNA	623853.3
auNGA	550158.9
LA50	1
LGA50	1
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

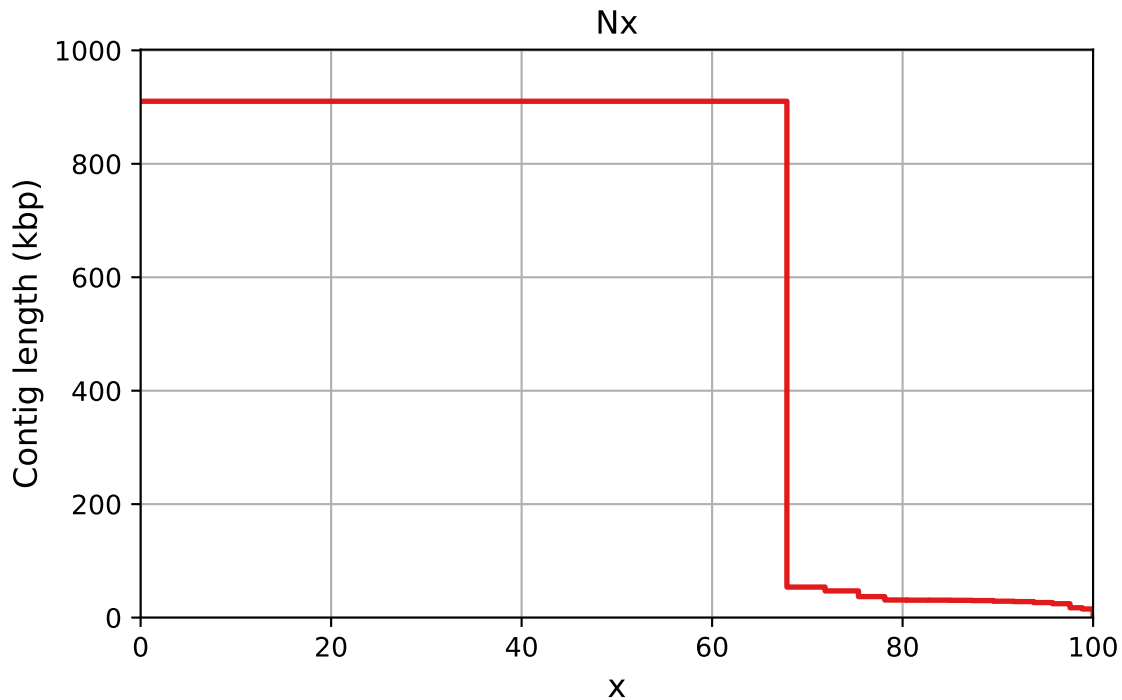
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# misassemblies	4
# contig misassemblies	4
# c. relocations	1
# c. translocations	3
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	46260
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	6305
# indels	419
# indels (<= 5 bp)	363
# indels (> 5 bp)	56
Indels length	2610

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

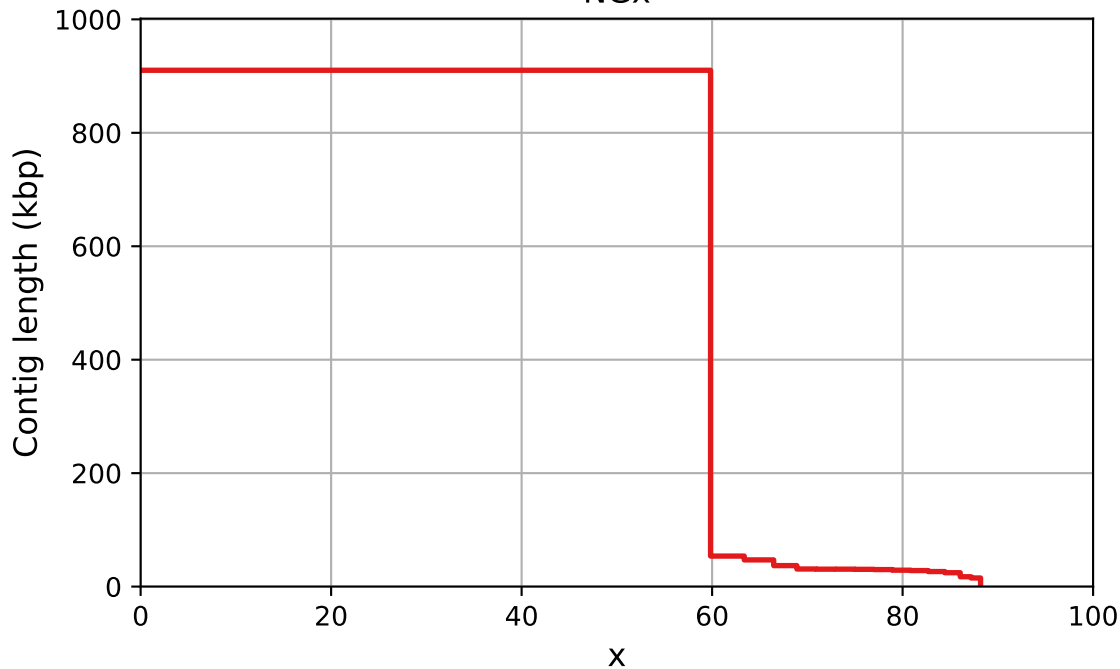
	GCF_040819585.1_PFhe_I_PB_III_cons_genomic
# fully unaligned contigs	3
Fully unaligned length	73812
# partially unaligned contigs	5
Partially unaligned length	66916
# N's	0

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).

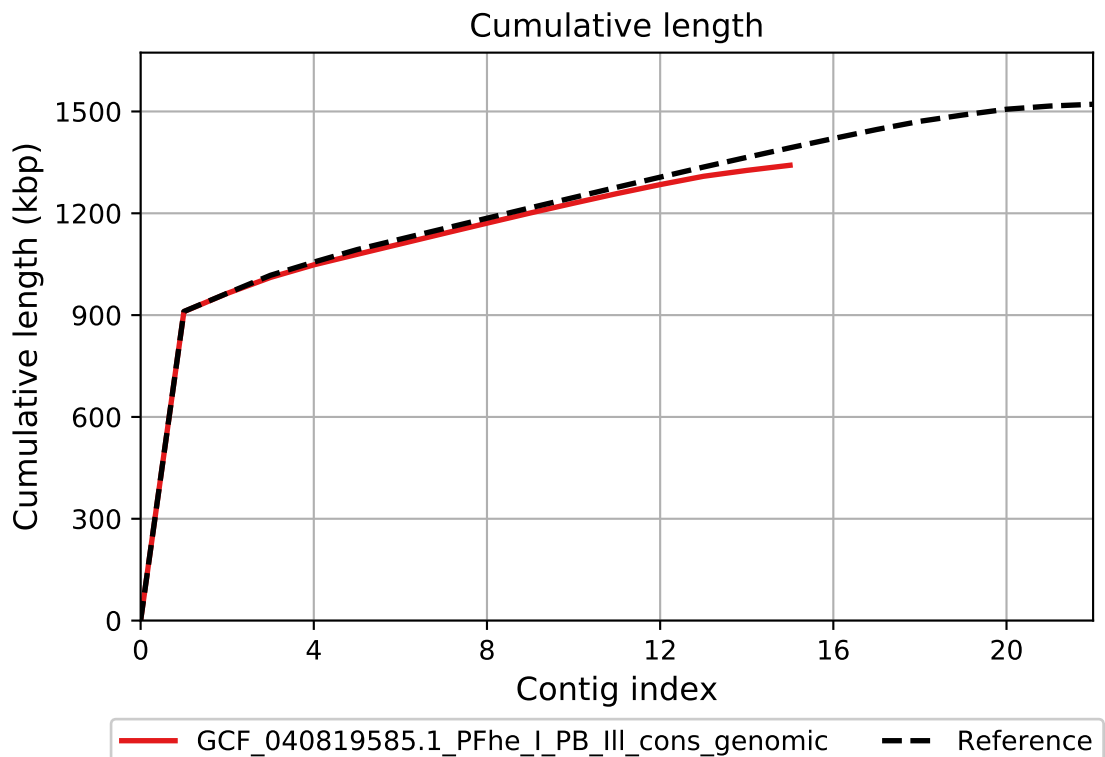


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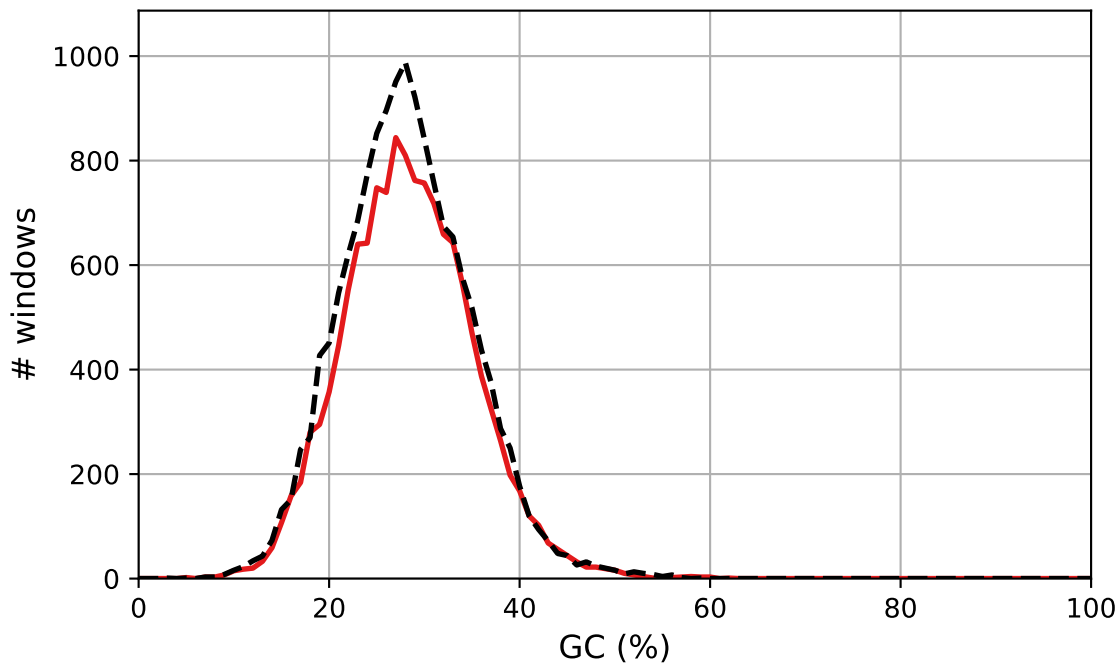
NGx



— GCF_040819585.1_PFhe_I_PB_III_cons_genomic

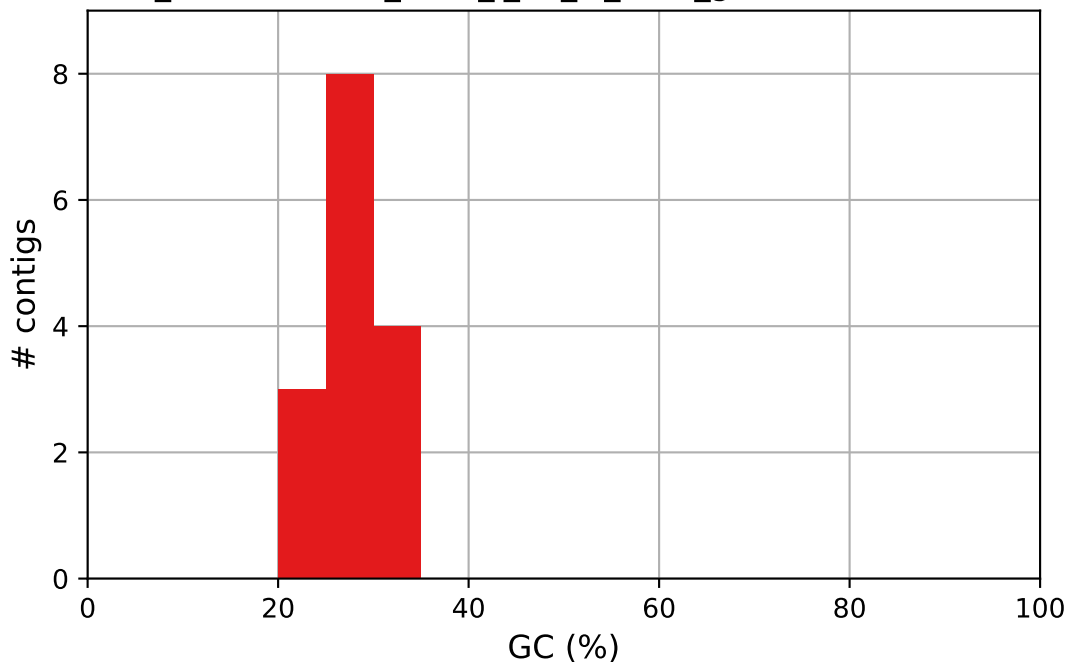


GC content



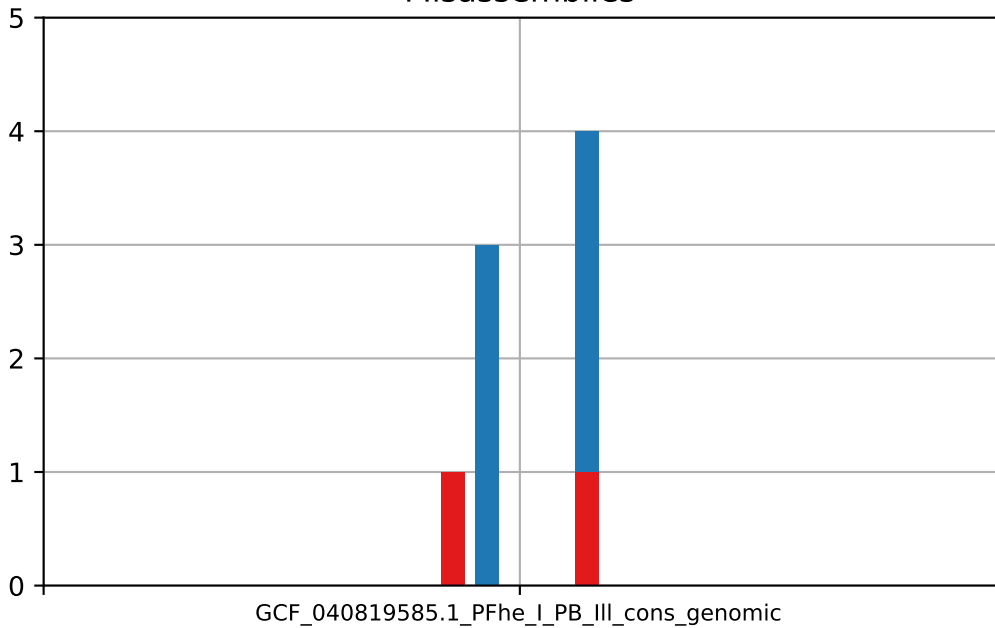
— GCF_040819585.1_PFhe_I_PB_III_cons_genomic - - Reference

GCF_040819585.1_PFhe_I_PB_III_cons_genomic GC content



GCF_040819585.1_PFhe_I_PB_III_cons_genomic

Misassemblies

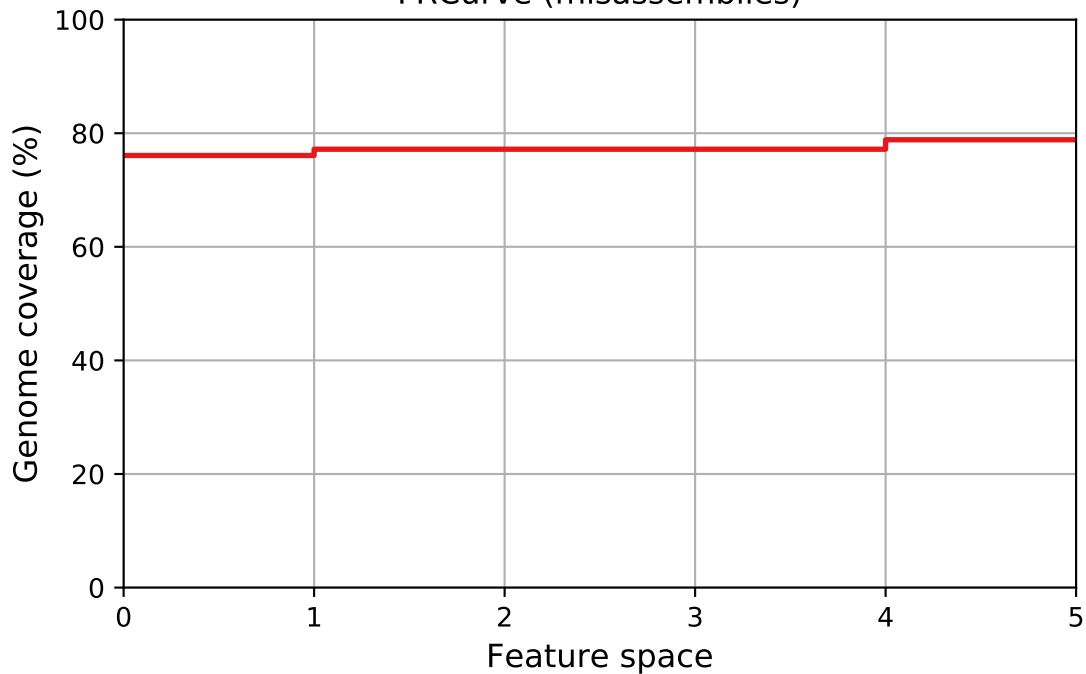


relocations



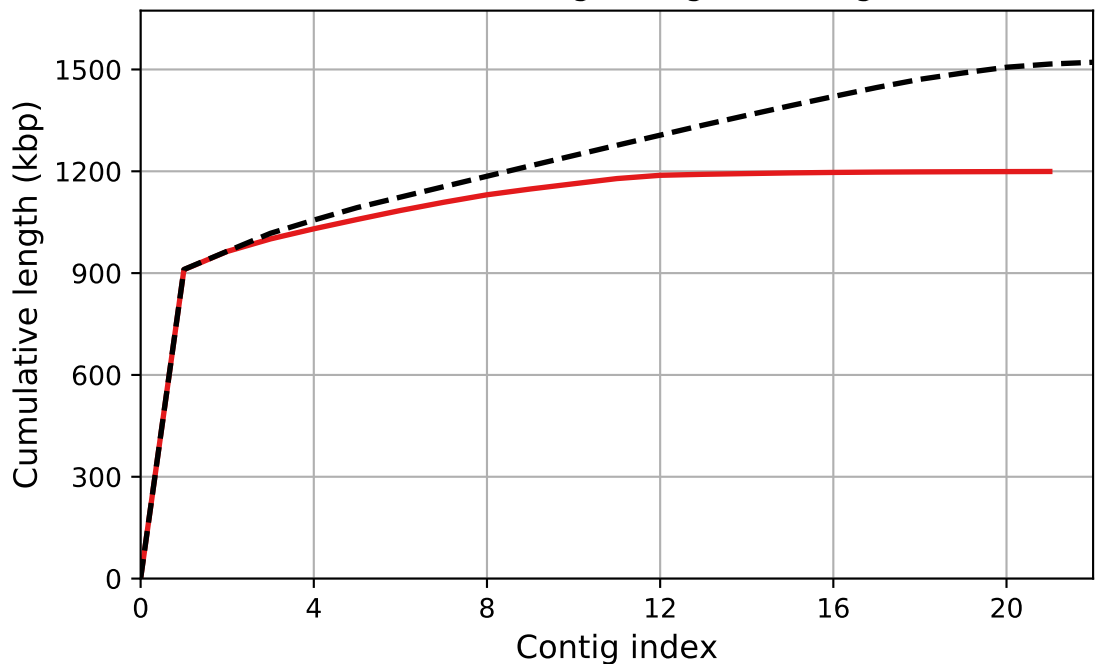
translocations

FRCurve (misassemblies)



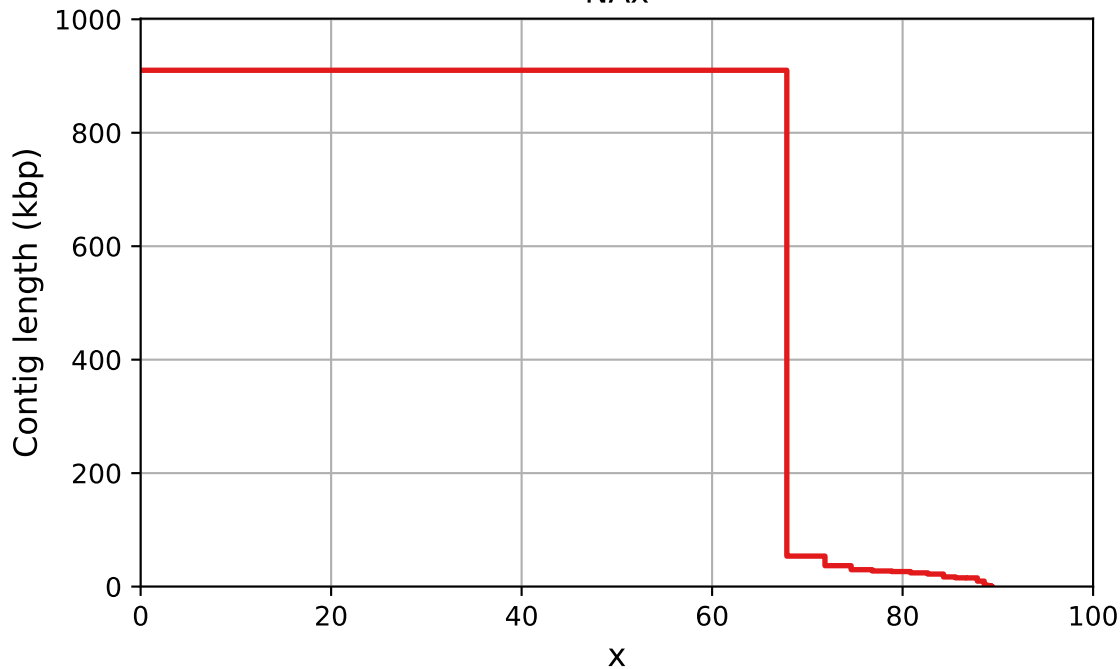
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Cumulative length (aligned contigs)



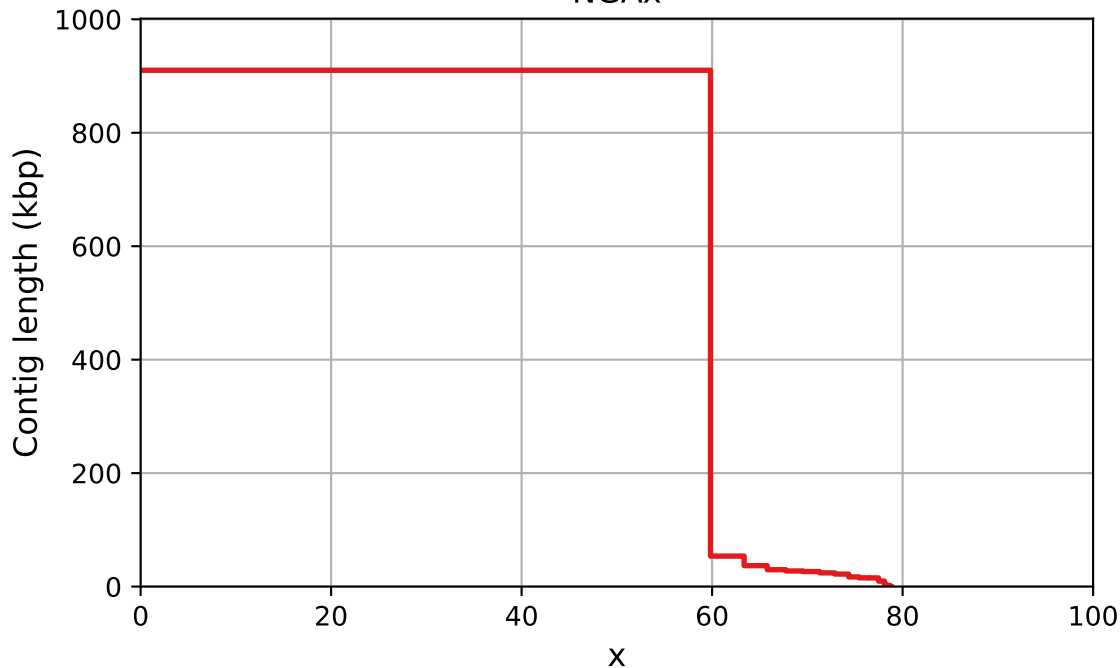
— GCF_040819585.1_PFhe_I_PB_III_cons_genomic - - Reference

NAx

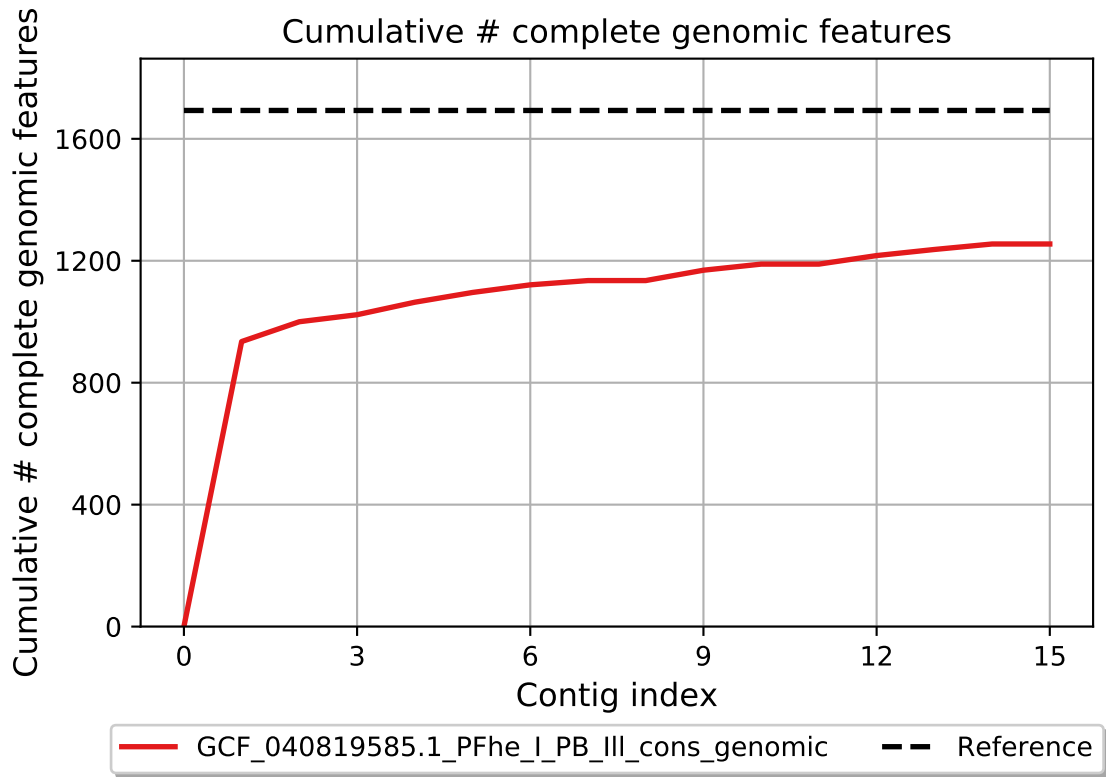


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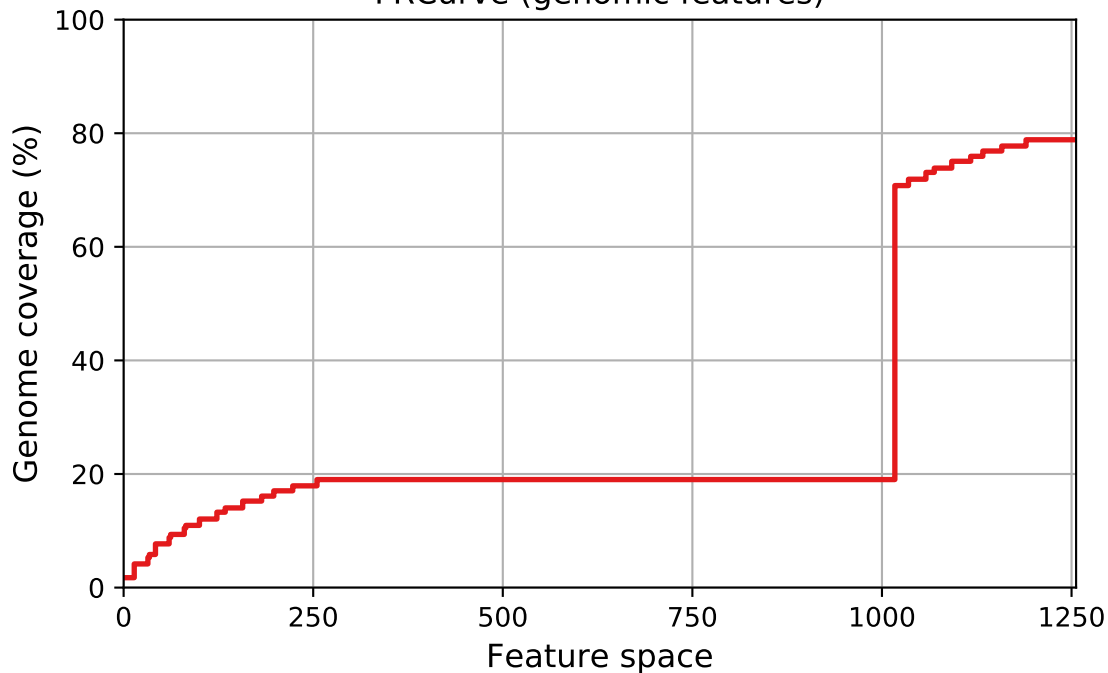
NGAx



— GCF_040819585.1_PFhe_I_PB_III_cons_genomic



FRCurve (genomic features)



— GCF_040819585.1_PFhe_I_PB_III_cons_genomic