

Report

GCA_032595755.1_ASM3259575v1_genomic	
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1006563
Total length (>= 1000 bp)	1006563
Total length (>= 5000 bp)	1006563
Total length (>= 10000 bp)	1006563
Total length (>= 25000 bp)	988428
Total length (>= 50000 bp)	961940
# contigs	4
Largest contig	910071
Total length	1006563
Reference length	1521208
GC (%)	28.39
Reference GC (%)	28.18
N50	910071
NG50	910071
N90	910071
NG90	-
auN	826525.6
auNG	546901.0
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	23
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	7287
Genome fraction (%)	62.696
Duplication ratio	1.000
# N's per 100 kbp	4547.55
# mismatches per 100 kbp	586.83
# indels per 100 kbp	24.44
# genomic features	962 + 42 part
Largest alignment	862433
Total aligned length	953433
NA50	862433
NGA50	862433
NA90	51806
NGA90	-
auNA	742464.6
auNGA	491278.9
LA50	1
LGA50	1
LA90	2
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

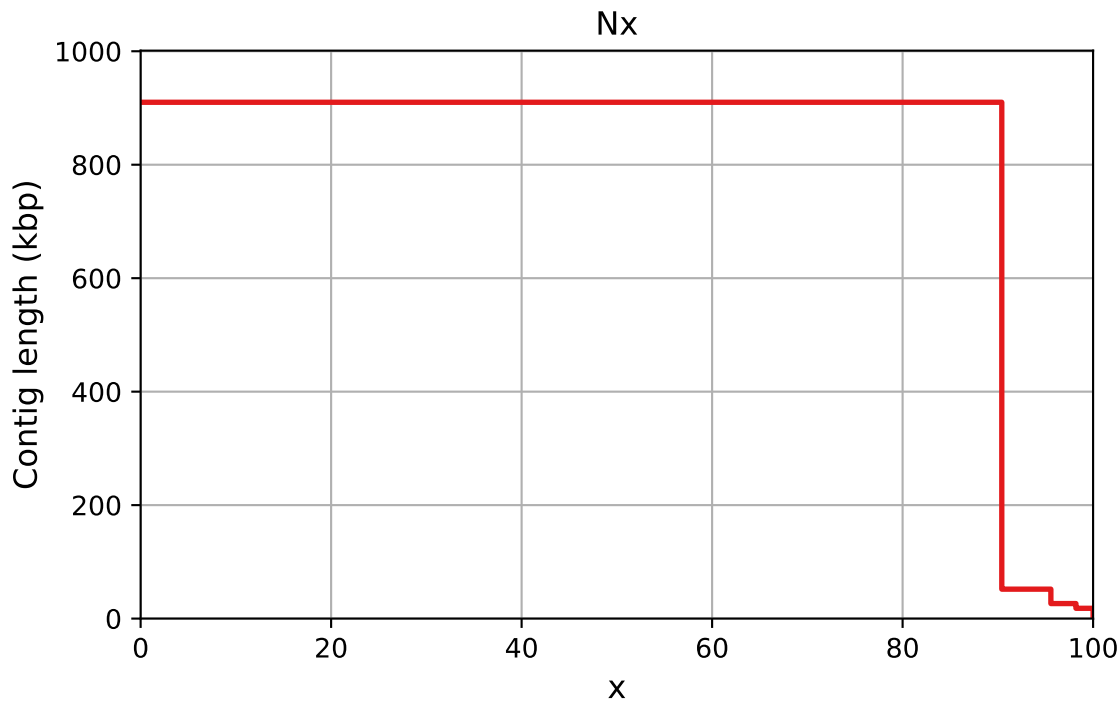
	GCA_032595755.1_ASM3259575v1_genomic
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	23
# unaligned mis. contigs	0
# mismatches	5595
# indels	233
# indels (<= 5 bp)	208
# indels (> 5 bp)	25
Indels length	1083

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

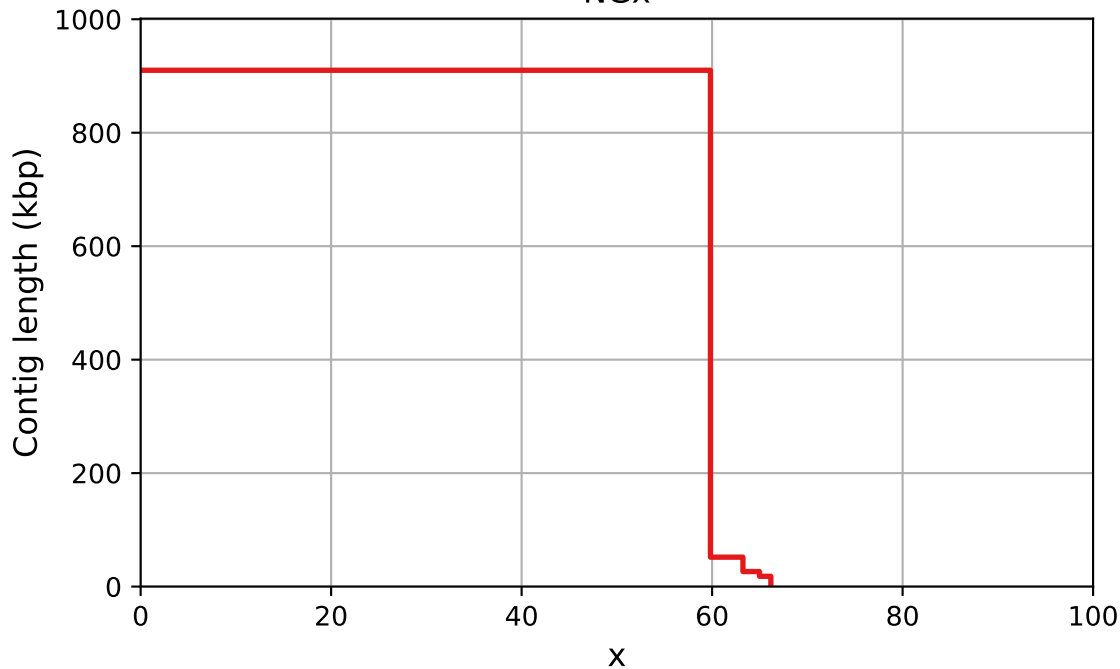
	GCA_032595755.1_ASM3259575v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	7287
# N's	45774

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).

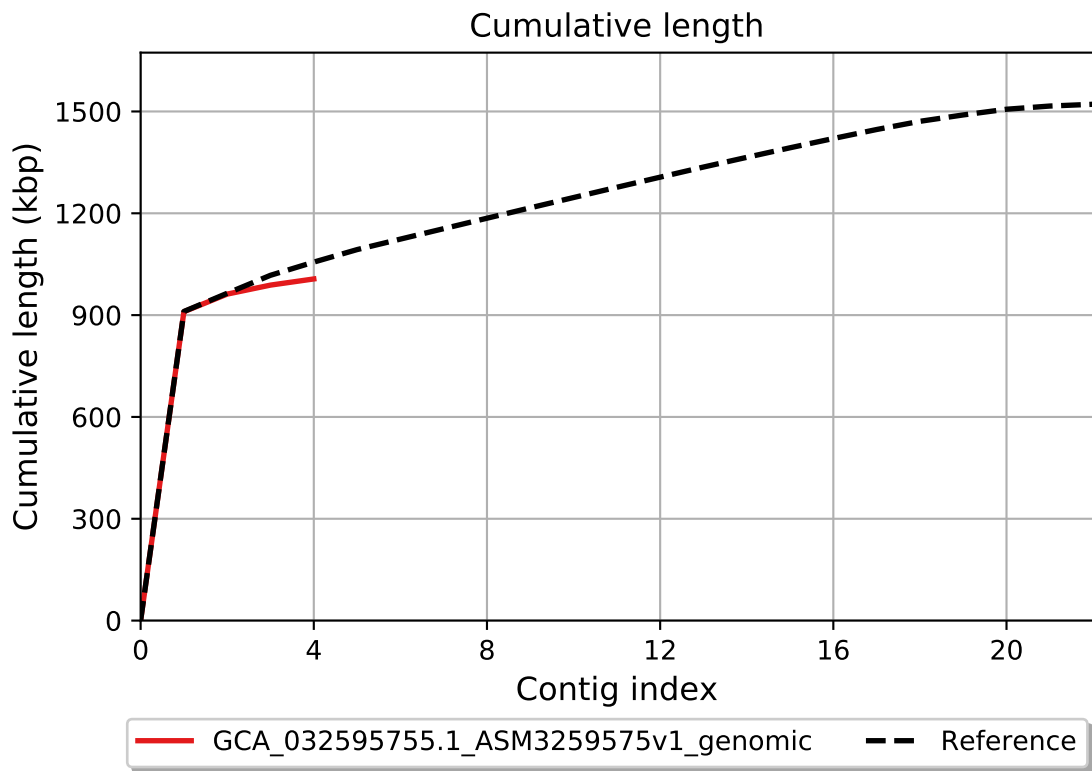


— GCA_032595755.1_ASM3259575v1_genomic

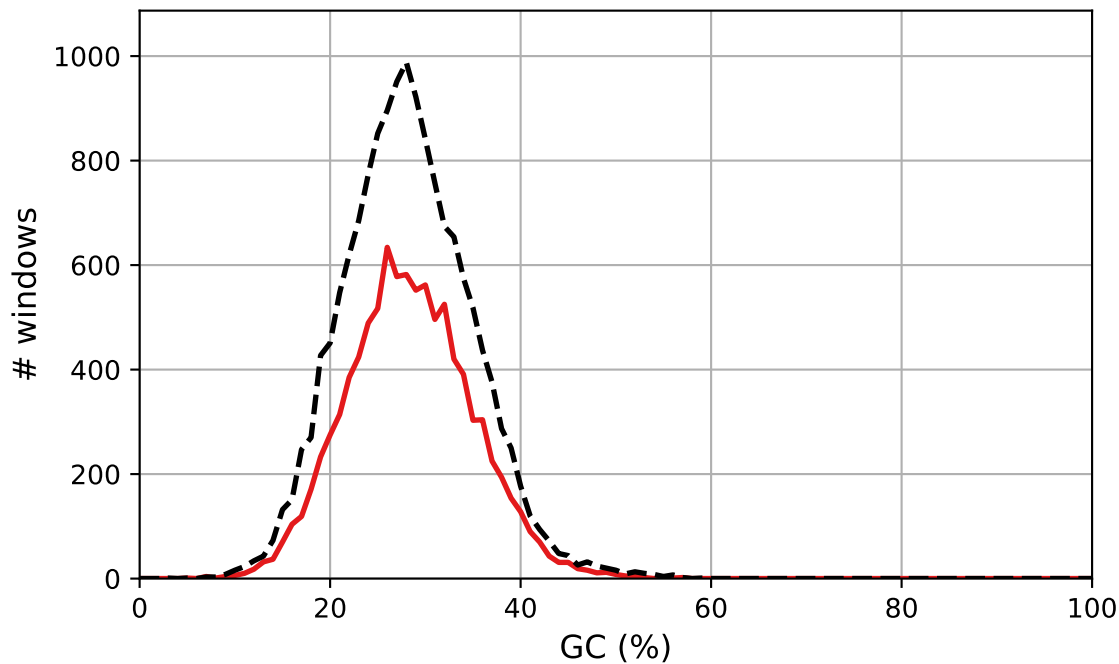
NGx



— GCA_032595755.1_ASM3259575v1_genomic



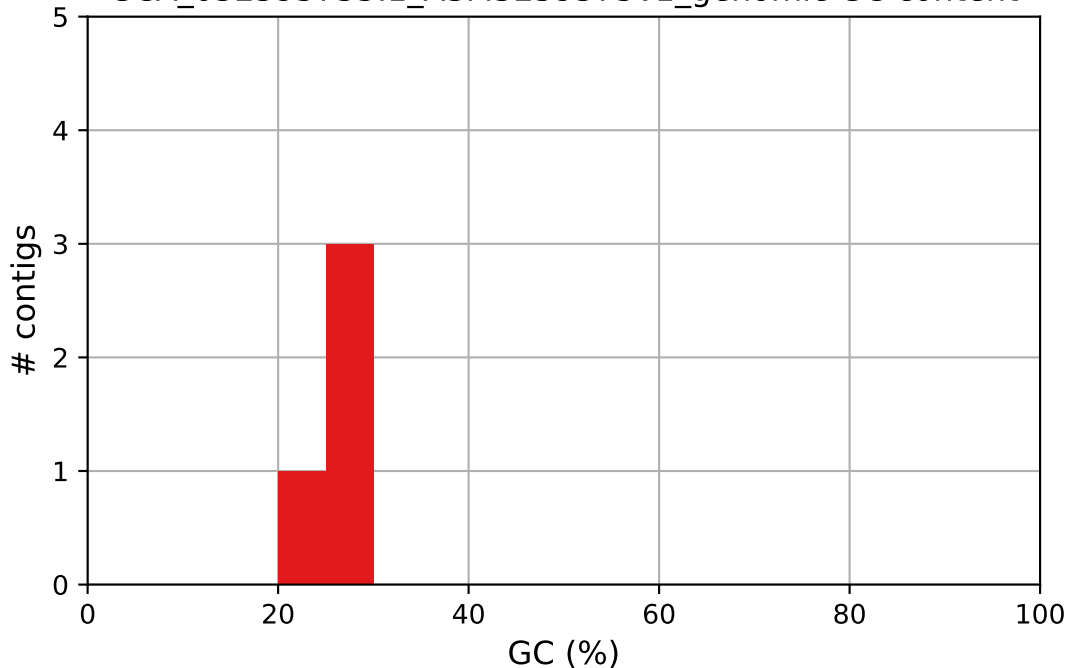
GC content



GCA_032595755.1_ASM3259575v1_genomic

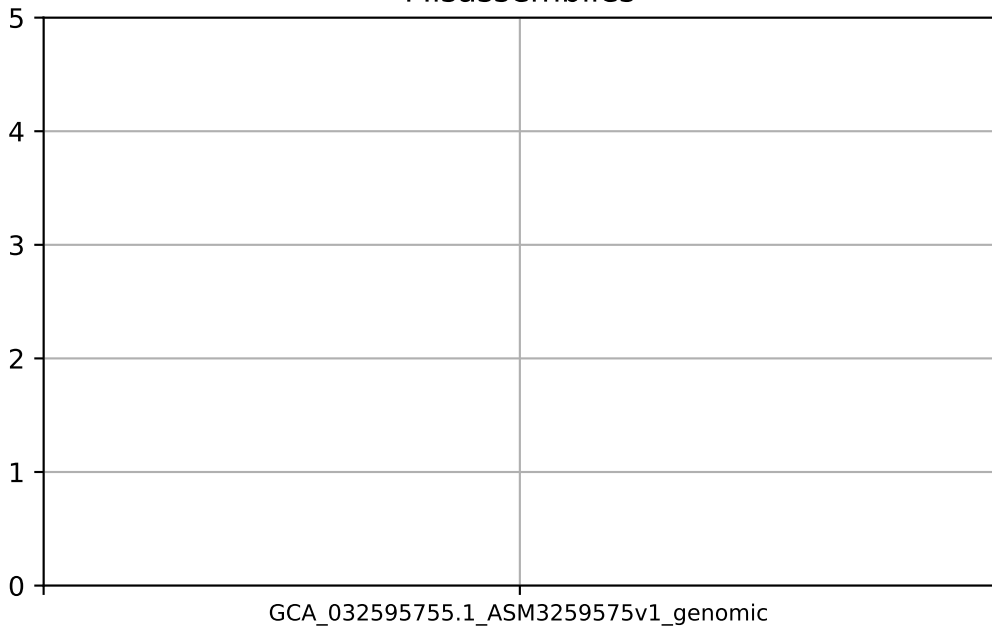
Reference

GCA_032595755.1_ASM3259575v1_genomic GC content

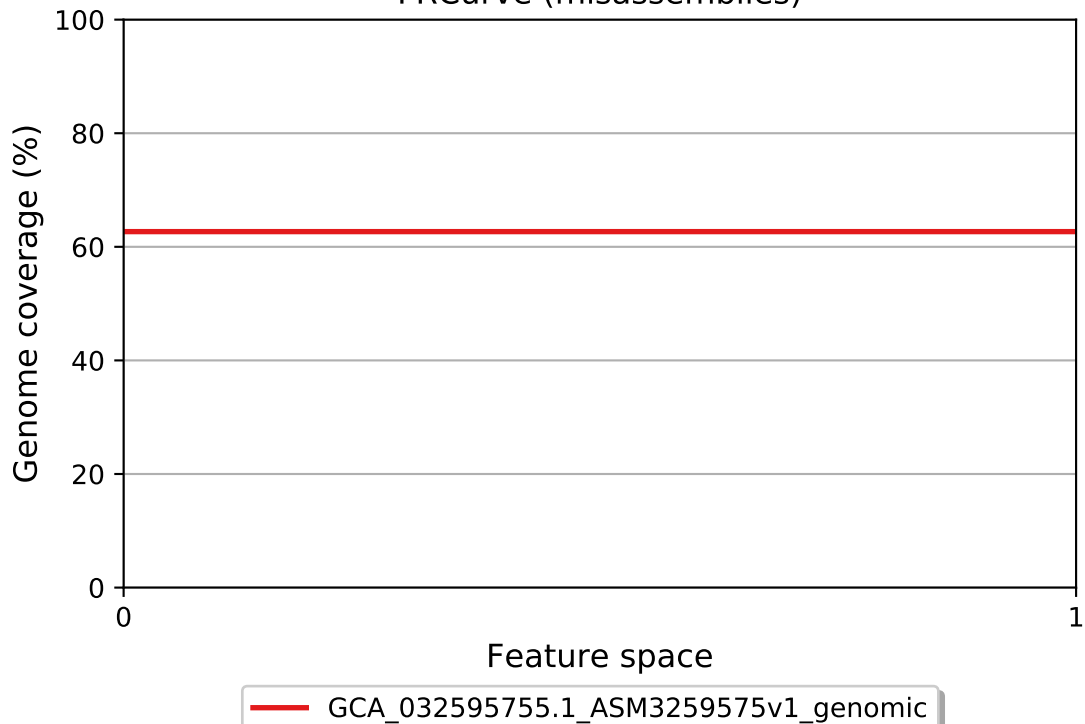


GCA_032595755.1_ASM3259575v1_genomic

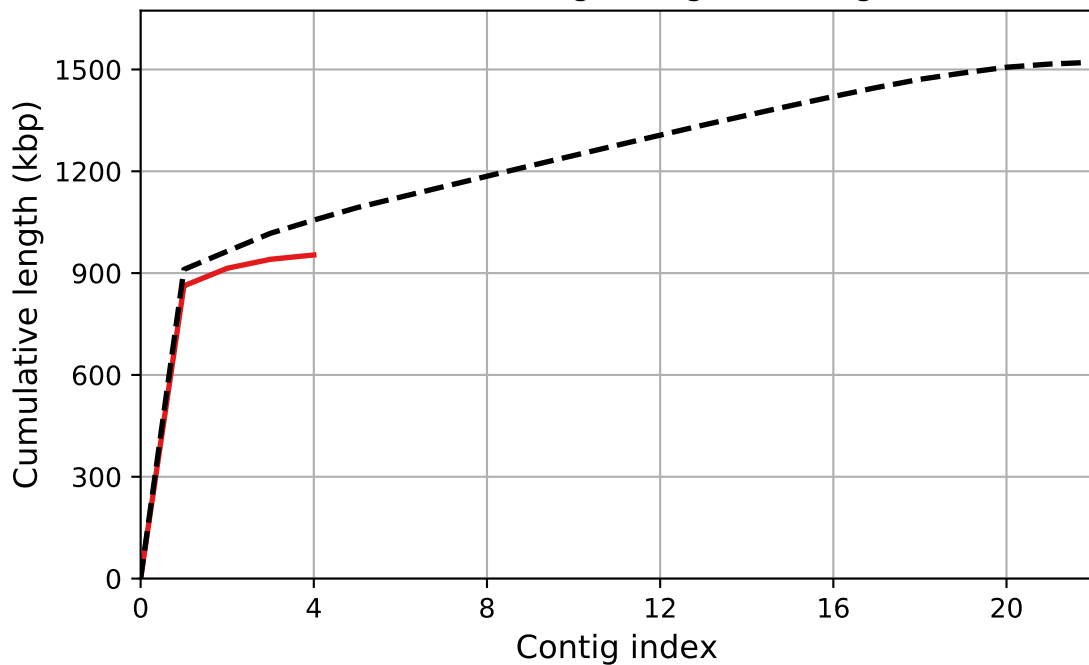
Misassemblies



FRCurve (misassemblies)



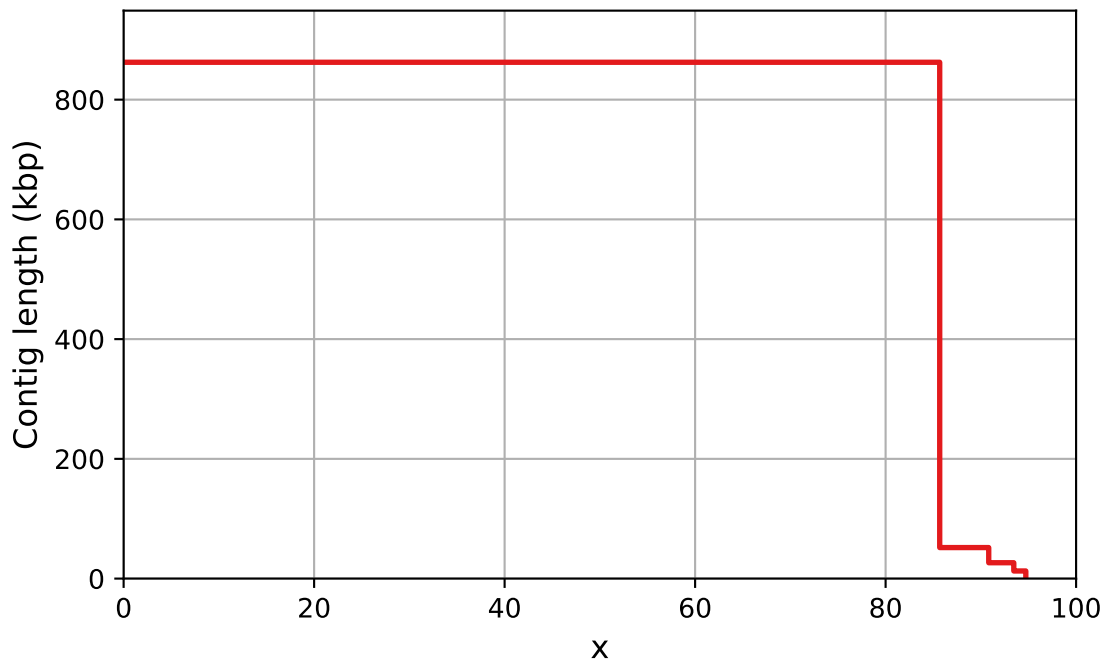
Cumulative length (aligned contigs)



GCA_032595755.1_ASM3259575v1_genomic

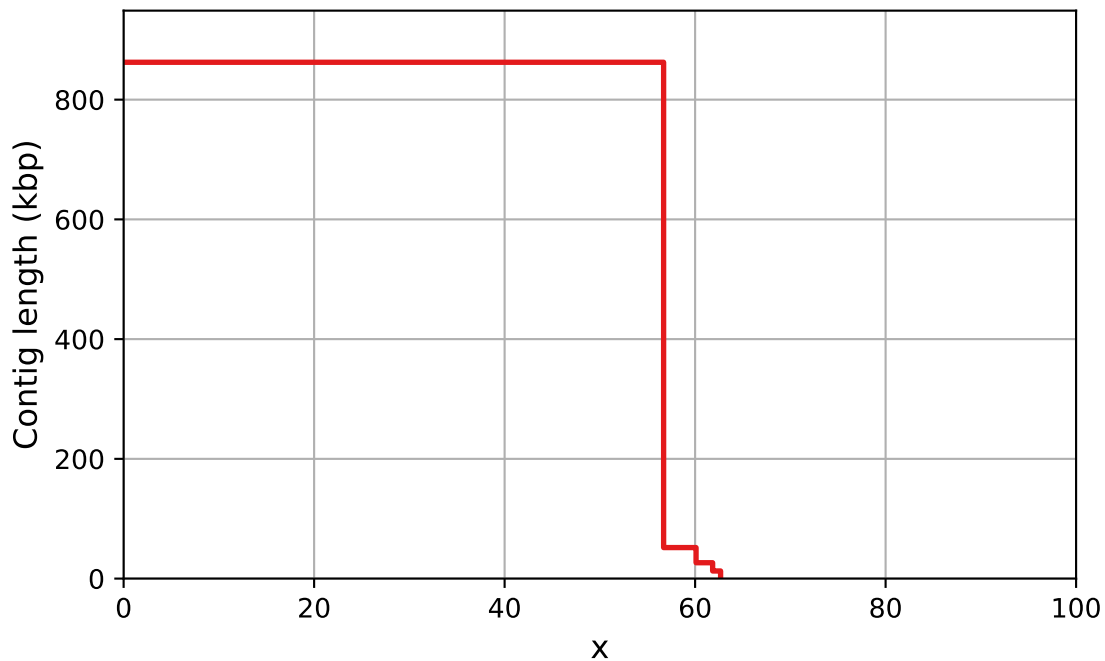
Reference

NAx

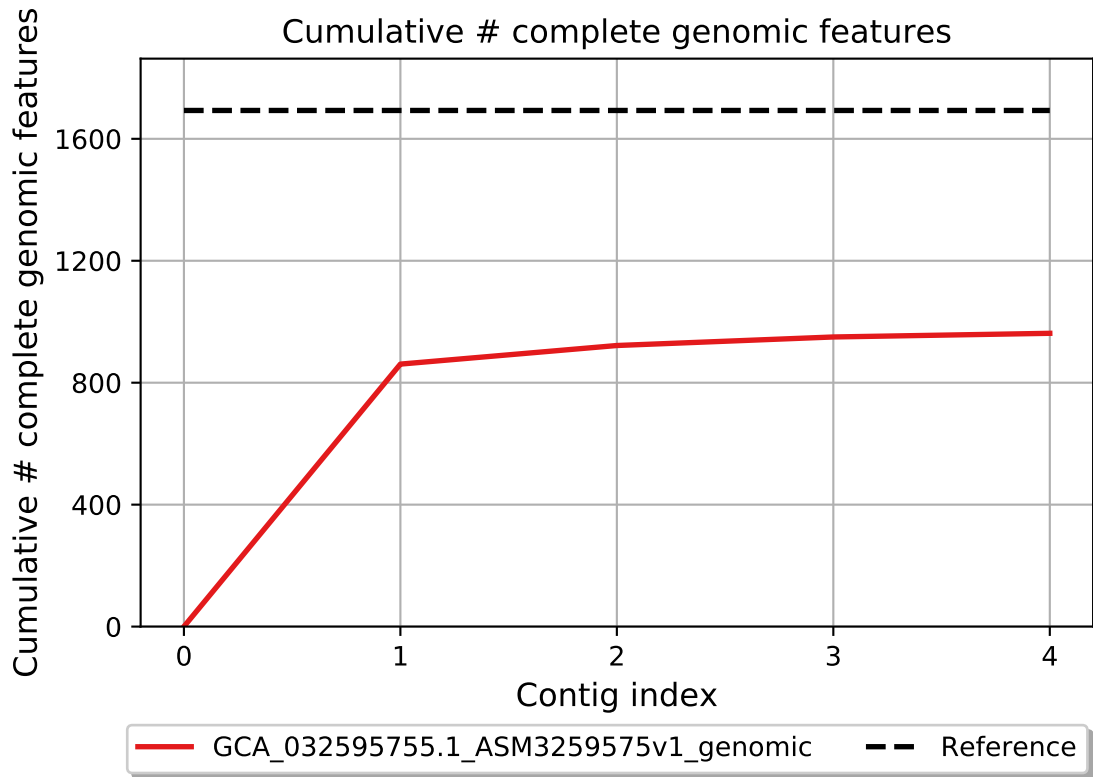


— GCA_032595755.1_ASM3259575v1_genomic

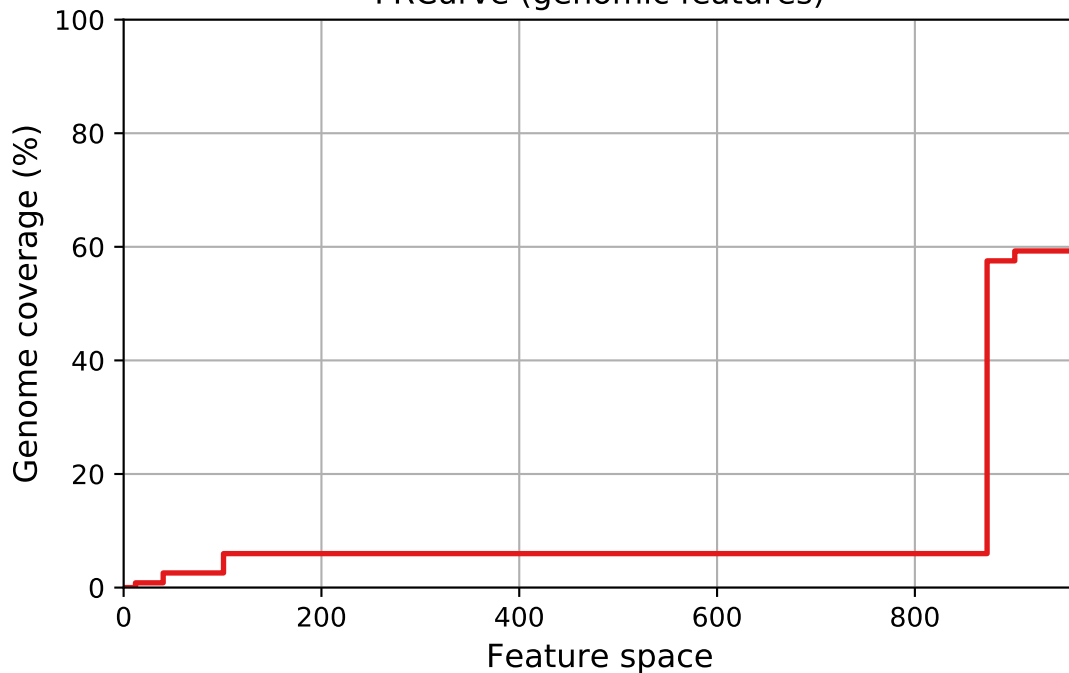
NGAx



— GCA_032595755.1_ASM3259575v1_genomic



FRCurve (genomic features)



— GCA_032595755.1_ASM3259575v1_genomic