Report

	UNY193P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1403883
Total length (>= 1000 bp)	1403883
Total length (>= 5000 bp)	1403883
Total length (>= 10000 bp)	1389234
Total length (>= 25000 bp)	1346097
Total length (>= 50000 bp)	964090
# contigs	19
Largest contig	910086
Total length	1403883
Reference length	1521208
GC (%)	28.38
Reference GC (%)	28.18
N50	910086
NG50	910086
N90	27704
NG90	24809
auN	600849.4
auNG	554508.2
L50	1
LG50	1
L90	12
LG90	16
# misassemblies	10
# misassembled contigs	6
Misassembled contigs length	182795
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	2 + 12 part
Unaligned length	183613
Genome fraction (%)	76.995
Duplication ratio	1.037
# N's per 100 kbp	0.00
# mismatches per 100 kbp	769.19
# indels per 100 kbp	46.76
# genomic features	1223 + 37 part
Largest alignment	904873
Total aligned length	1214653
NA50	904873
NGA50	904873
NA90	-
NGA90	-
auNA	588240.9
auNGA	542872.1
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

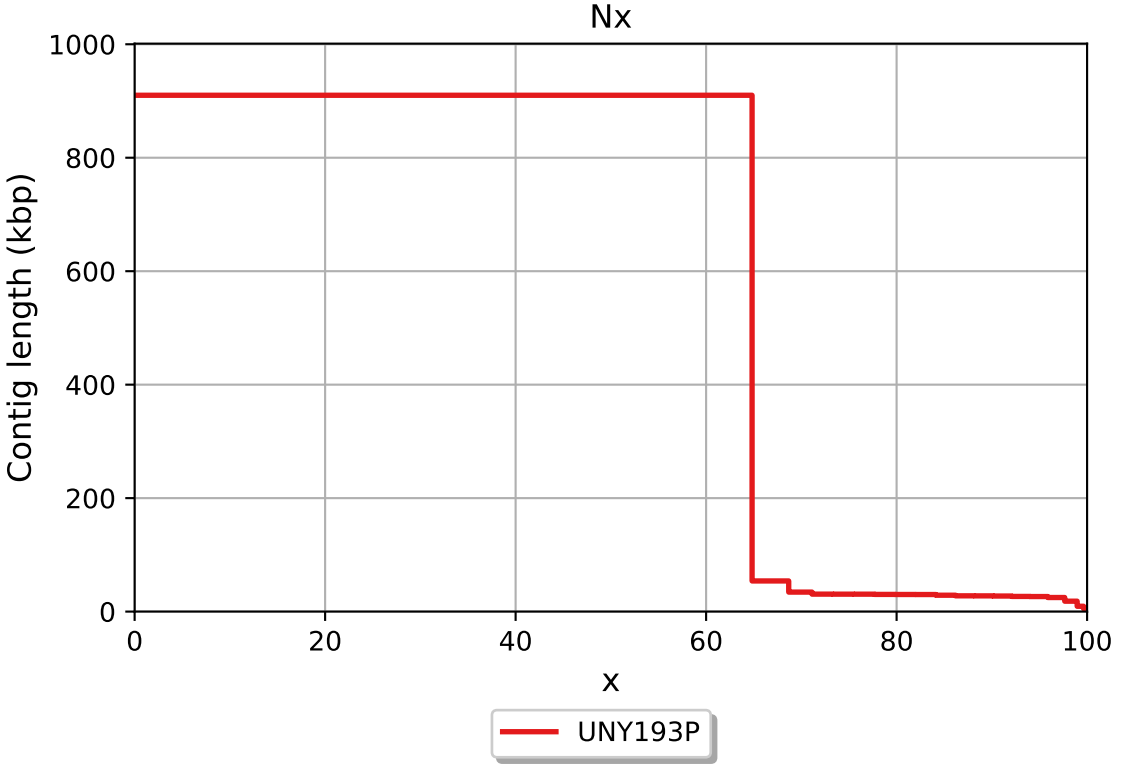
	UNY193P
# misassemblies	10
# contig misassemblies	10
# c. relocations	2
# c. translocations	8
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	182795
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	9343
# indels	568
# indels (<= 5 bp)	524
# indels (> 5 bp)	44
Indels length	1989

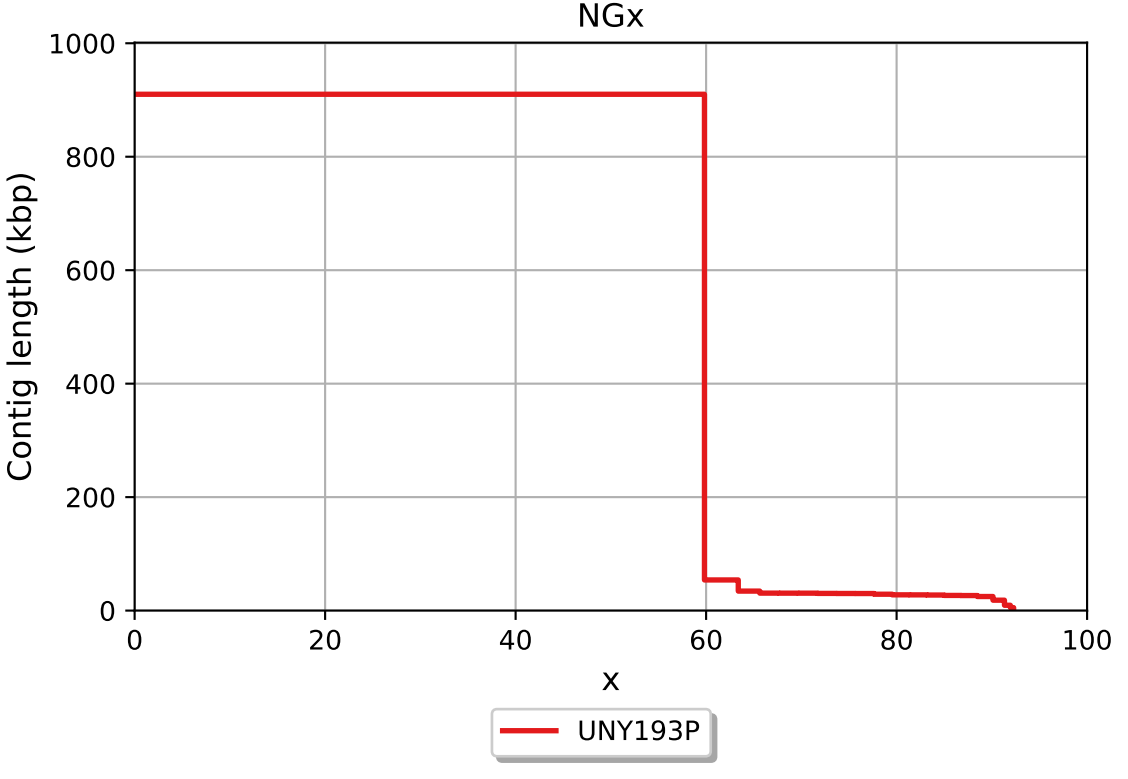
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

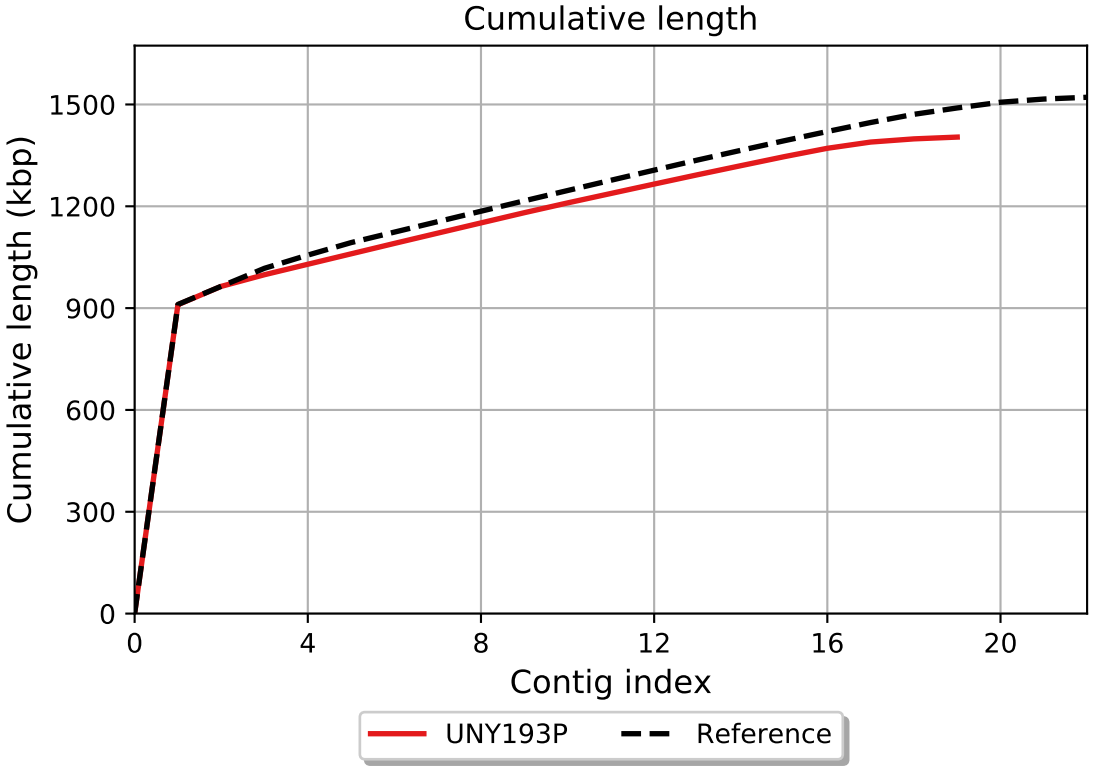
Unaligned report

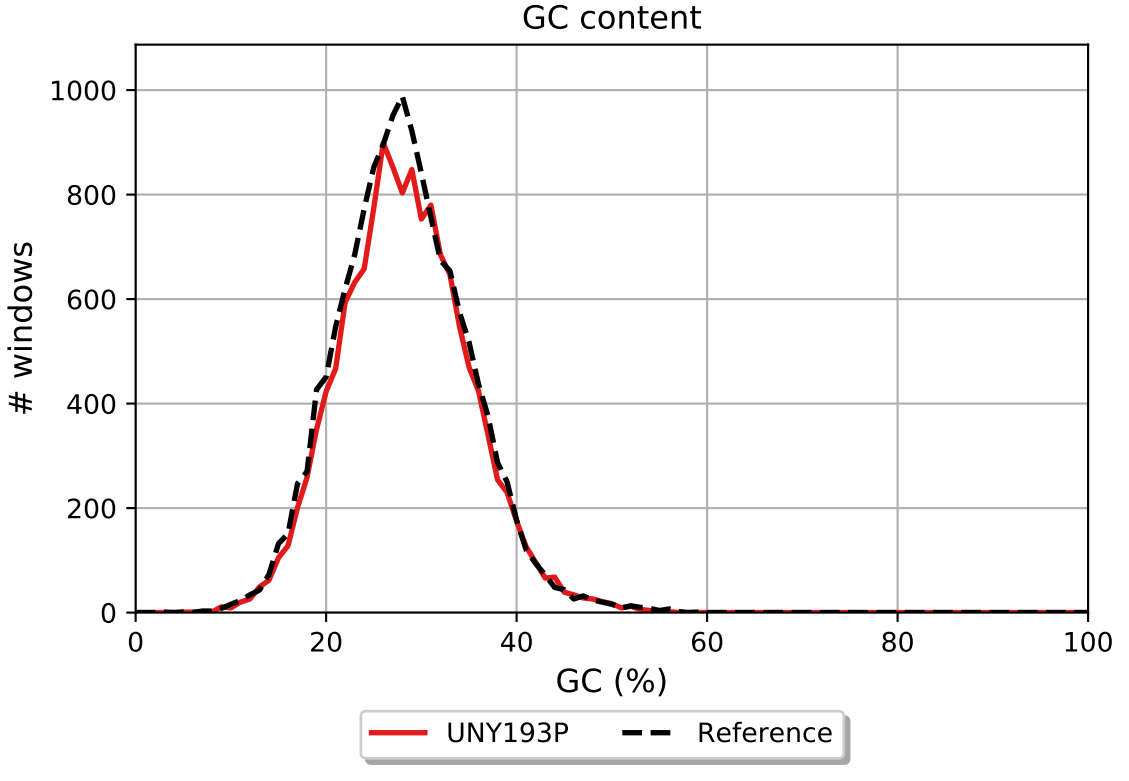
	UNY193P
# fully unaligned contigs	2
Fully unaligned length	57852
# partially unaligned contigs	12
Partially unaligned length	125761
# N's	0

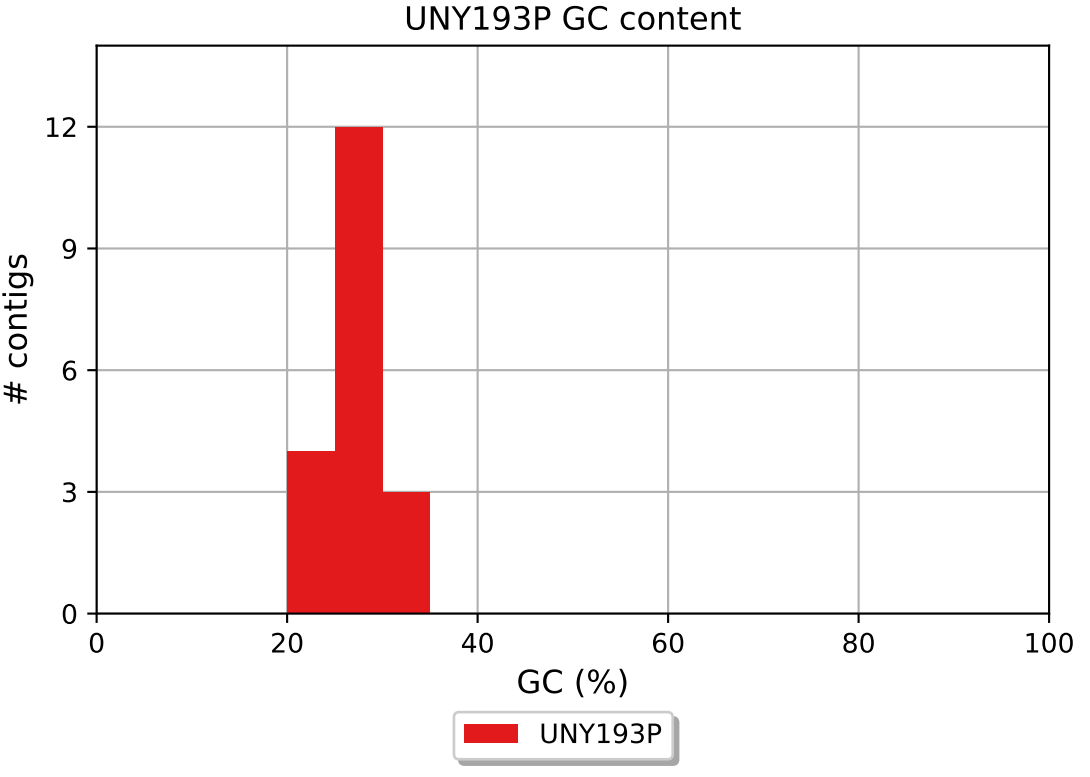
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

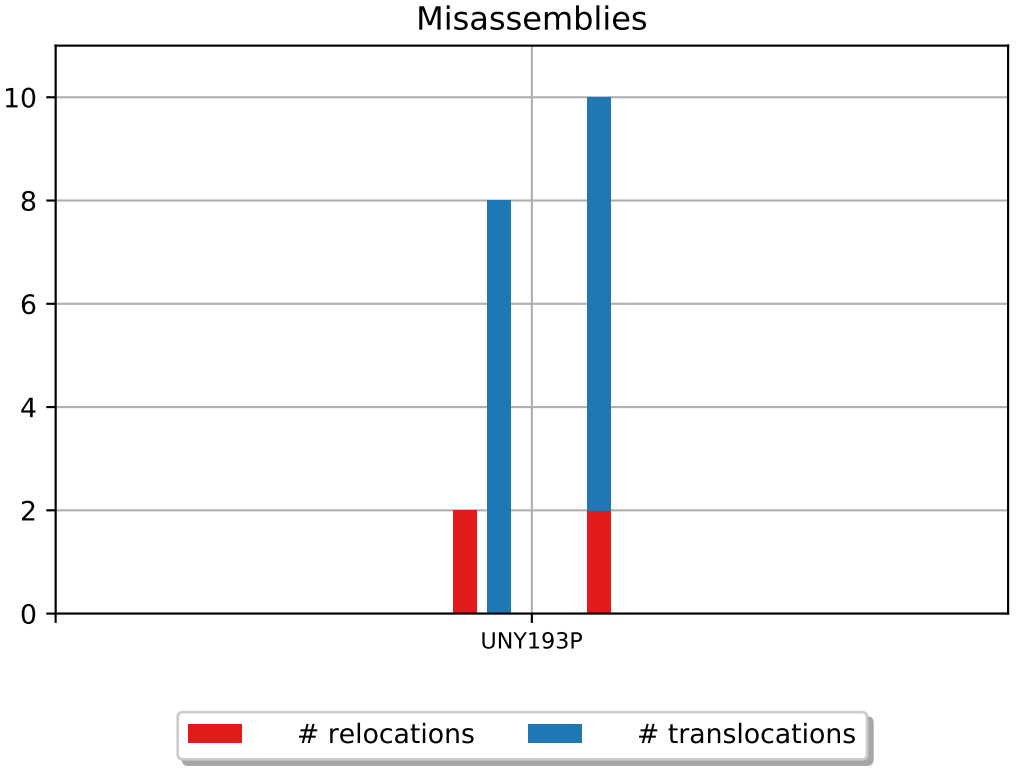

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UNY193P

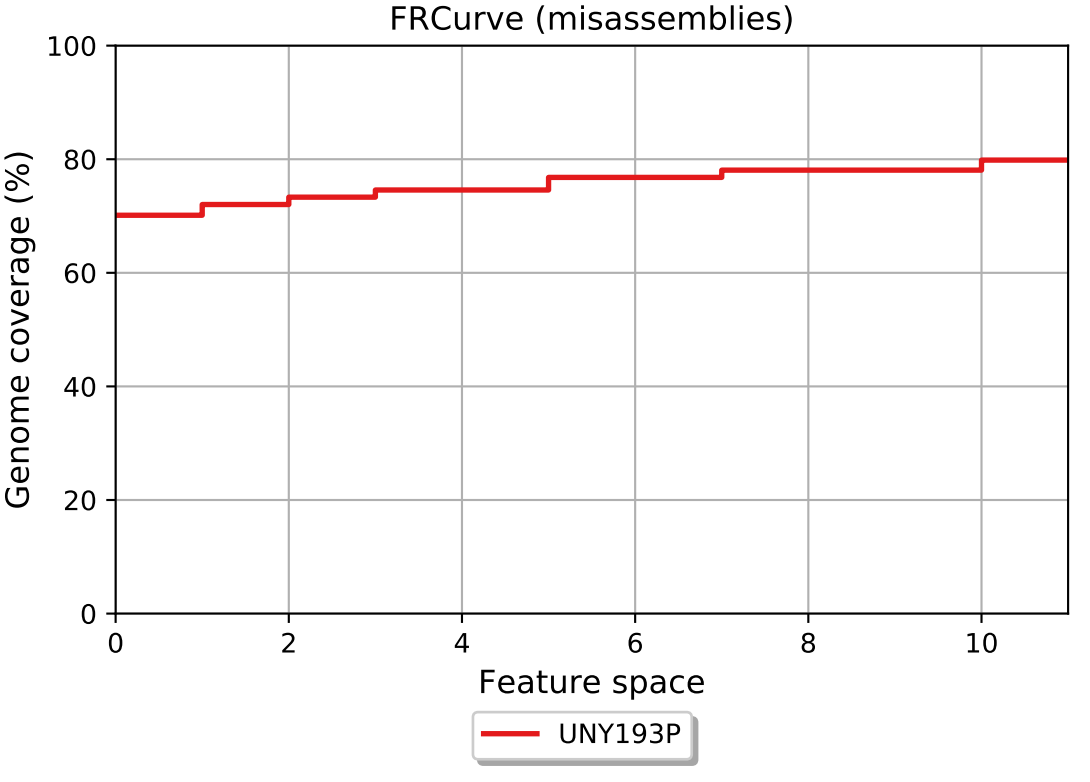

NGx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
UNY193P

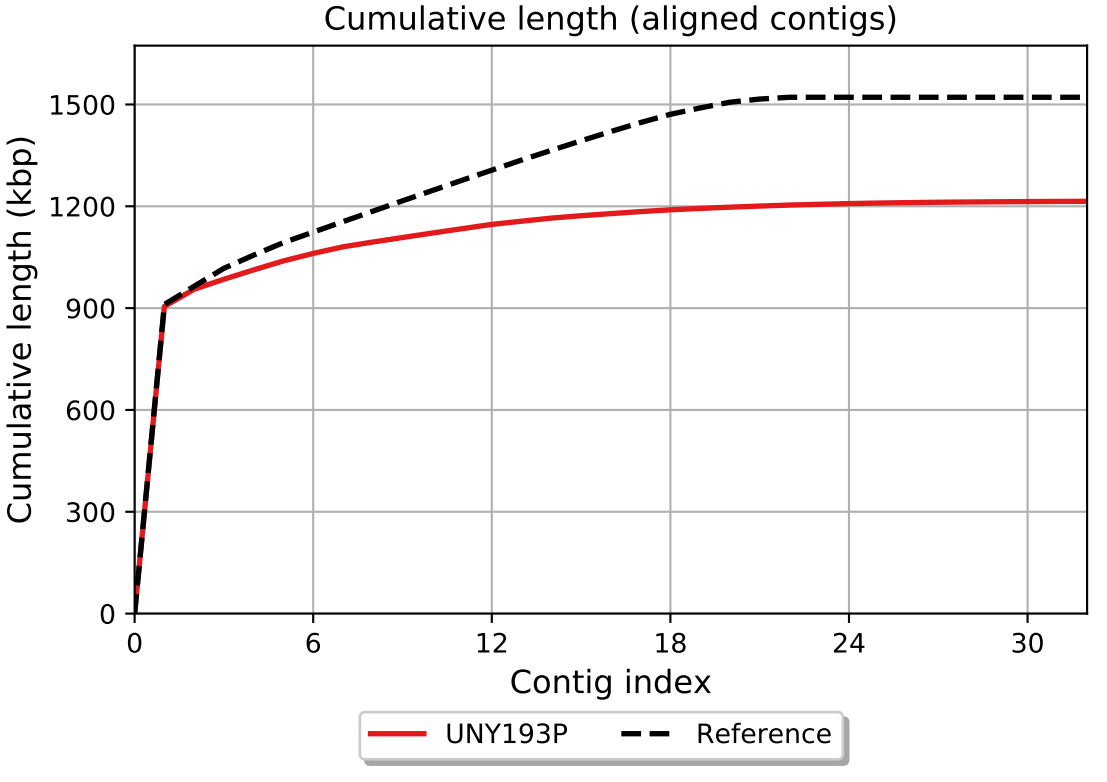

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UNY193P
Reference

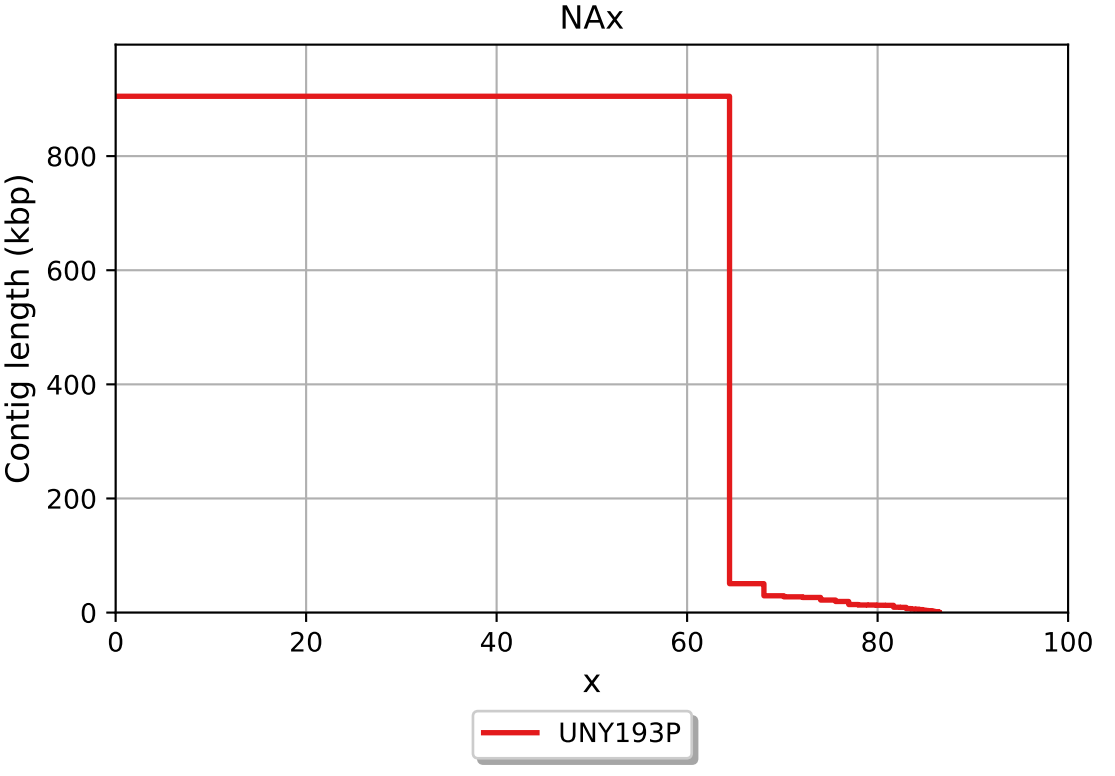

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
UNY193P
Reference

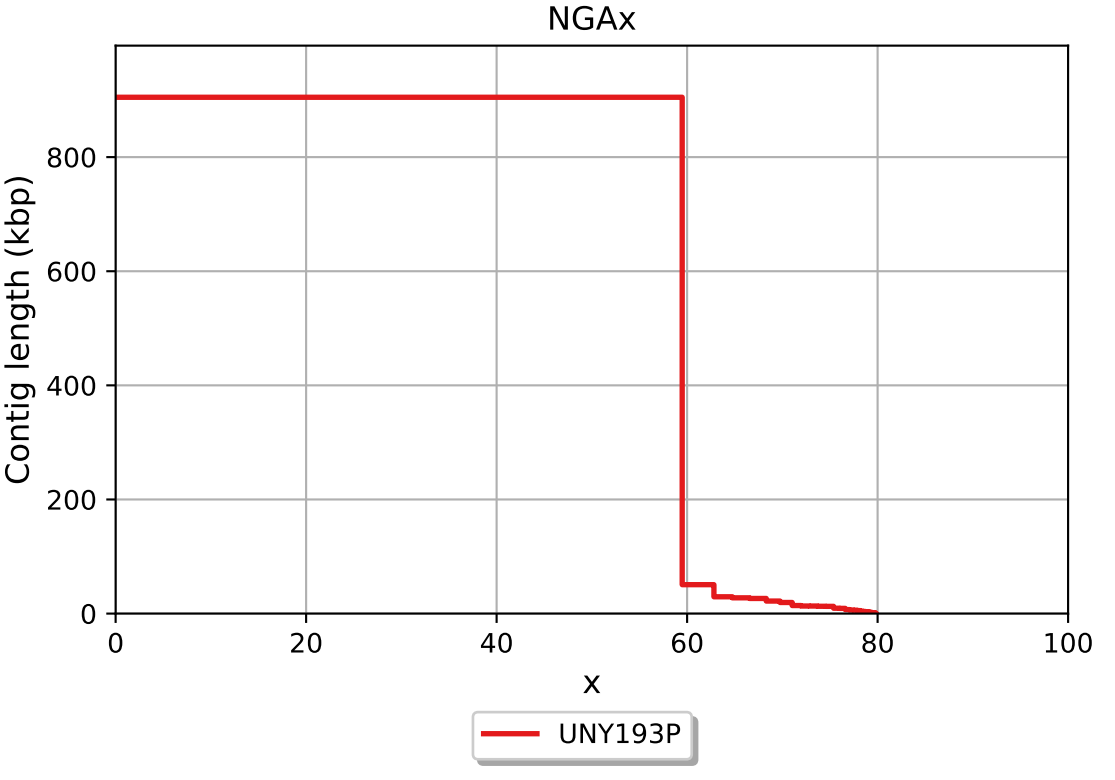

UNY193P GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
UNY193P

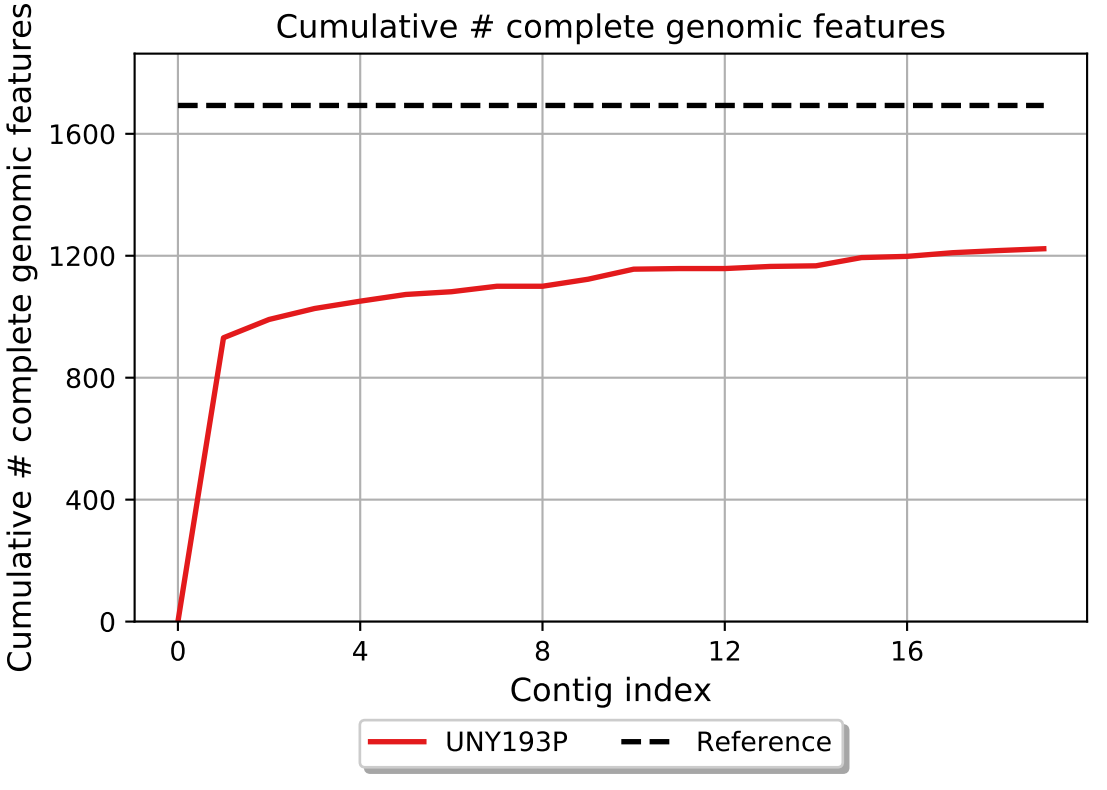

Misassemblies
10
8
6
4
2
0
UNY193P
relocations
translocations

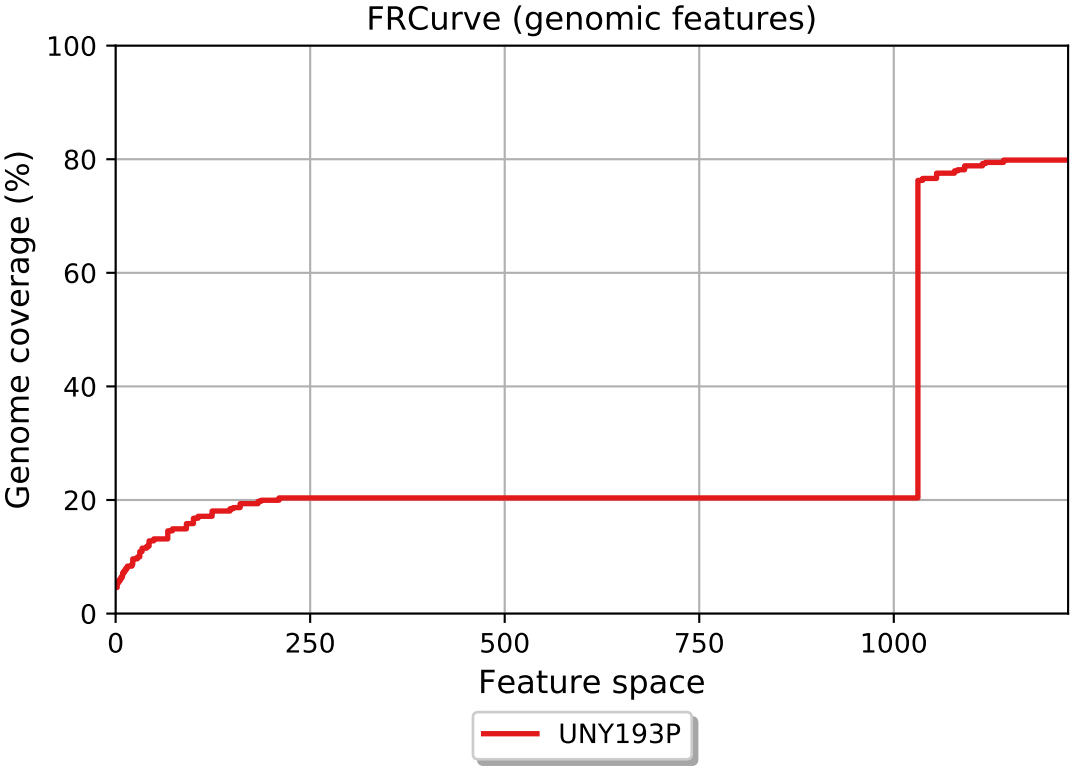

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
UNY193P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
6
12
18
24
30
Contig index
UNY193P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY193P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY193P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
UNY193P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
UNY193P