Report

	UNY1128P
# contigs (>= 0 bp)	277
# contigs (>= 1000 bp)	30
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1488312
Total length (>= 1000 bp)	1431447
Total length (>= 5000 bp)	1407708
Total length (>= 10000 bp)	1393600
Total length (>= 25000 bp)	1273967
Total length (>= 50000 bp)	1093396
# contigs	43
Largest contig	709546
Total length	1440836
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	213832
NG50	213832
N90	20737
NG90	15263
auN	393279.6
auNG	372500.9
L50	2
LG50	2
L90	13
LG90	17
# misassemblies	27
# misassembled contigs	8
Misassembled contigs length	938889
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	8 + 16 part
Unaligned length	173847
Genome fraction (%)	81.650
Duplication ratio	1.017
# N's per 100 kbp	0.90
# mismatches per 100 kbp	828.82
# indels per 100 kbp	65.41
# genomic features	1305 + 64 part
Largest alignment	696081
Total aligned length	1262754
NA50	213816
NGA50	213816
NA90	-
NGA90	-
auNA	372768.3
auNGA	353073.4
LA50	2
LGA50	2
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

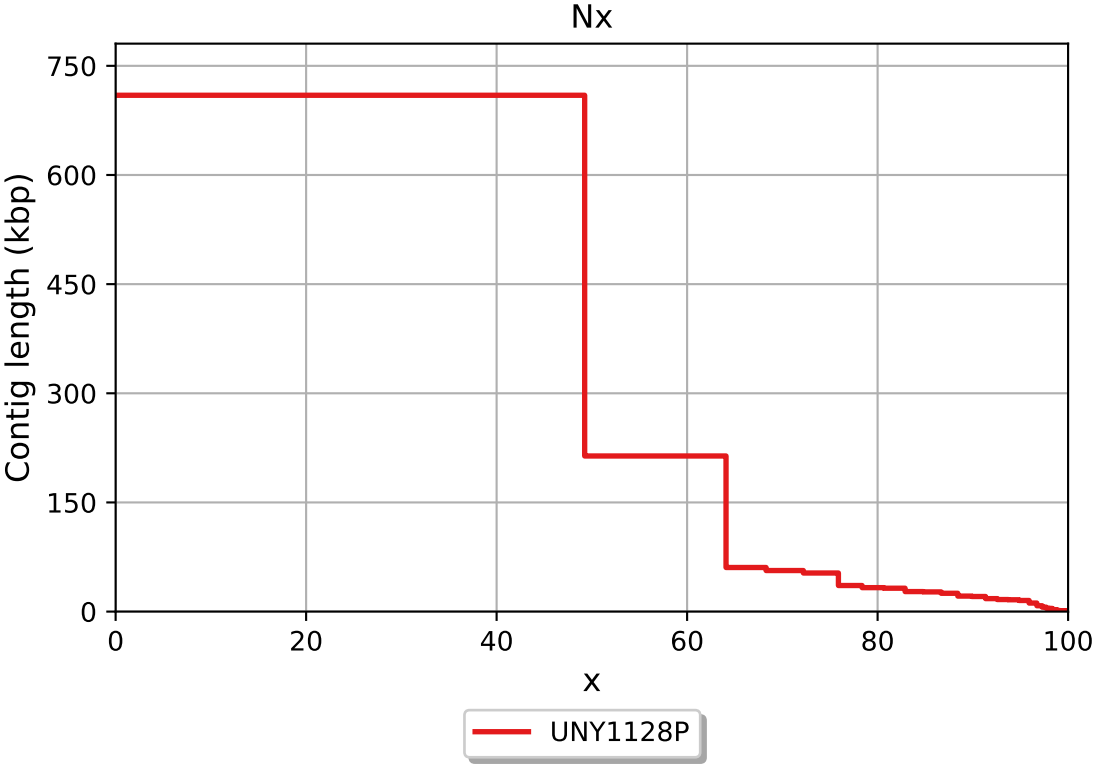
	UNY1128P
# misassemblies	27
# contig misassemblies	27
# c. relocations	5
# c. translocations	22
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	938889
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	10466
# indels	826
# indels (<= 5 bp)	761
# indels (> 5 bp)	65
Indels length	3067

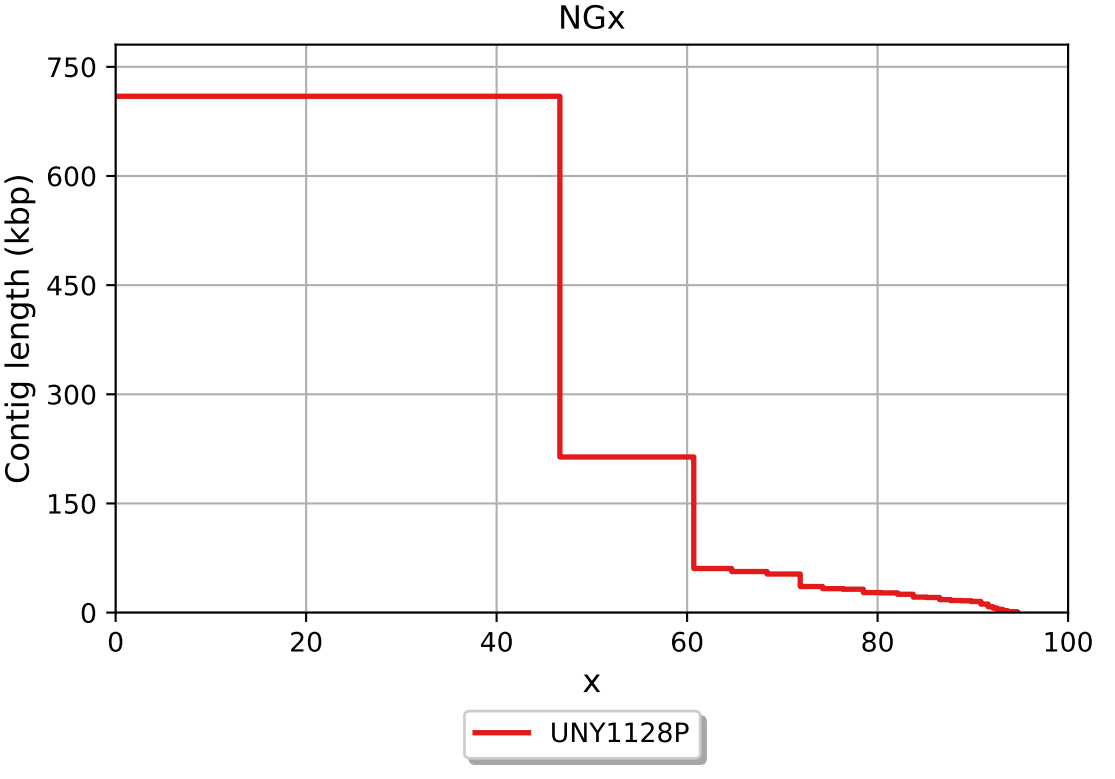
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

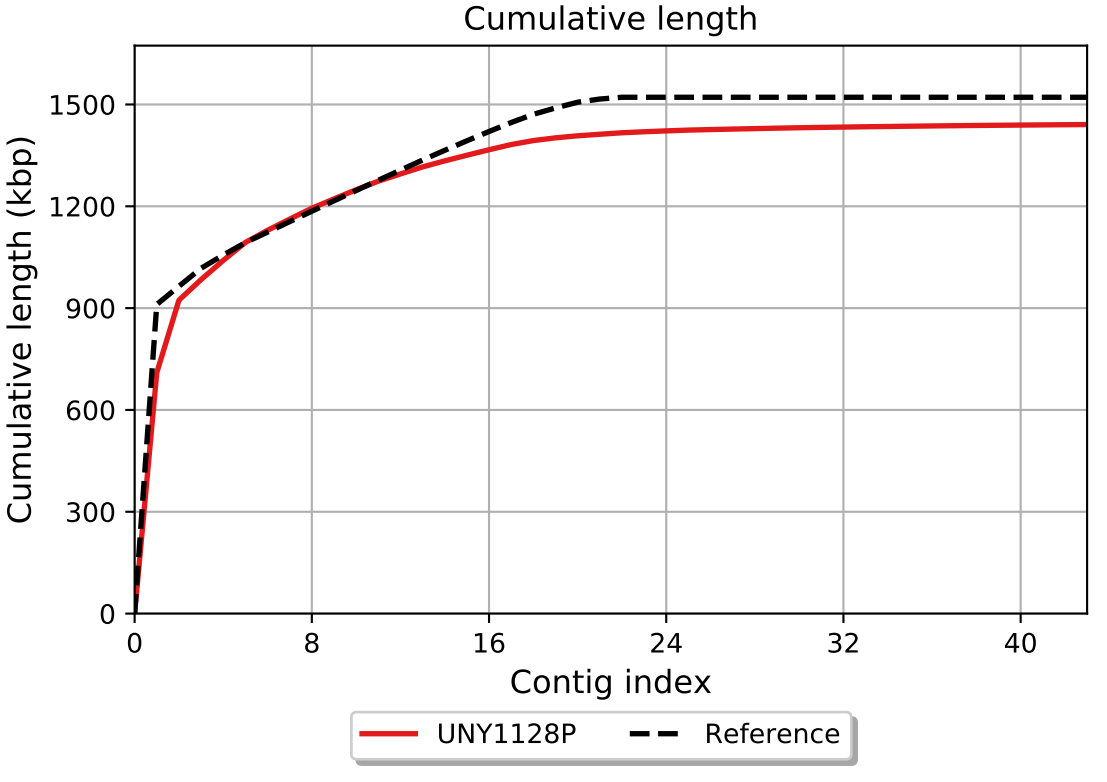
Unaligned report

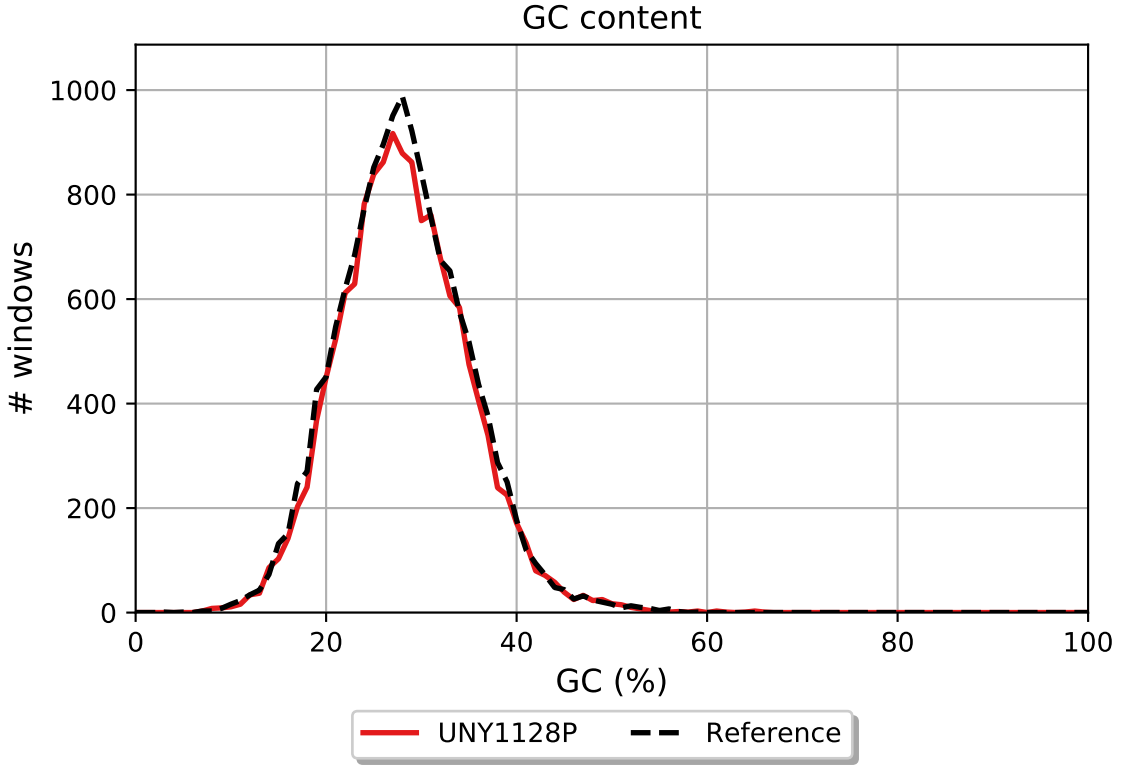
	UNY1128P
# fully unaligned contigs	8
Fully unaligned length	13375
# partially unaligned contigs	16
Partially unaligned length	160472
# N's	13

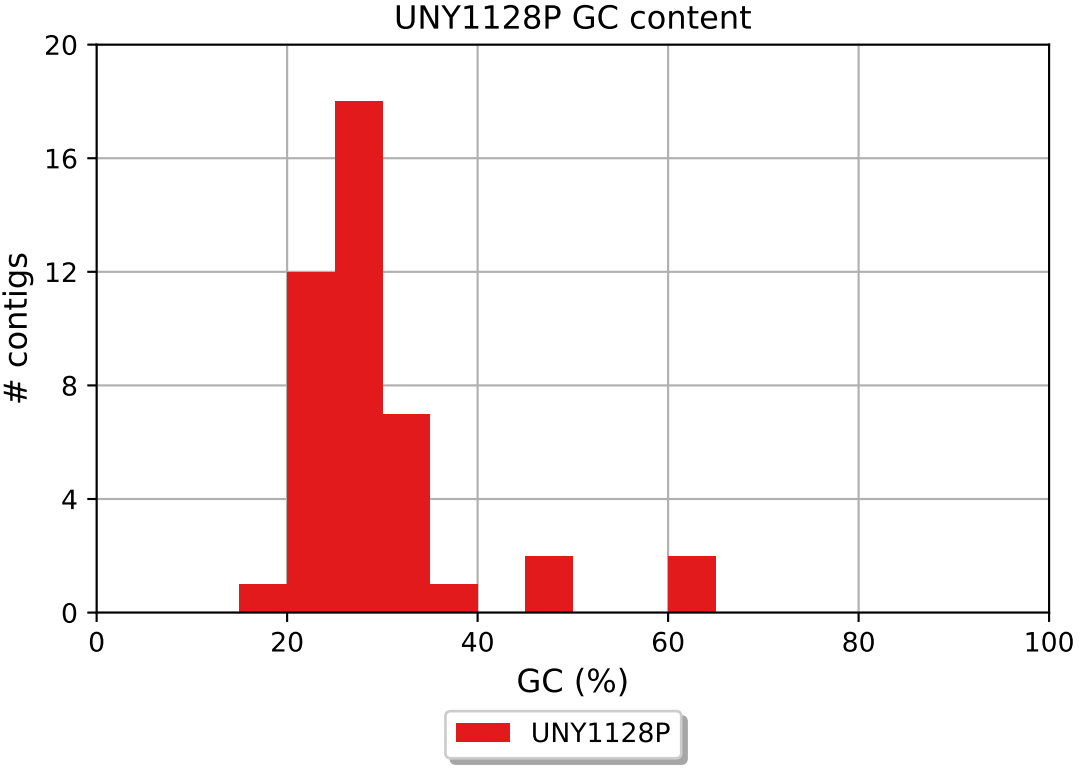
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
UNY1128P

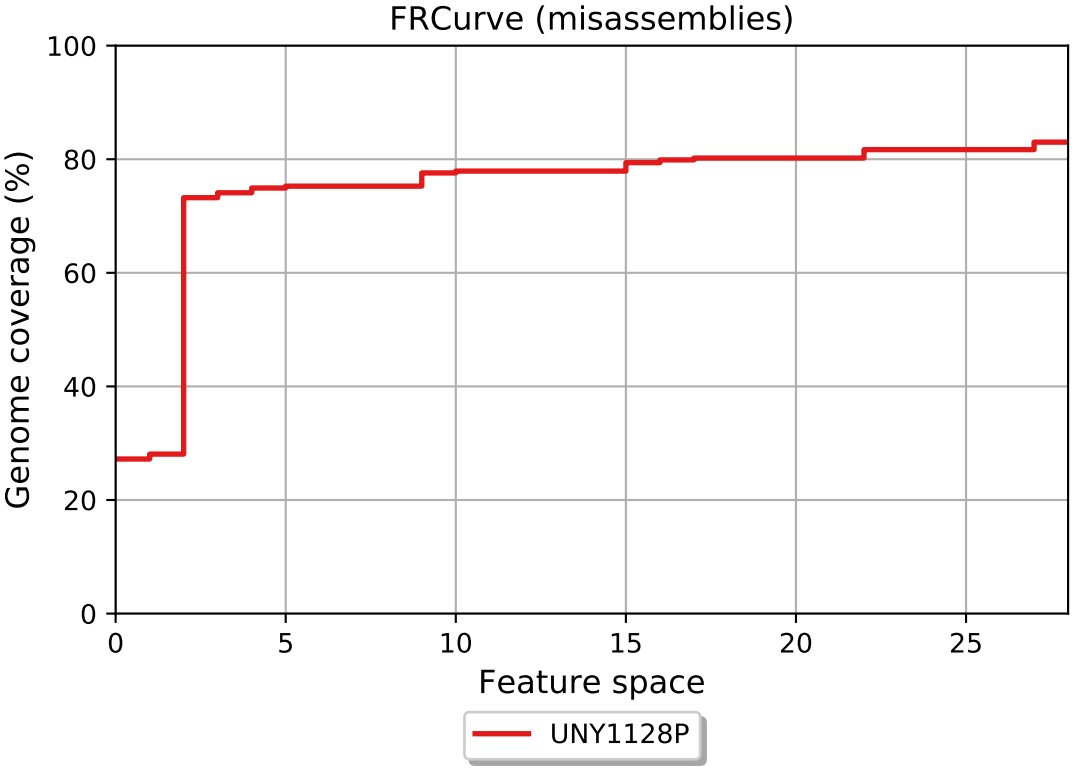

NGx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
UNY1128P

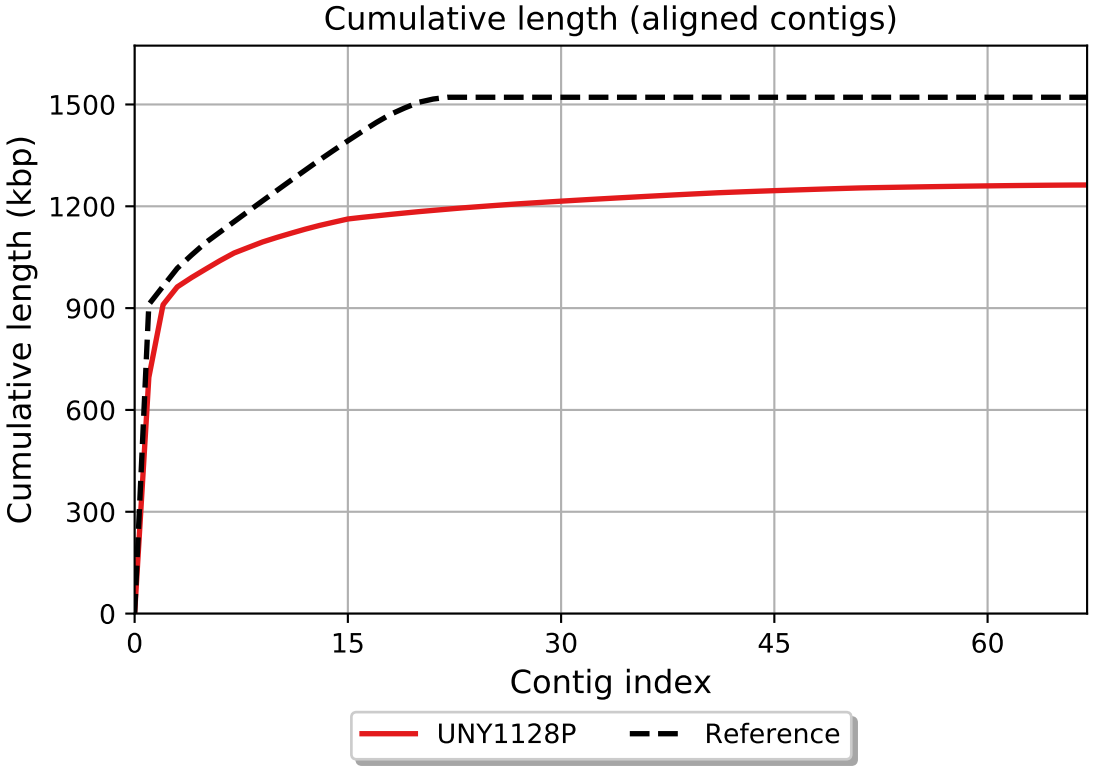

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
UNY1128P
Reference

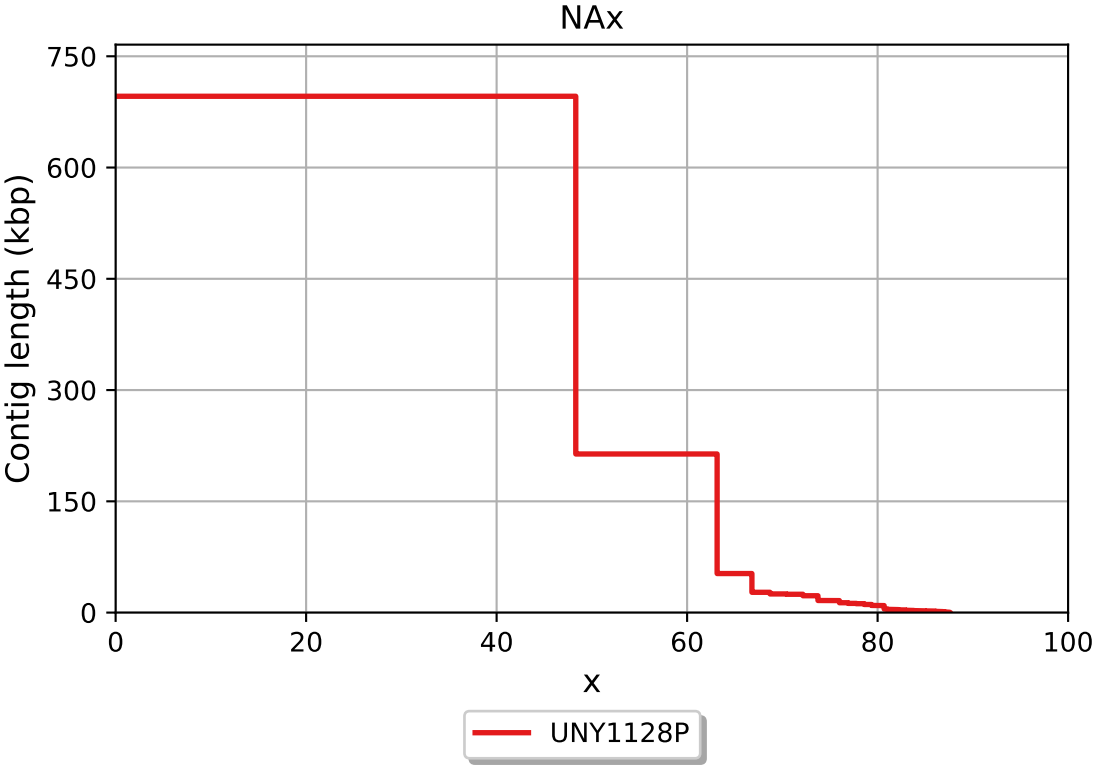

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
UNY1128P
Reference

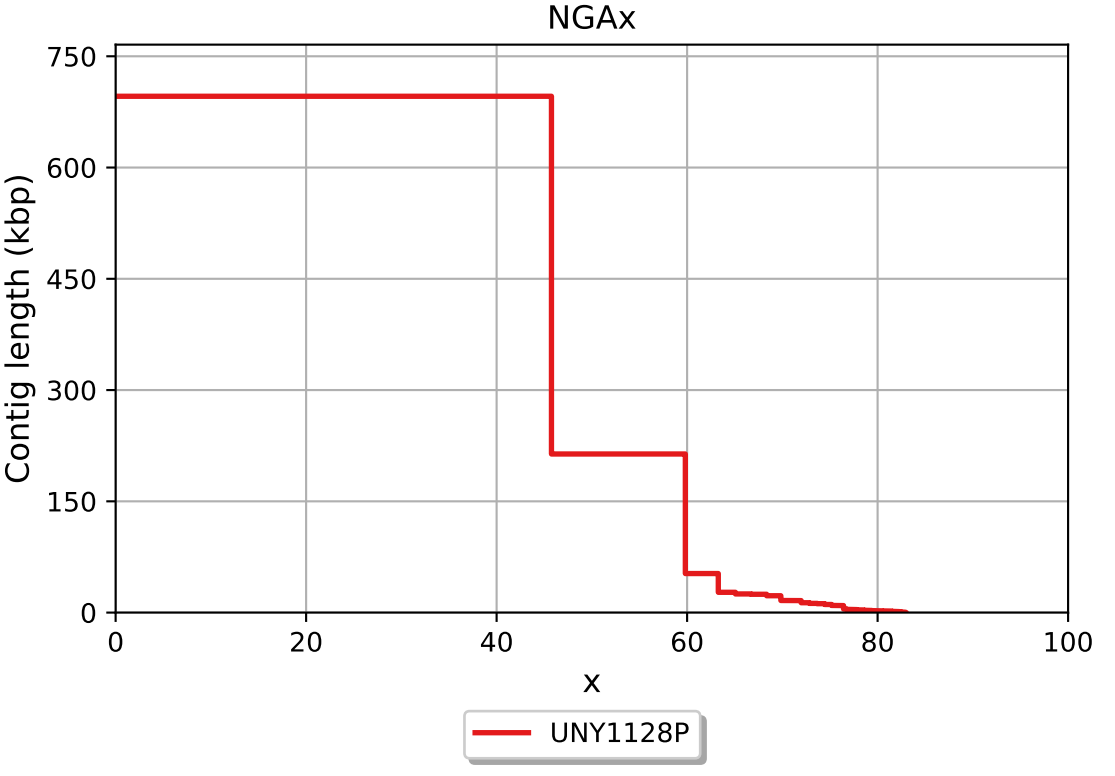

UNY1128P GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
UNY1128P

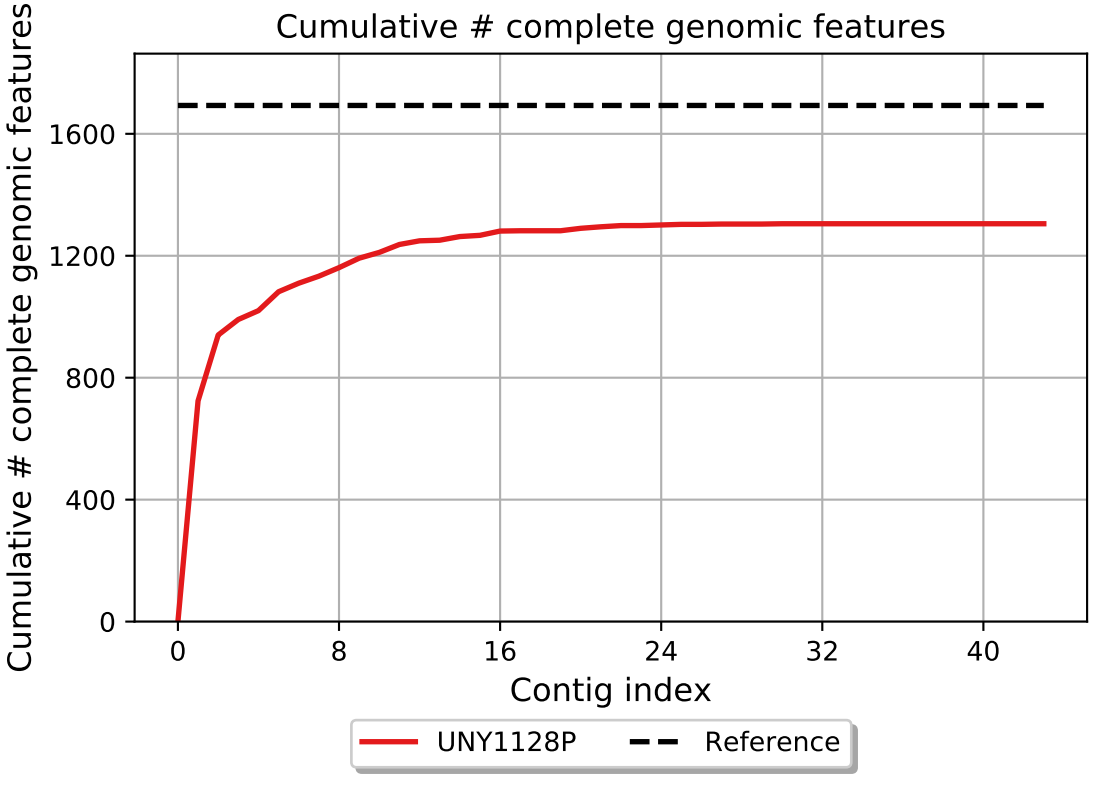
Misassemblies
30
25
20
15
10
5
0
UNY1128P
relocations
translocations

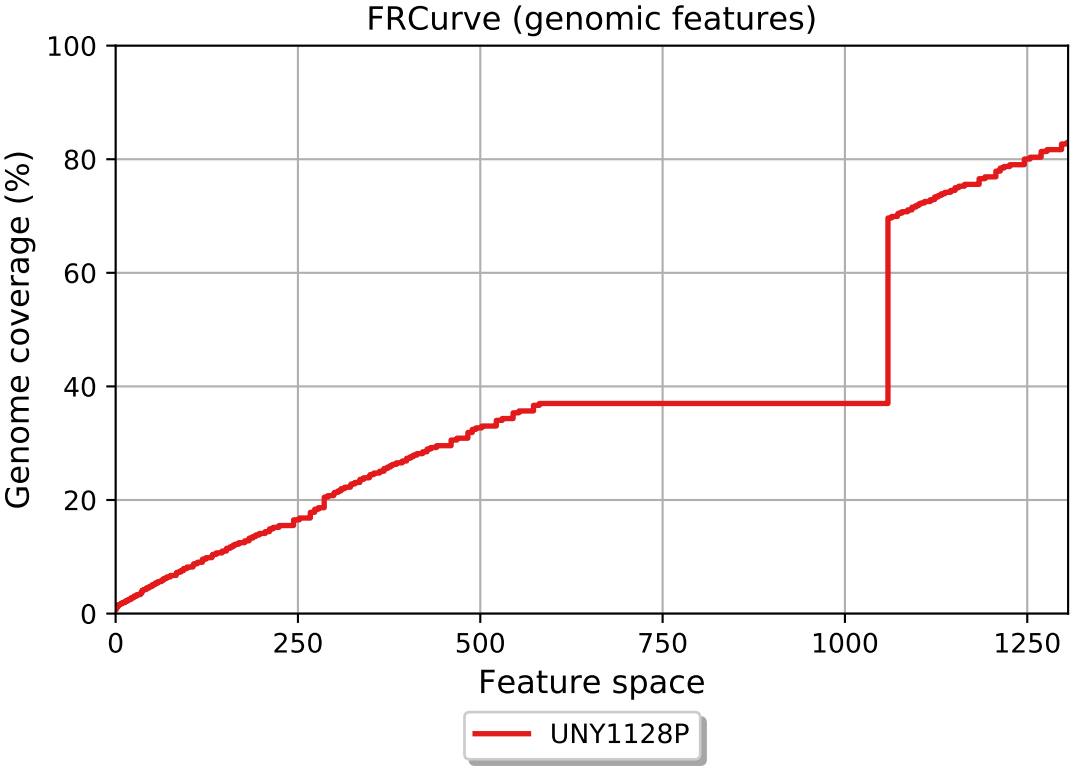

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
UNY1128P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
15
30
45
60
Contig index
UNY1128P
Reference


NAx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
UNY1128P


NGAx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
UNY1128P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
8
16
24
32
40
Contig index
UNY1128P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
UNY1128P