Report

	UNY208P
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1413253
Total length (>= 1000 bp)	1413253
Total length (>= 5000 bp)	1413253
Total length (>= 10000 bp)	1413253
Total length (>= 25000 bp)	1287173
Total length (>= 50000 bp)	966596
# contigs	19
Largest contig	912713
Total length	1413253
Reference length	1521208
GC (%)	28.35
Reference GC (%)	28.18
N50	912713
NG50	912713
N90	25503
NG90	21337
auN	600072.0
auNG	557486.9
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	14
# misassembled contigs	6
Misassembled contigs length	187224
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	0 + 16 part
Unaligned length	185167
Genome fraction (%)	78.520
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	772.90
# indels per 100 kbp	41.67
# genomic features	1262 + 35 part
Largest alignment	904987
Total aligned length	1223835
NA50	904987
NGA50	904987
NA90	-
NGA90	-
auNA	584040.7
auNGA	542593.3
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

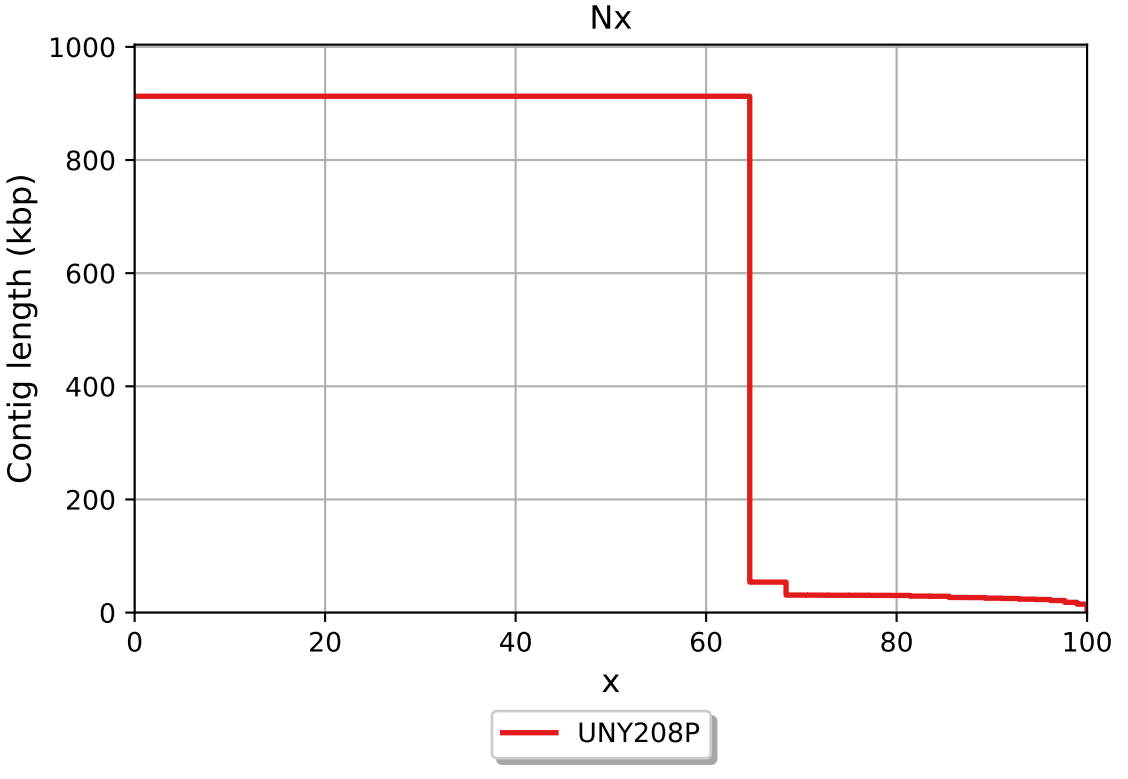
	UNY208P
# misassemblies	14
# contig misassemblies	14
# c. relocations	3
# c. translocations	11
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	187224
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	9459
# indels	510
# indels (<= 5 bp)	459
# indels (> 5 bp)	51
Indels length	2269

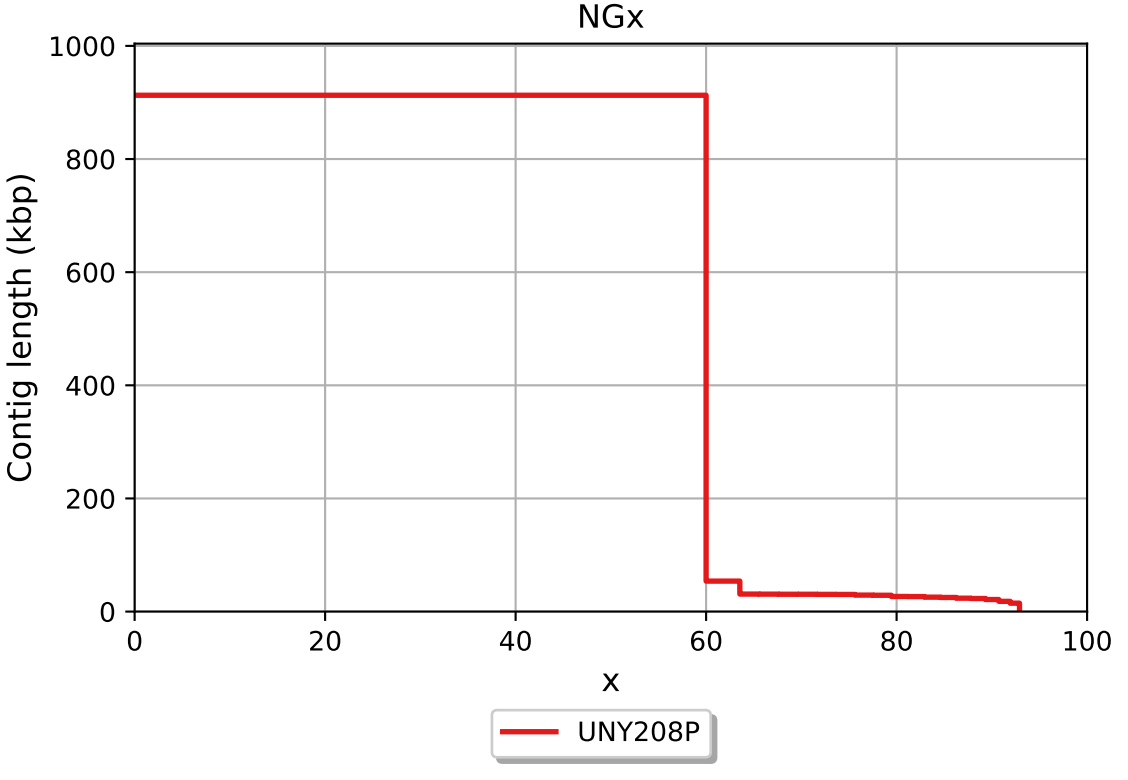
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

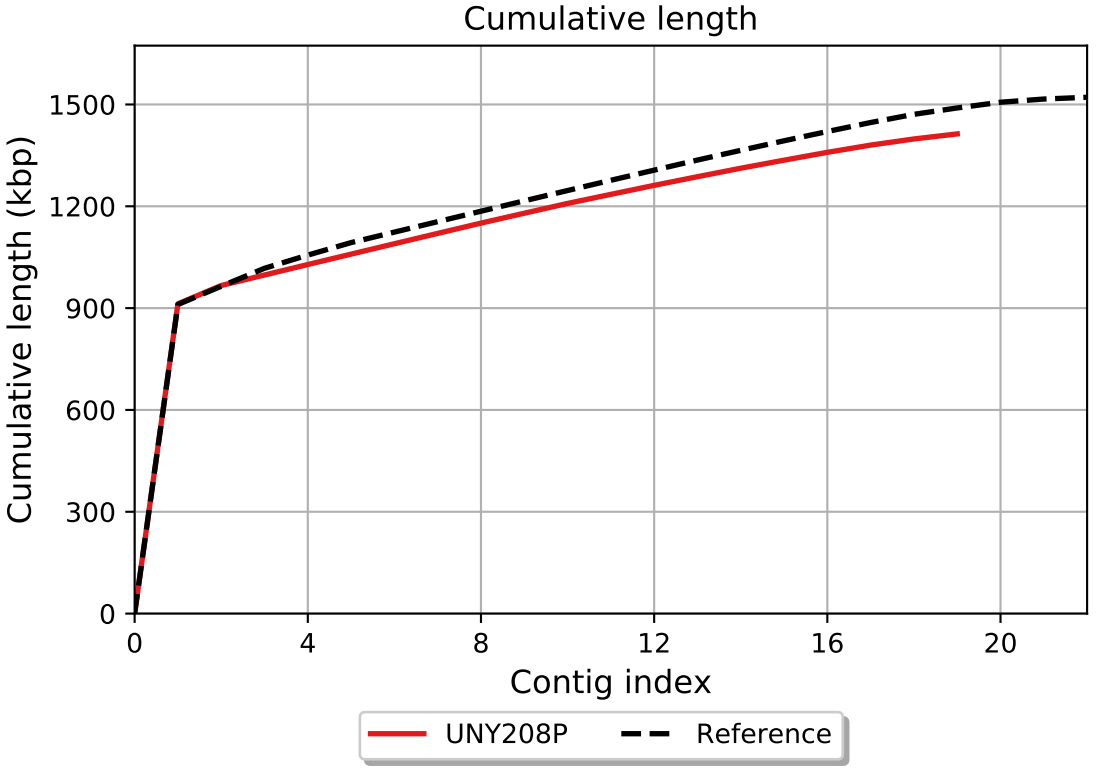
Unaligned report

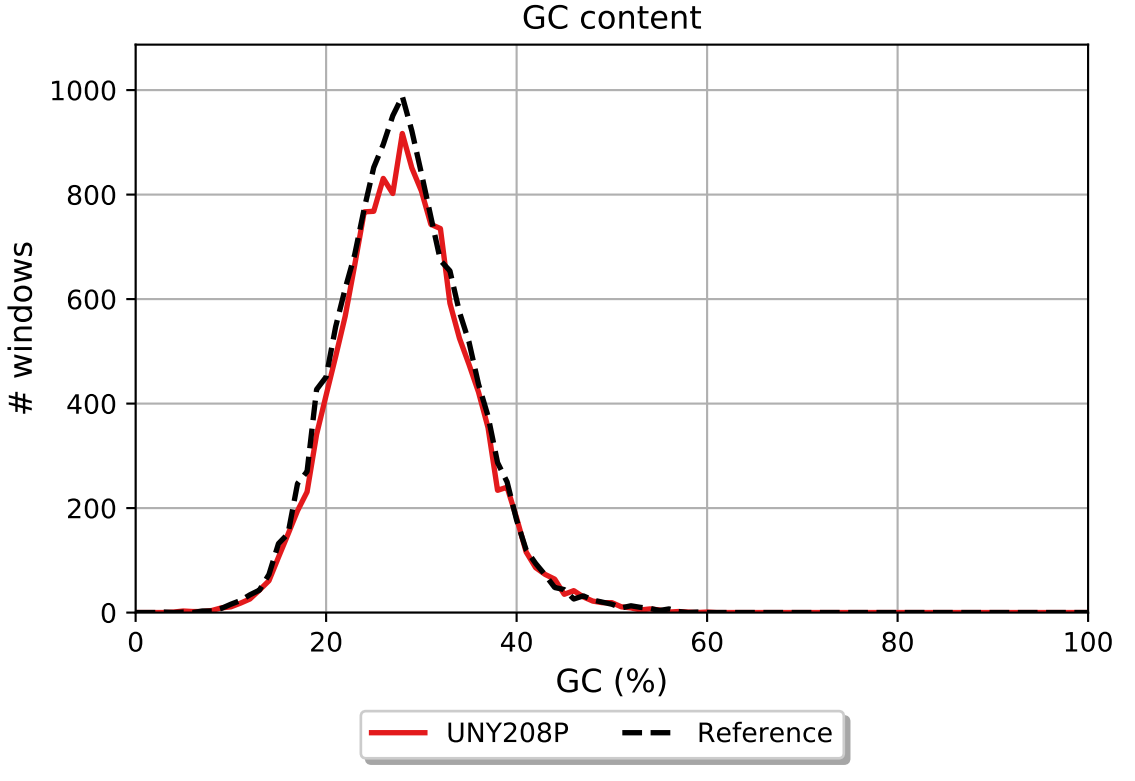
	UNY208P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
Partially unaligned length	185167
# N's	0

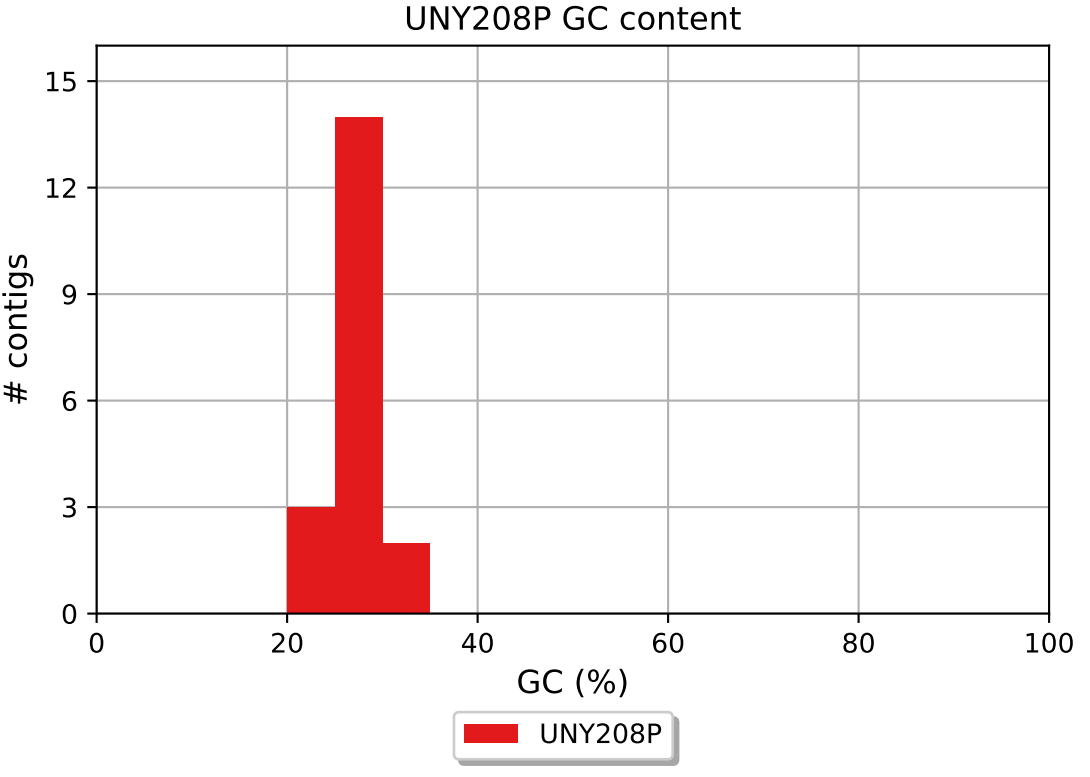
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

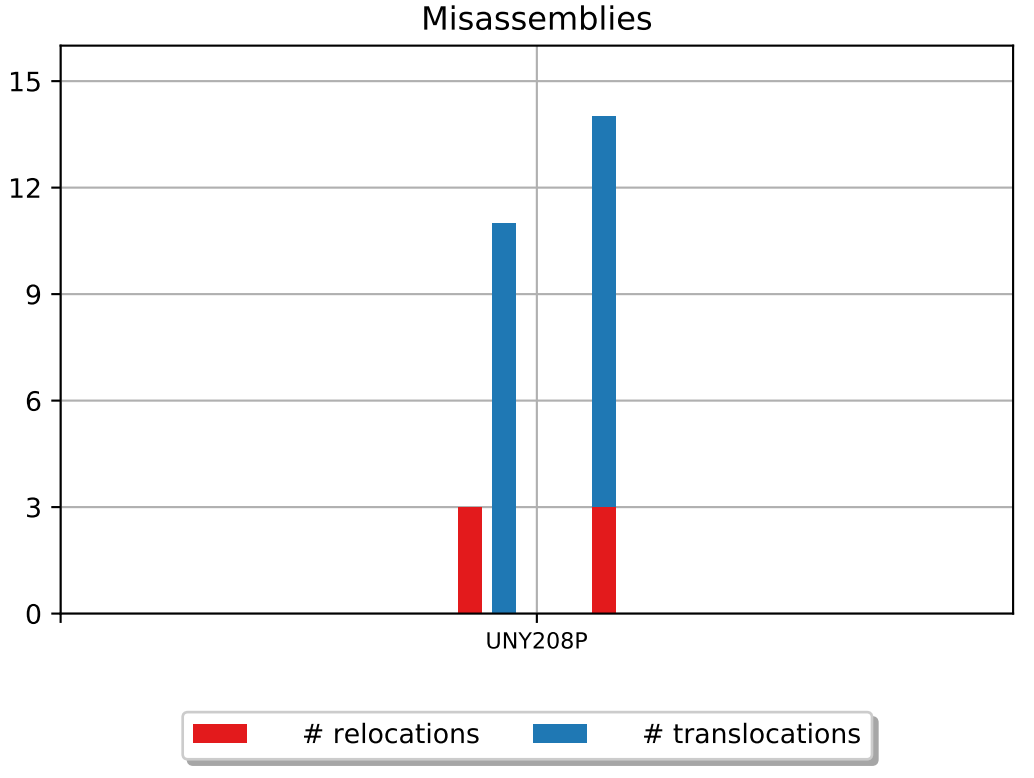

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UNY208P

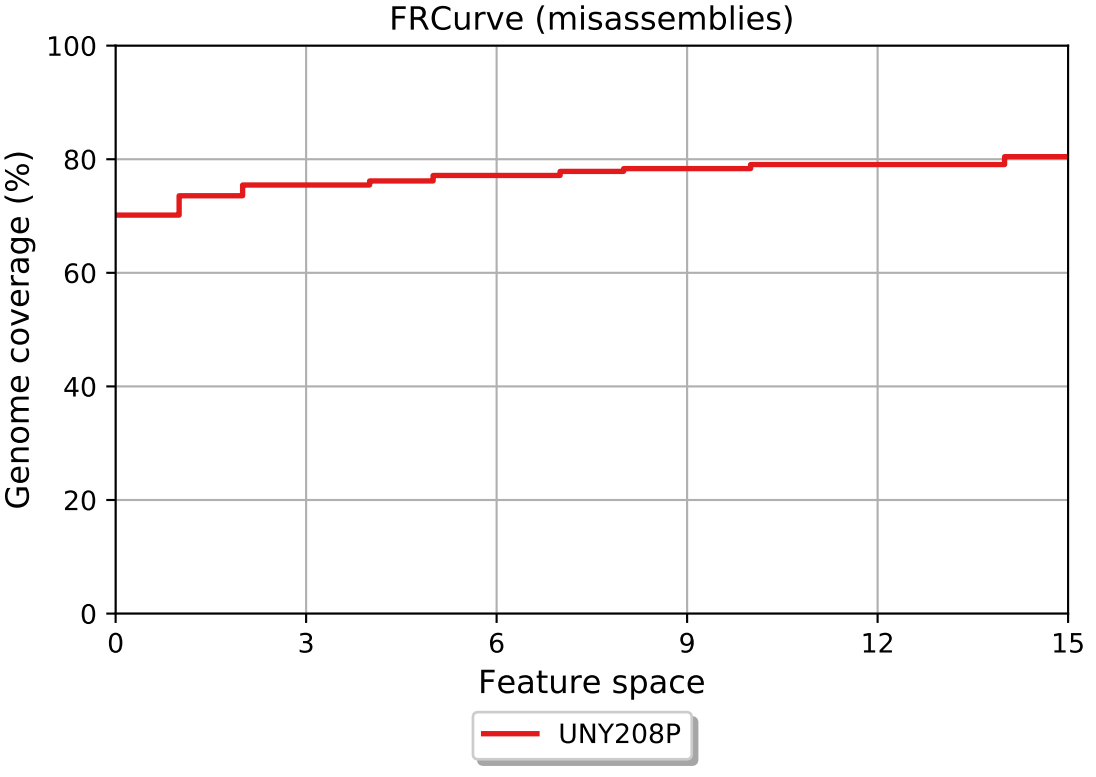

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UNY208P

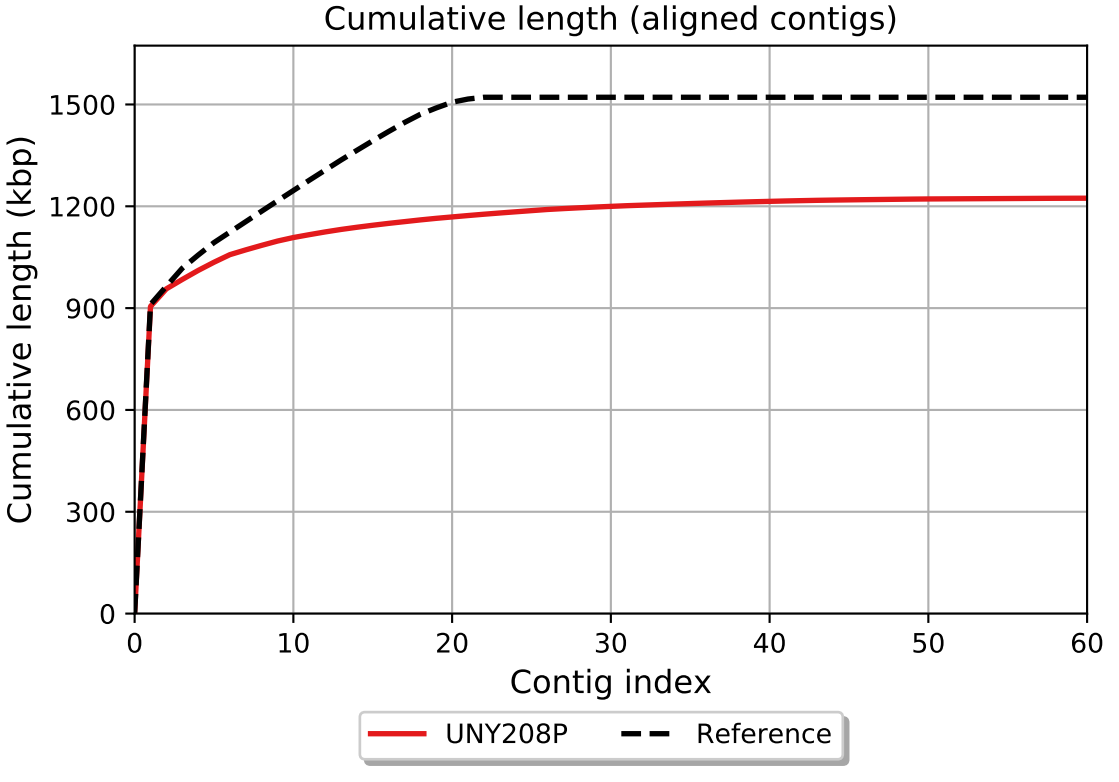

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UNY208P
Reference

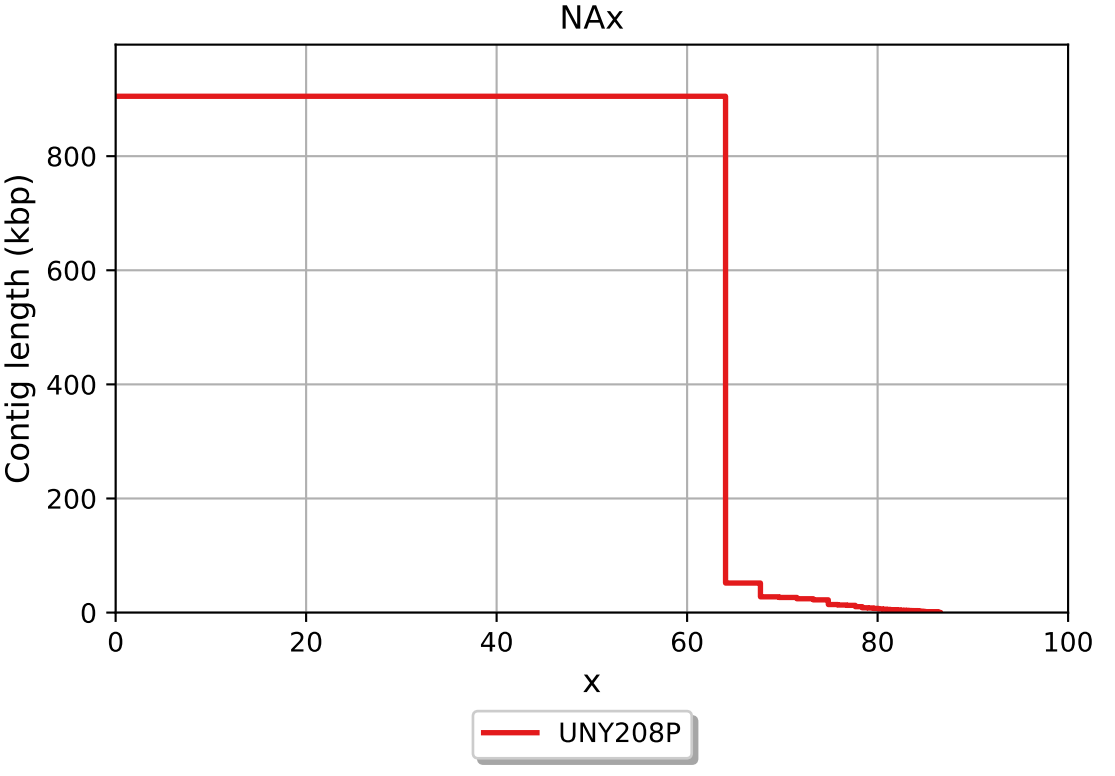

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
UNY208P
Reference

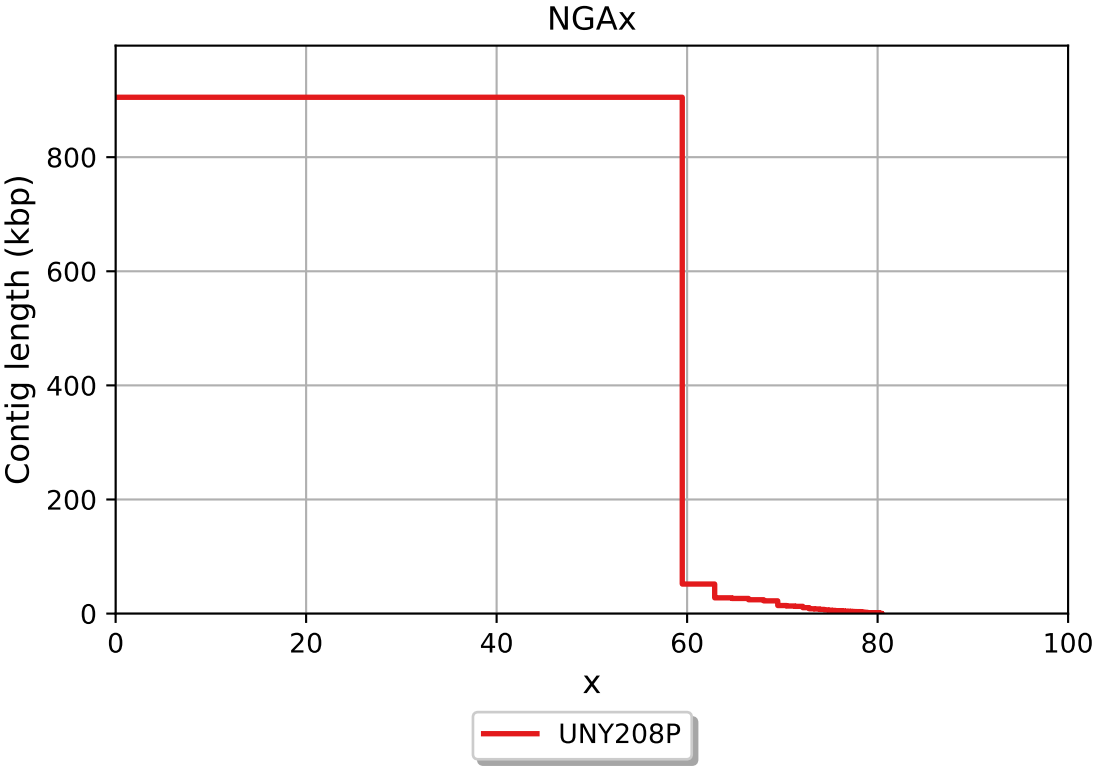

UNY208P GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
UNY208P

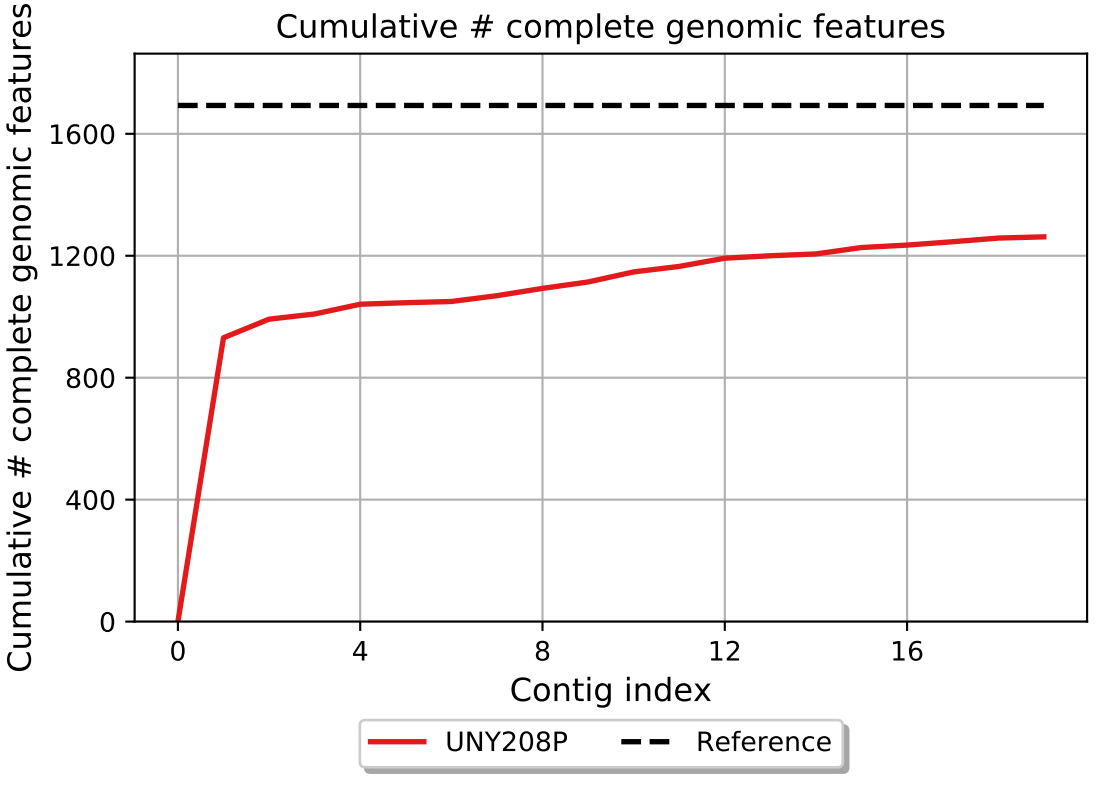

Misassemblies
15
12
9
6
3
0
UNY208P
relocations
translocations

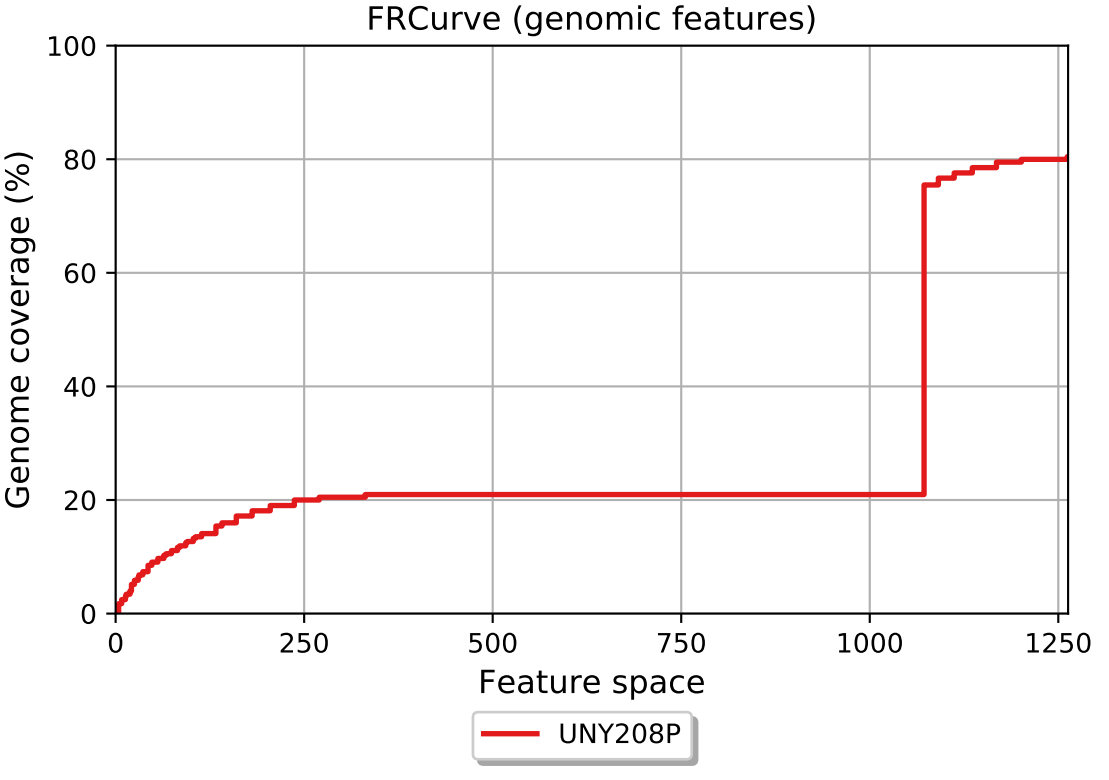

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
UNY208P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
10
20
30
40
50
60
Contig index
UNY208P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY208P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY208P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
UNY208P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
UNY208P