Report

	UNY169P
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1346761
Total length (>= 1000 bp)	1346761
Total length (>= 5000 bp)	1346761
Total length (>= 10000 bp)	1338039
Total length (>= 25000 bp)	1259766
Total length (>= 50000 bp)	956581
# contigs	17
Largest contig	902773
Total length	1346761
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	902773
NG50	902773
N90	27768
NG90	-
auN	615412.7
auNG	544839.3
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	18
# misassembled contigs	9
Misassembled contigs length	266473
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	1 + 13 part
Unaligned length	120825
Genome fraction (%)	80.421
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	855.10
# indels per 100 kbp	53.06
# genomic features	1267 + 57 part
Largest alignment	902593
Total aligned length	1225119
NA50	902593
NGA50	902593
NA90	2241
NGA90	-
auNA	610379.1
auNGA	540382.9
LA50	1
LGA50	1
LA90	26
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

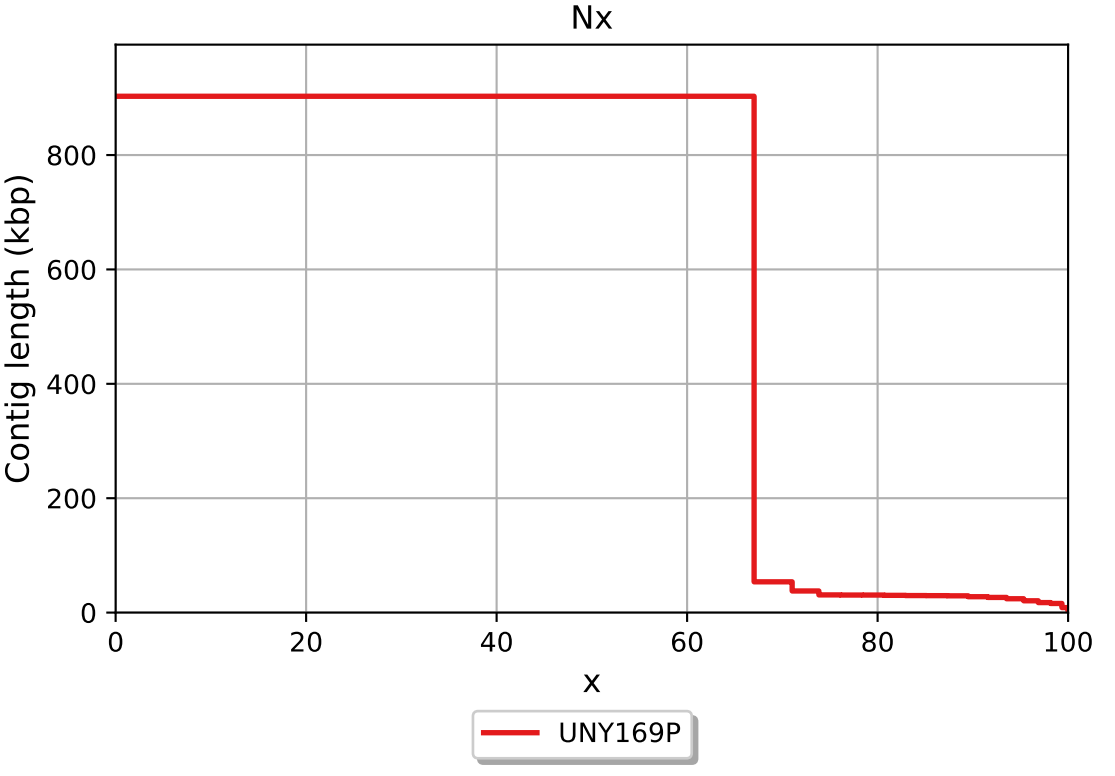
	UNY169P
# misassemblies	18
# contig misassemblies	18
# c. relocations	6
# c. translocations	12
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	266473
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	10476
# indels	650
# indels (<= 5 bp)	580
# indels (> 5 bp)	70
Indels length	3129

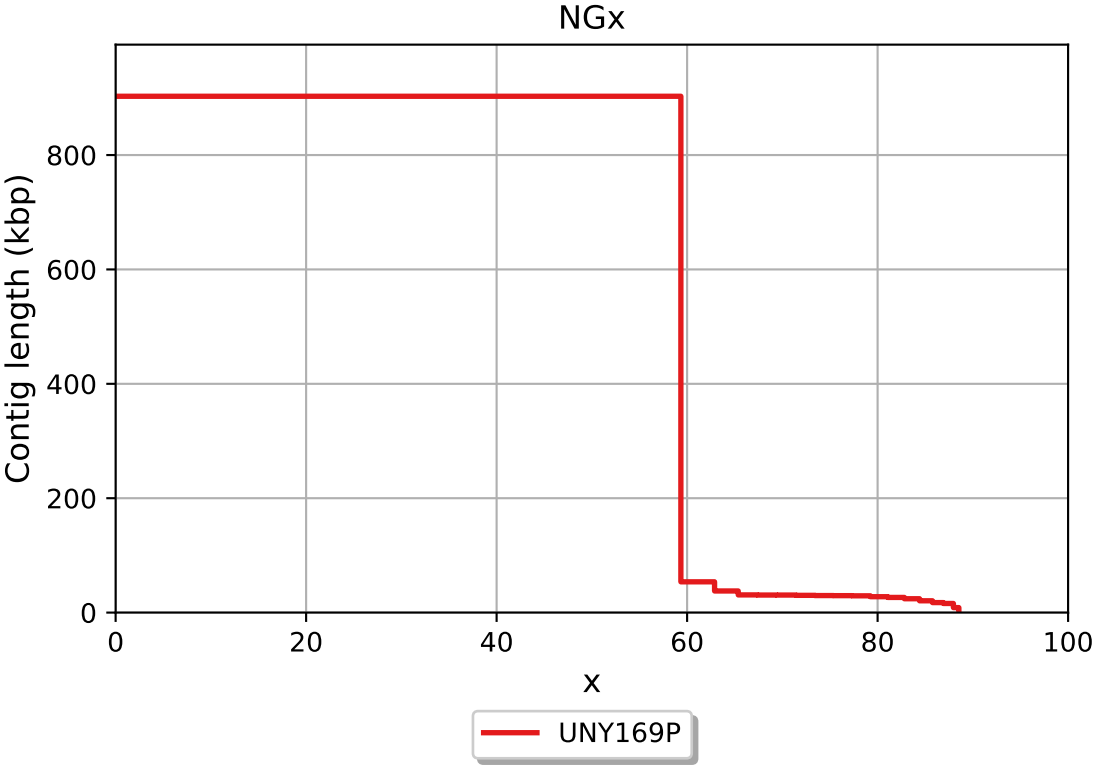
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

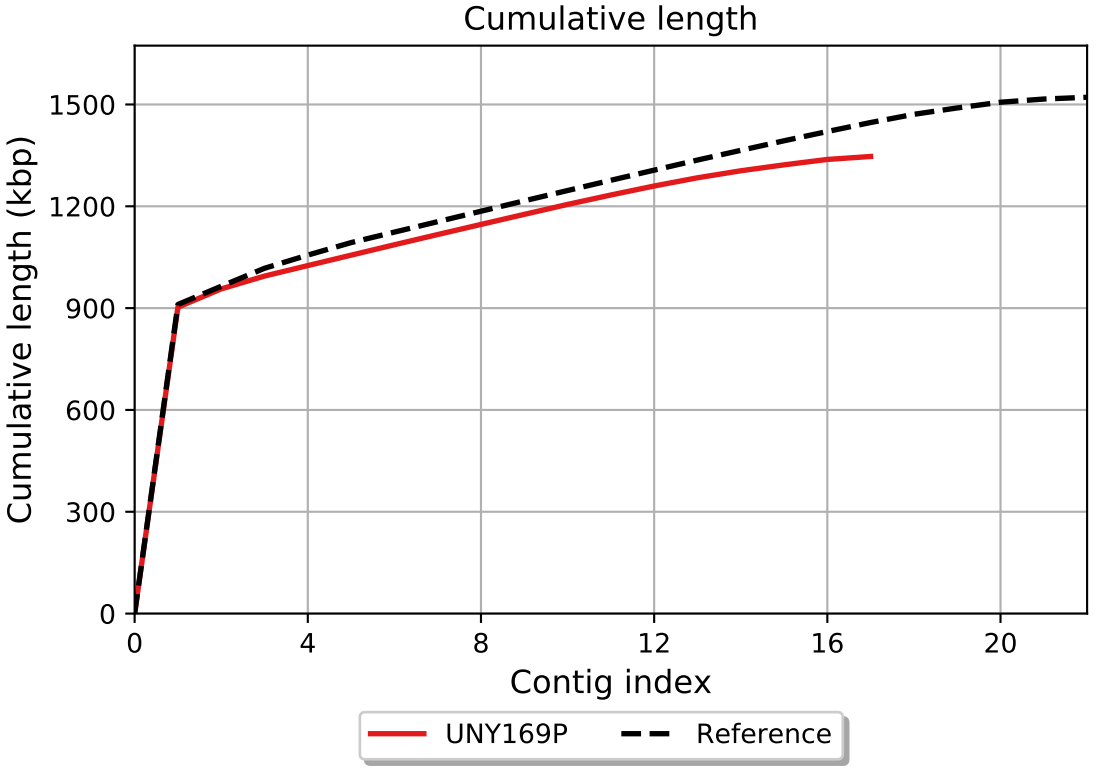
Unaligned report

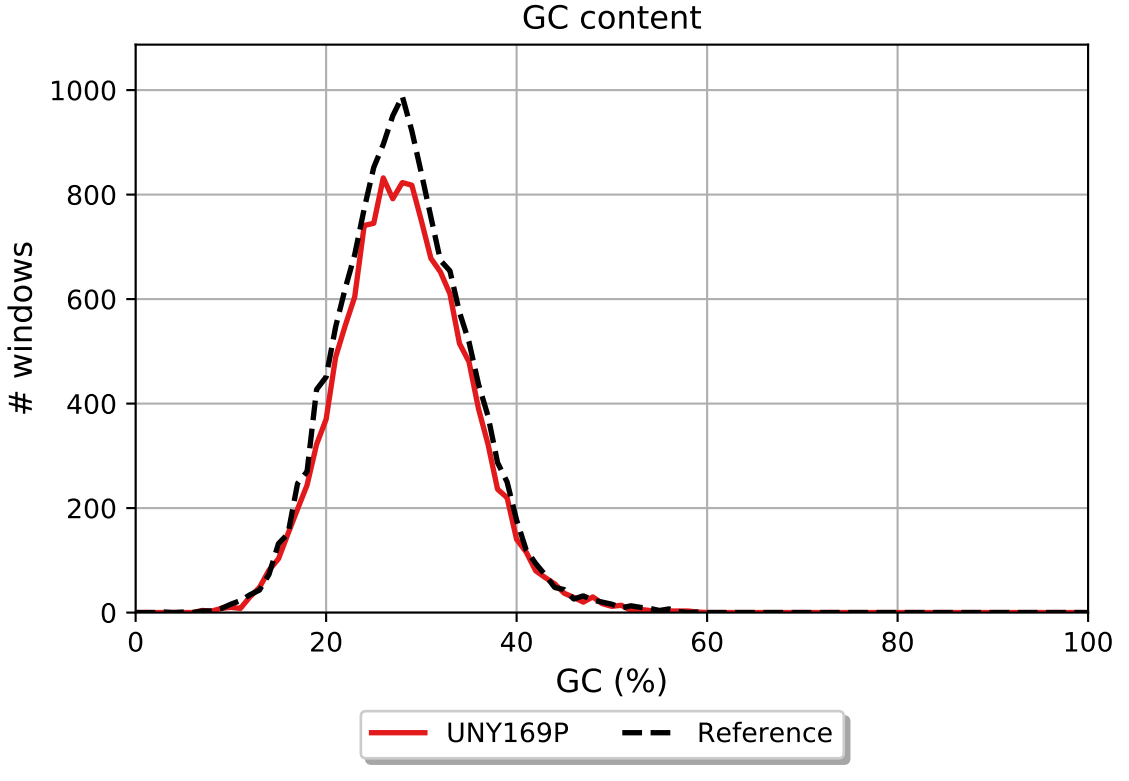
	UNY169P
# fully unaligned contigs	1
Fully unaligned length	27768
# partially unaligned contigs	13
Partially unaligned length	93057
# N's	0

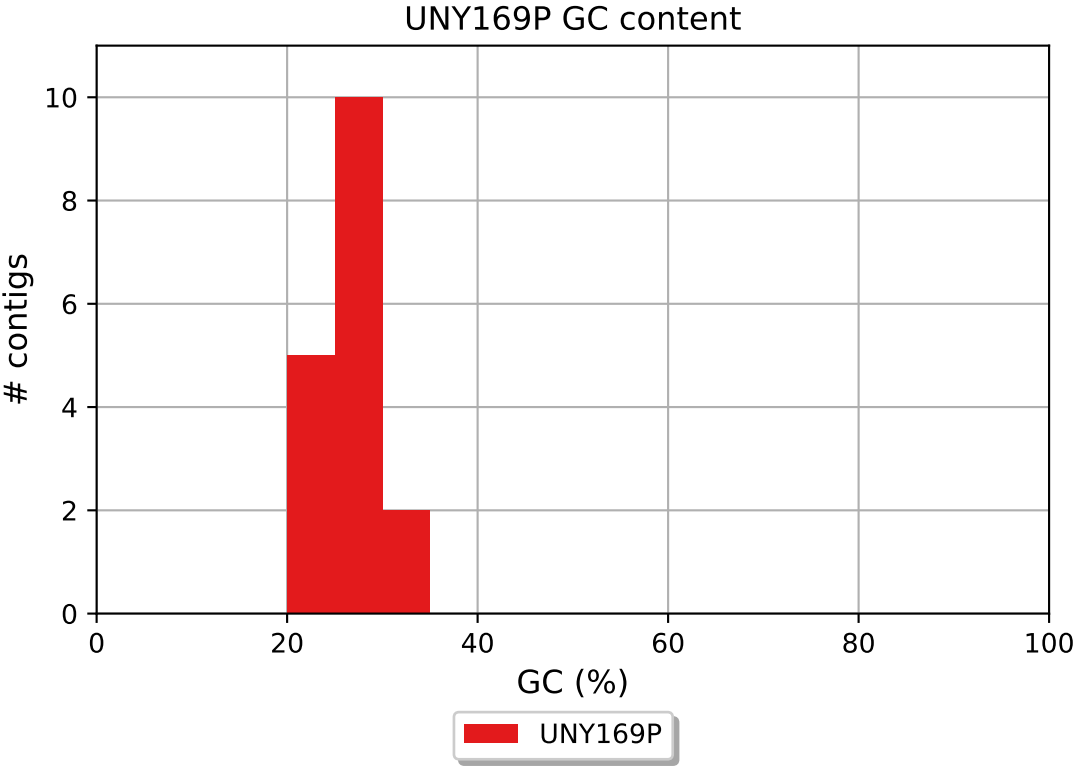
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

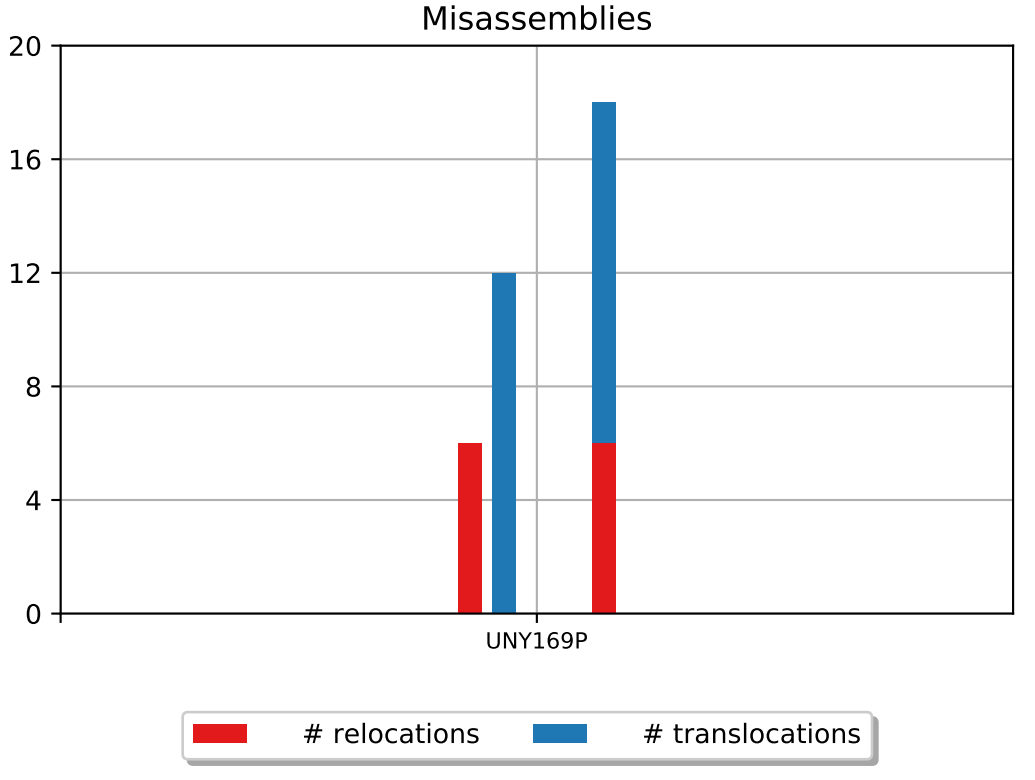

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY169P

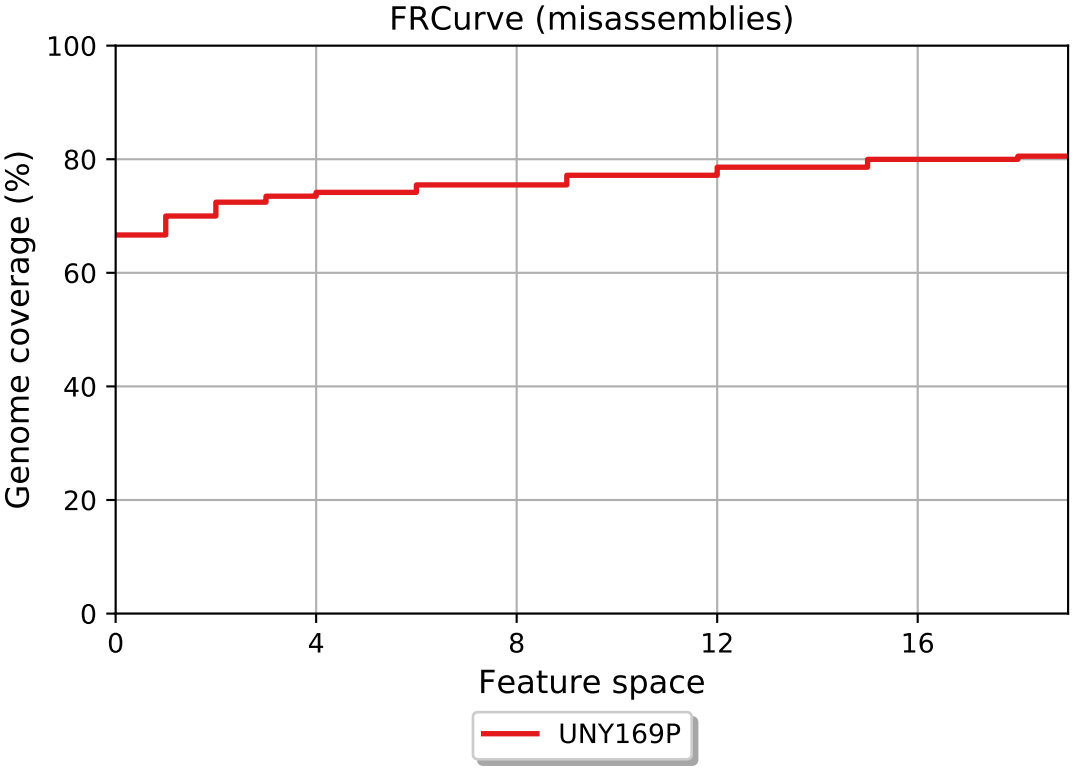

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY169P

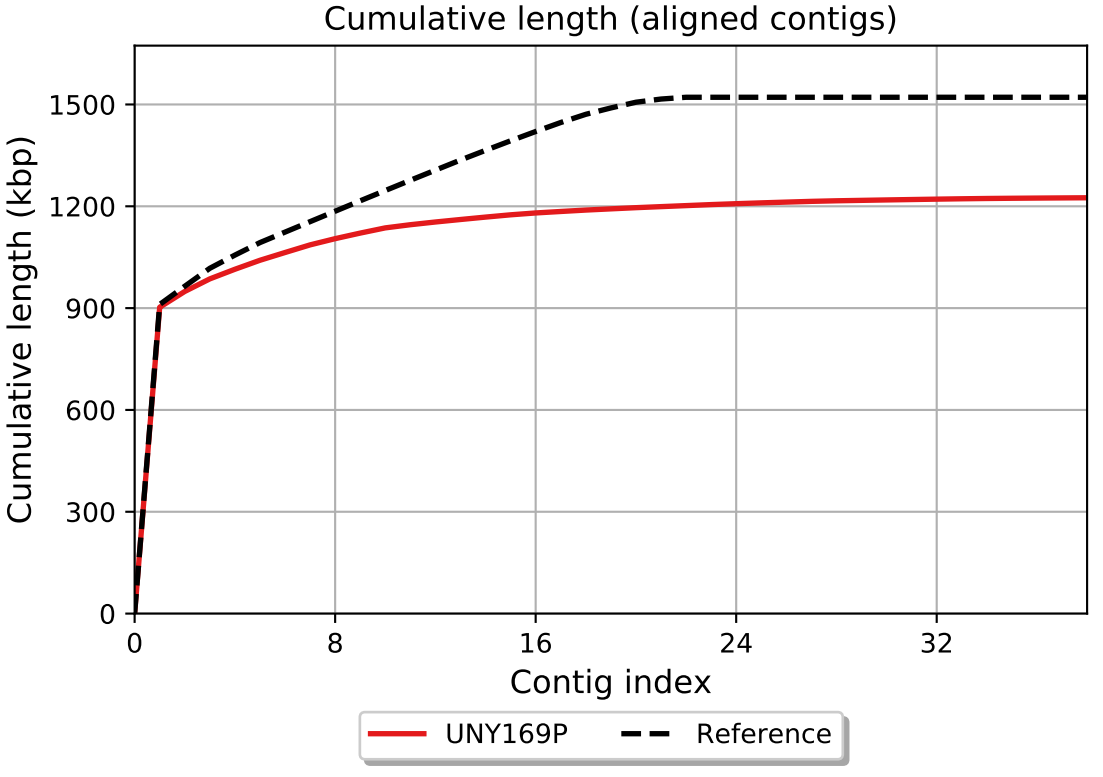

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UNY169P
Reference

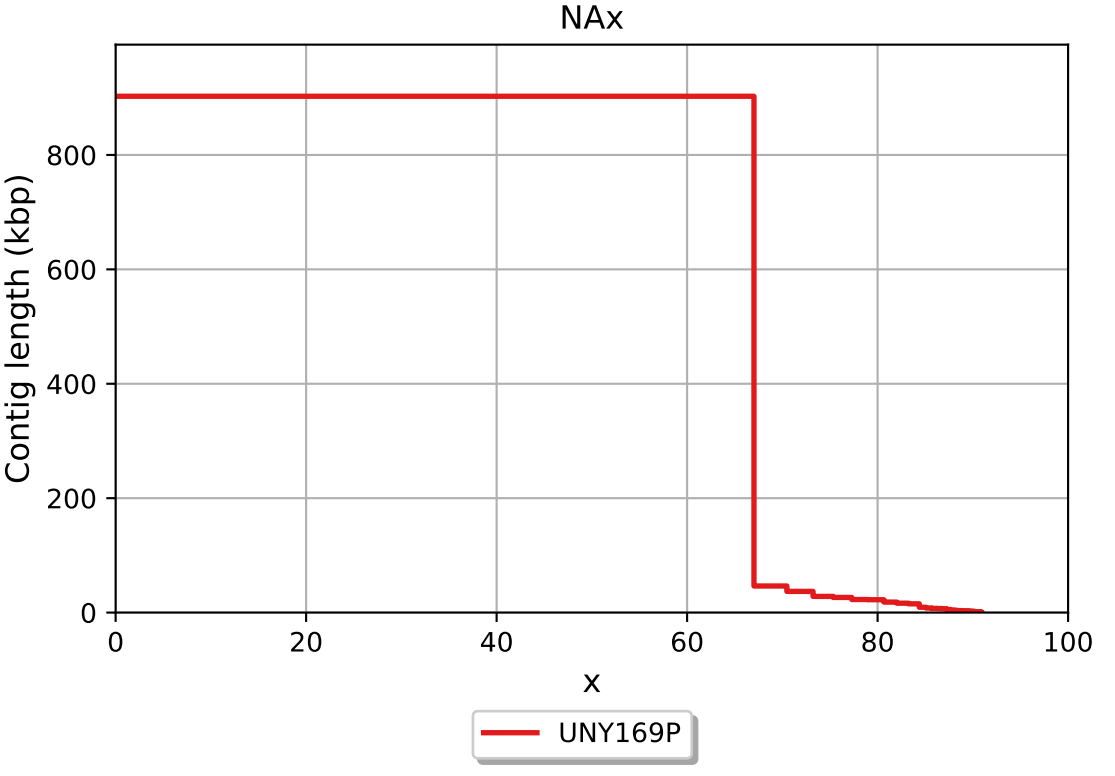

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
UNY169P
Reference

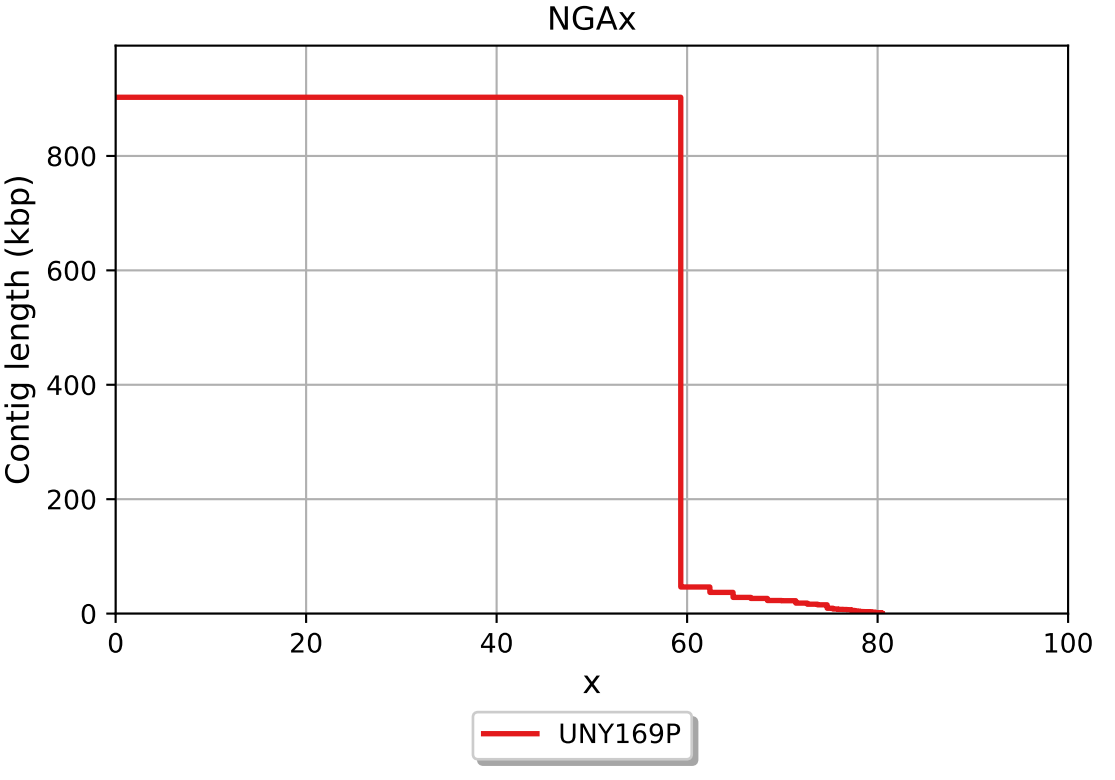

UNY169P GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
UNY169P

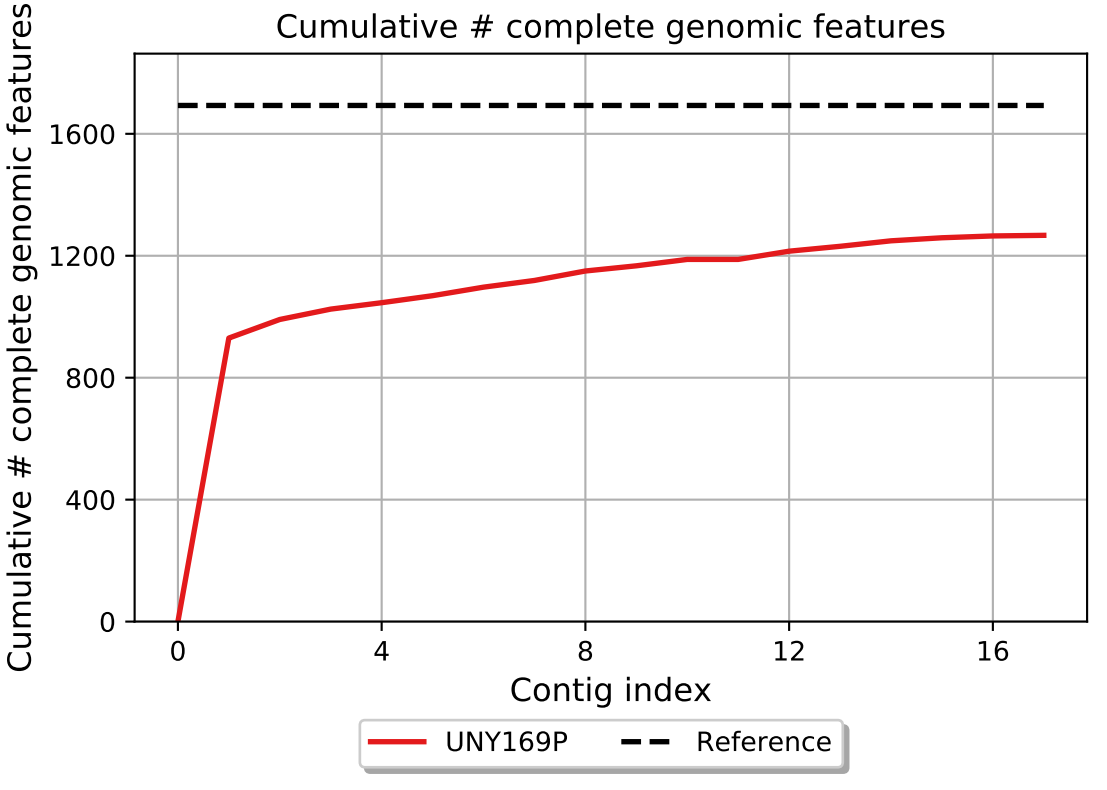

Misassemblies
20
16
12
8
4
0
UNY169P
relocations
translocations

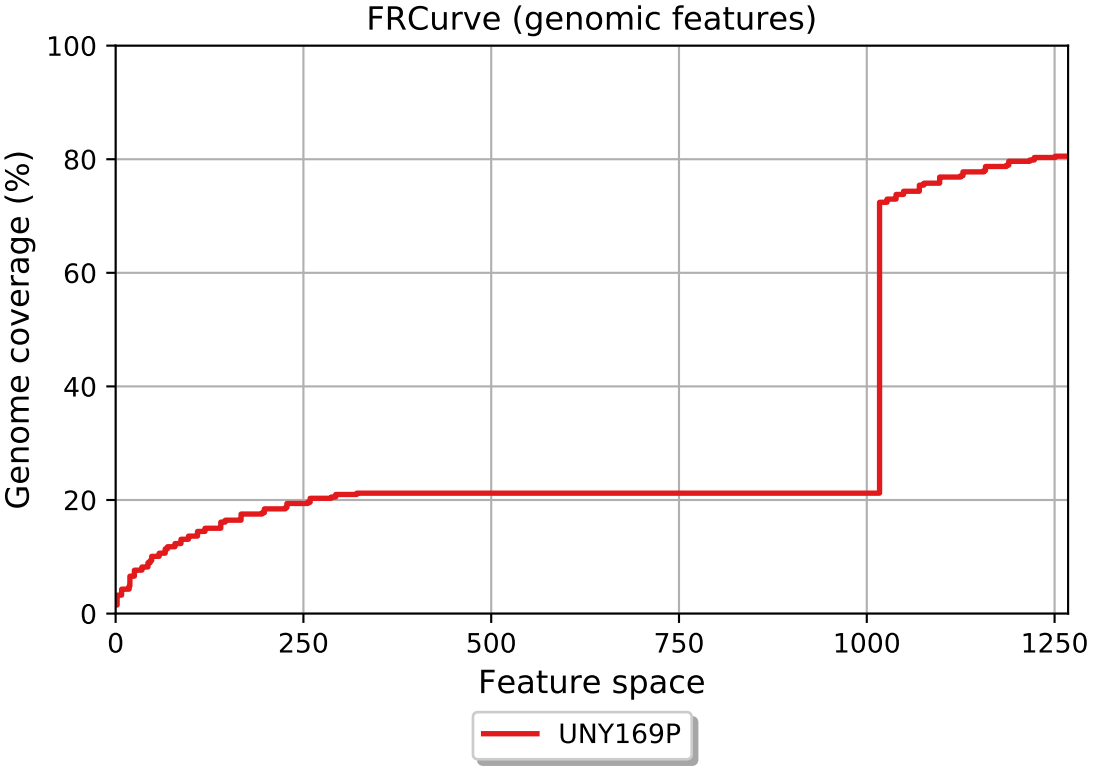

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
Feature space
UNY169P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
Contig index
UNY169P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY169P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UNY169P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
UNY169P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
UNY169P