Report

	UWI283P
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1332290
Total length (>= 1000 bp)	1332290
Total length (>= 5000 bp)	1332290
Total length (>= 10000 bp)	1332290
Total length (>= 25000 bp)	1225449
Total length (>= 50000 bp)	957131
# contigs	16
Largest contig	903355
Total length	1332290
Reference length	1521208
GC (%)	28.25
Reference GC (%)	28.18
N50	903355
NG50	903355
N90	26531
NG90	-
auN	622473.7
auNG	545169.0
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	20
# misassembled contigs	8
Misassembled contigs length	240737
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 10 part
Unaligned length	135937
Genome fraction (%)	77.217
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	872.33
# indels per 100 kbp	51.52
# genomic features	1223 + 49 part
Largest alignment	903176
Total aligned length	1195764
NA50	903176
NGA50	903176
NA90	-
NGA90	-
auNA	617040.0
auNGA	540410.2
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

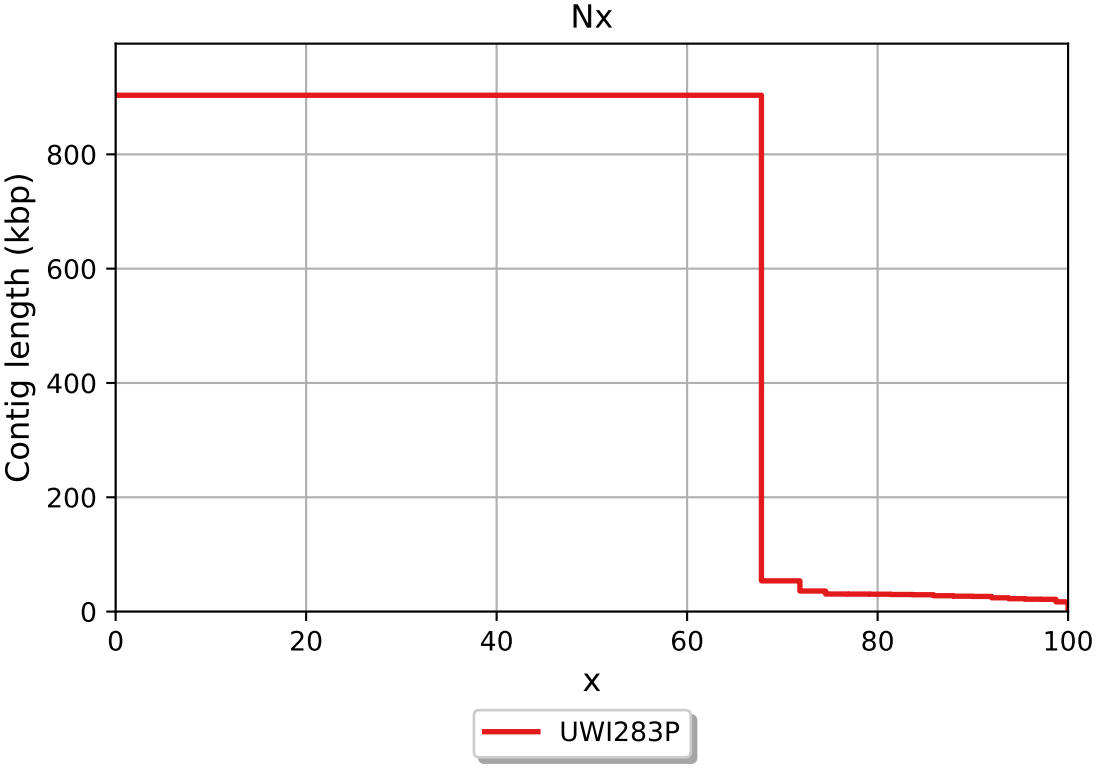
	UWI283P
# misassemblies	20
# contig misassemblies	20
# c. relocations	2
# c. translocations	18
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	240737
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	10431
# indels	616
# indels (<= 5 bp)	538
# indels (> 5 bp)	78
Indels length	2521

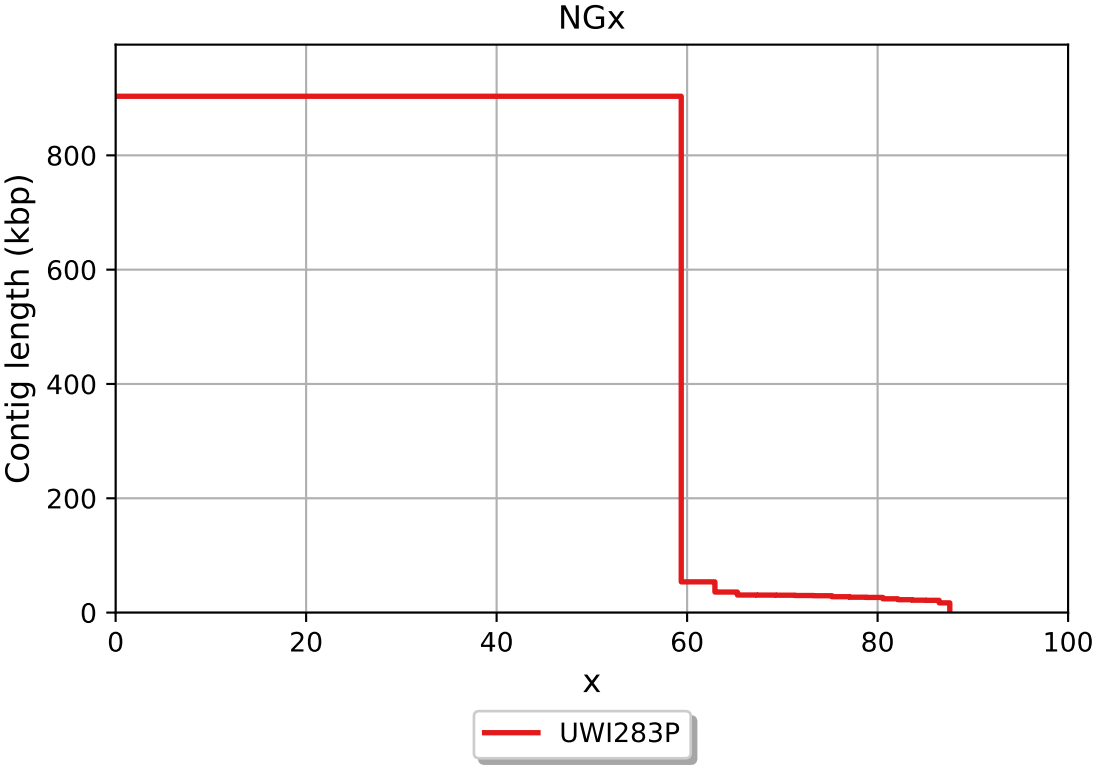
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

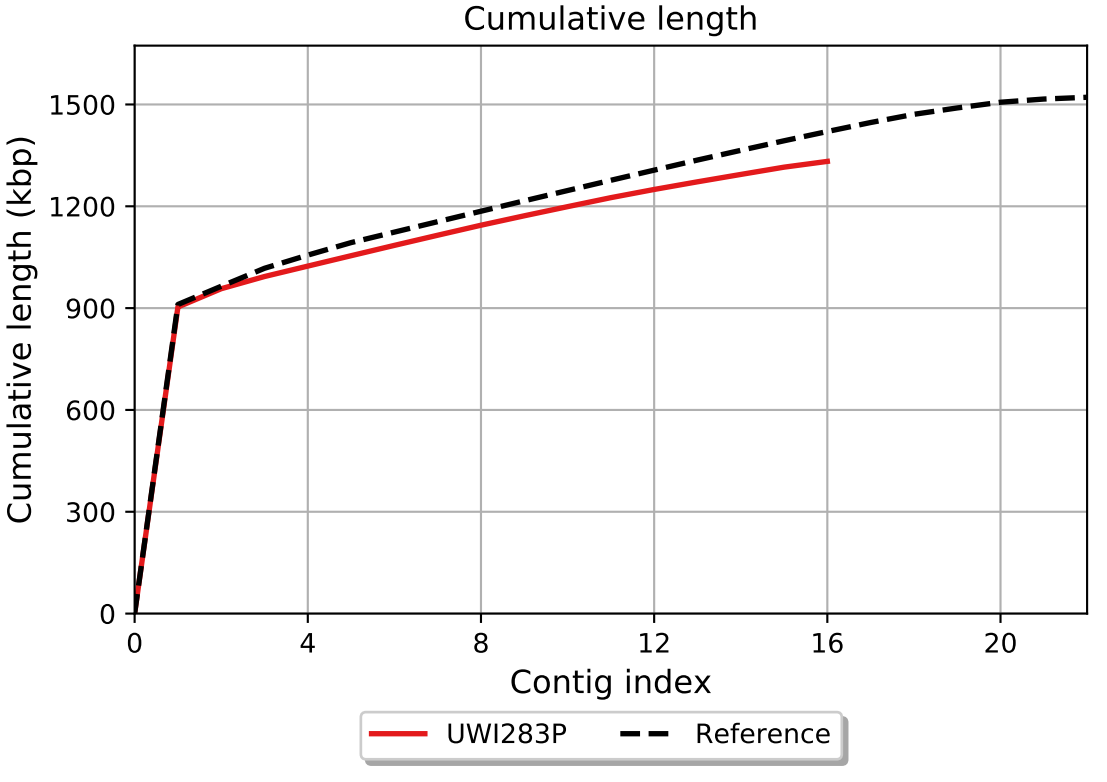
Unaligned report

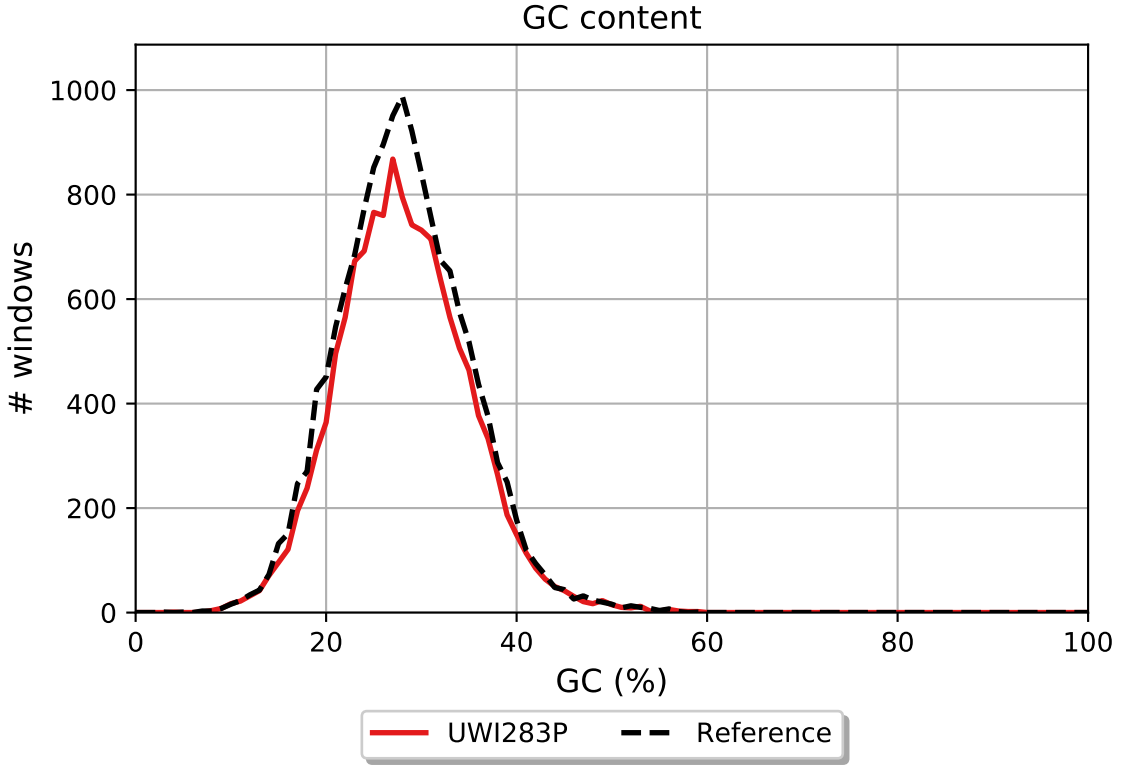
	UWI283P
# fully unaligned contigs	2
Fully unaligned length	63704
# partially unaligned contigs	10
Partially unaligned length	72233
# N's	0

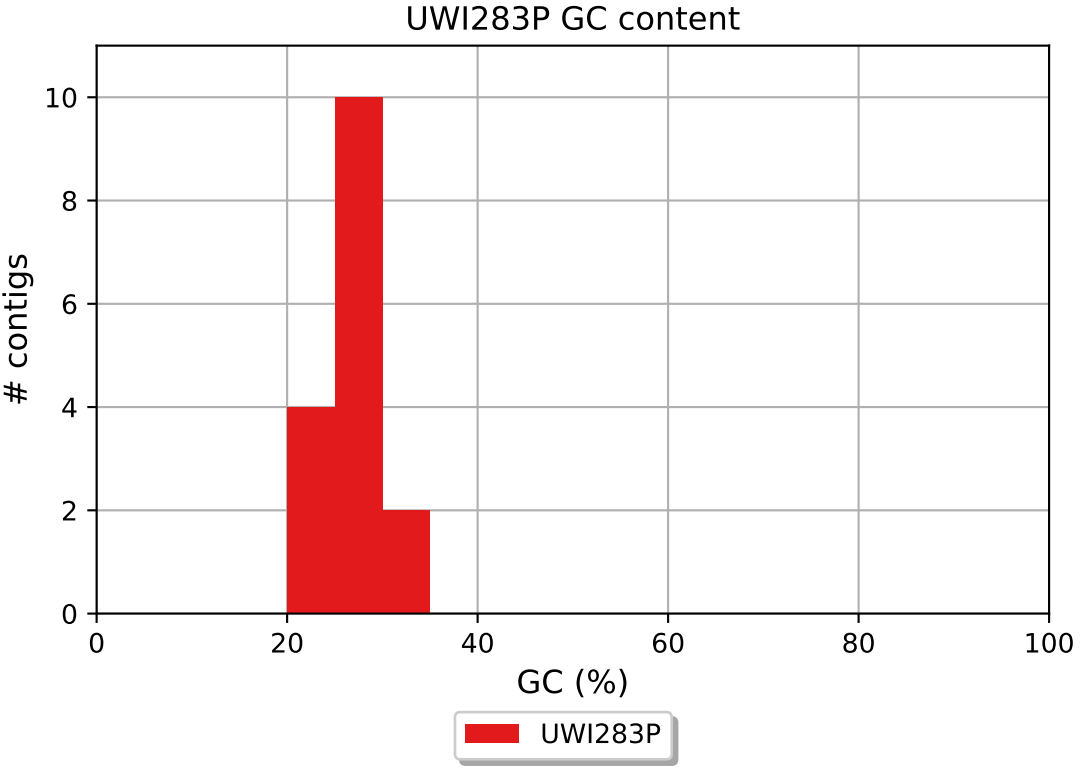
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI283P

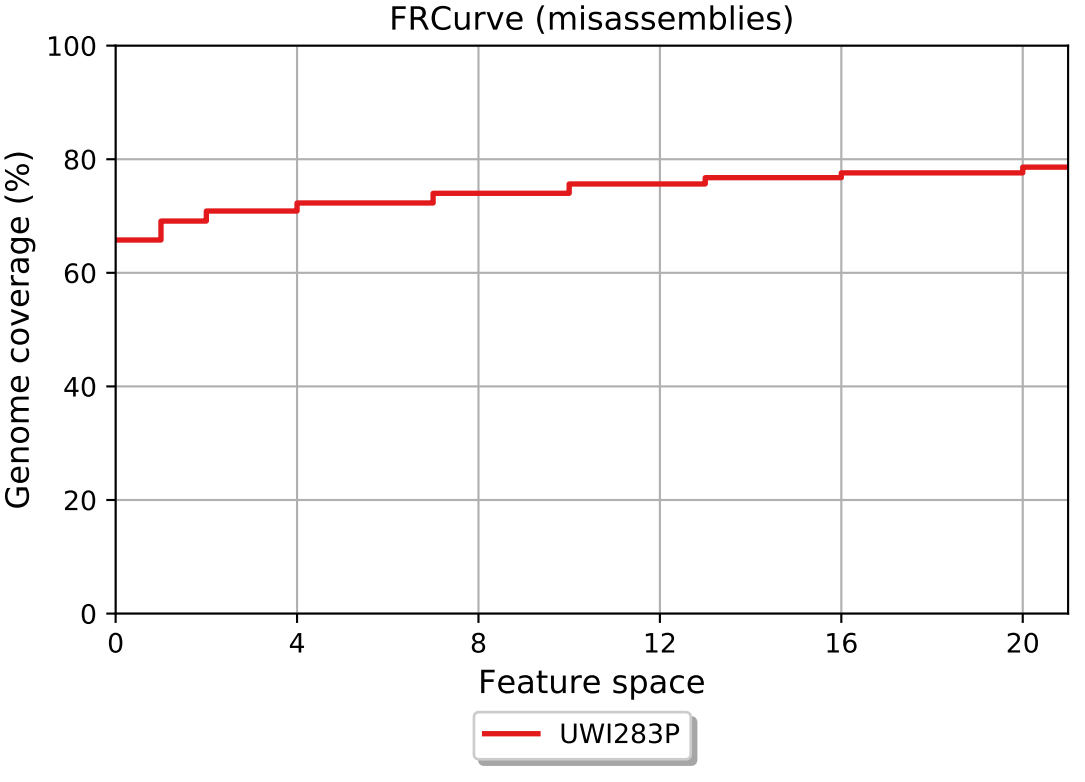

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI283P

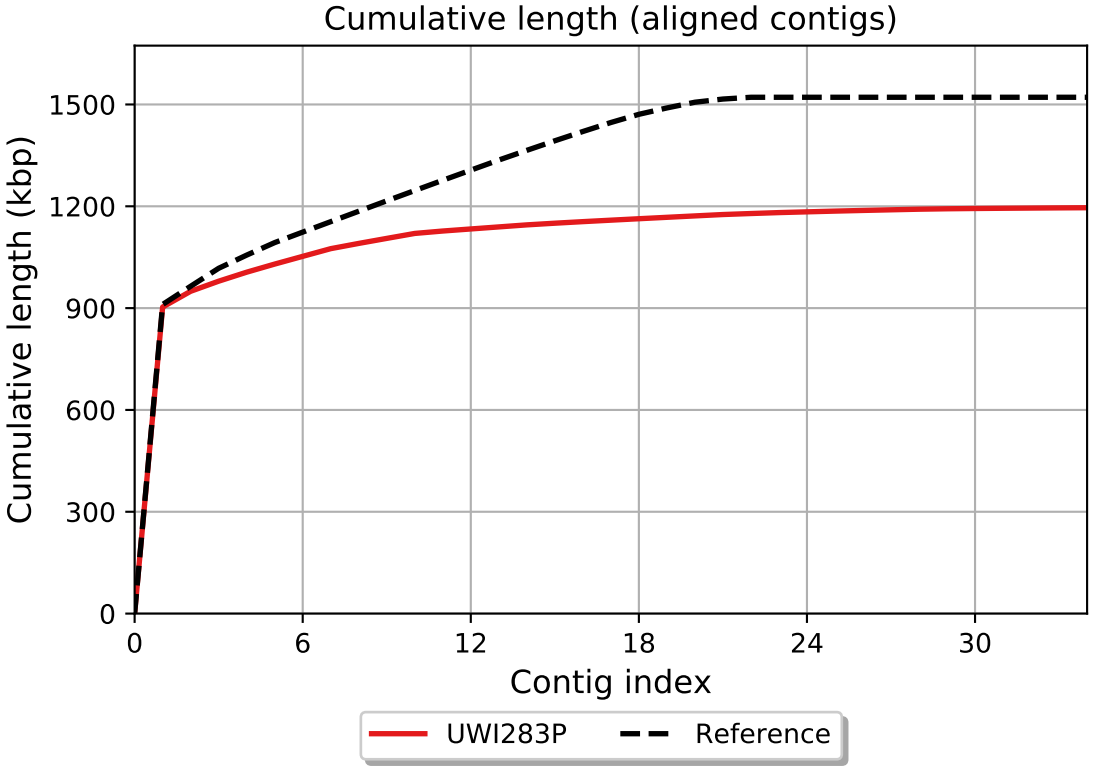

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UWI283P
Reference

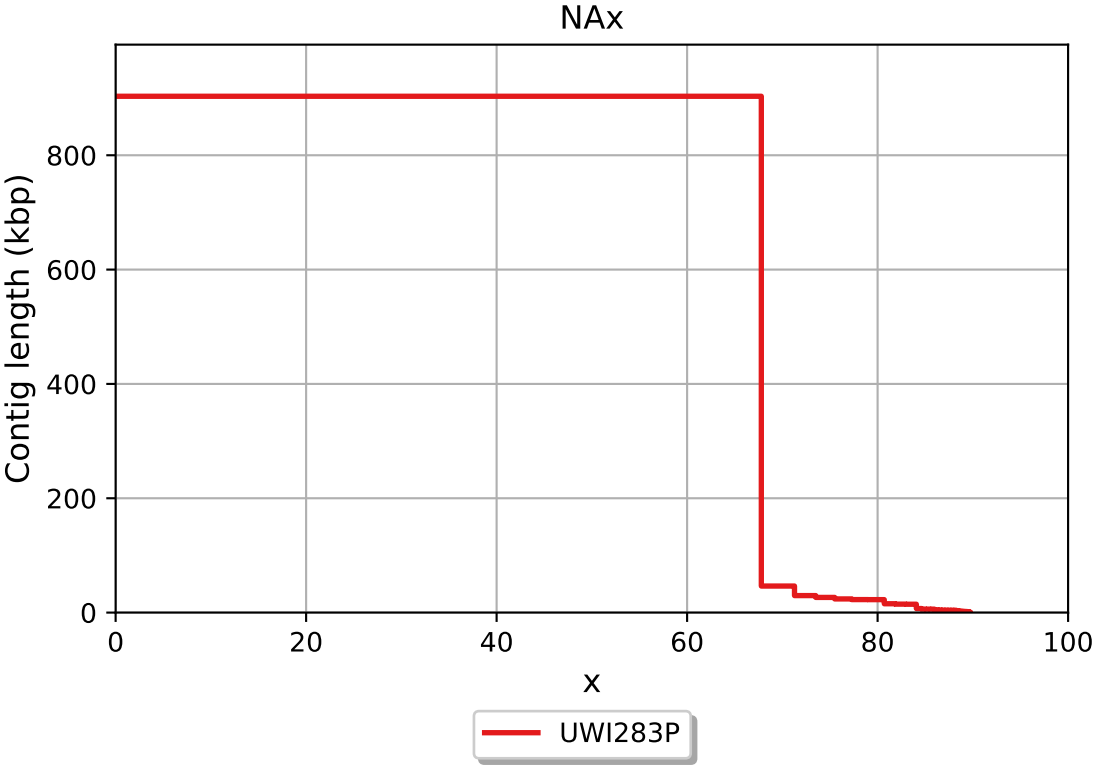

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
UWI283P
Reference

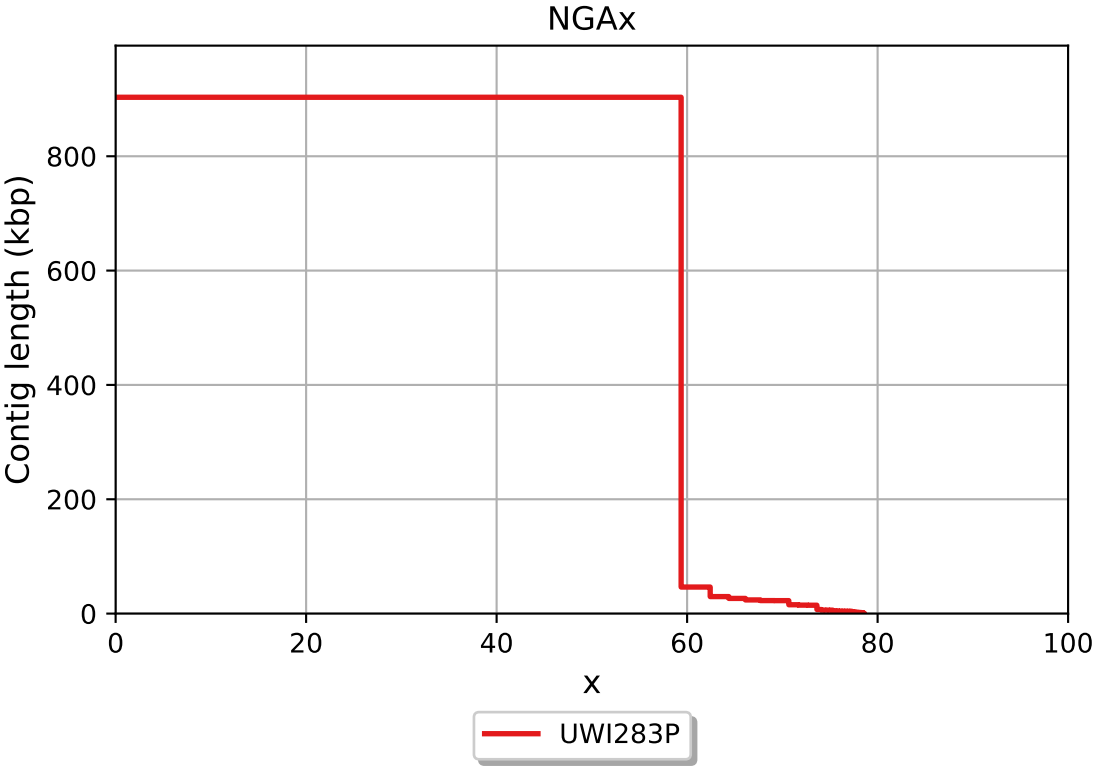

UWI283P GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
UWI283P

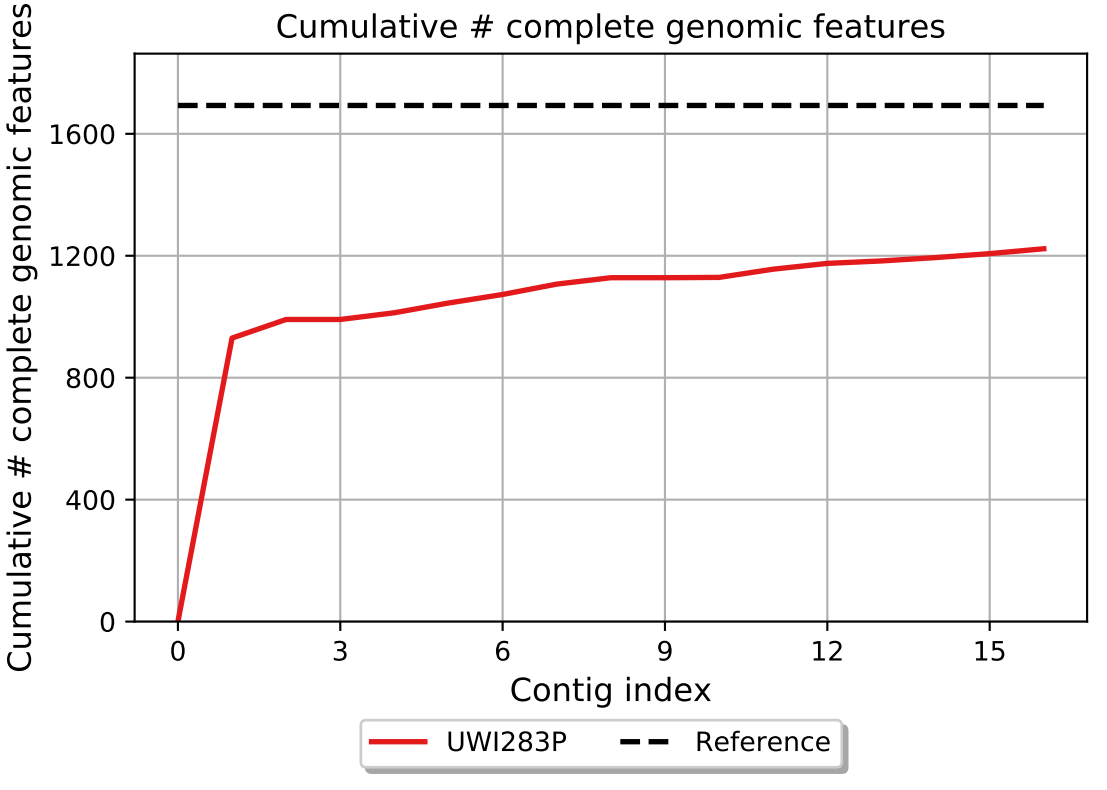
Misassemblies
20
16
12
8
4
0
UWI283P
relocations
translocations

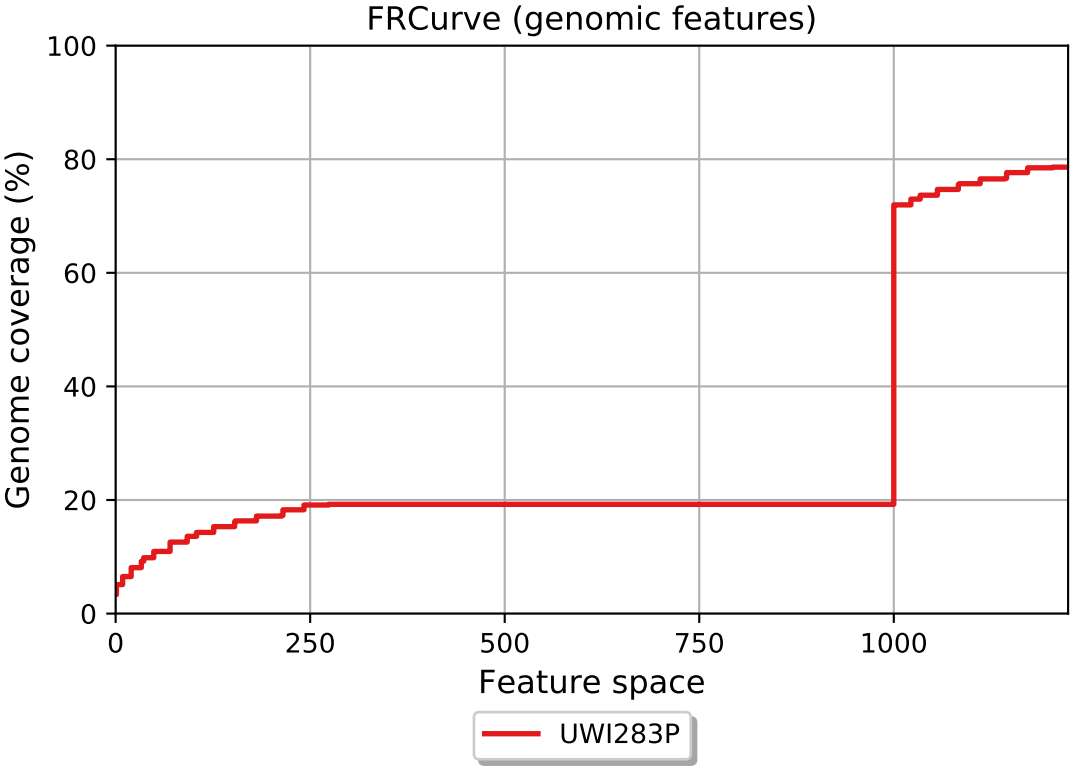

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
UWI283P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
6
12
18
24
30
Contig index
UWI283P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI283P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI283P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
3
6
9
12
15
Contig index
UWI283P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
UWI283P