Report

	UWI247P
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1359286
Total length (>= 1000 bp)	1359286
Total length (>= 5000 bp)	1359286
Total length (>= 10000 bp)	1359286
Total length (>= 25000 bp)	1256549
Total length (>= 50000 bp)	966184
# contigs	17
Largest contig	912339
Total length	1359286
Reference length	1521208
GC (%)	28.17
Reference GC (%)	28.18
N50	912339
NG50	912339
N90	26785
NG90	-
auN	622310.7
auNG	556070.1
L50	1
LG50	1
L90	11
LG90	-
# misassemblies	16
# misassembled contigs	7
Misassembled contigs length	203780
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 14 part
Unaligned length	169312
Genome fraction (%)	76.947
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	747.05
# indels per 100 kbp	44.21
# genomic features	1225 + 38 part
Largest alignment	904616
Total aligned length	1183061
NA50	904616
NGA50	904616
NA90	-
NGA90	-
auNA	606430.8
auNGA	541880.5
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

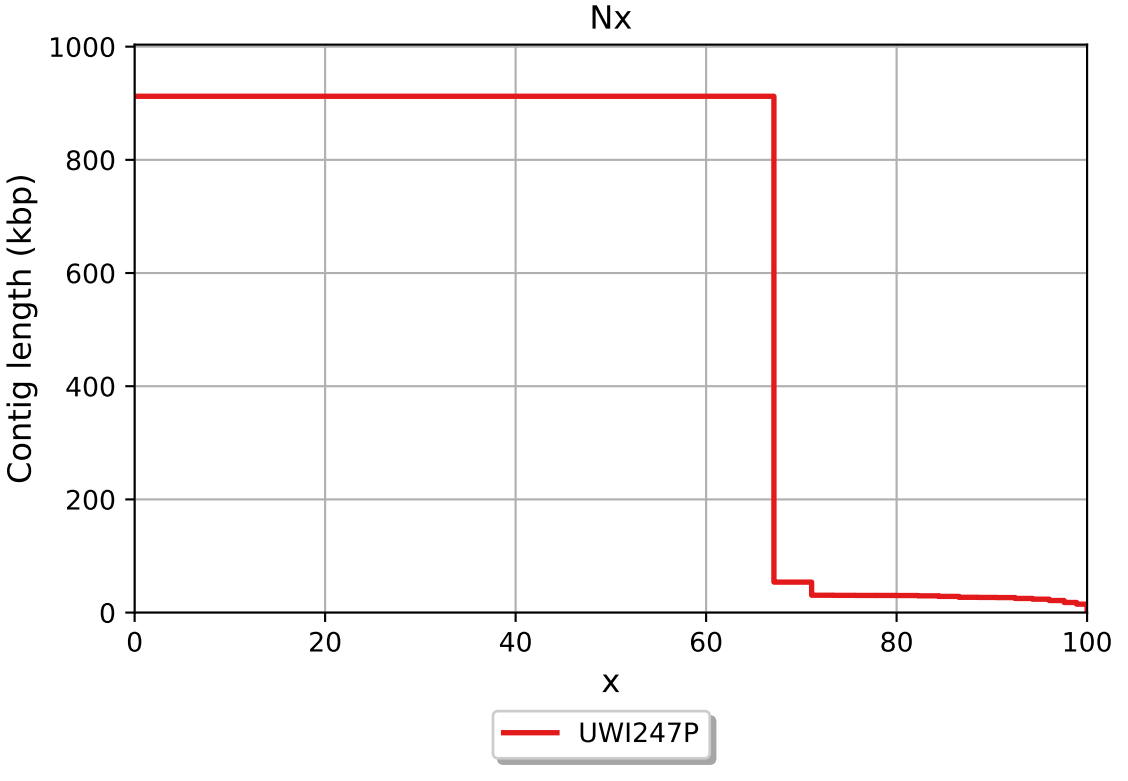
	UWI247P
# misassemblies	16
# contig misassemblies	16
# c. relocations	3
# c. translocations	13
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	203780
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	8838
# indels	523
# indels (<= 5 bp)	467
# indels (> 5 bp)	56
Indels length	2445

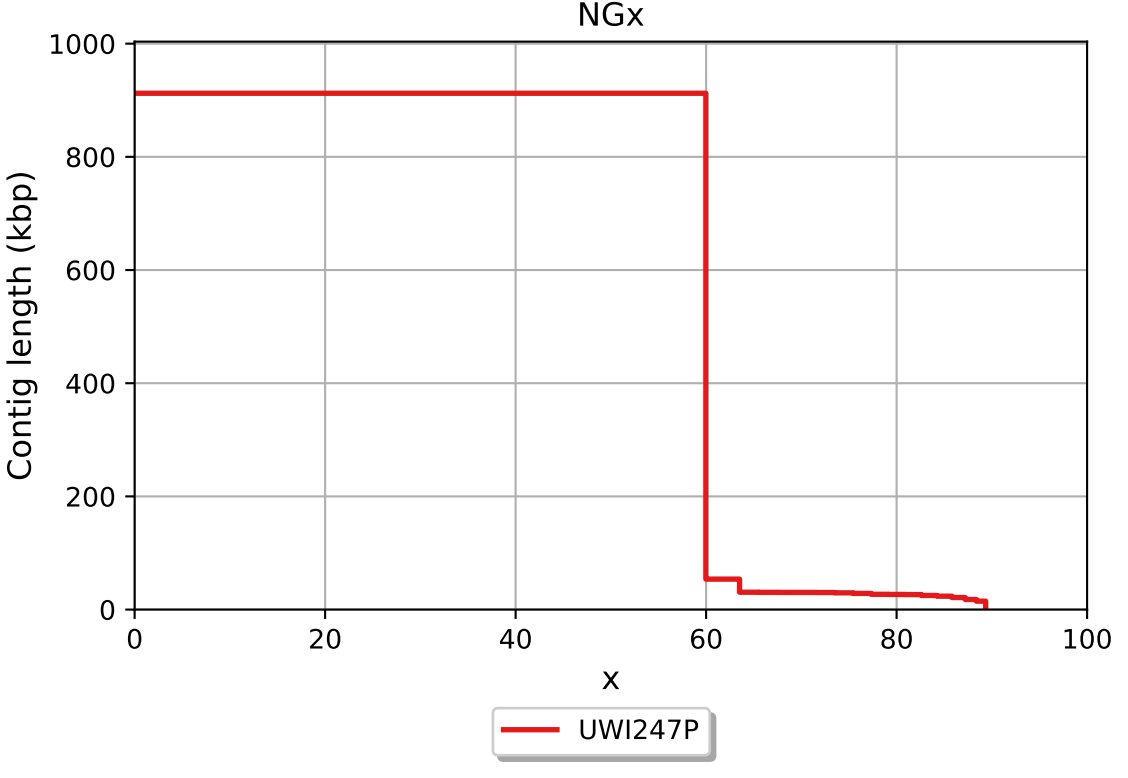
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

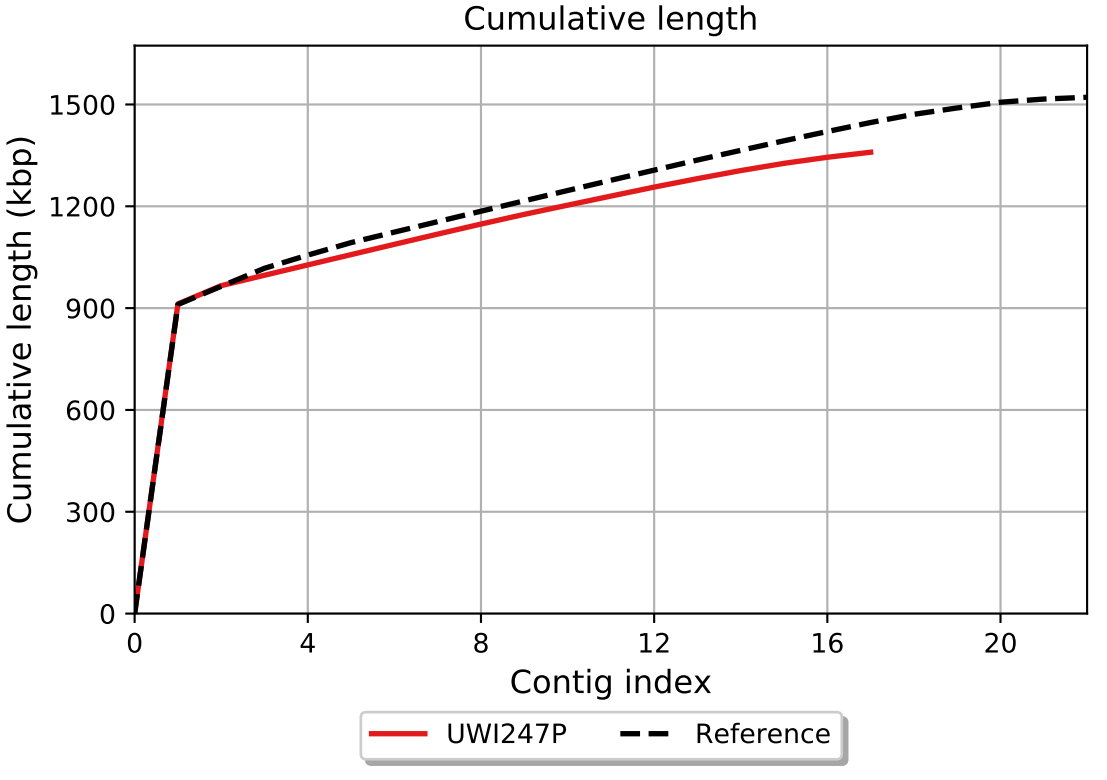
Unaligned report

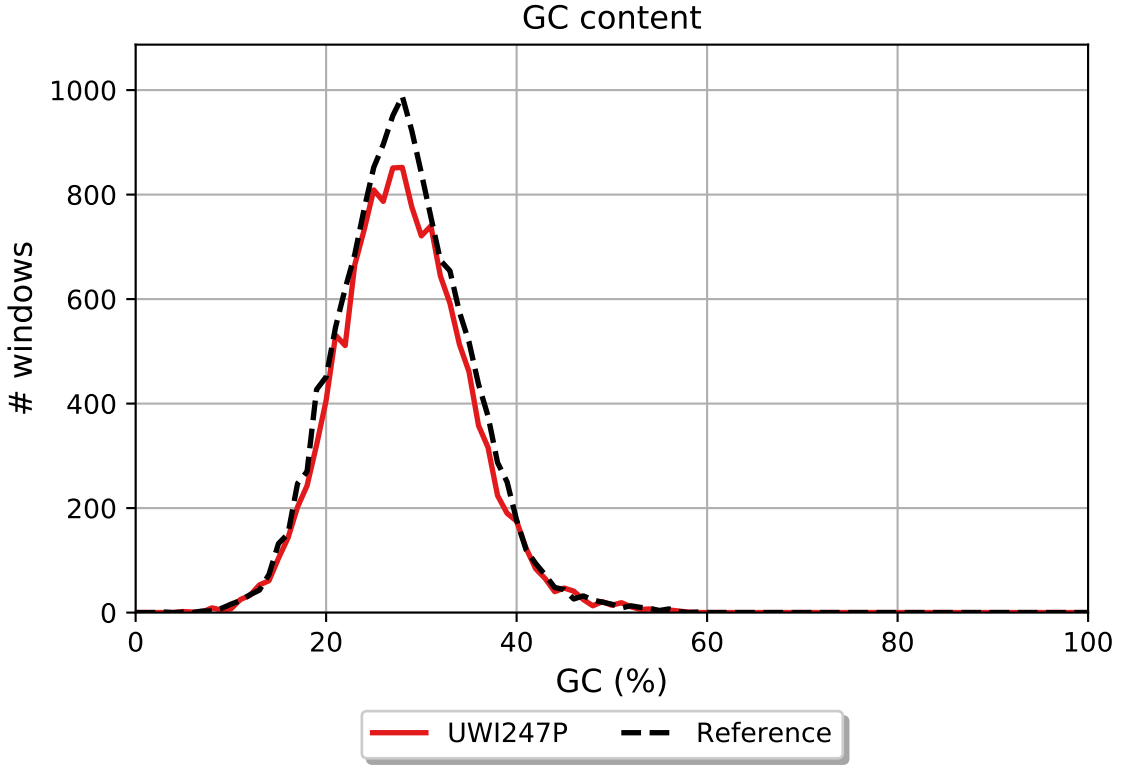
	UWI247P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	169312
# N's	0

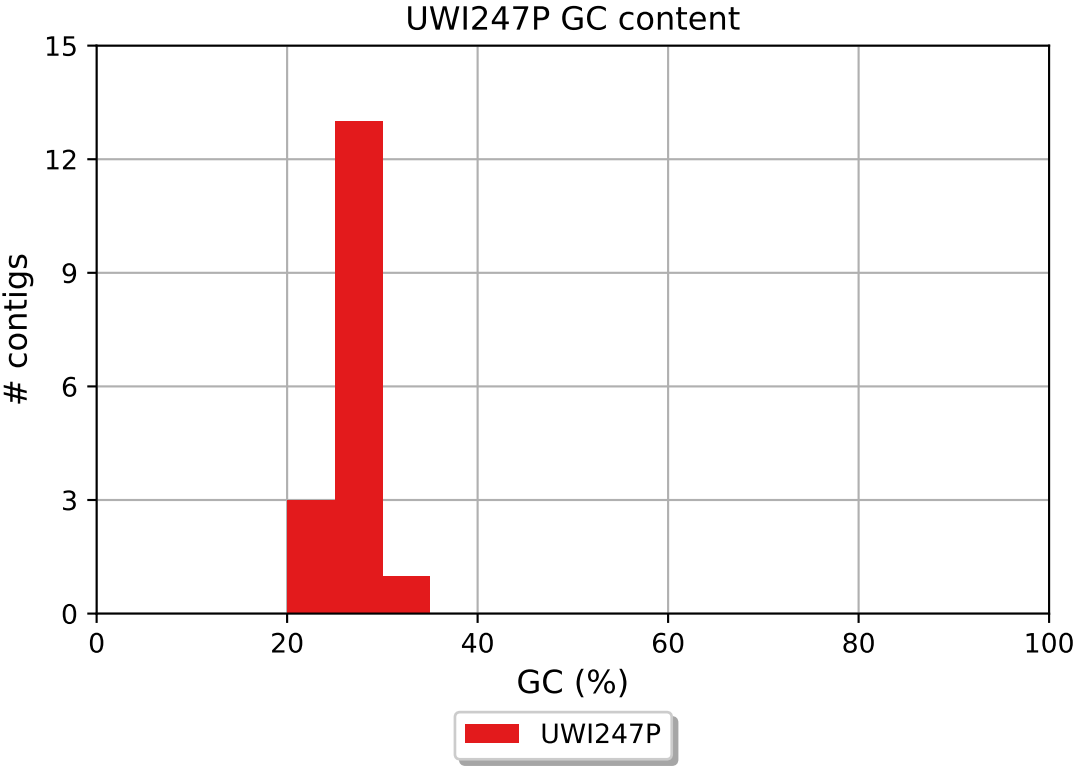
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

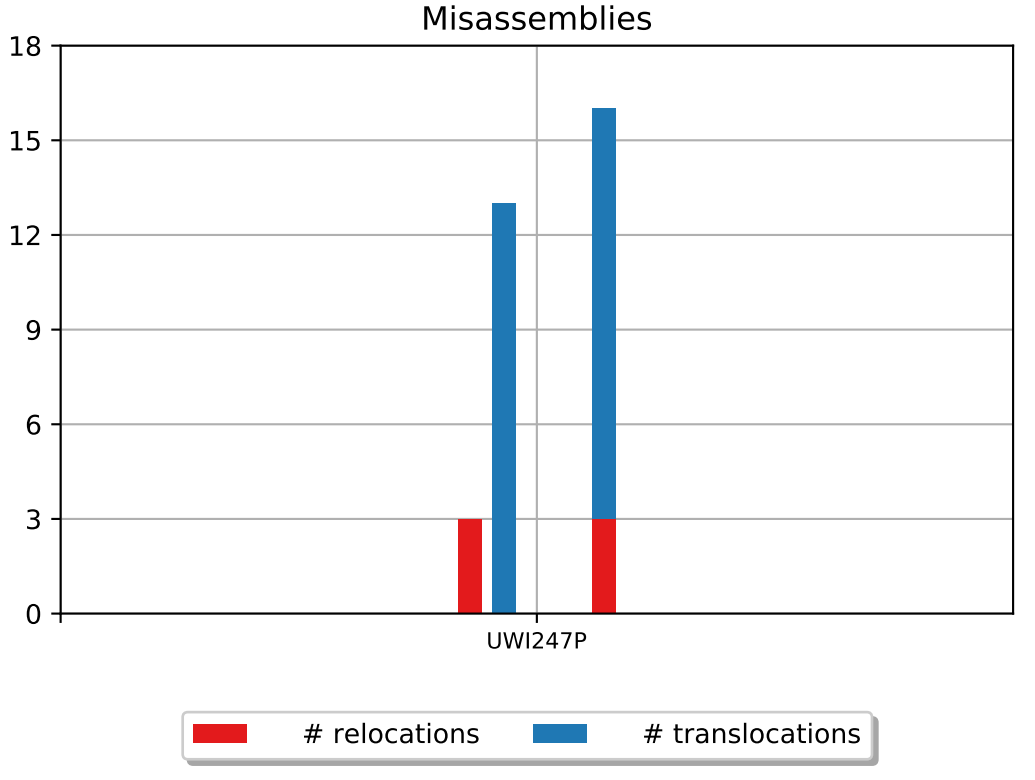

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UWI247P

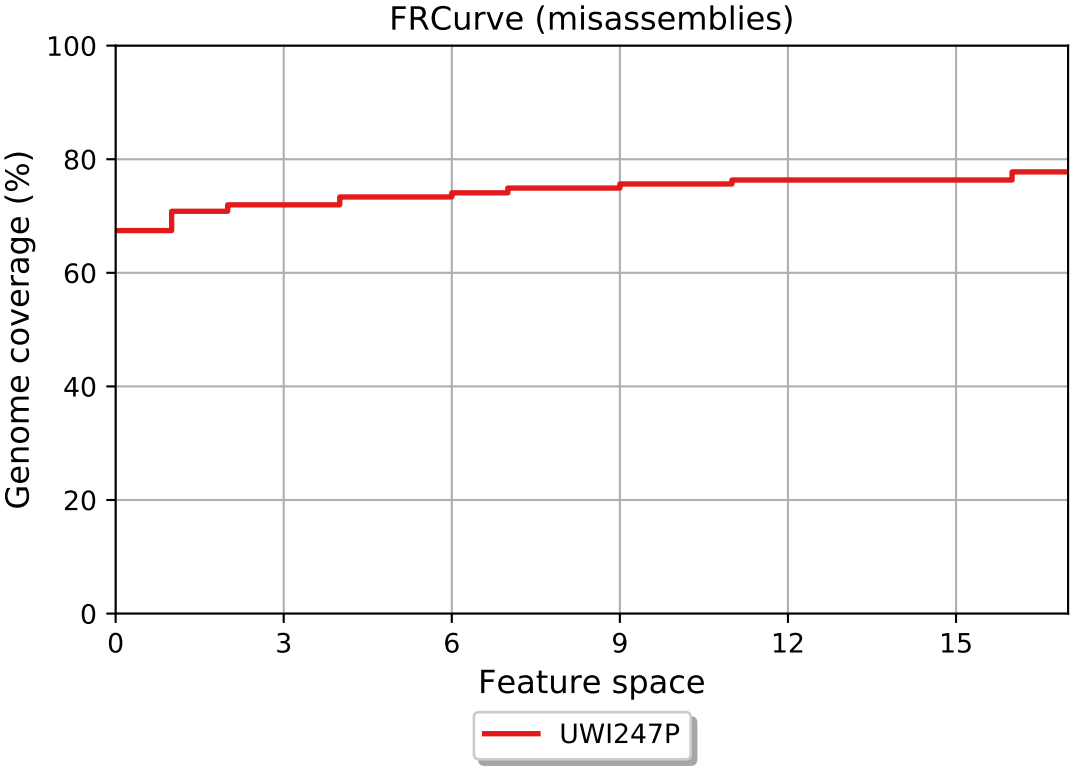

NGx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
UWI247P

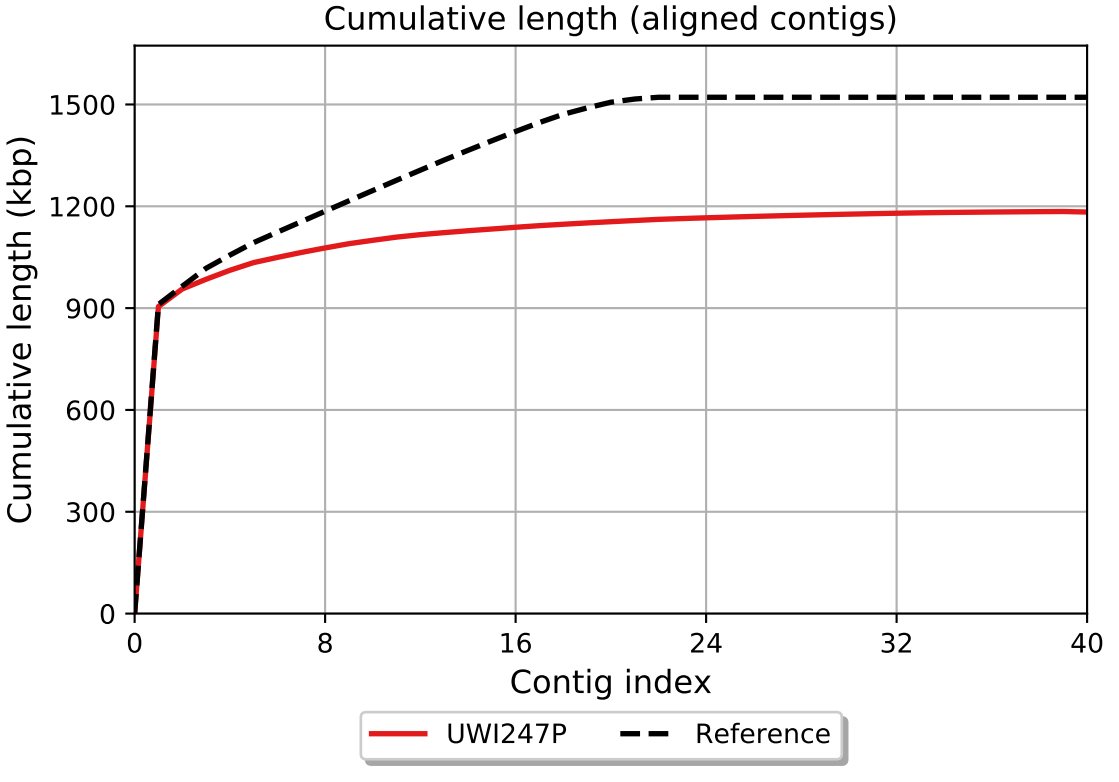

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UWI247P
Reference

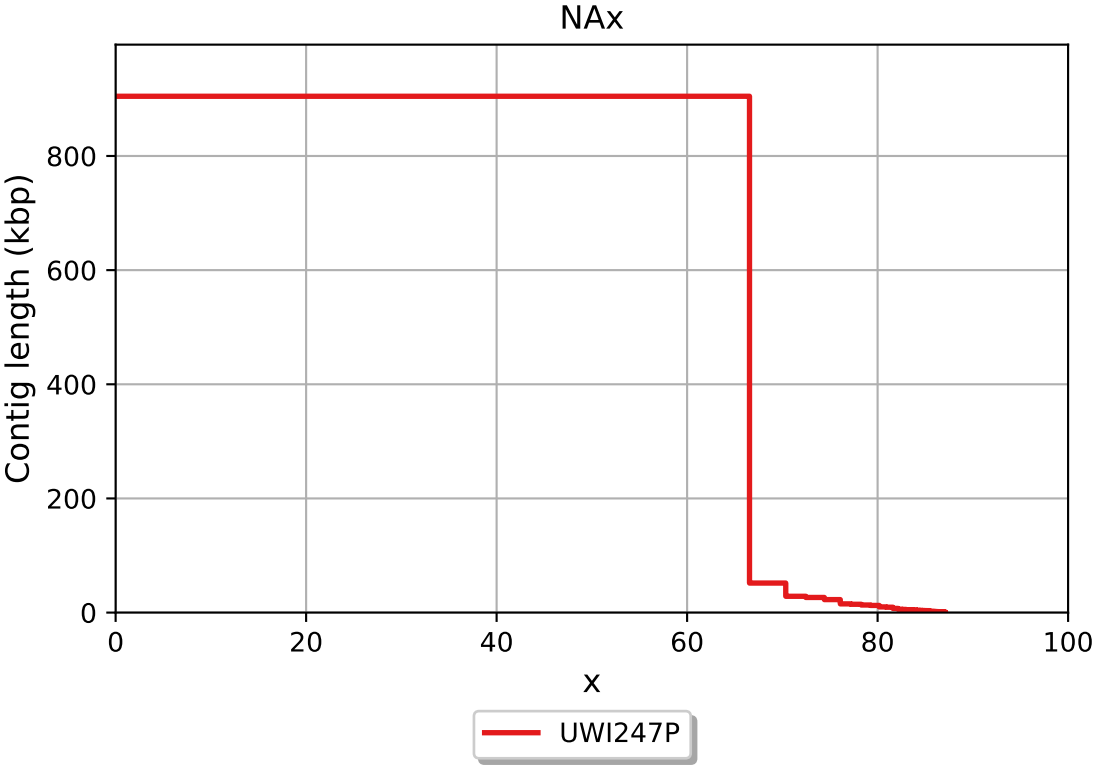

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
UWI247P
Reference

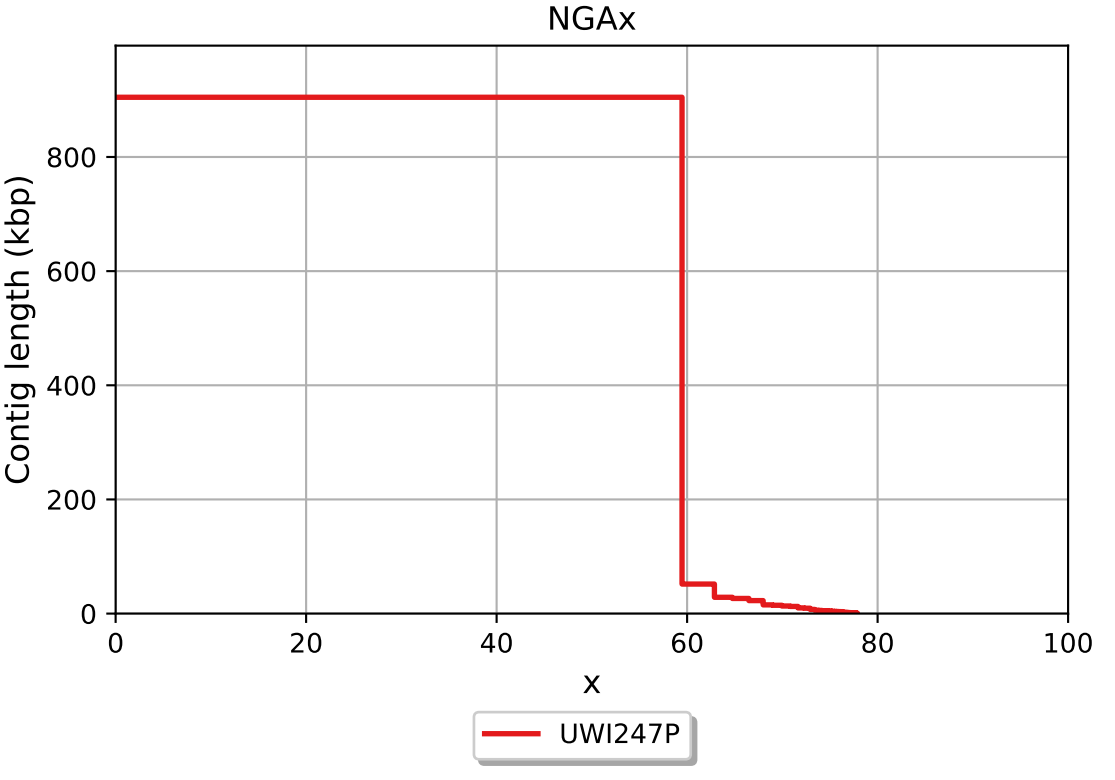

UWI247P GC content
15
12
9
6
3
0
contigs
0
20
40
60
80
100
GC (%)
UWI247P

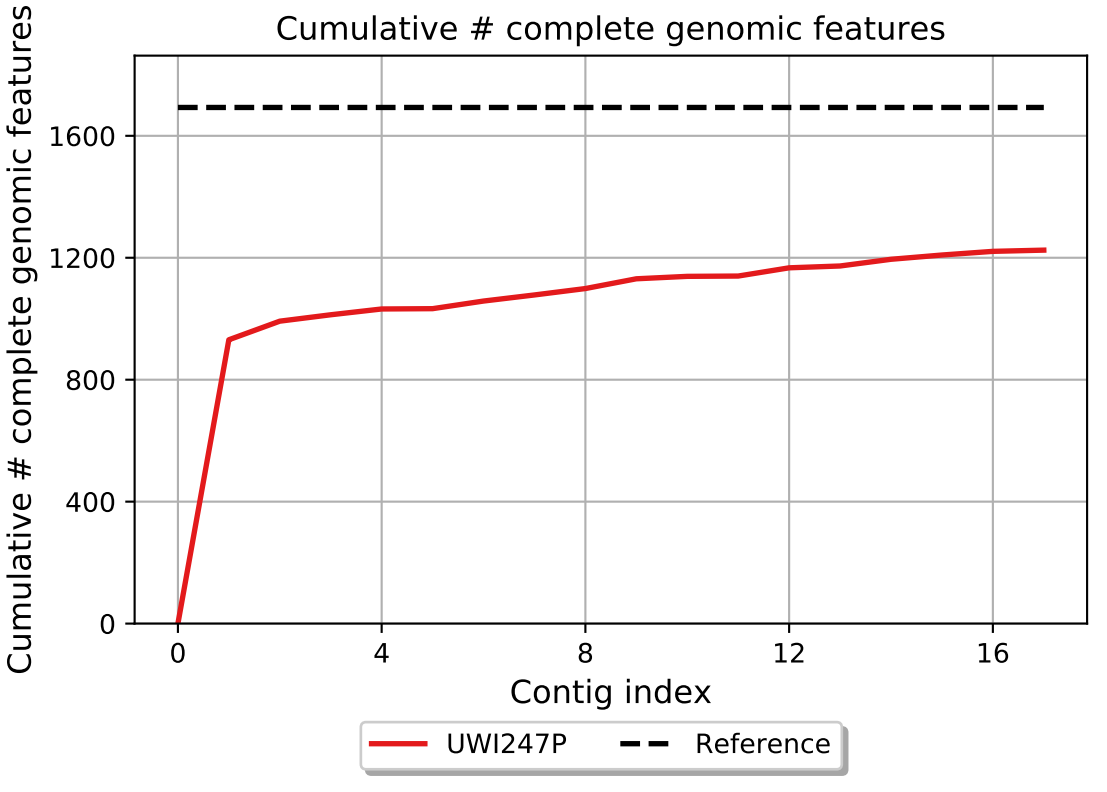

Misassemblies
18
15
12
9
6
3
0
UWI247P
relocations
translocations

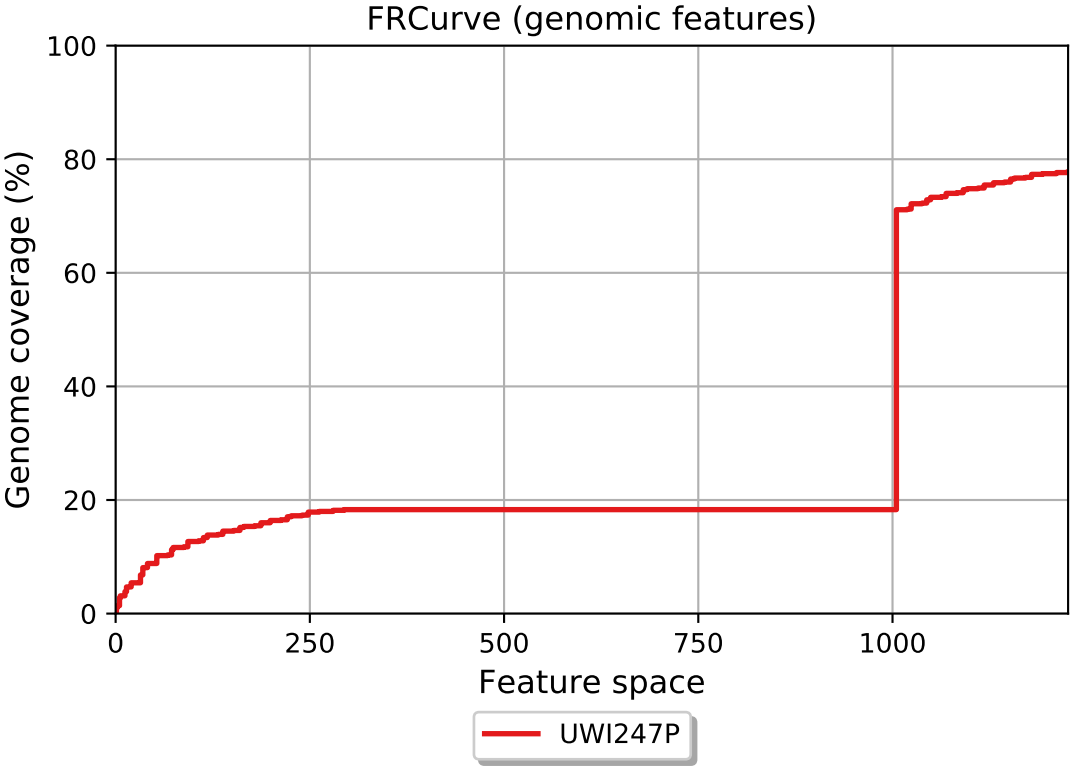

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
UWI247P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
UWI247P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI247P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI247P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
UWI247P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
UWI247P