Report

	UWI248P
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1387586
Total length (>= 1000 bp)	1387586
Total length (>= 5000 bp)	1387586
Total length (>= 10000 bp)	1387586
Total length (>= 25000 bp)	1284700
Total length (>= 50000 bp)	963799
# contigs	18
Largest contig	910022
Total length	1387586
Reference length	1521208
GC (%)	28.19
Reference GC (%)	28.18
N50	910022
NG50	910022
N90	26763
NG90	18037
auN	607246.6
auNG	553906.4
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	18
# misassembled contigs	8
Misassembled contigs length	234336
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 15 part
Unaligned length	185552
Genome fraction (%)	76.972
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	784.23
# indels per 100 kbp	52.06
# genomic features	1227 + 36 part
Largest alignment	904617
Total aligned length	1196589
NA50	904617
NGA50	904617
NA90	-
NGA90	-
auNA	594095.4
auNGA	541910.4
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

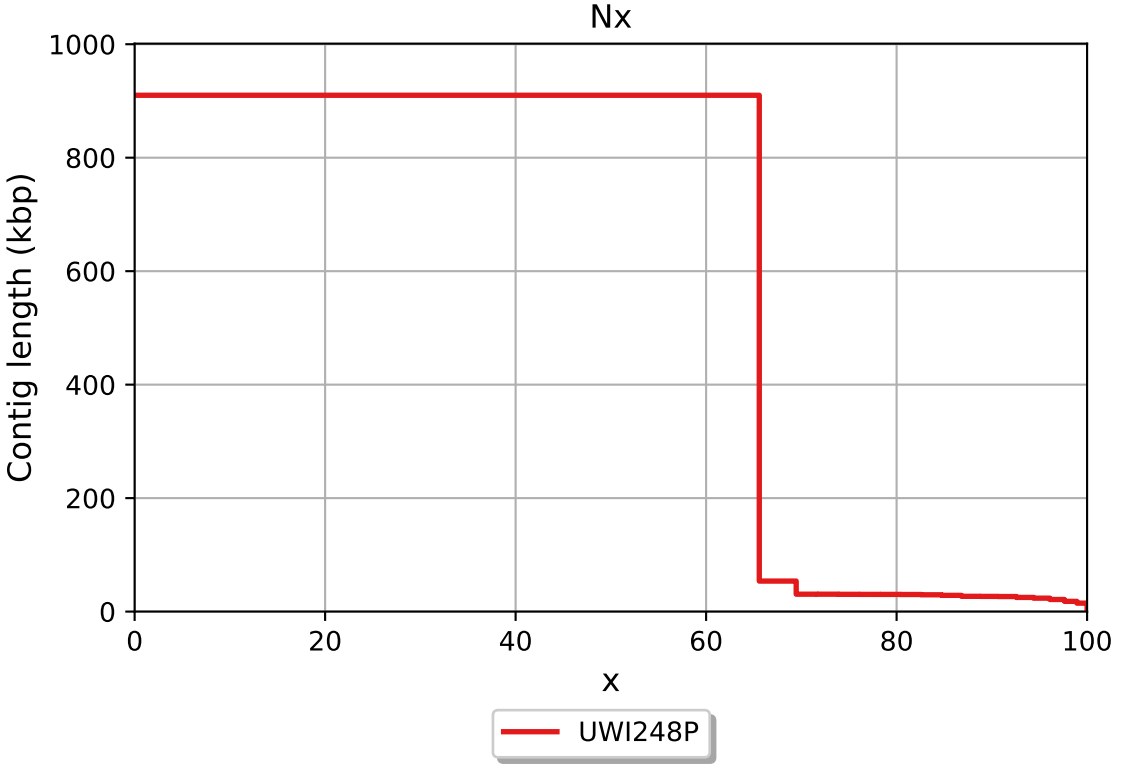
	UWI248P
# misassemblies	18
# contig misassemblies	18
# c. relocations	3
# c. translocations	15
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	234336
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9384
# indels	623
# indels (<= 5 bp)	565
# indels (> 5 bp)	58
Indels length	2685

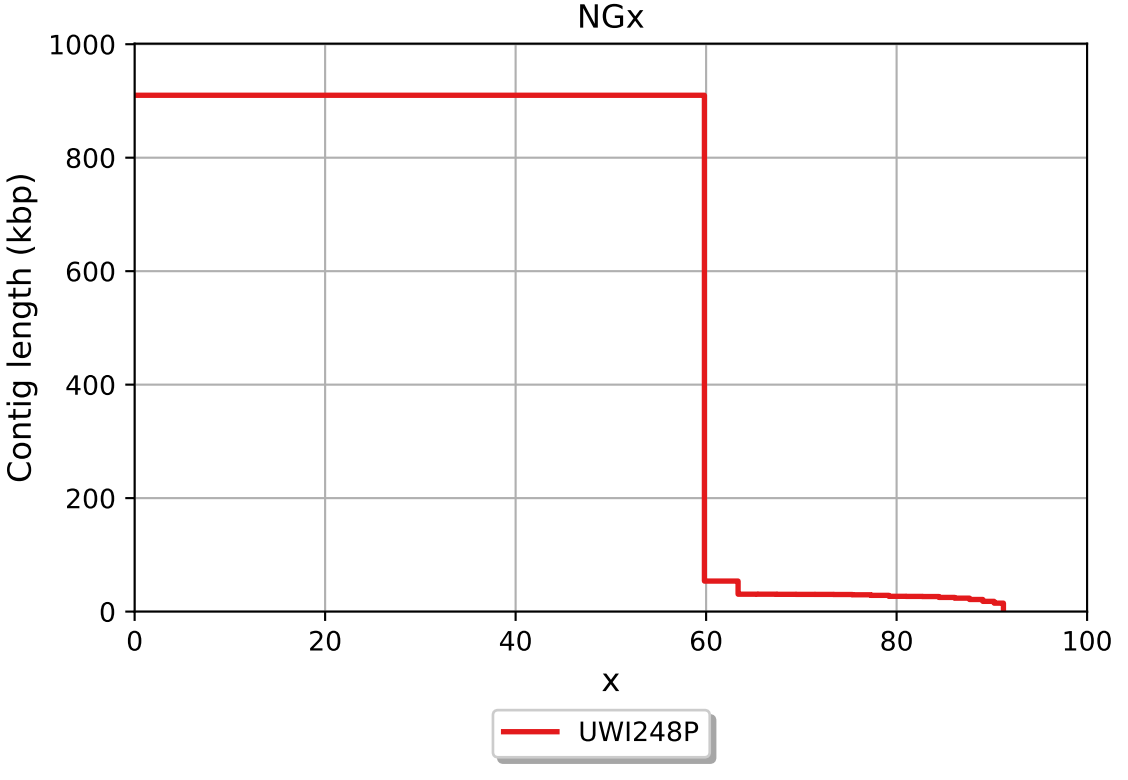
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

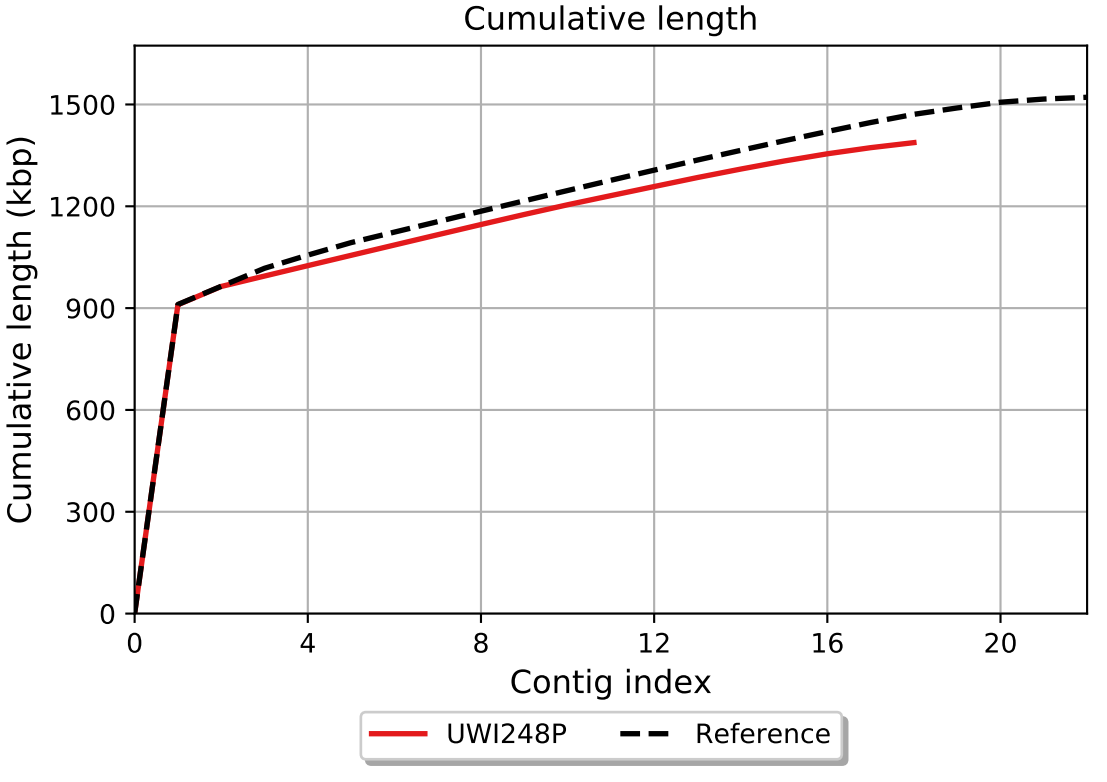
Unaligned report

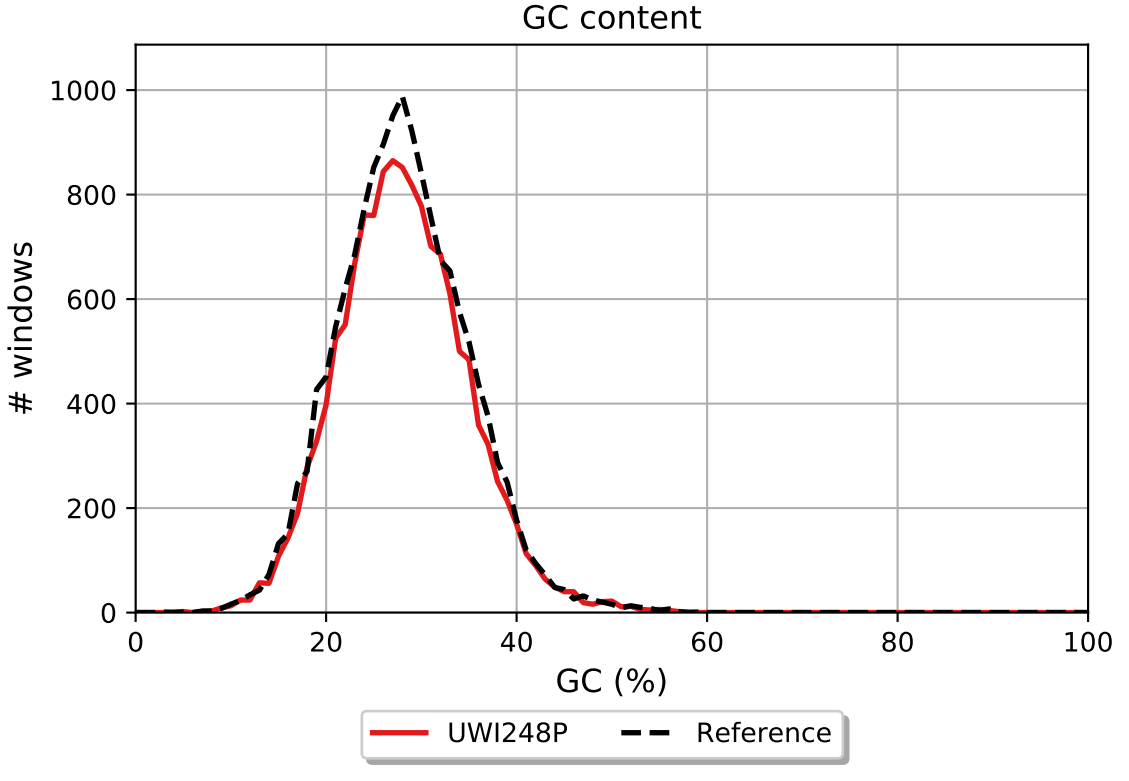
	UWI248P
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	185552
# N's	0

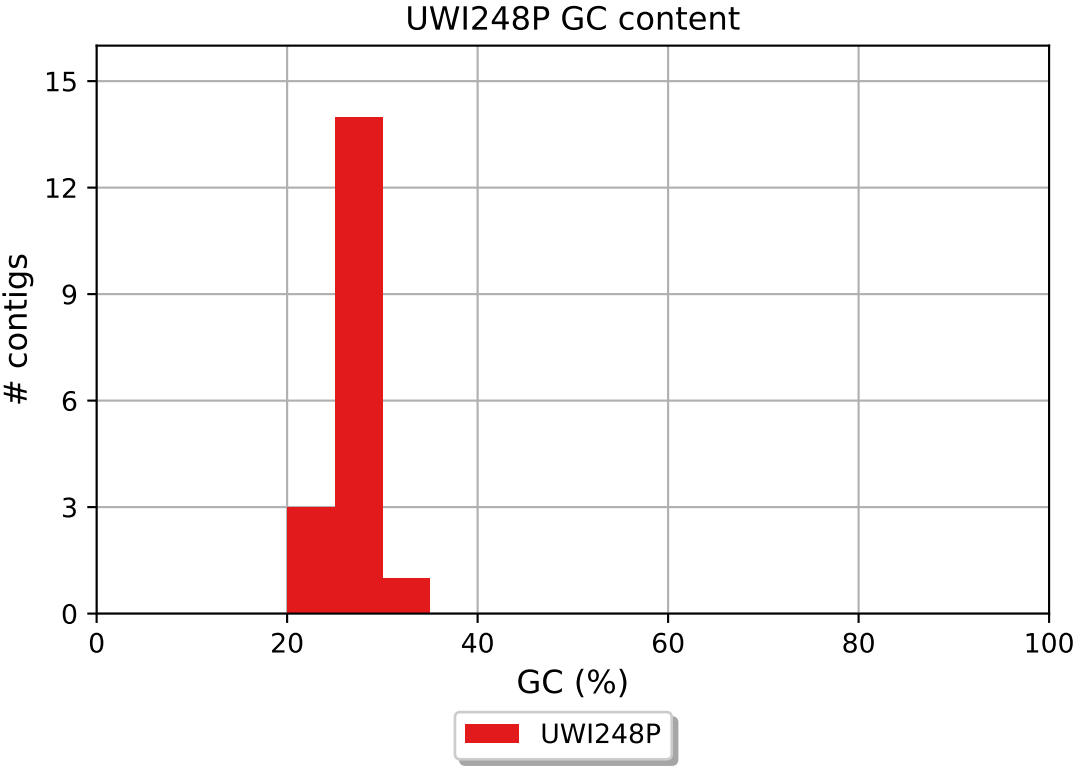
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

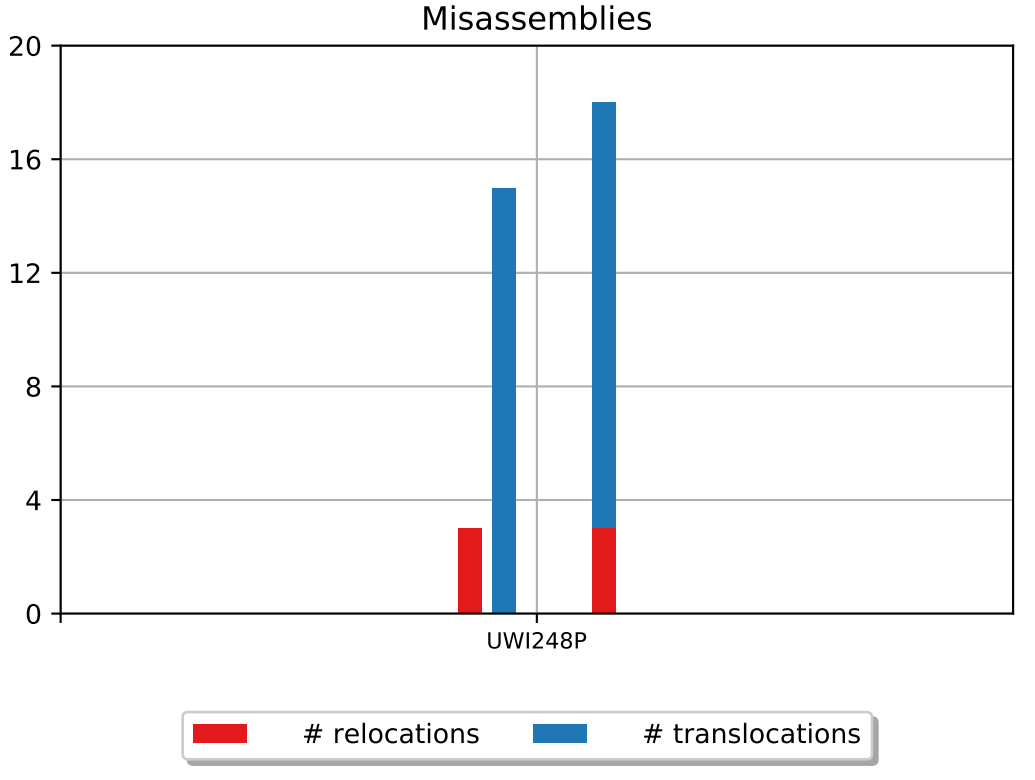

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UWI248P

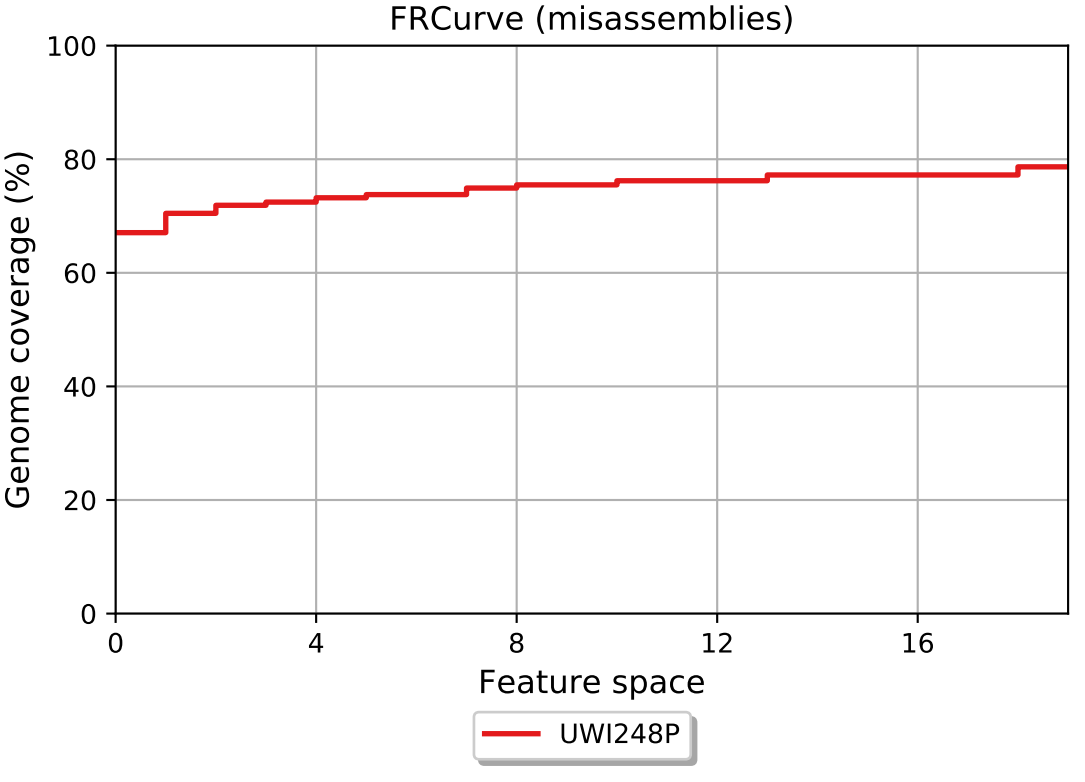

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
UWI248P

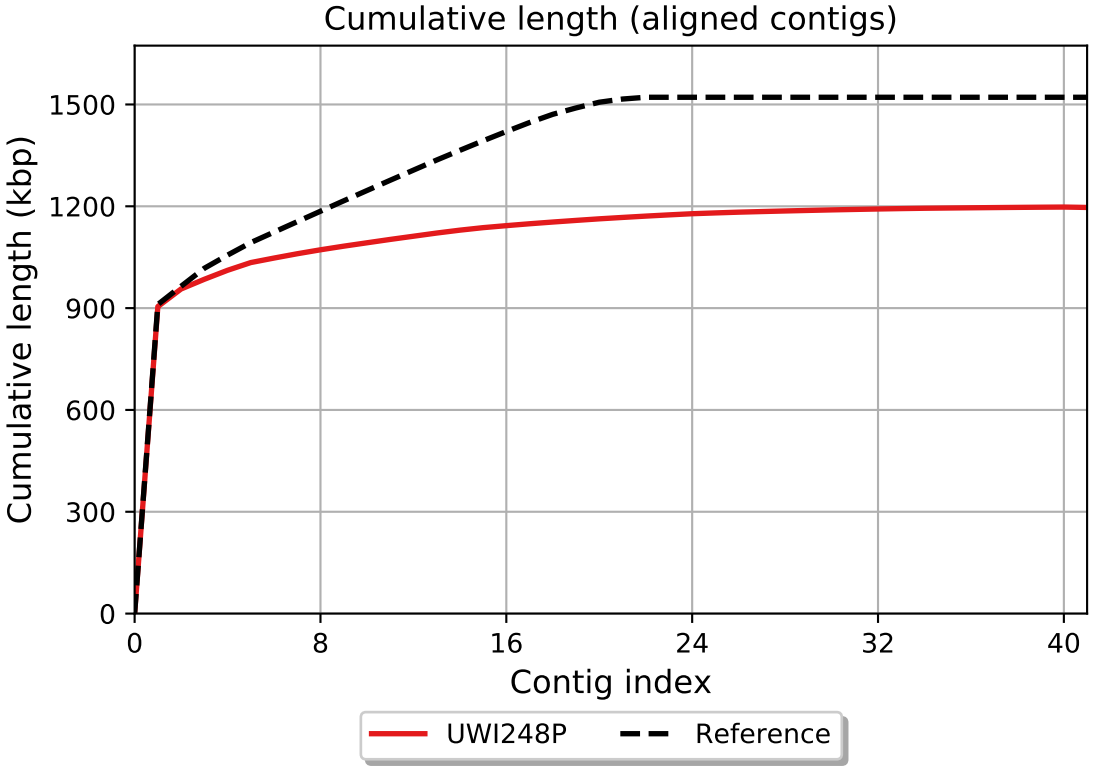

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
UWI248P
Reference

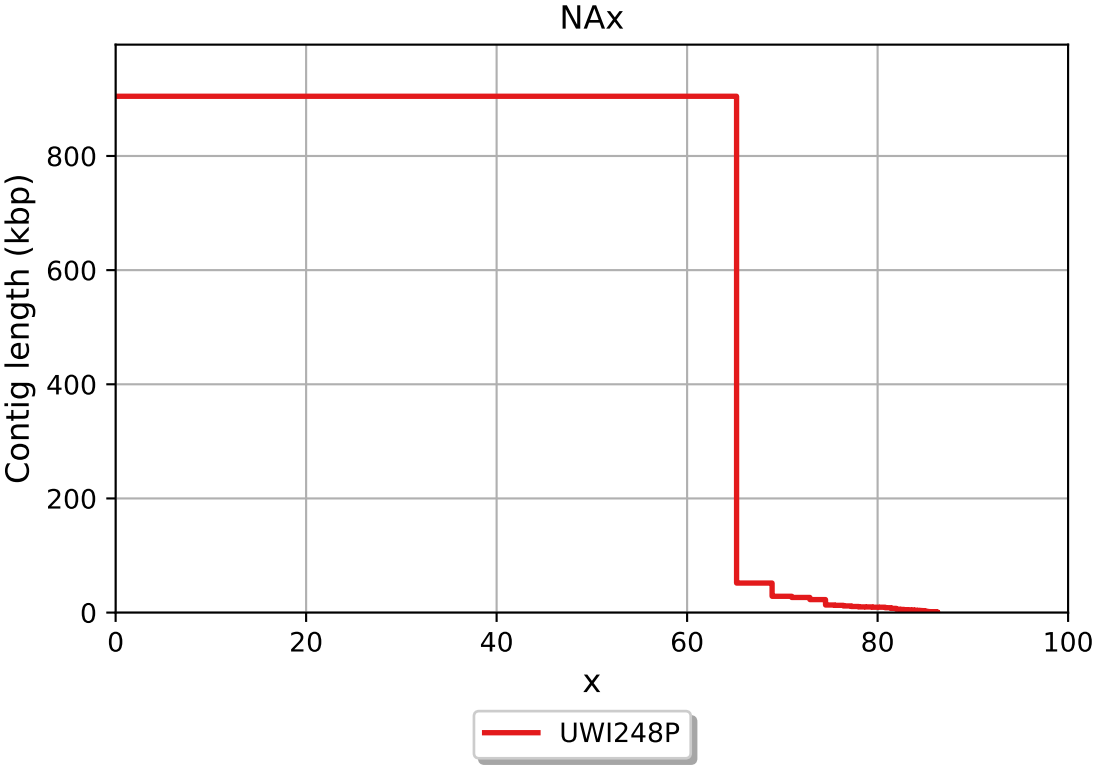

GC content
windows
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
UWI248P
Reference

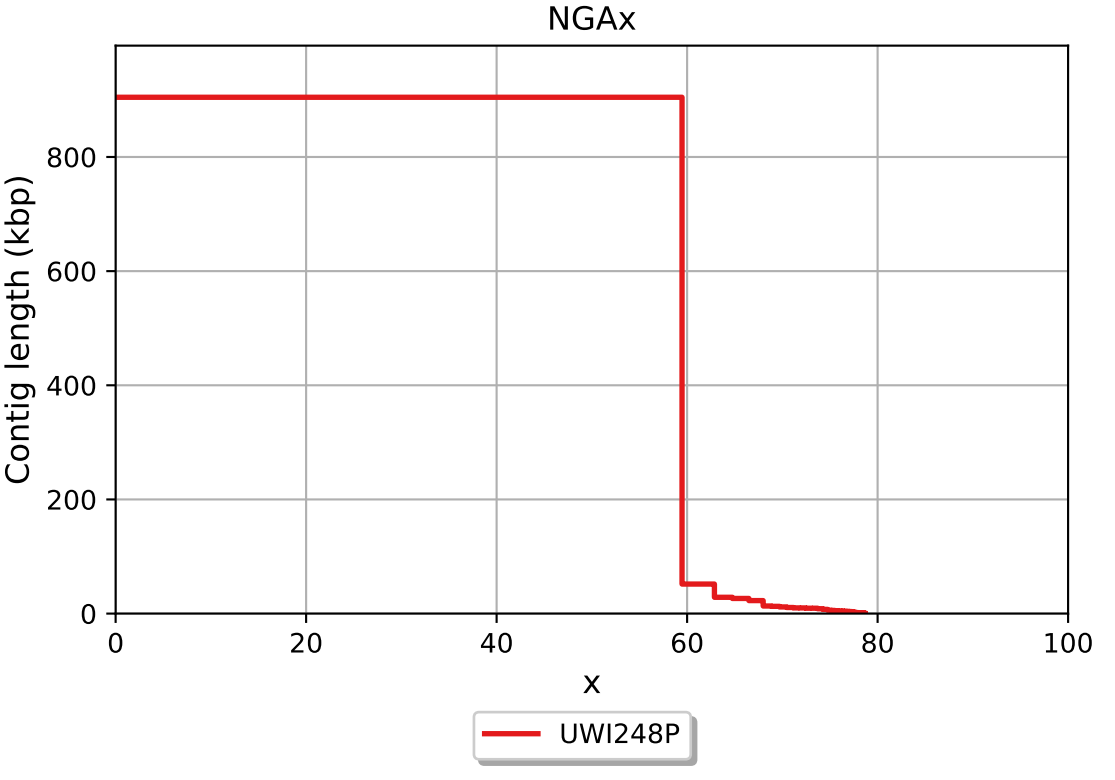

UWI248P GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
UWI248P

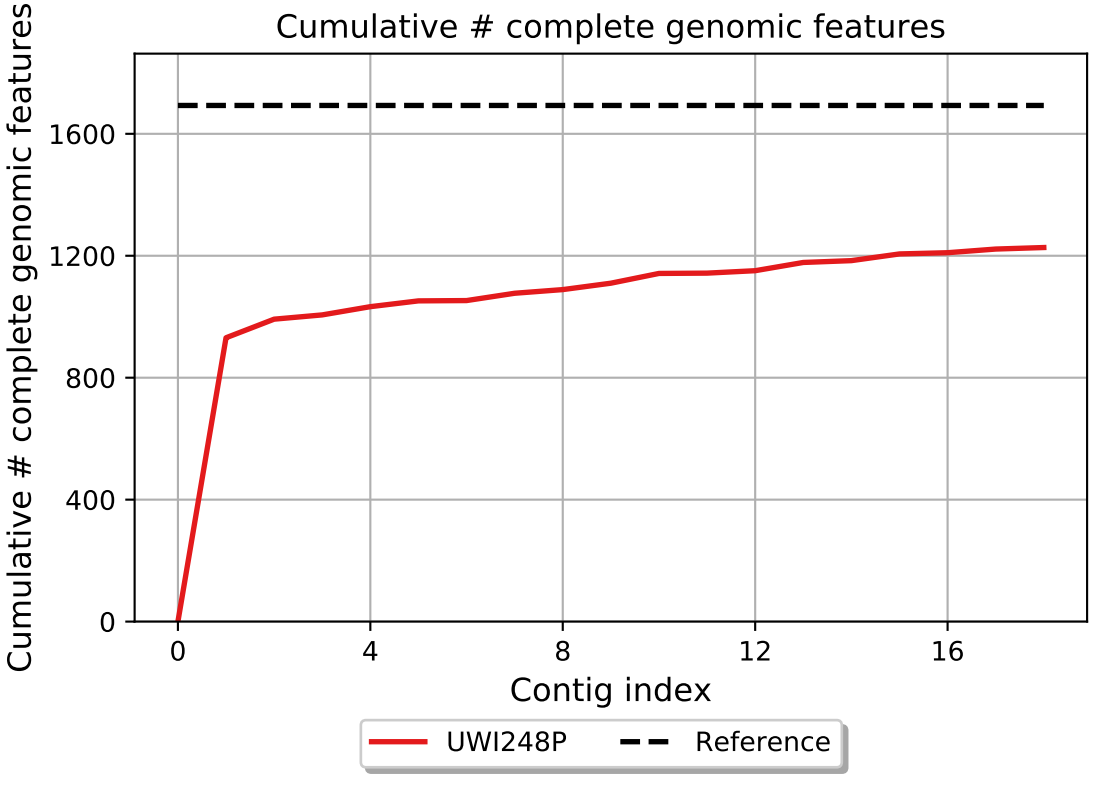

Misassemblies
20
16
12
8
4
0
UWI248P
relocations
translocations

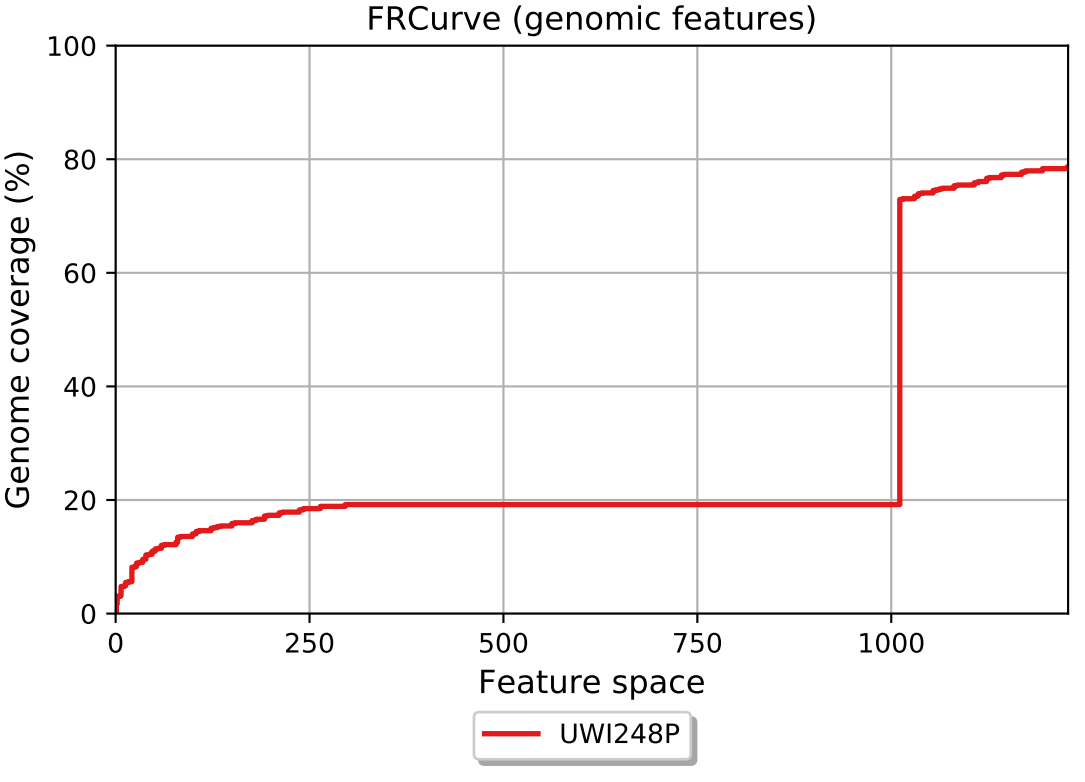

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
Feature space
UWI248P


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
8
16
24
32
40
Contig index
UWI248P
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI248P


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
UWI248P


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
4
8
12
16
Contig index
UWI248P
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
Feature space
UWI248P