Report

	XYZ459H
# contigs (>= 0 bp)	24
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	1272095
Total length (>= 1000 bp)	1269813
Total length (>= 5000 bp)	1266365
Total length (>= 10000 bp)	1248489
Total length (>= 25000 bp)	1169398
Total length (>= 50000 bp)	903233
# contigs	22
Largest contig	903233
Total length	1271424
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	903233
NG50	903233
N90	26537
NG90	-
auN	649068.4
auNG	542490.7
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	8
# misassembled contigs	5
Misassembled contigs length	101197
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	3 + 10 part
Unaligned length	118769
Genome fraction (%)	75.191
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	757.97
# indels per 100 kbp	44.71
# genomic features	1182 + 44 part
Largest alignment	903158
Total aligned length	1151892
NA50	903158
NGA50	903158
NA90	1842
NGA90	-
auNA	645585.2
auNGA	539579.4
LA50	1
LGA50	1
LA90	19
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

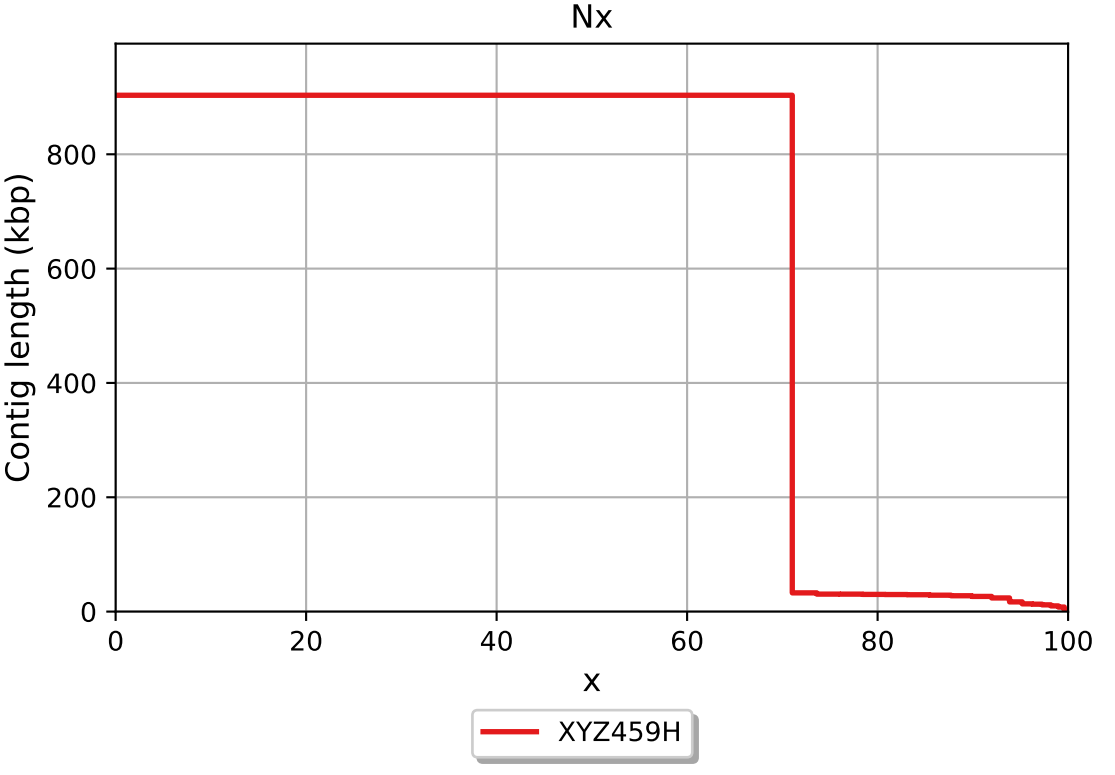
	XYZ459H
# misassemblies	8
# contig misassemblies	8
# c. relocations	2
# c. translocations	6
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	101197
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	8731
# indels	515
# indels (<= 5 bp)	442
# indels (> 5 bp)	73
Indels length	2518

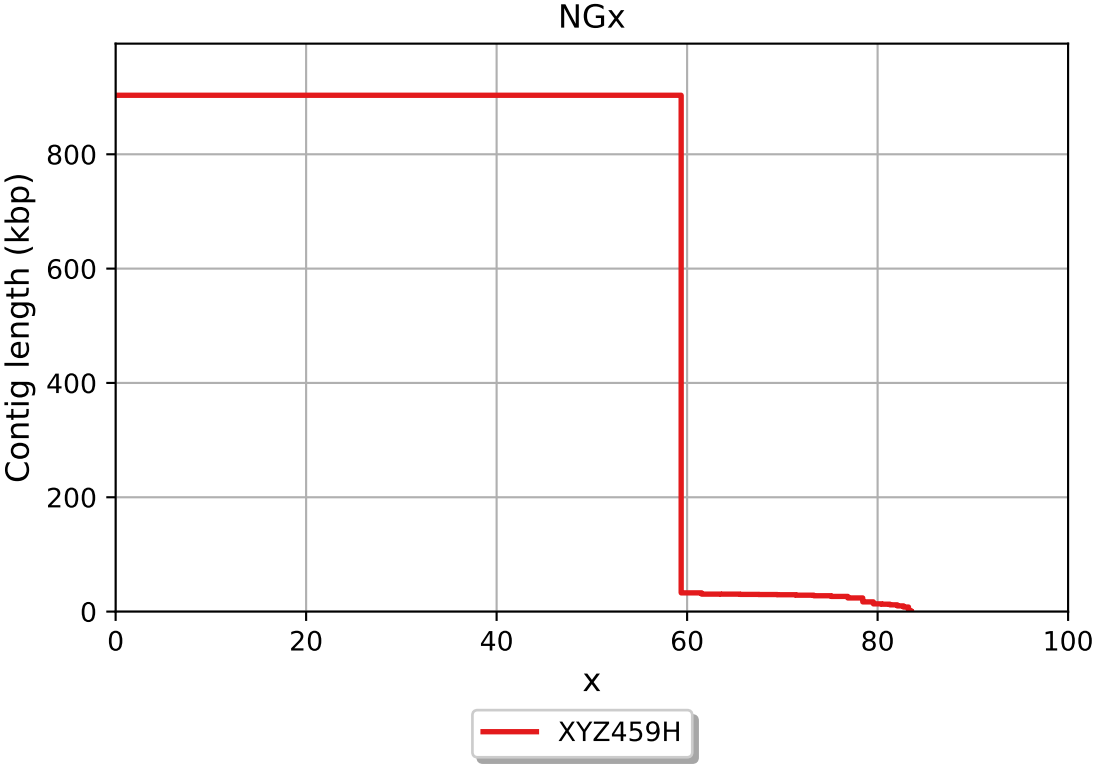
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

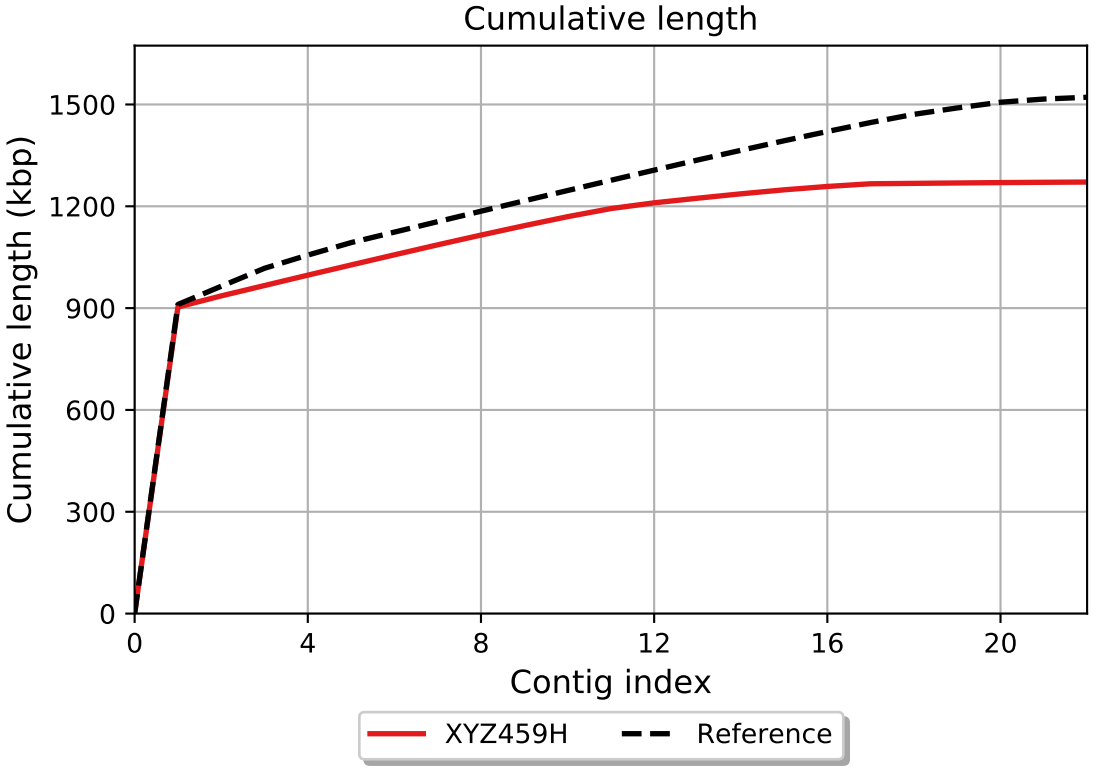
Unaligned report

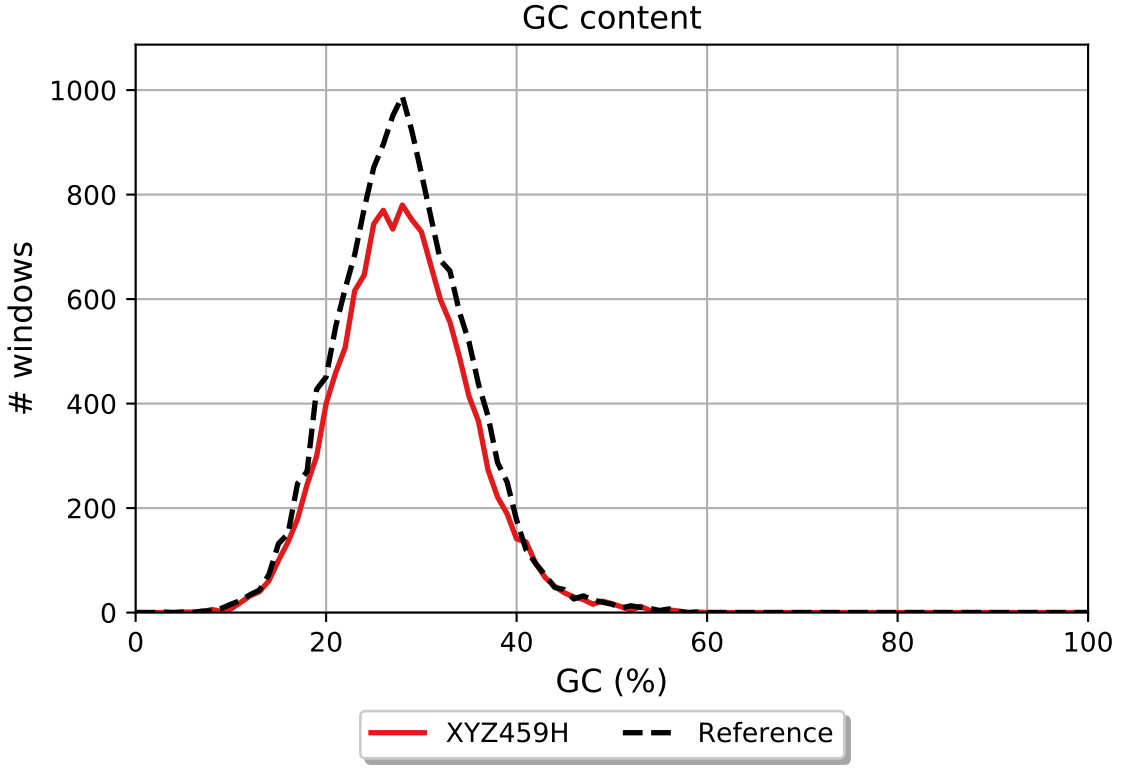
	XYZ459H
# fully unaligned contigs	3
Fully unaligned length	61191
# partially unaligned contigs	10
Partially unaligned length	57578
# N's	0

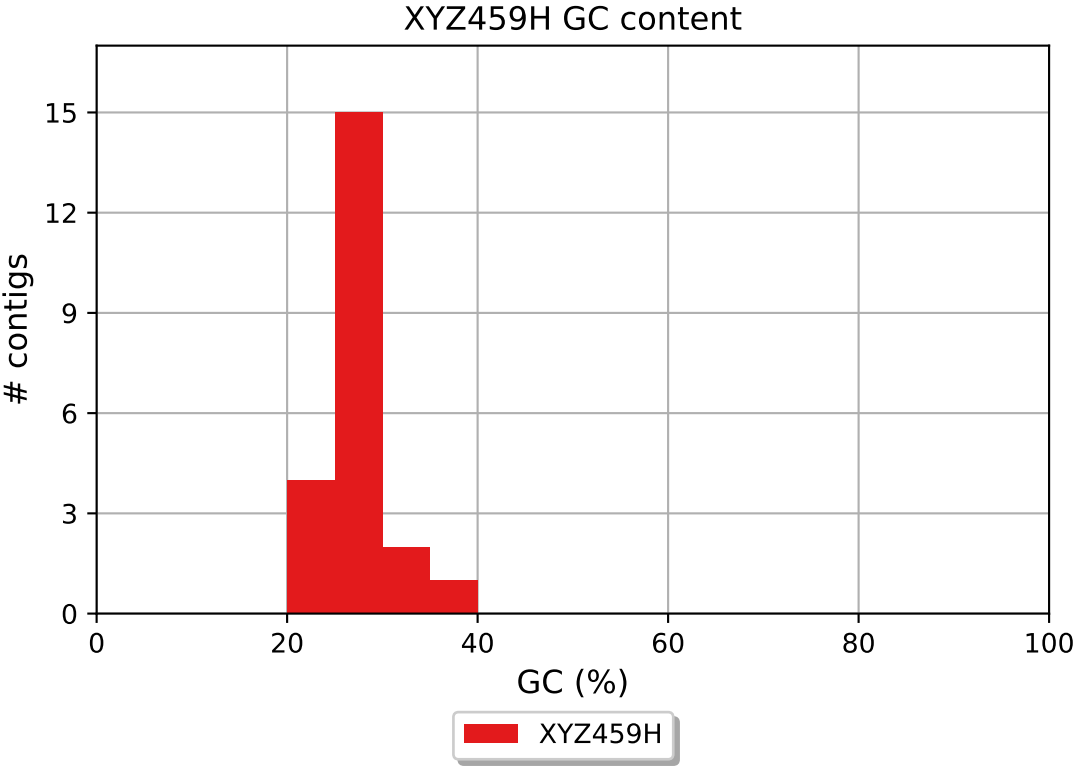
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

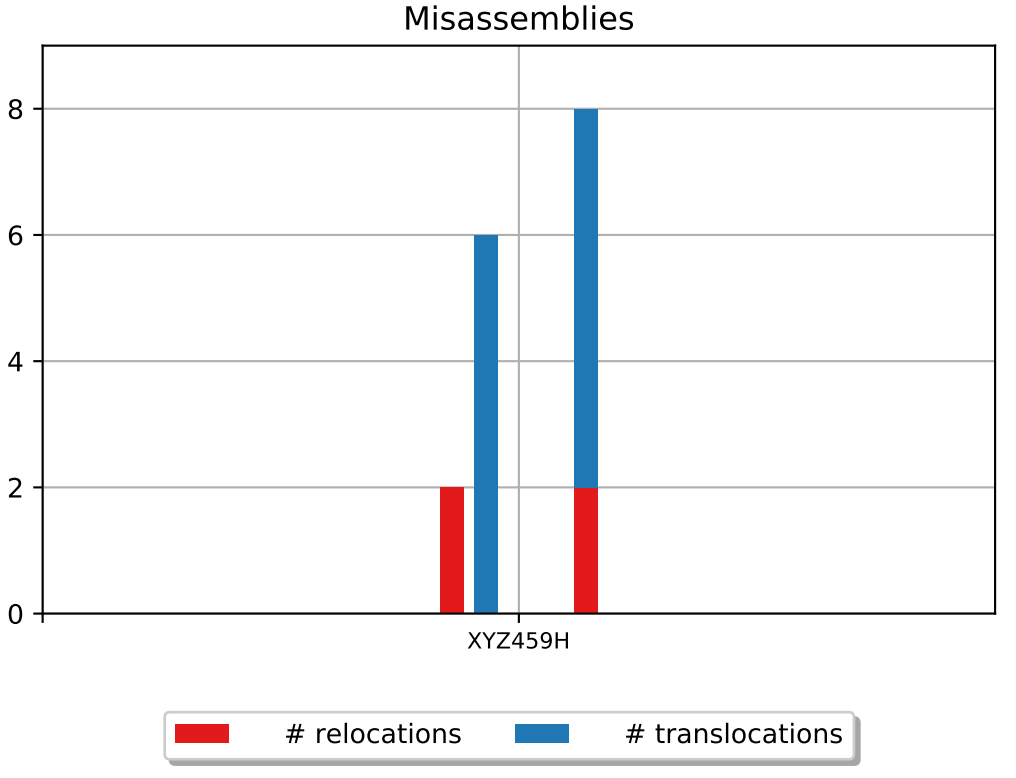

Nx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
XYZ459H

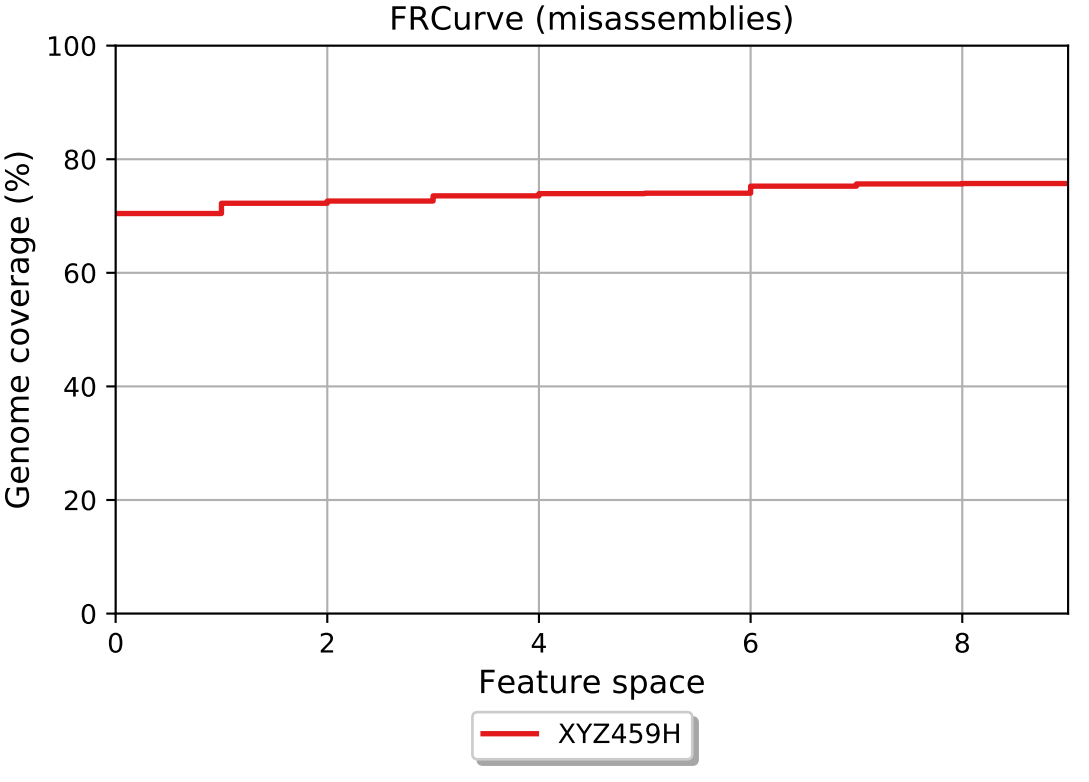

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
XYZ459H

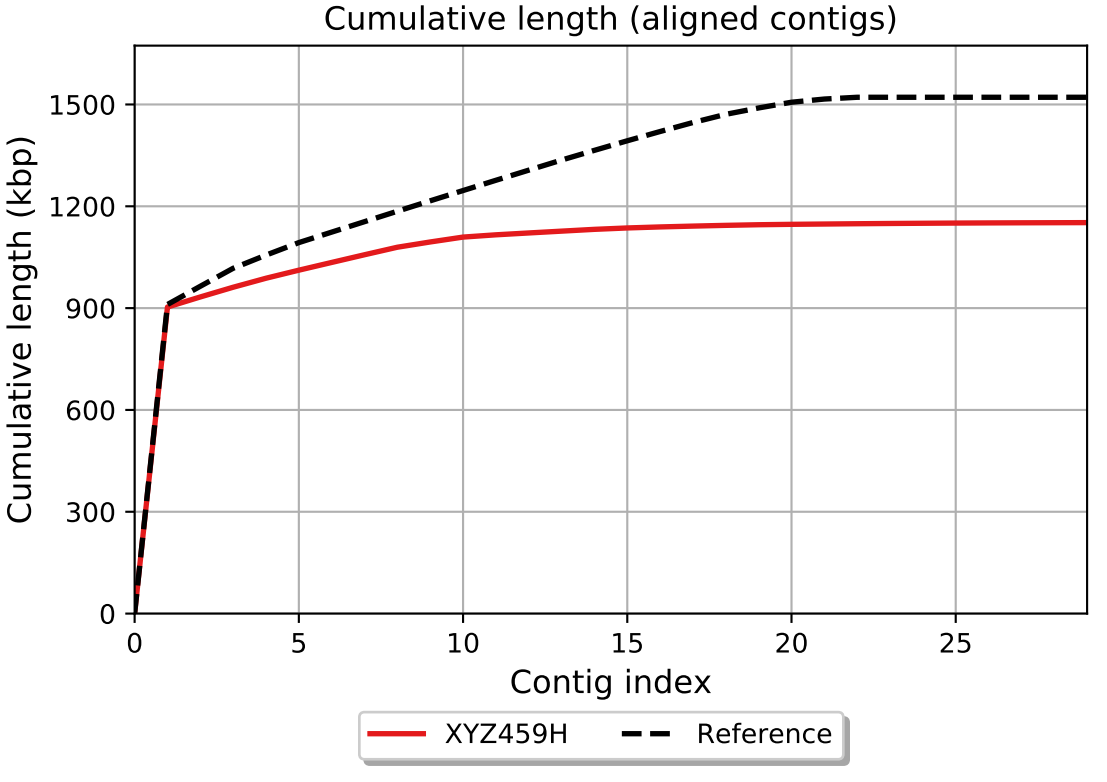

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
XYZ459H
Reference

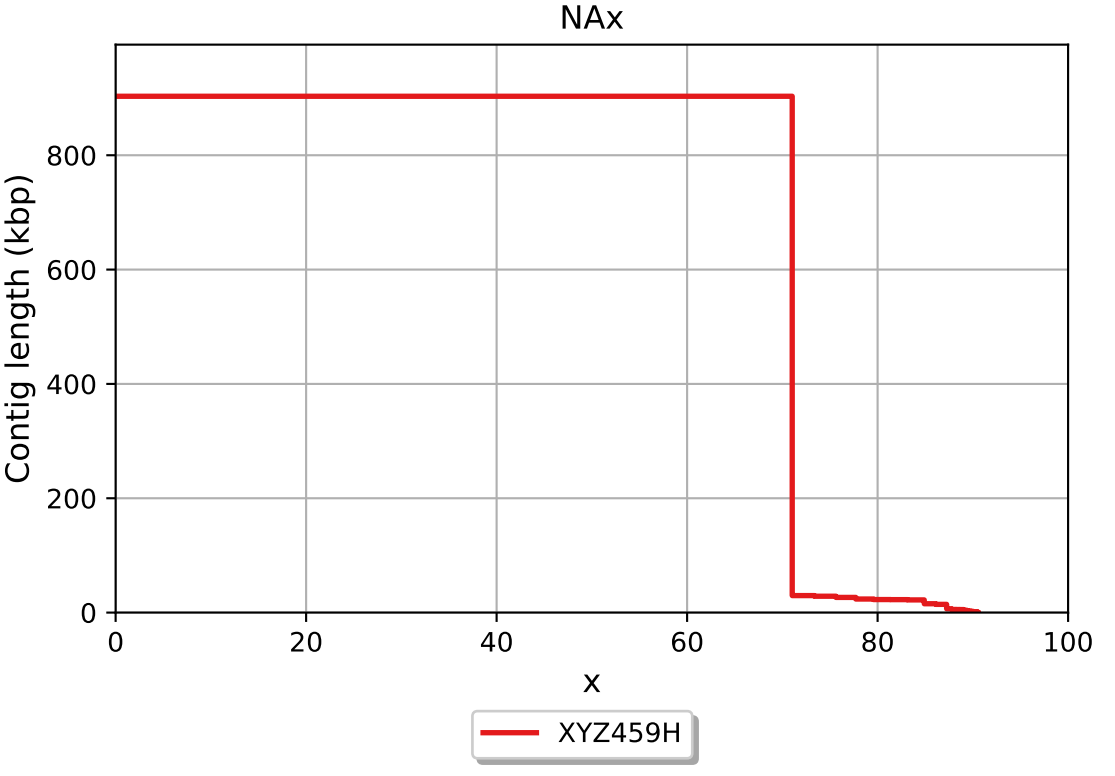

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
XYZ459H
Reference

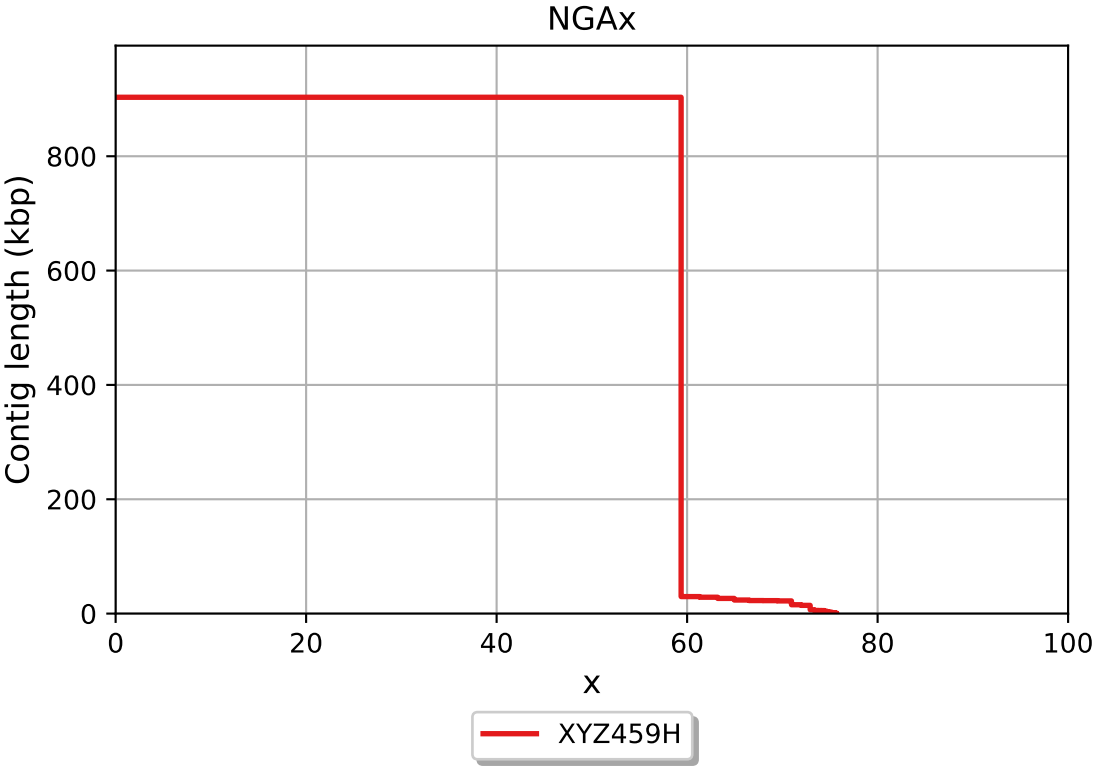

XYZ459H GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
XYZ459H

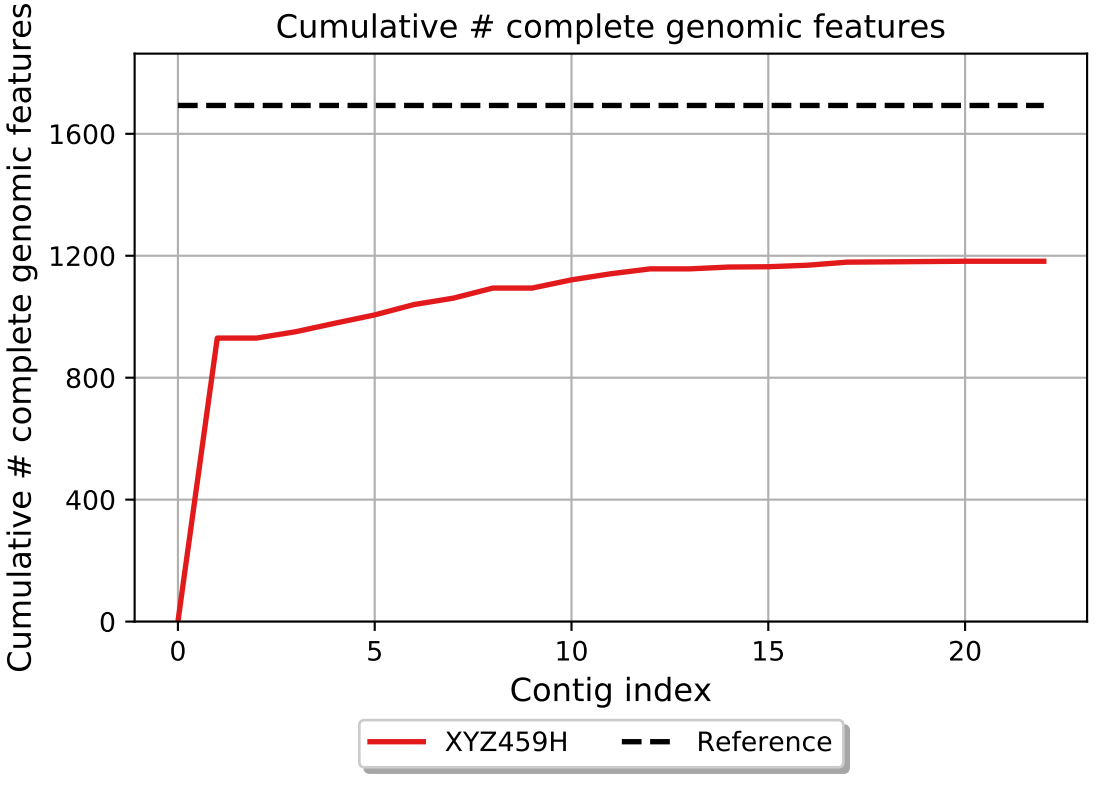

Misassemblies
8
6
4
2
0
XYZ459H
relocations
translocations

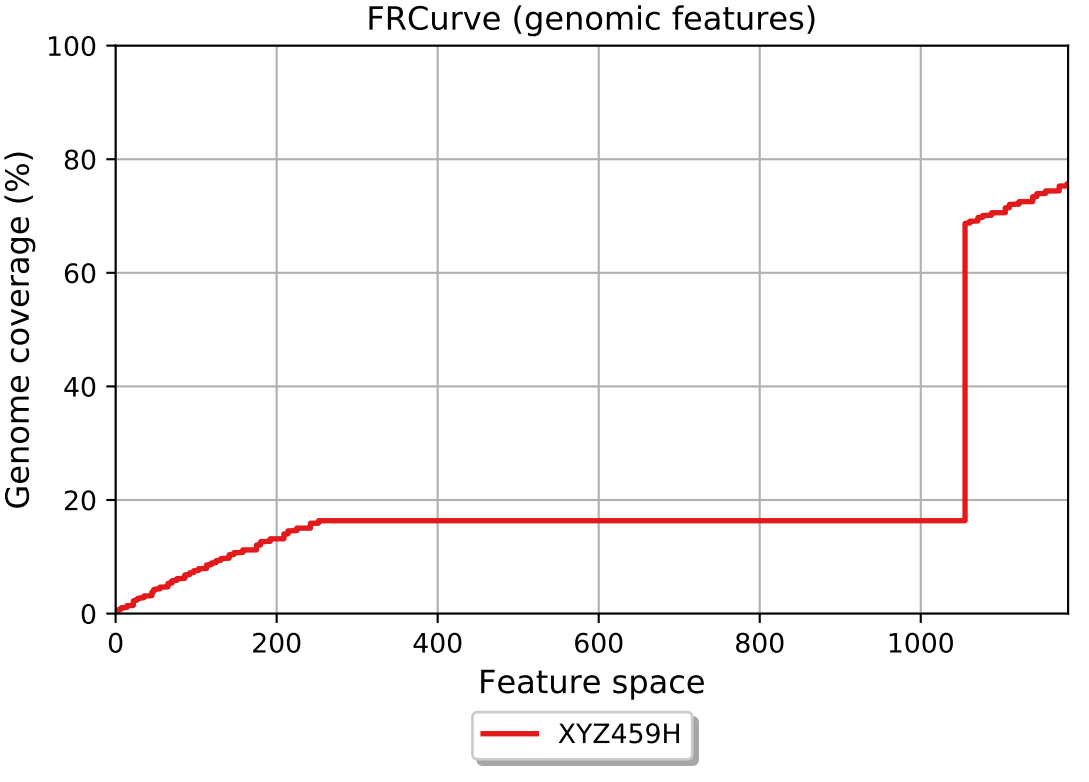

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
Feature space
XYZ459H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
5
10
15
20
25
Contig index
XYZ459H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
XYZ459H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
XYZ459H


Cumulative # complete genomic features
Cumulative # complete genomic features
1600
1200
800
400
0
0
5
10
15
20
Contig index
XYZ459H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
XYZ459H