Report

	ESI36H
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1182078
Total length (>= 1000 bp)	1182078
Total length (>= 5000 bp)	1174817
Total length (>= 10000 bp)	1174817
Total length (>= 25000 bp)	1131930
Total length (>= 50000 bp)	1019108
# contigs	11
Largest contig	909934
Total length	1182078
Reference length	1521208
GC (%)	28.21
Reference GC (%)	28.18
N50	909934
NG50	909934
N90	28638
NG90	-
auN	709008.6
auNG	550946.0
L50	1
LG50	1
L90	5
LG90	-
# misassemblies	14
# misassembled contigs	4
Misassembled contigs length	142865
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 7 part
Unaligned length	67218
Genome fraction (%)	72.107
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	738.26
# indels per 100 kbp	33.18
# genomic features	1139 + 32 part
Largest alignment	904537
Total aligned length	1109088
NA50	904537
NGA50	904537
NA90	7401
NGA90	-
auNA	696317.0
auNGA	541083.8
LA50	1
LGA50	1
LA90	9
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

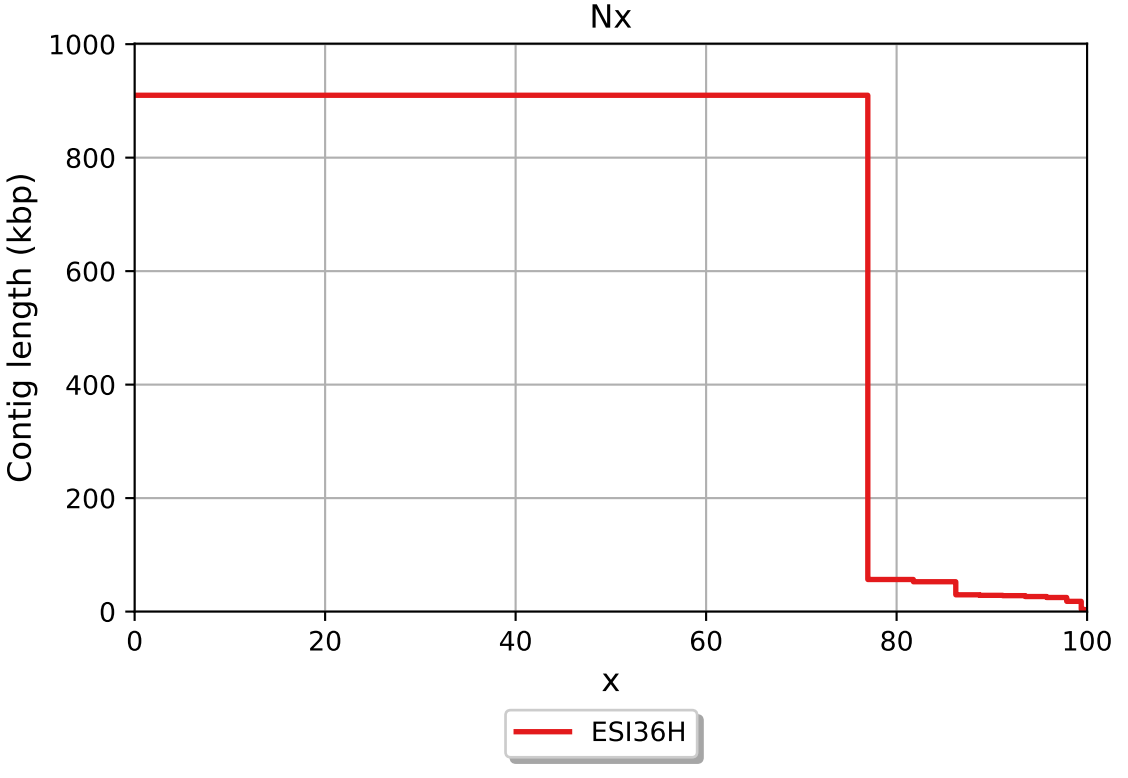
	ESI36H
# misassemblies	14
# contig misassemblies	14
# c. relocations	2
# c. translocations	12
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	4
Misassembled contigs length	142865
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	8188
# indels	368
# indels (<= 5 bp)	326
# indels (> 5 bp)	42
Indels length	1713

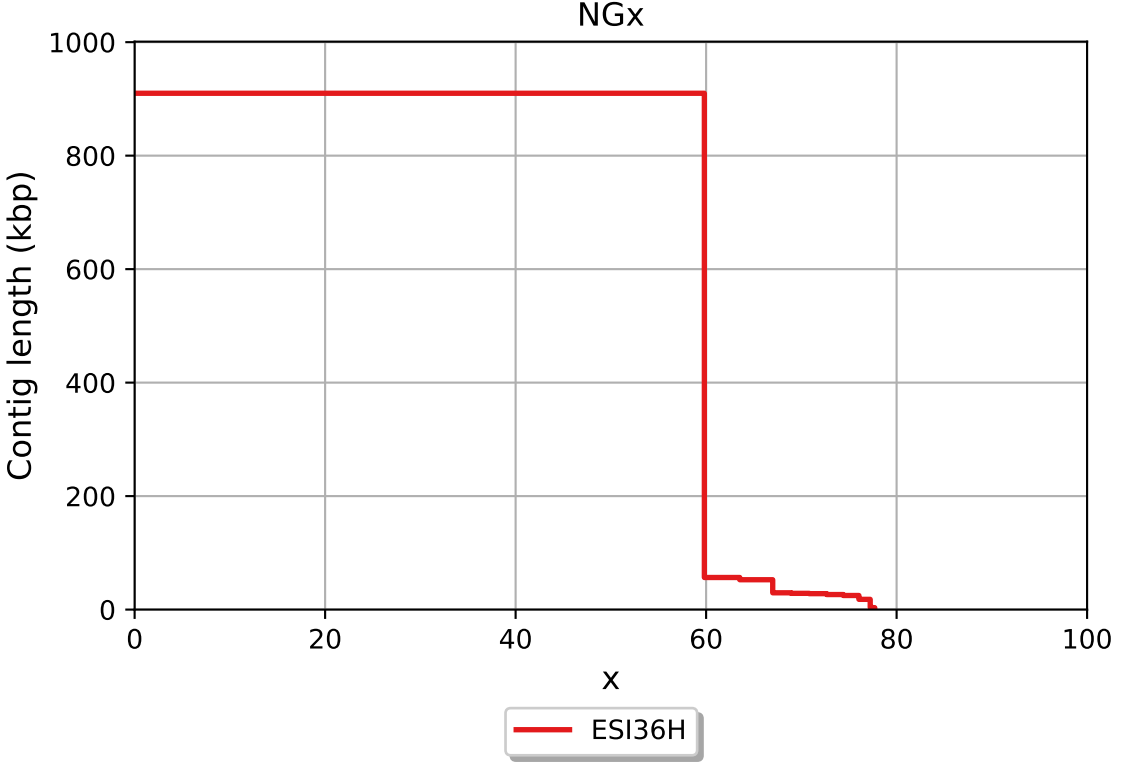
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

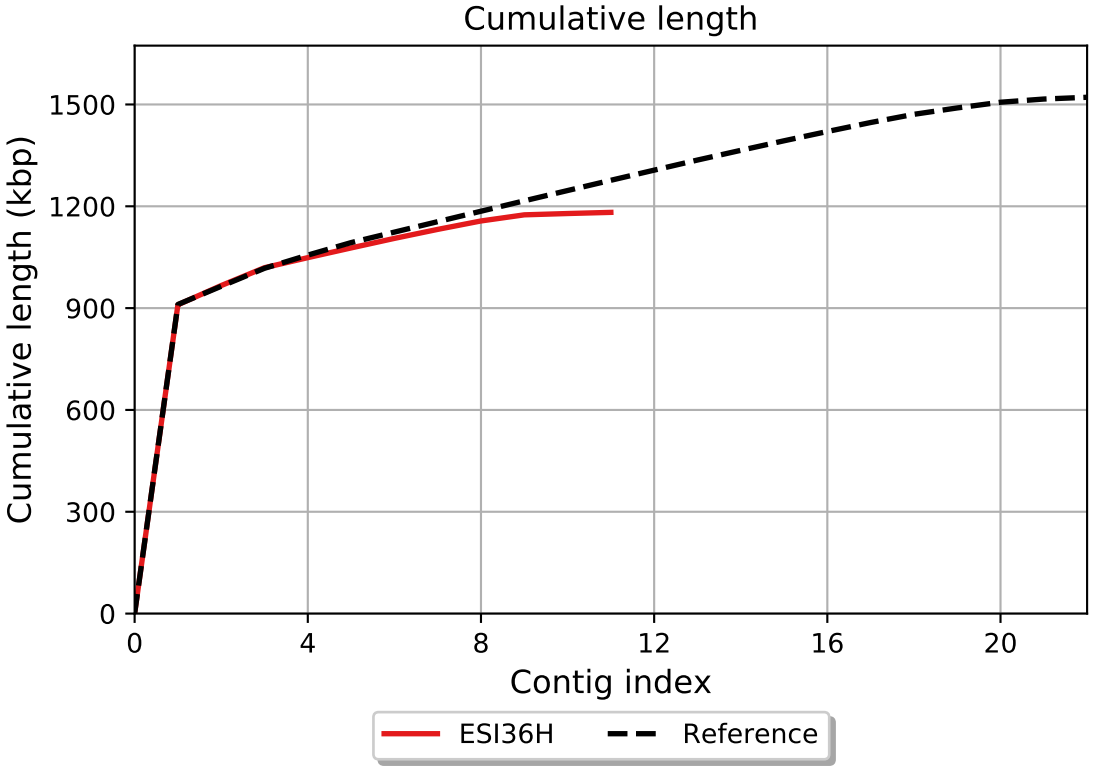
Unaligned report

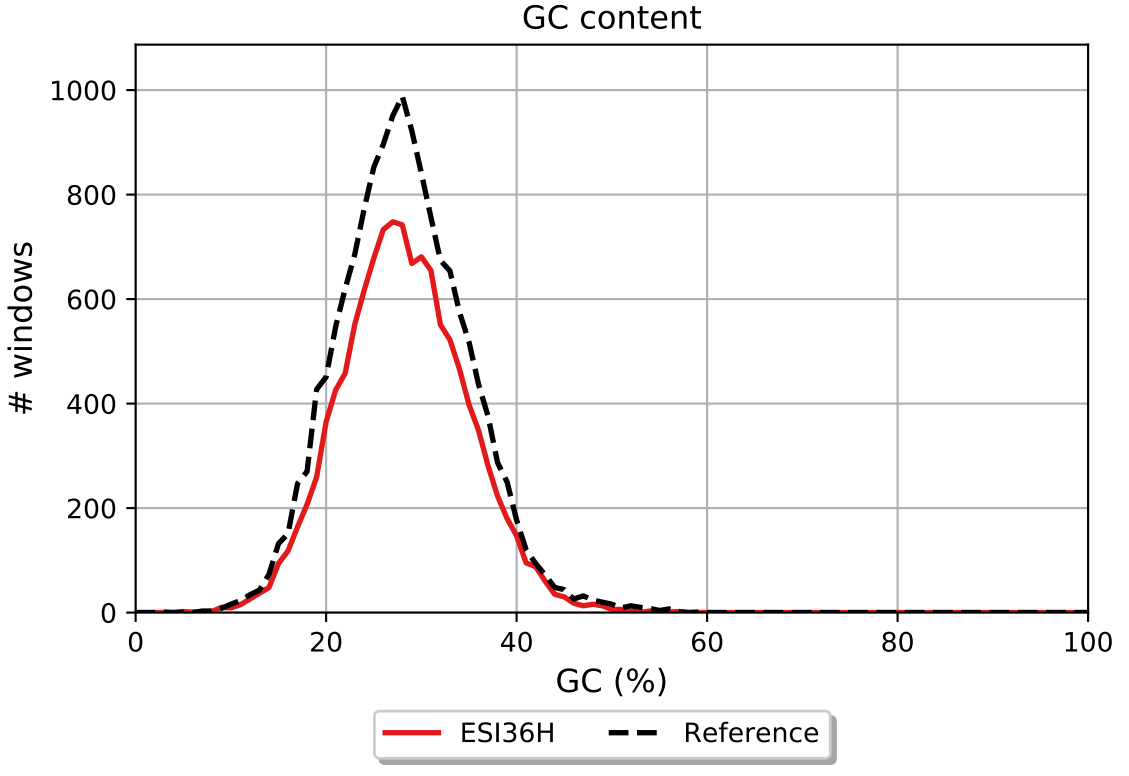
	ESI36H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	67218
# N's	0

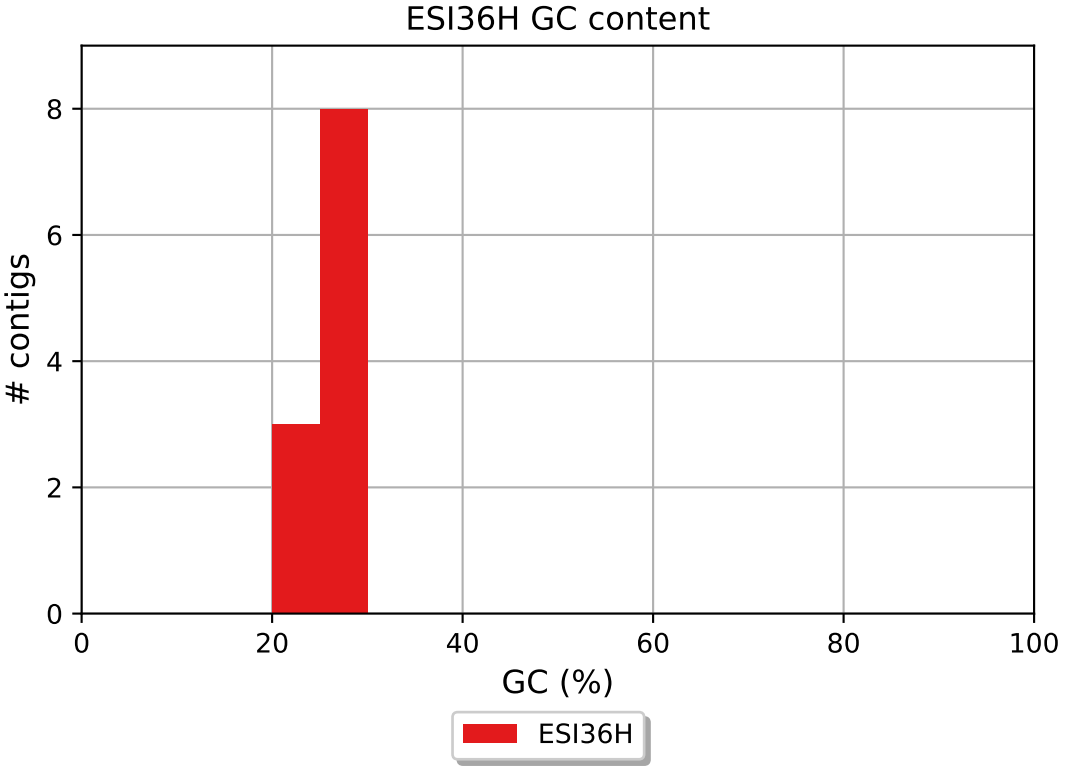
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

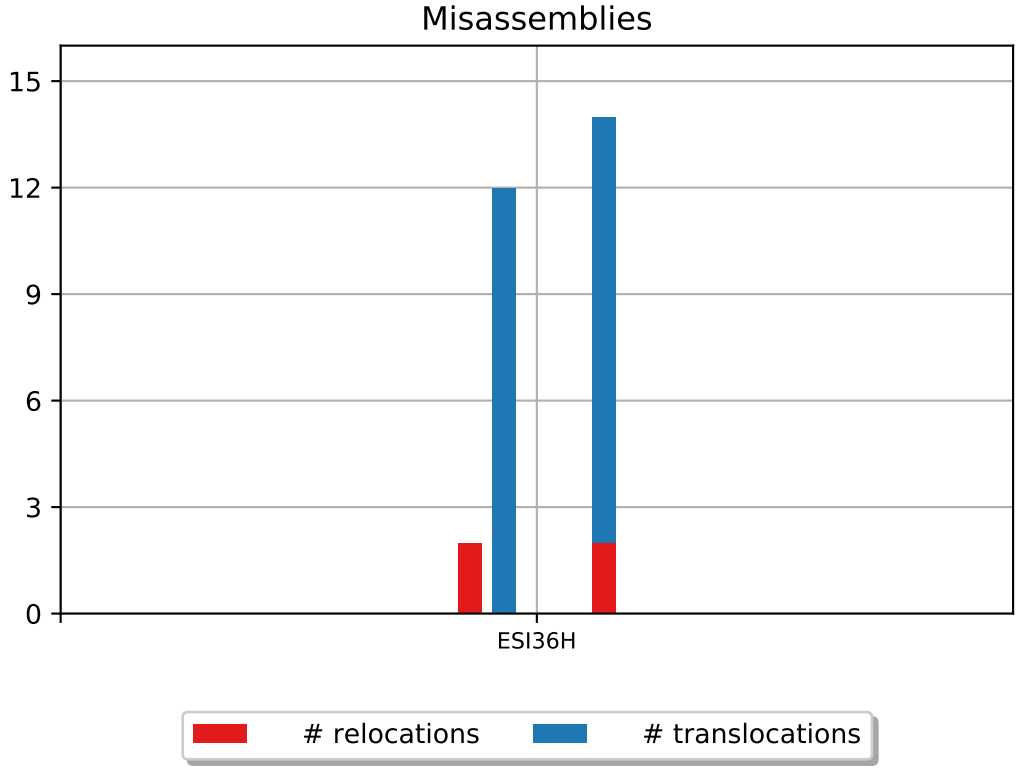

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
ESI36H

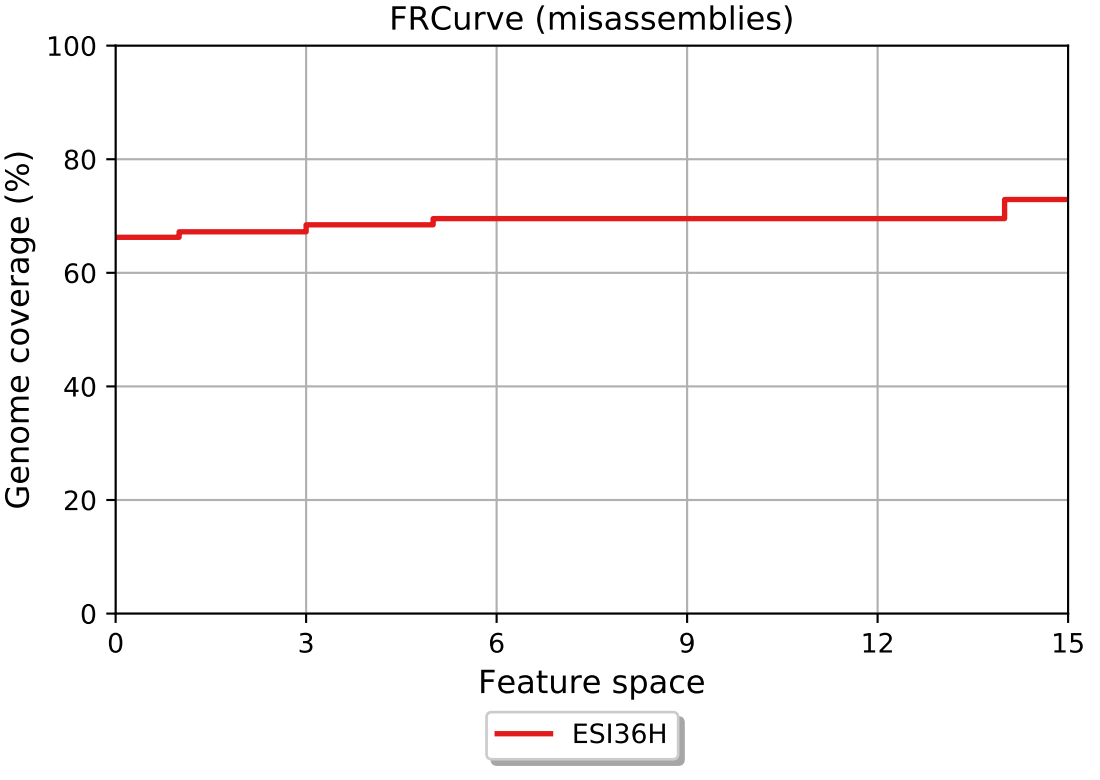

NGx
1000
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
ESI36H

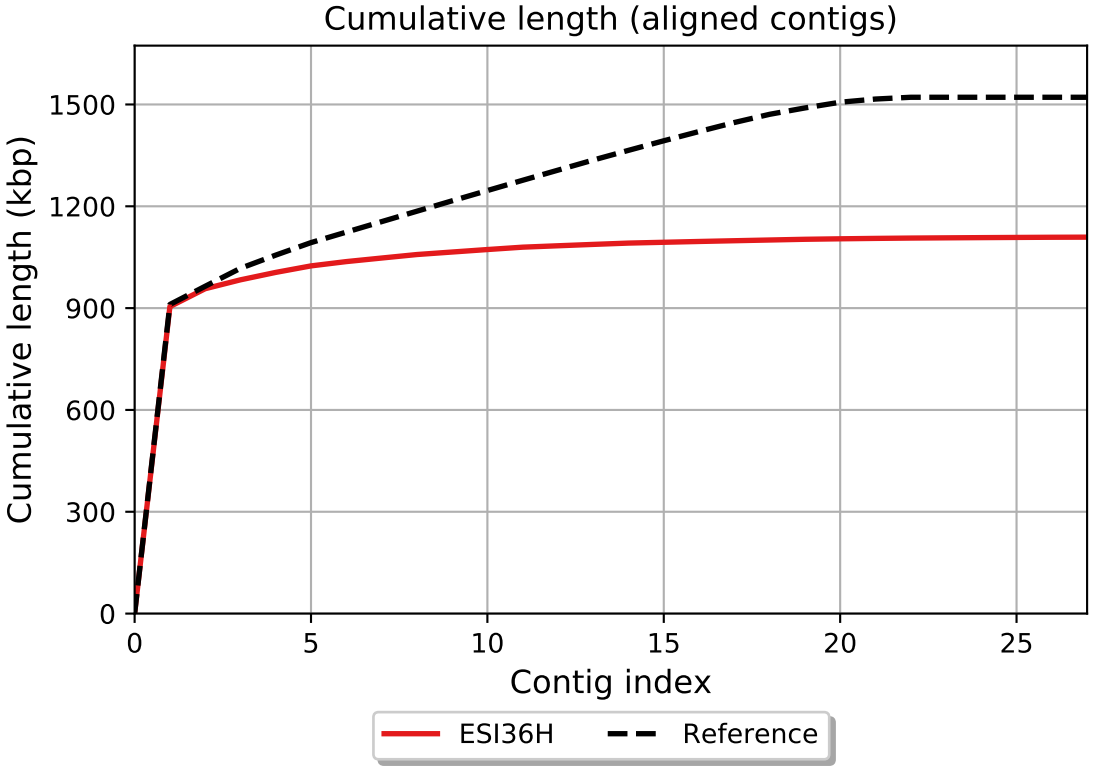

Cumulative length
Cumulative length (kbp)
1500
1200
900
600
300
0
0
4
8
12
16
20
Contig index
ESI36H
Reference

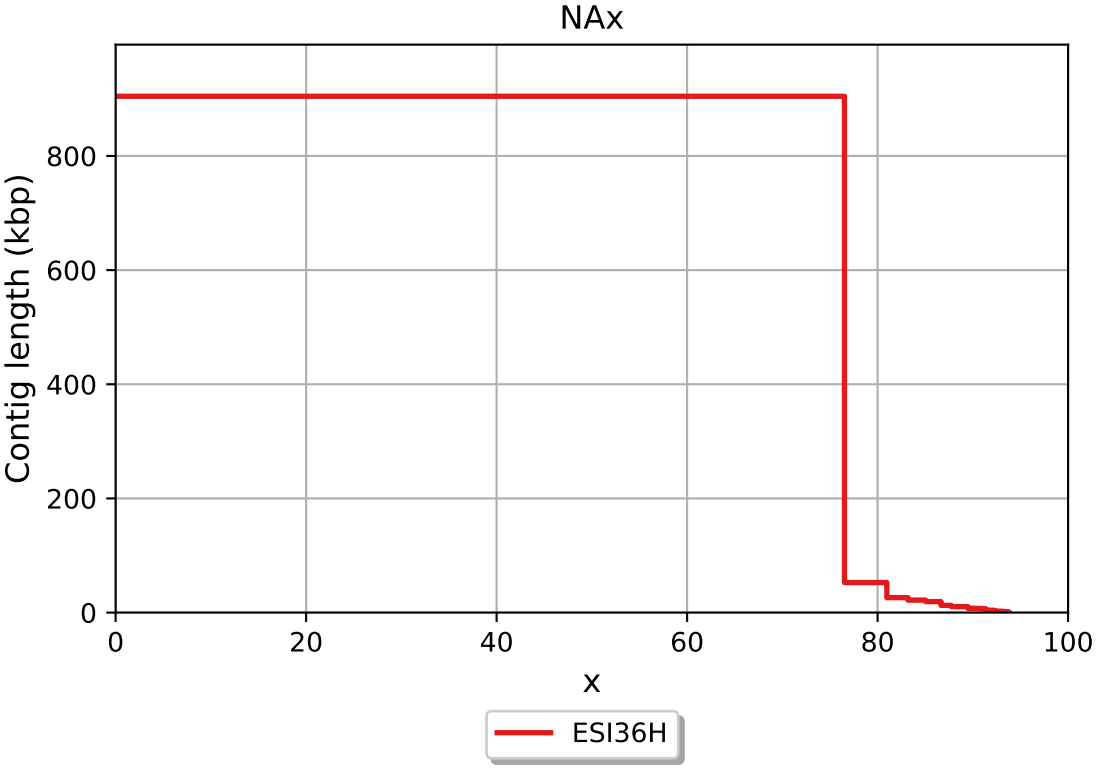

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
ESI36H
Reference

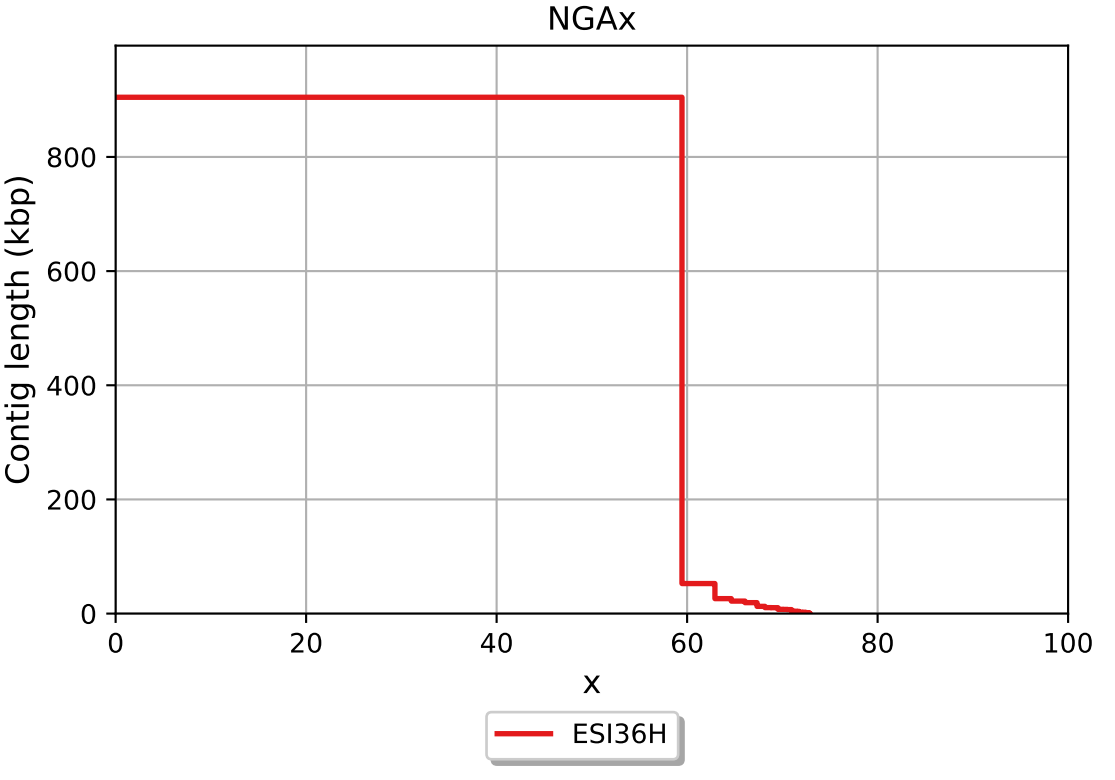

ESI36H GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
ESI36H

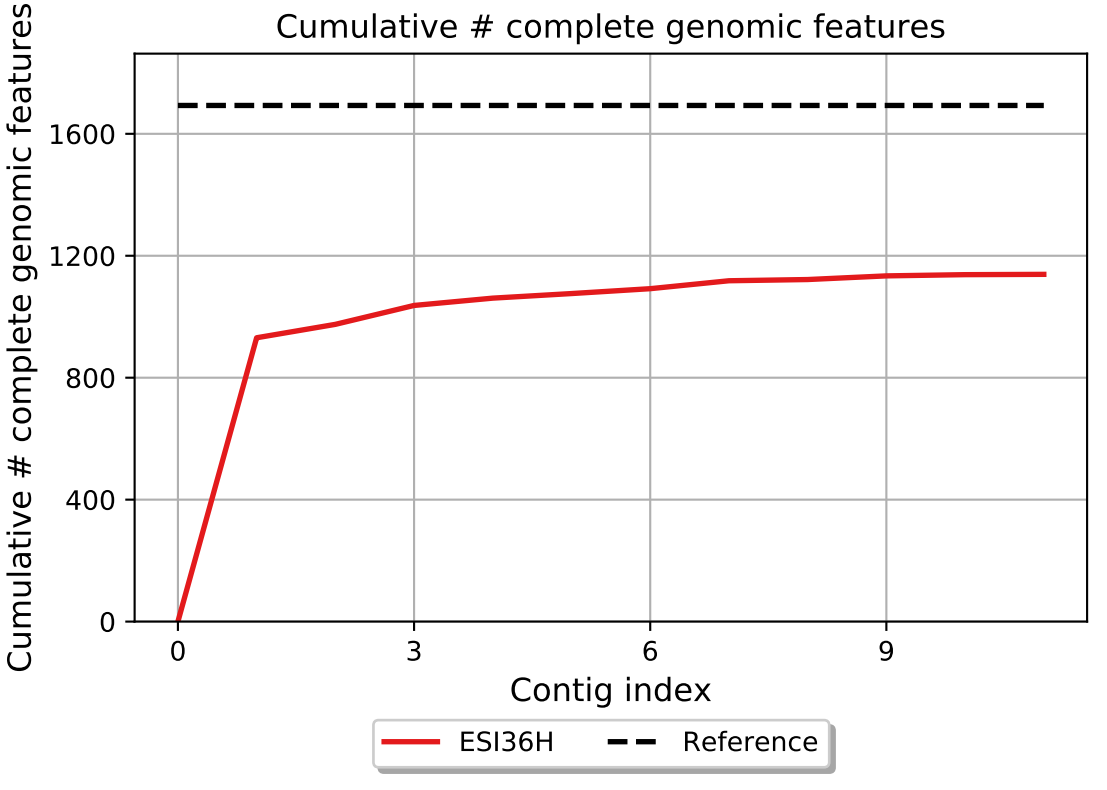

Misassemblies
15
12
9
6
3
0
ESI36H
relocations
translocations

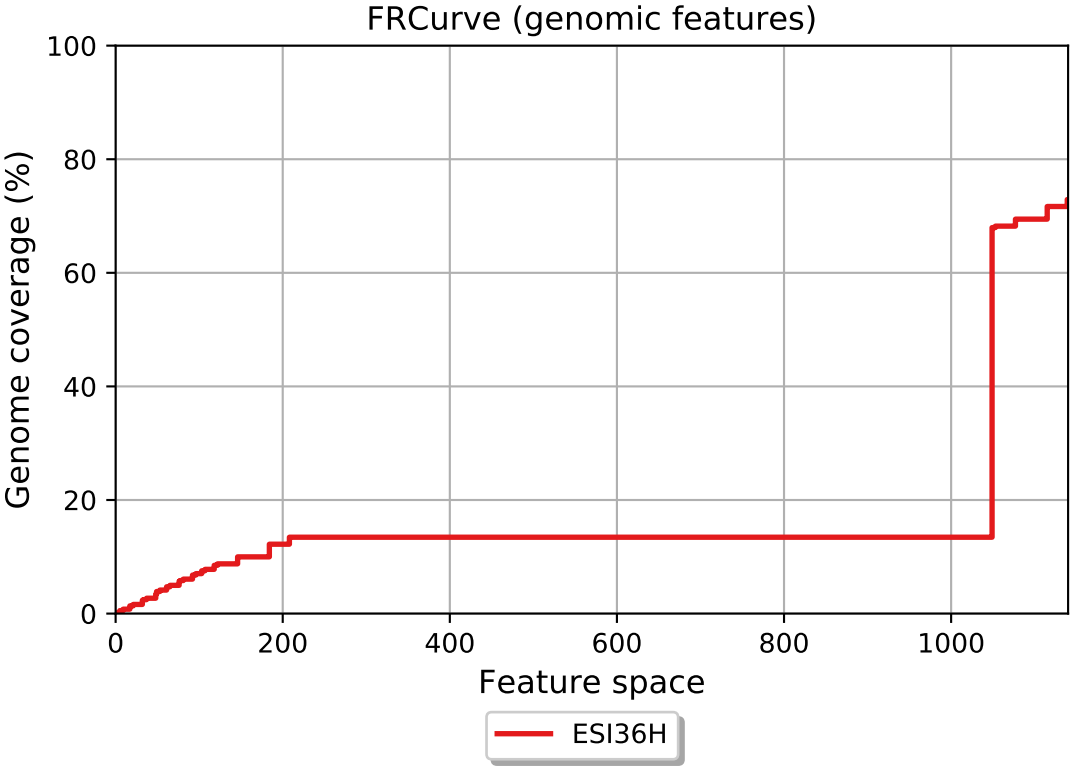

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
ESI36H


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
5
10
15
20
25
Contig index
ESI36H
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
ESI36H


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
ESI36H


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
3
6
9
Contig index
ESI36H
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
200
400
600
800
1000
Feature space
ESI36H