Report

	K89HH
# contigs (>= 0 bp)	150
# contigs (>= 1000 bp)	66
# contigs (>= 5000 bp)	32
# contigs (>= 10000 bp)	25
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1557782
Total length (>= 1000 bp)	1522401
Total length (>= 5000 bp)	1447581
Total length (>= 10000 bp)	1404448
Total length (>= 25000 bp)	1233769
Total length (>= 50000 bp)	826996
# contigs	98
Largest contig	552693
Total length	1545632
Reference length	1521208
GC (%)	28.05
Reference GC (%)	28.18
N50	274303
NG50	274303
N90	11525
NG90	15555
auN	257152.6
auNG	261281.4
L50	2
LG50	2
L90	24
LG90	22
# misassemblies	20
# misassembled contigs	14
Misassembled contigs length	802892
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	9 + 24 part
Unaligned length	144656
Genome fraction (%)	85.122
Duplication ratio	1.075
# N's per 100 kbp	0.00
# mismatches per 100 kbp	794.74
# indels per 100 kbp	55.63
# genomic features	1327 + 83 part
Largest alignment	437440
Total aligned length	1391393
NA50	115253
NGA50	115253
NA90	504
NGA90	994
auNA	187570.3
auNGA	190581.9
LA50	3
LGA50	3
LA90	102
LGA90	72

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

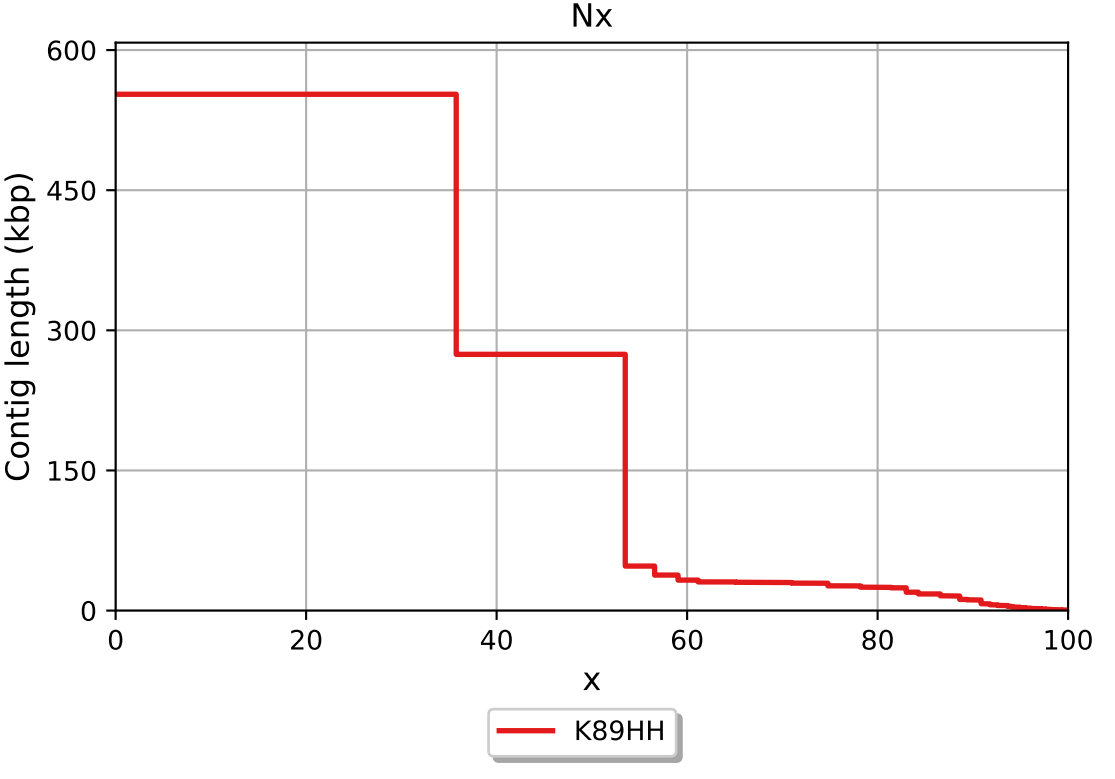
	K89HH
# misassemblies	20
# contig misassemblies	20
# c. relocations	5
# c. translocations	10
# c. inversions	5
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	14
Misassembled contigs length	802892
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	11058
# indels	774
# indels (<= 5 bp)	686
# indels (> 5 bp)	88
Indels length	4604

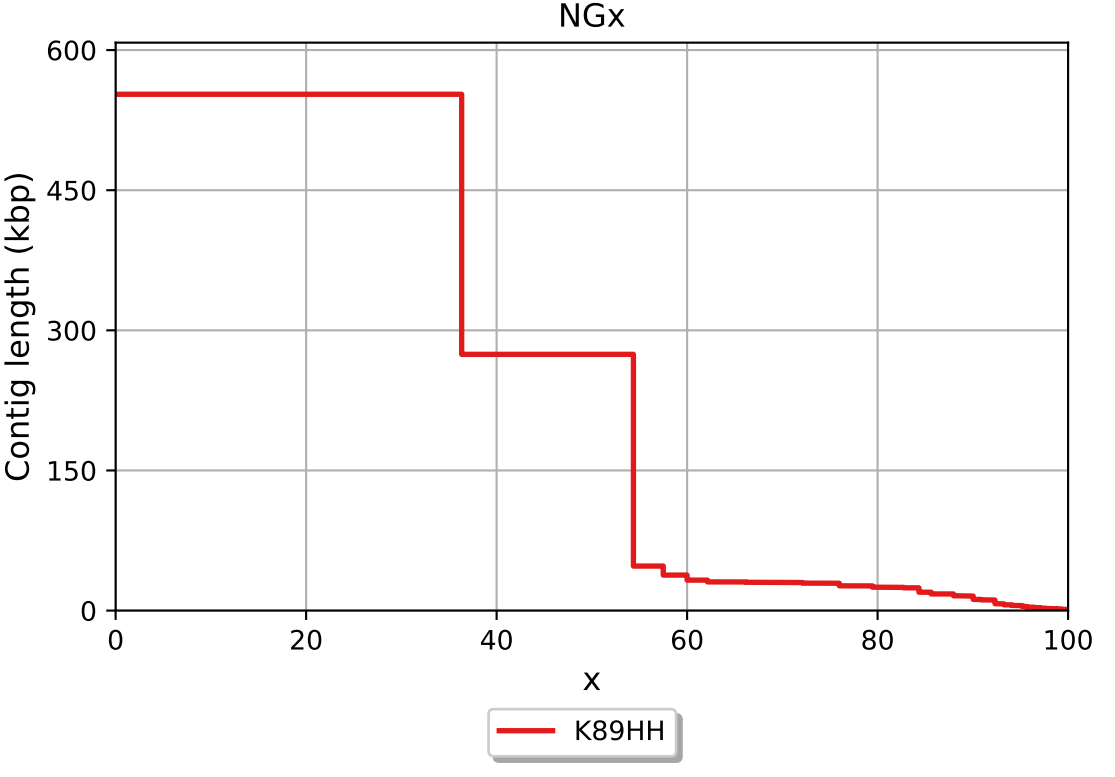
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

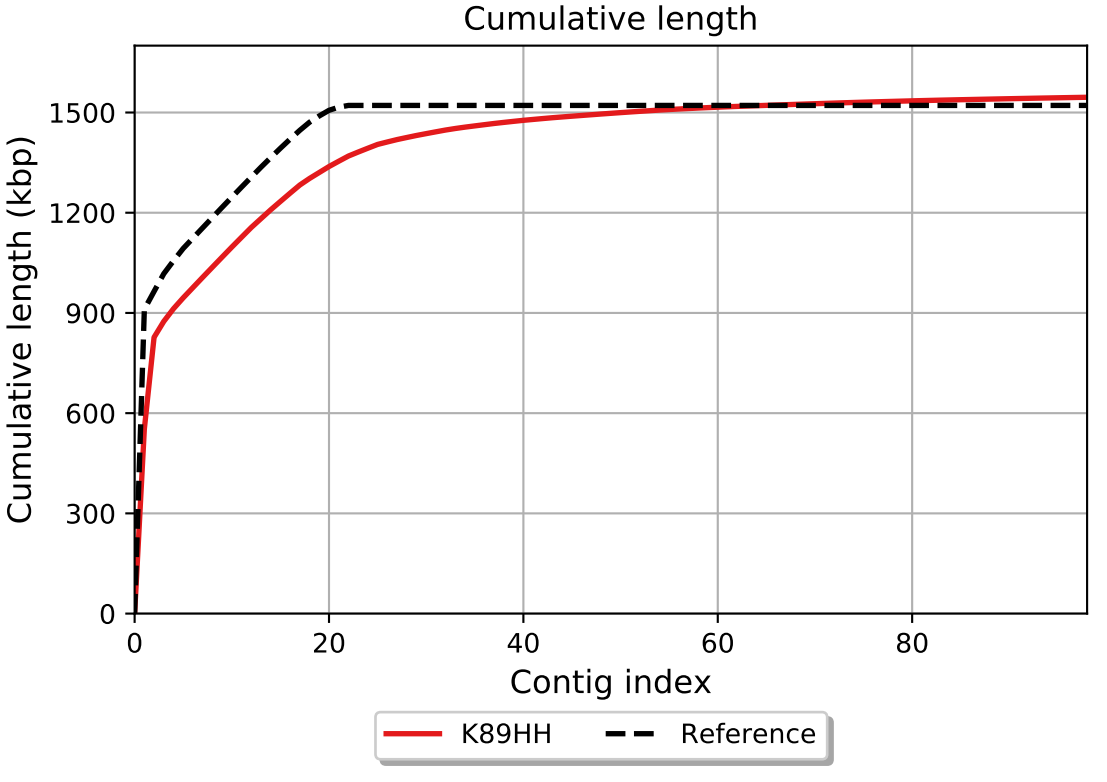
Unaligned report

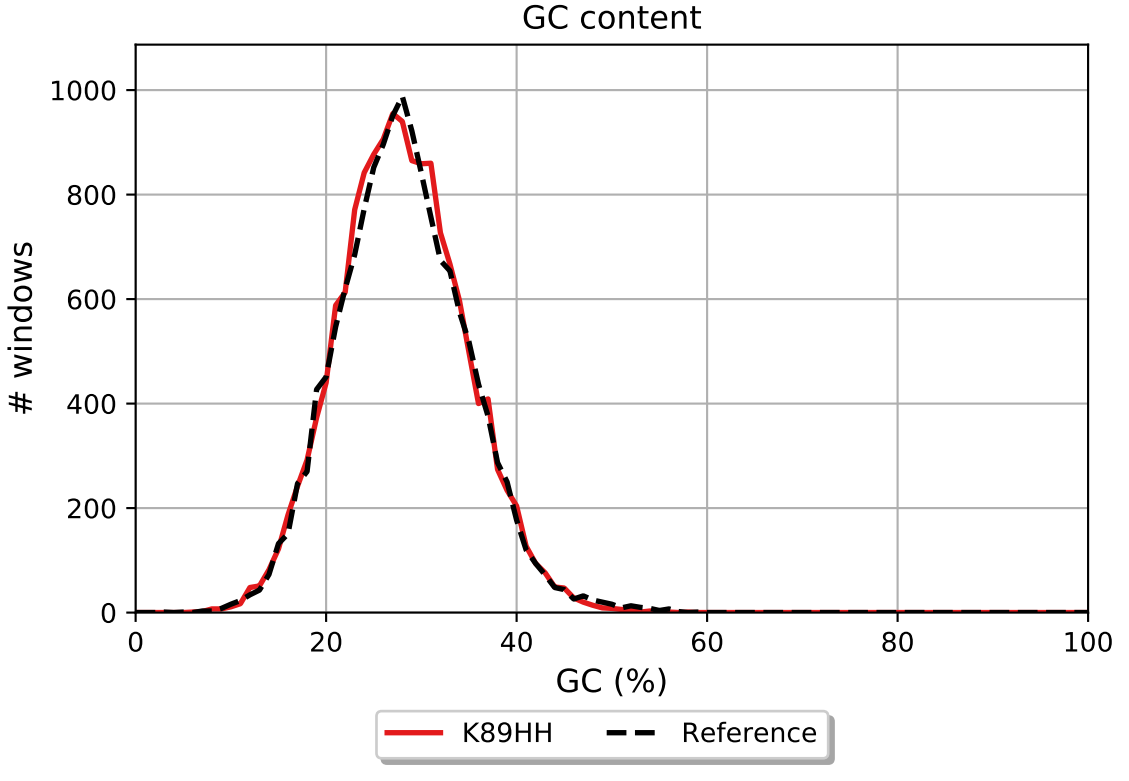
	K89HH
# fully unaligned contigs	9
Fully unaligned length	12104
# partially unaligned contigs	24
Partially unaligned length	132552
# N's	0

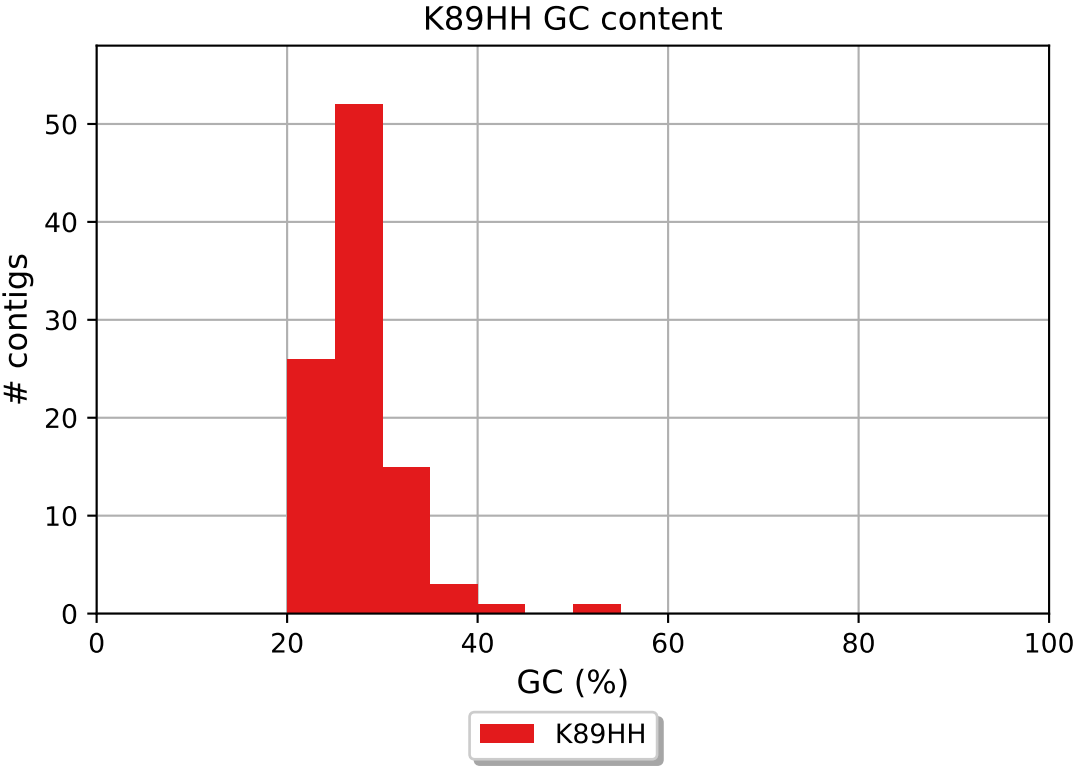
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

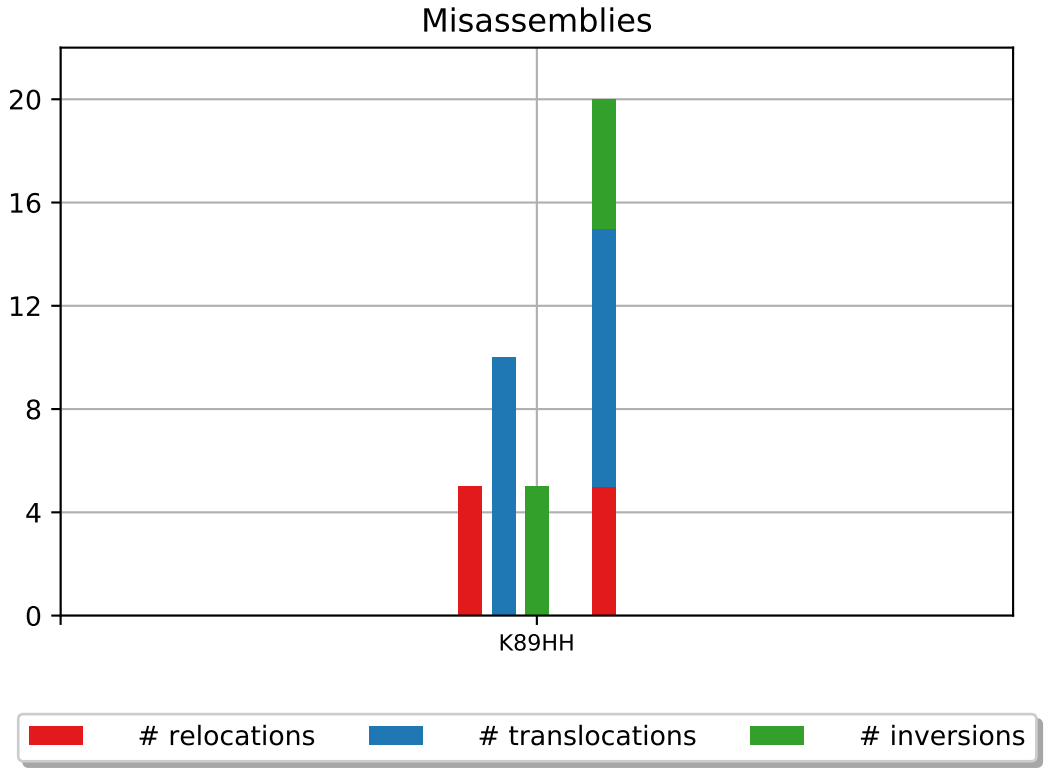

Nx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
K89HH

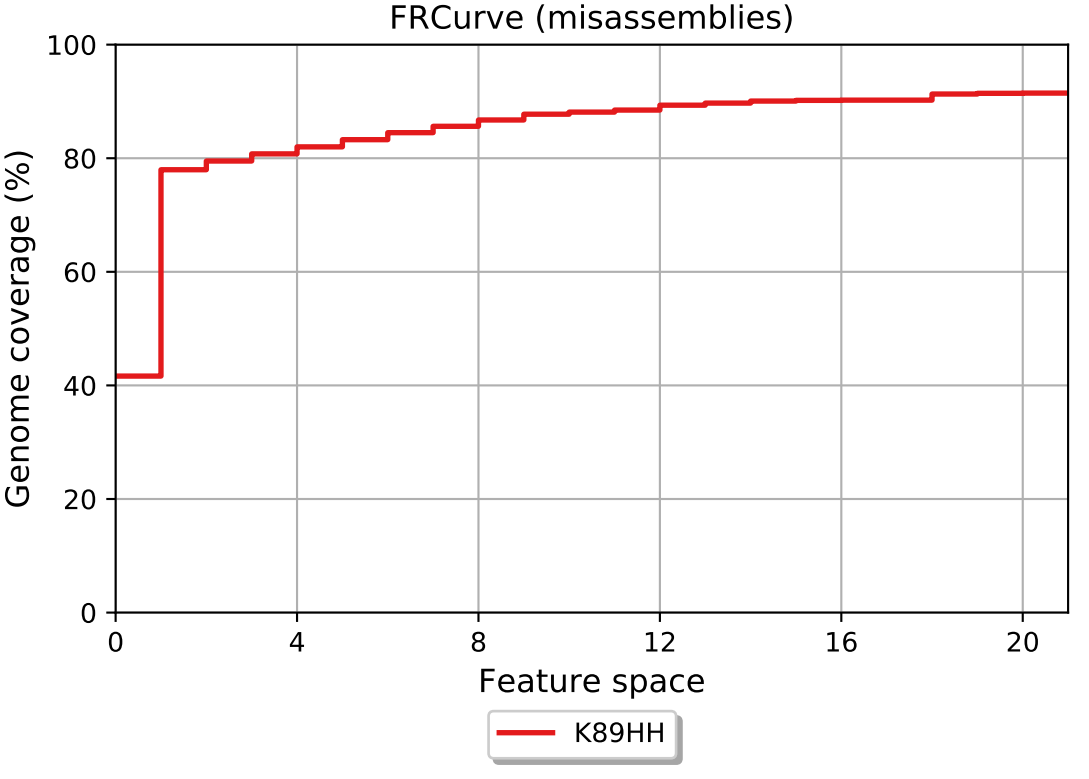

NGx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
K89HH

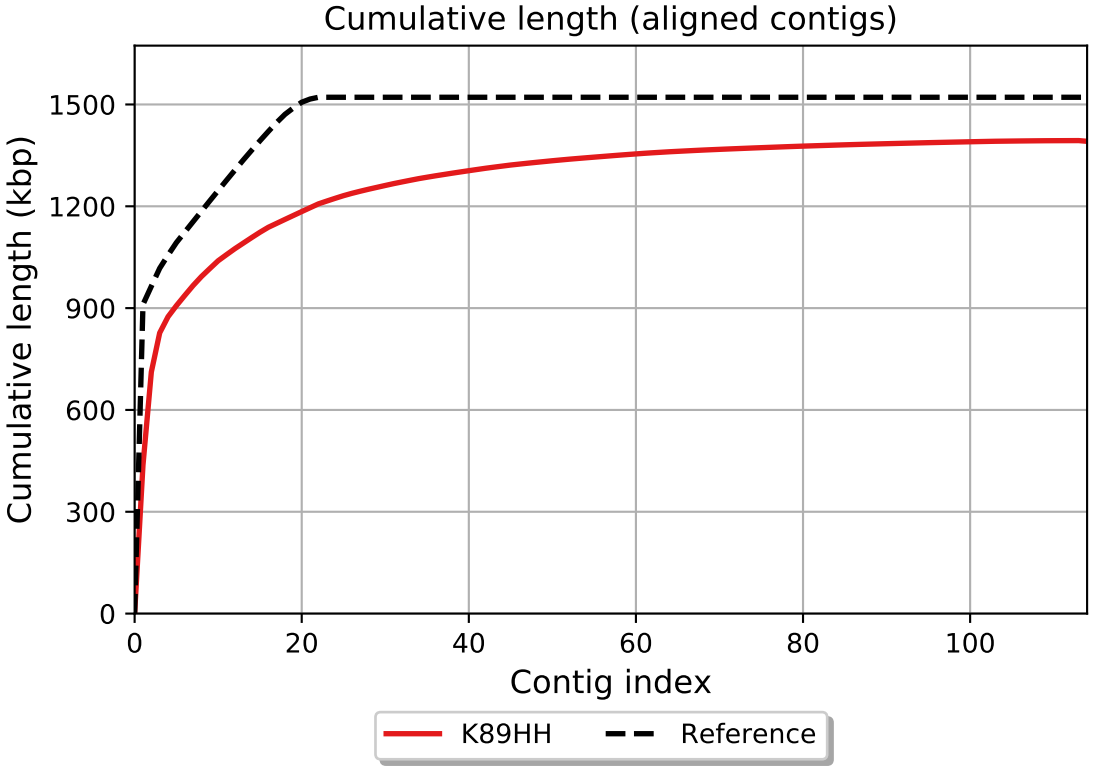

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
1500
0
20
40
60
80
Contig index
K89HH
Reference

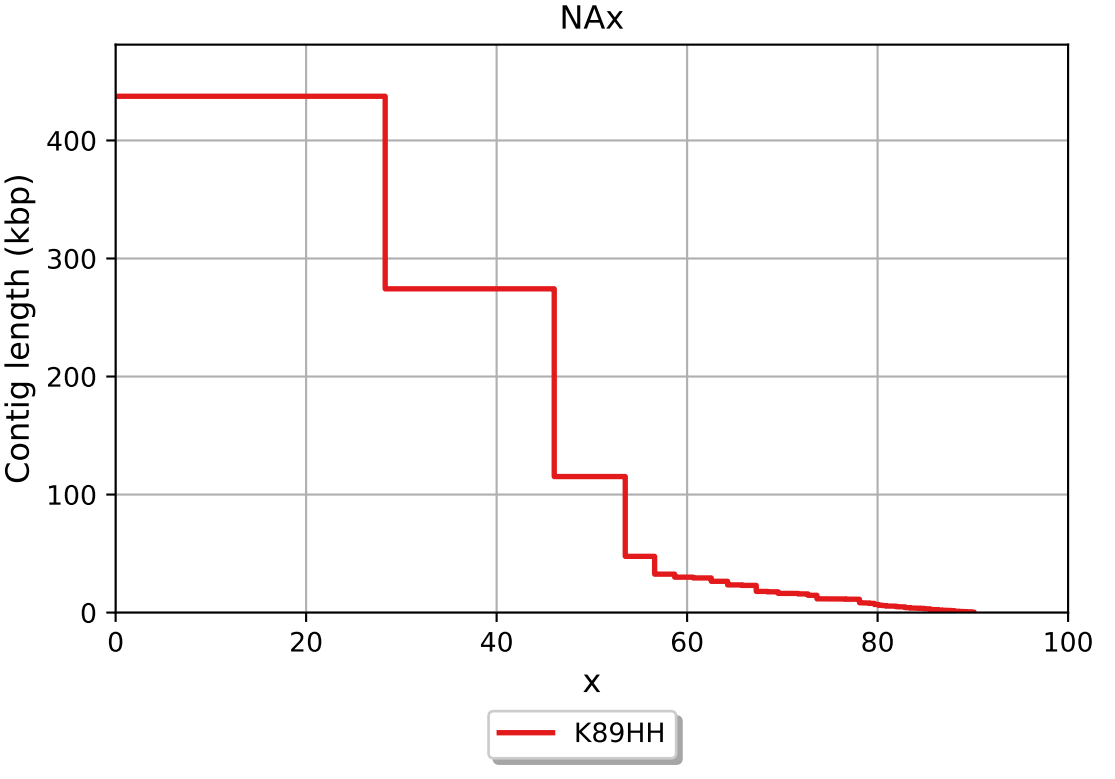

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
K89HH
Reference

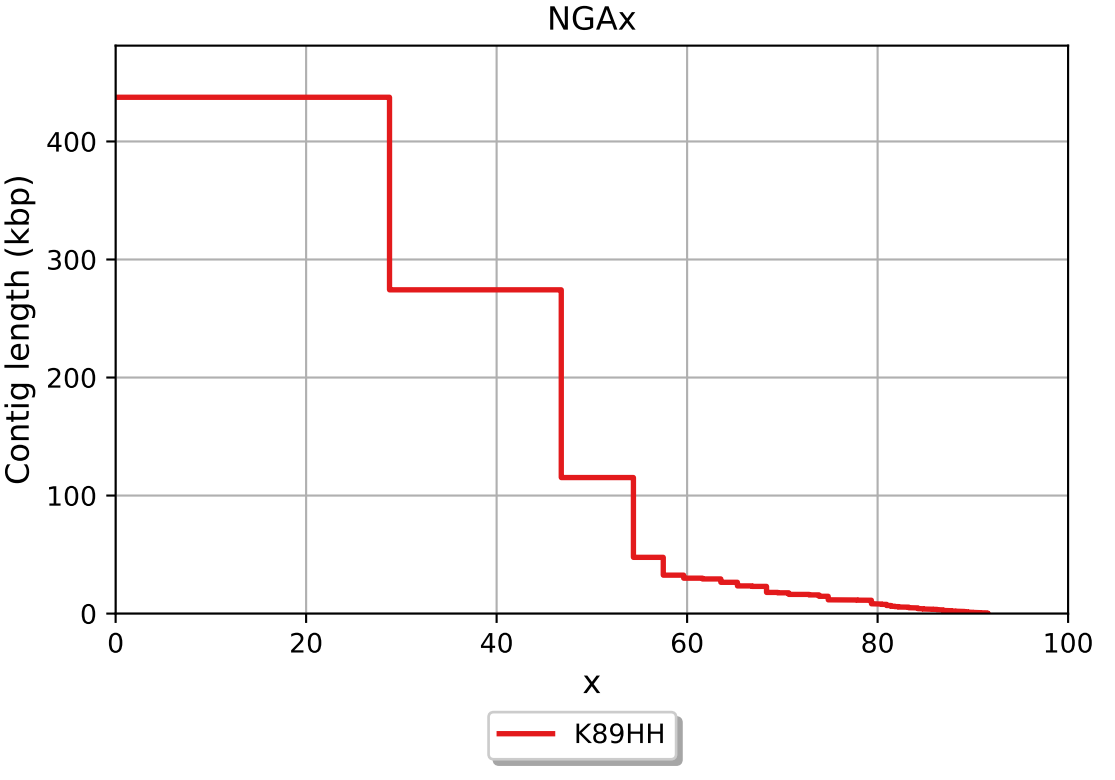

K89HH GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
K89HH

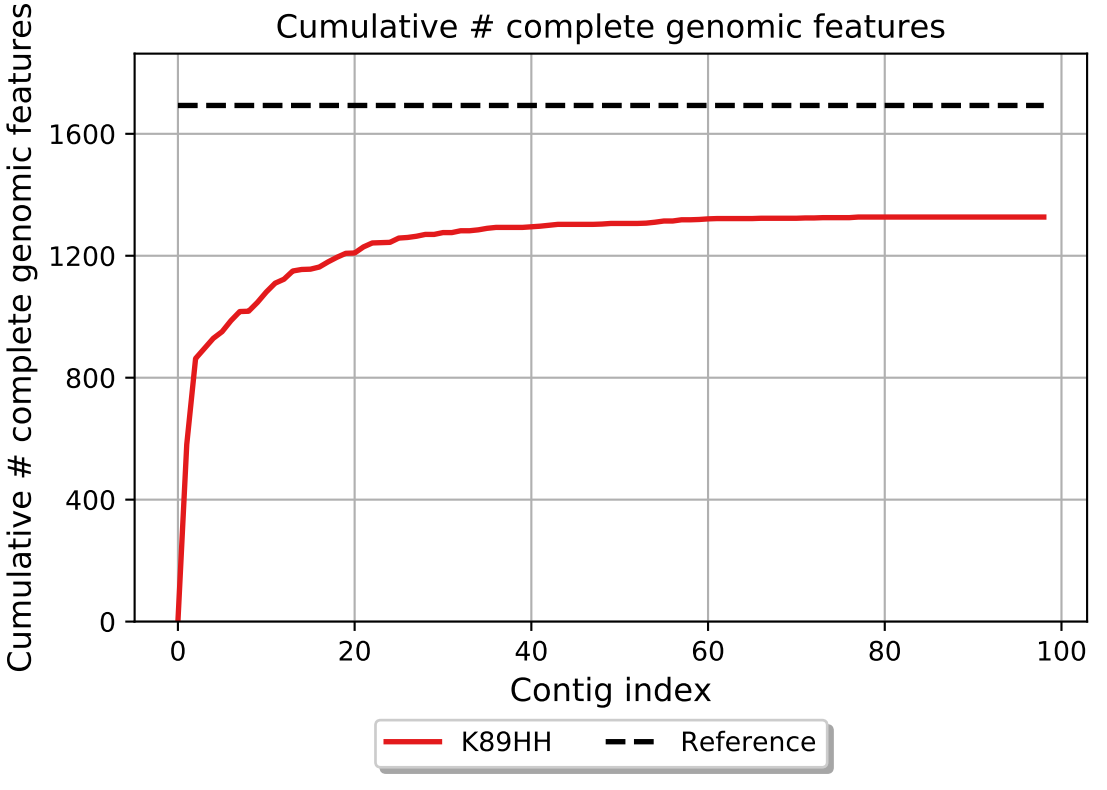

Misassemblies
20
16
12
8
4
0
K89HH
relocations
translocations
inversions

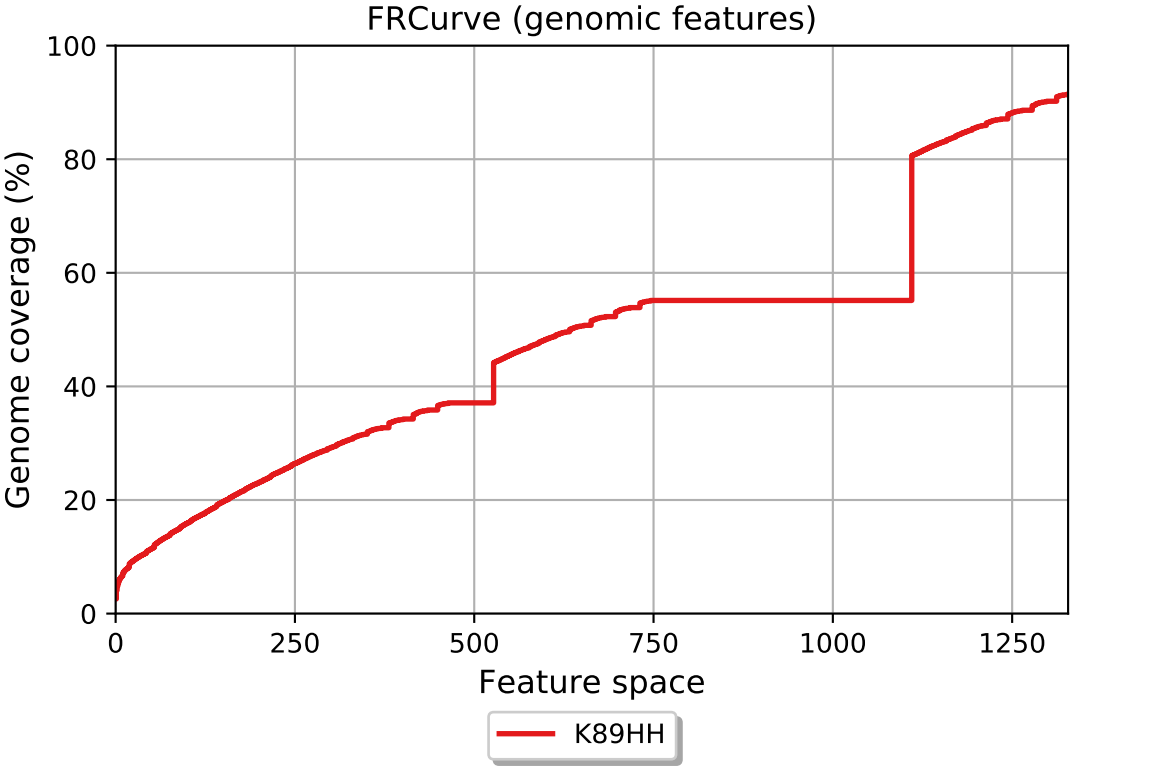

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
K89HH


Cumulative length (aligned contigs)
Cumulative length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
Contig index
K89HH
Reference


NAx
Contig length (kbp)
400
300
200
100
0
0
20
40
60
80
100
x
K89HH


NGAx
Contig length (kbp)
0
100
200
300
400
0
20
40
60
80
100
x
K89HH


Cumulative # complete genomic features
Cumulative # complete genomic features
0
400
800
1200
1600
0
20
40
60
80
100
Contig index
K89HH
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
250
500
750
1000
1250
Feature space
K89HH