Report

	E2348-69
# contigs (>= 0 bp)	2442
# contigs (>= 1000 bp)	156
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	5791762
Total length (>= 1000 bp)	5047942
Total length (>= 5000 bp)	4913543
Total length (>= 10000 bp)	4845903
Total length (>= 25000 bp)	4552658
Total length (>= 50000 bp)	3757801
# contigs	395
Largest contig	300313
Total length	5202412
Reference length	5046283
GC (%)	50.52
Reference GC (%)	50.52
N50	135065
NG50	135065
N90	20674
NG90	26342
auN	137006.7
auNG	141245.6
L50	13
LG50	13
L90	53
LG90	47
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	32395
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# unaligned contigs	303 + 1 part
Unaligned length	278081
Genome fraction (%)	97.577
Duplication ratio	1.000
# N's per 100 kbp	6.21
# mismatches per 100 kbp	1.18
# indels per 100 kbp	0.24
Largest alignment	300313
Total aligned length	4924201
NA50	135065
NGA50	135065
NA90	20674
NGA90	26342
auNA	136859.7
auNGA	141094.0
LA50	13
LGA50	13
LA90	53
LGA90	47

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

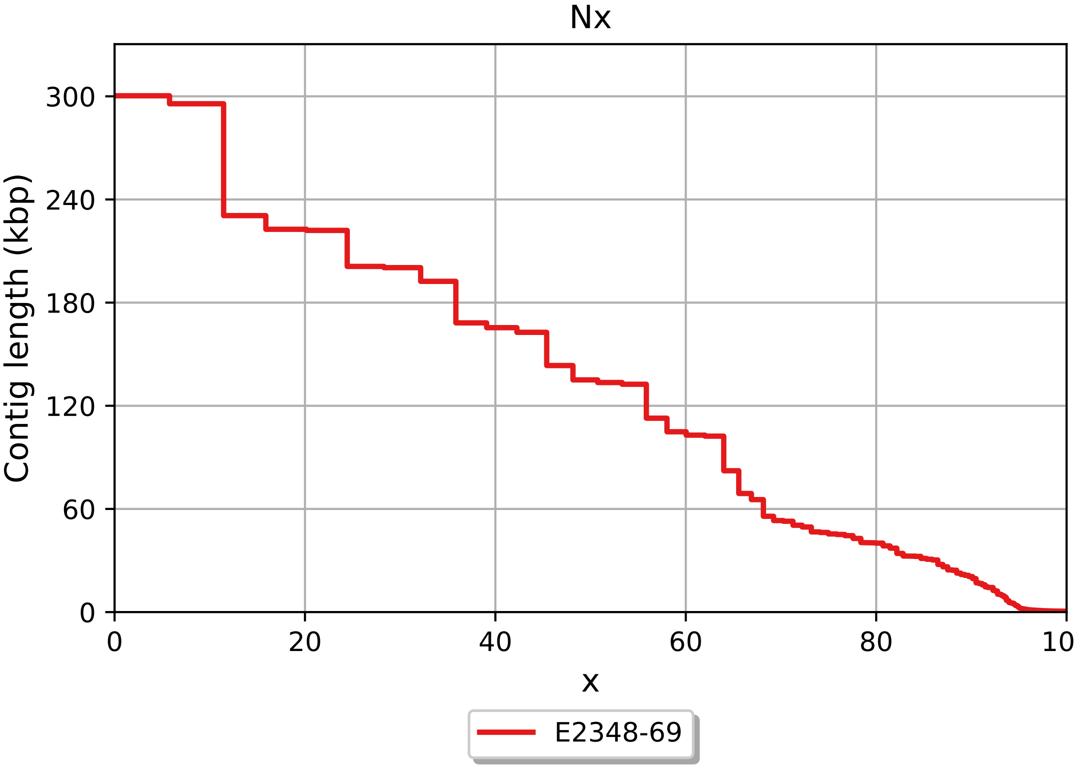
	E2348-69
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	32395
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# mismatches	58
# indels	12
# indels (<= 5 bp)	4
# indels (> 5 bp)	8
Indels length	995

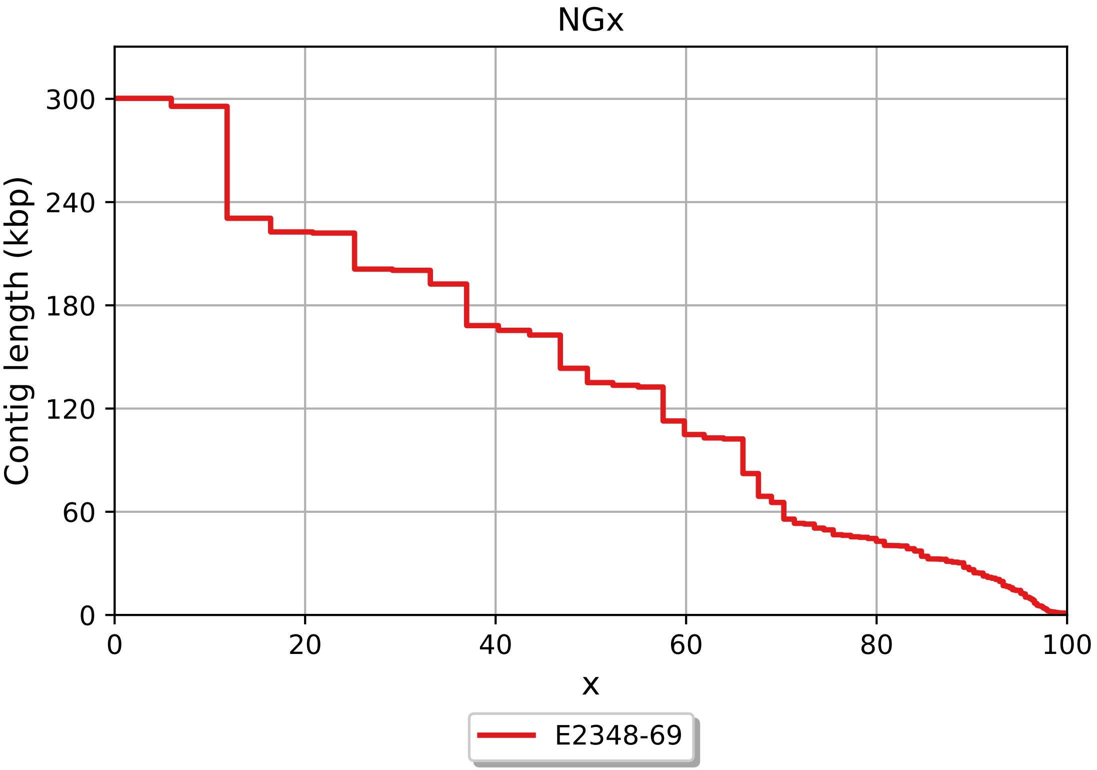
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

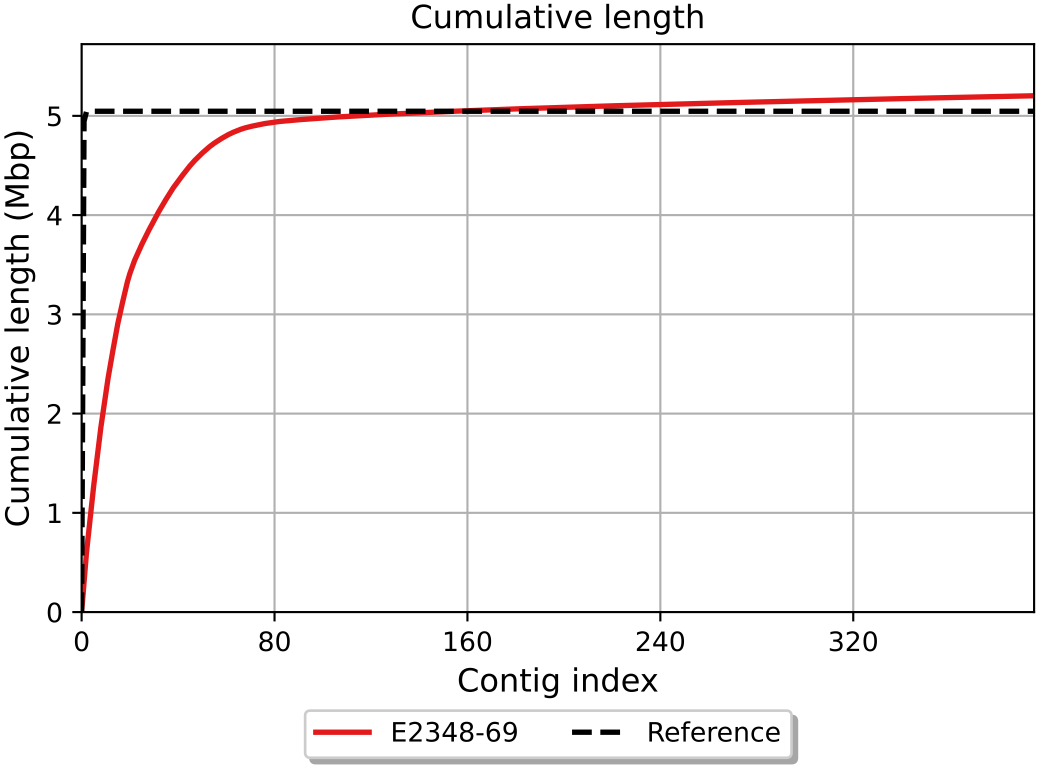
Unaligned report

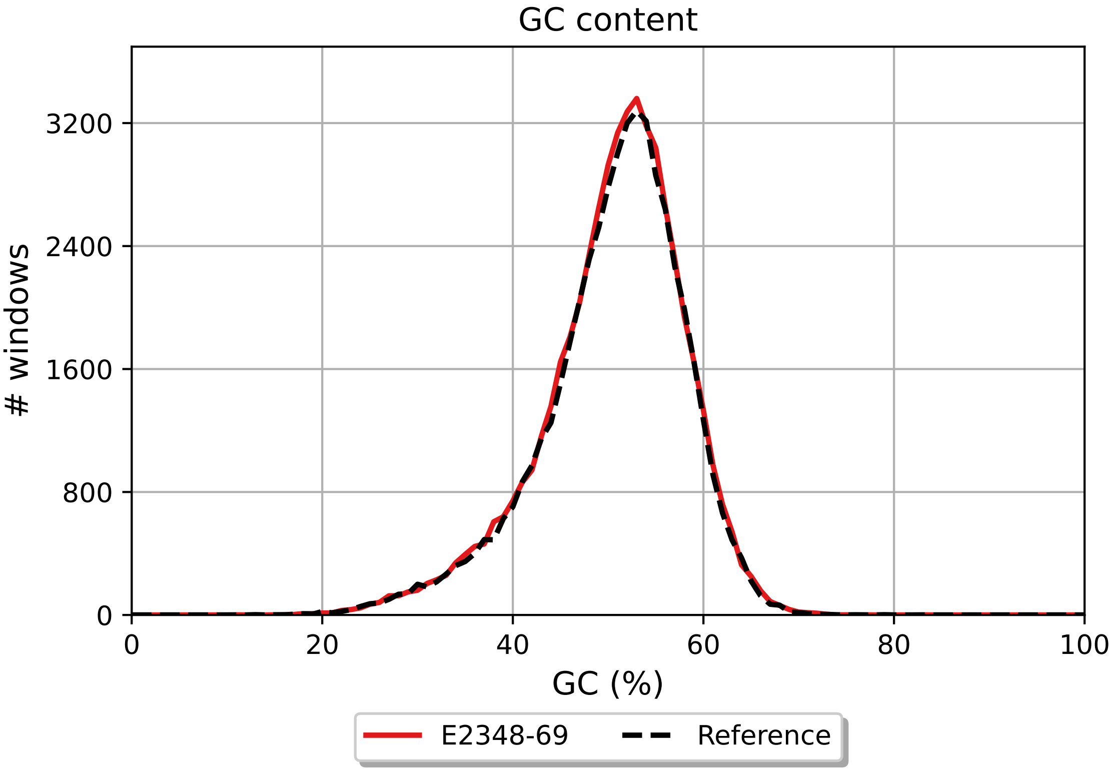
	E2348-69
# fully unaligned contigs	303
Fully unaligned length	276691
# partially unaligned contigs	1
Partially unaligned length	1390
# N's	323

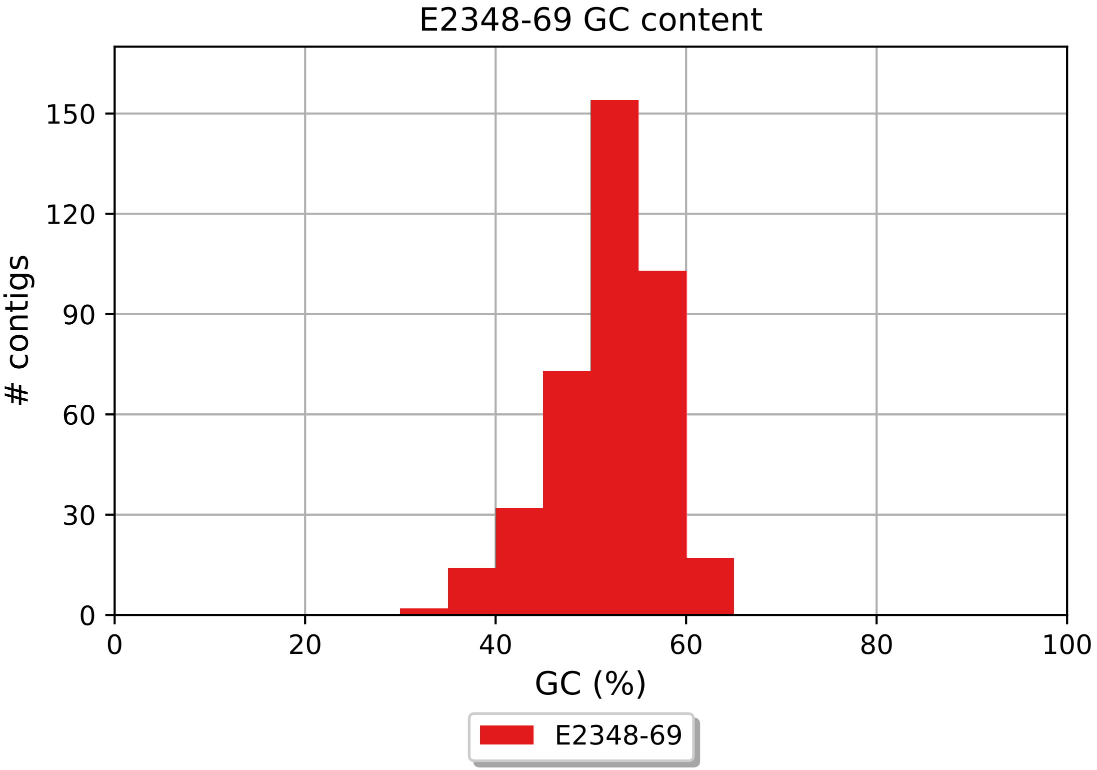
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

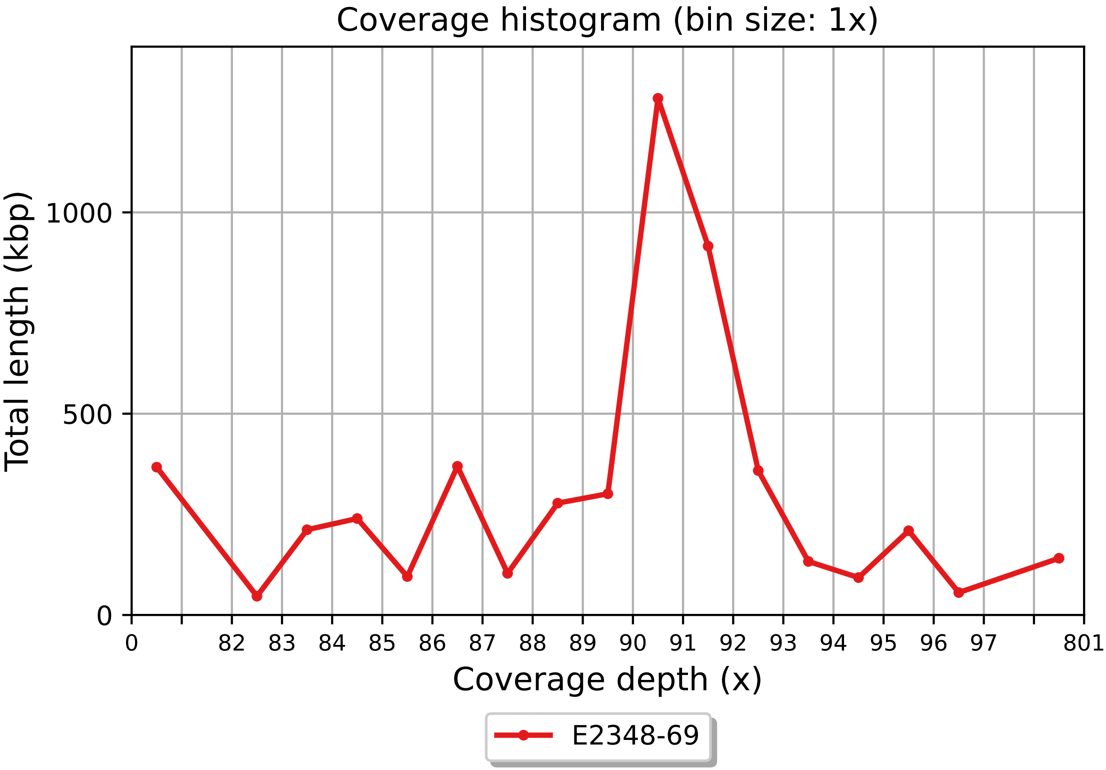

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
E2348-69

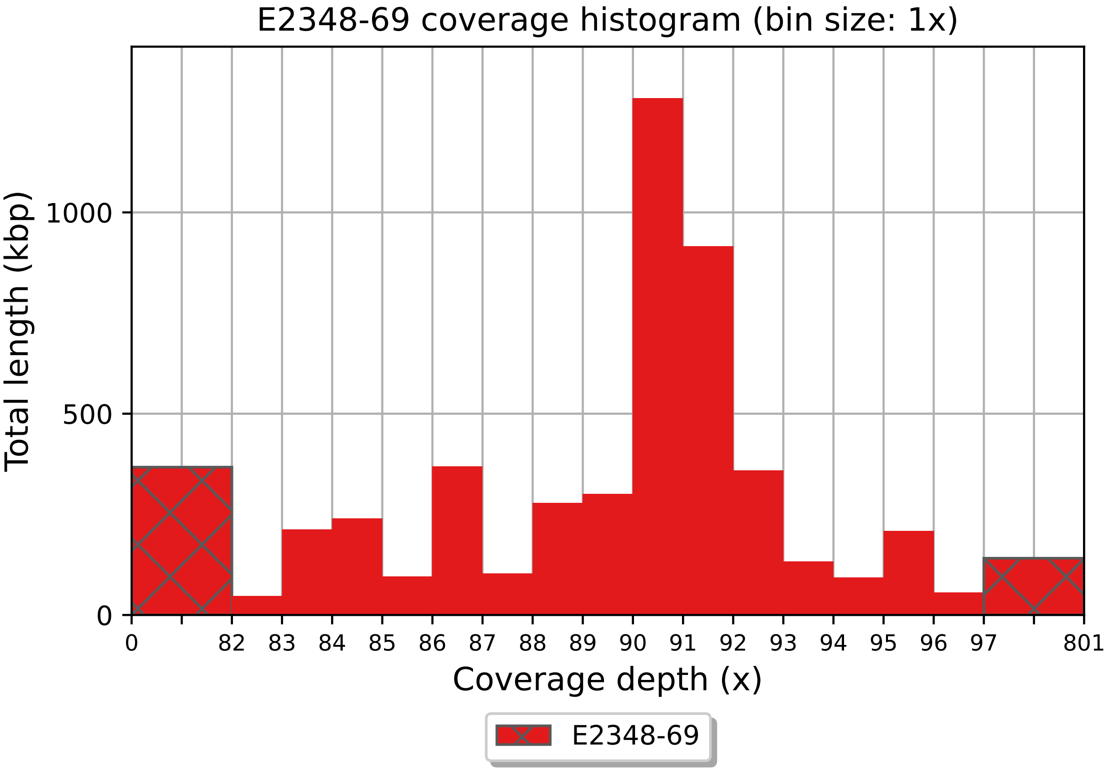

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
E2348-69

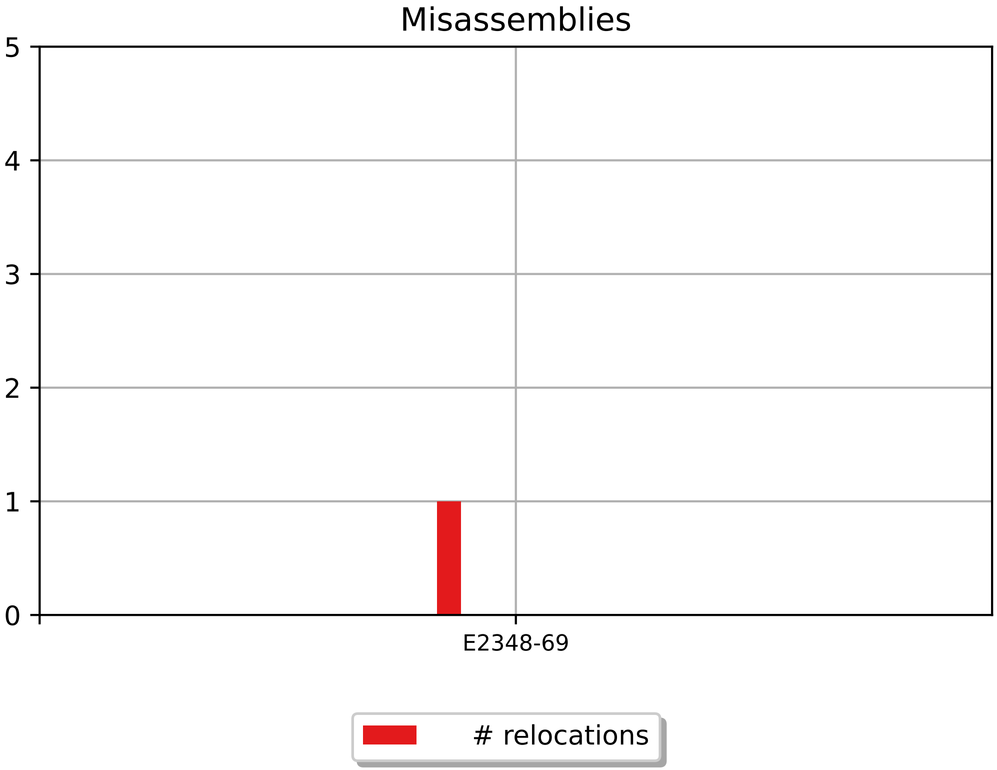

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
80
160
240
320
Contig index
E2348-69
Reference

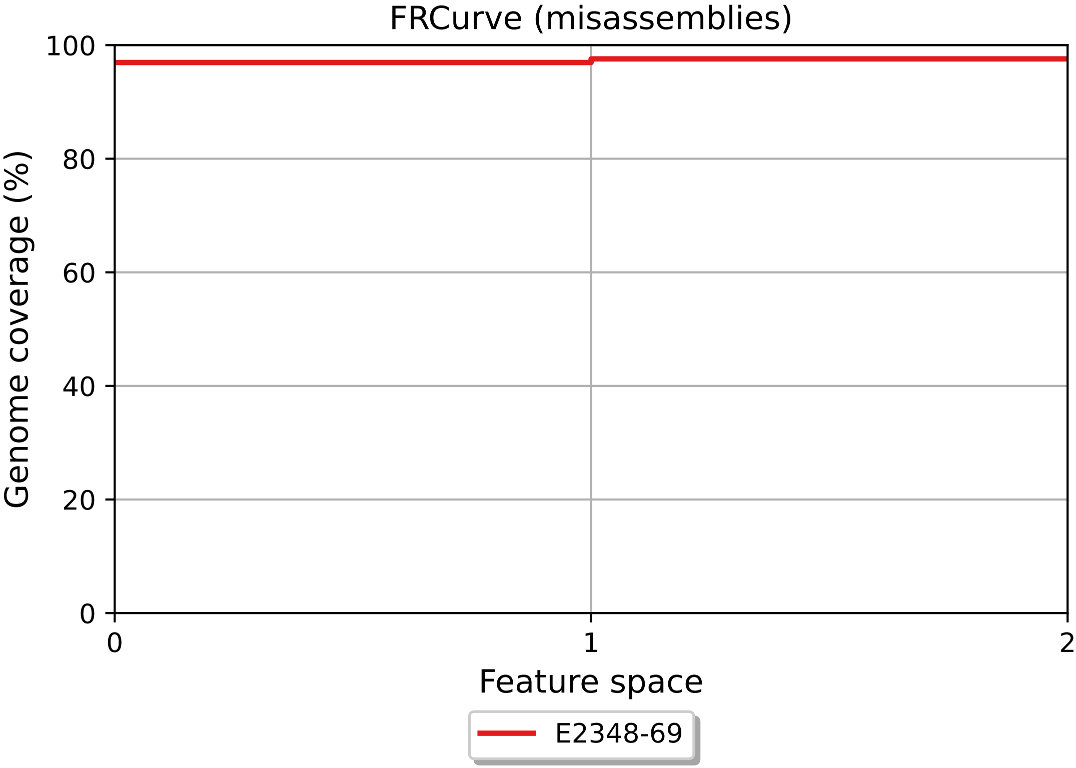

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
E2348-69
Reference

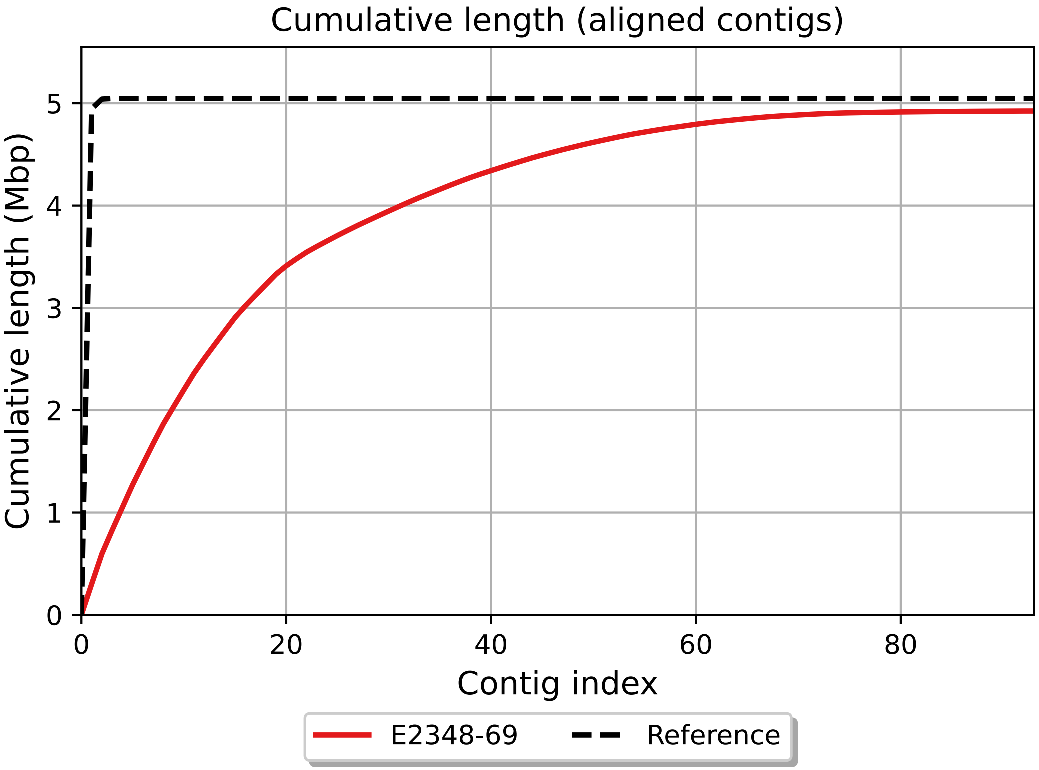

E2348-69 GC content
contigs
150
120
90
60
30
0
0
20
40
60
80
100
GC (%)
E2348-69

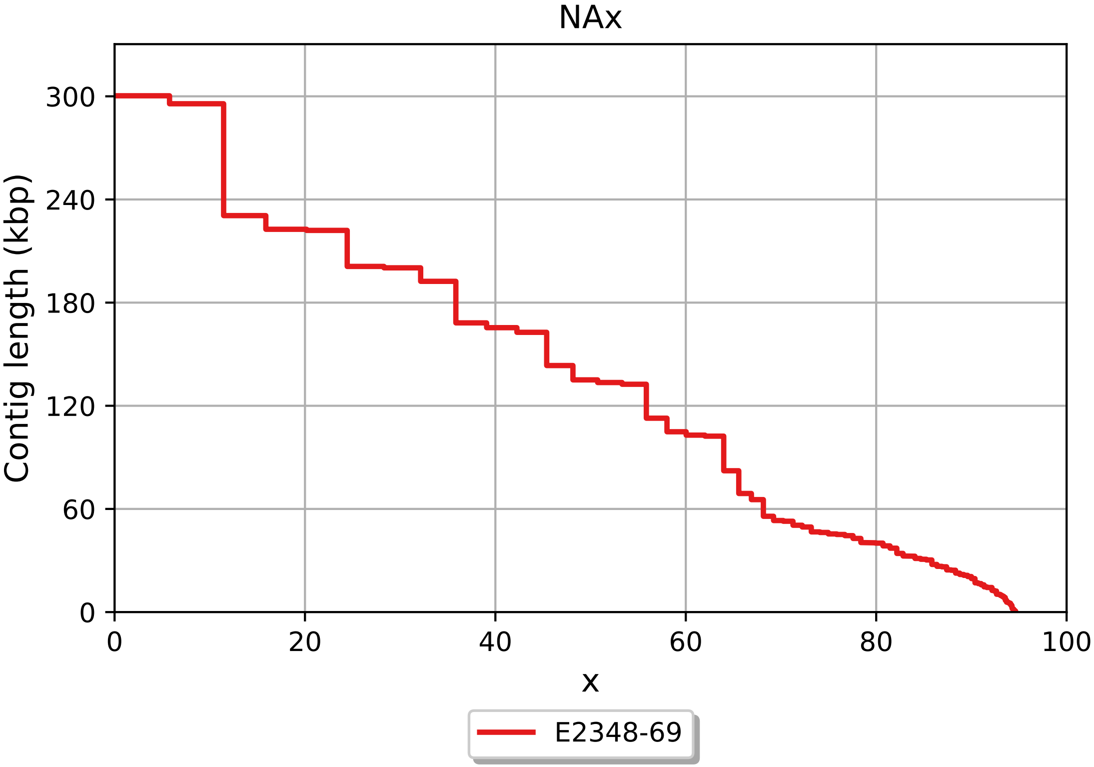

Coverage histogram (bin size: 1x)
Total length (kbp)
0
500
1000
0
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
801
Coverage depth (x)
E2348-69

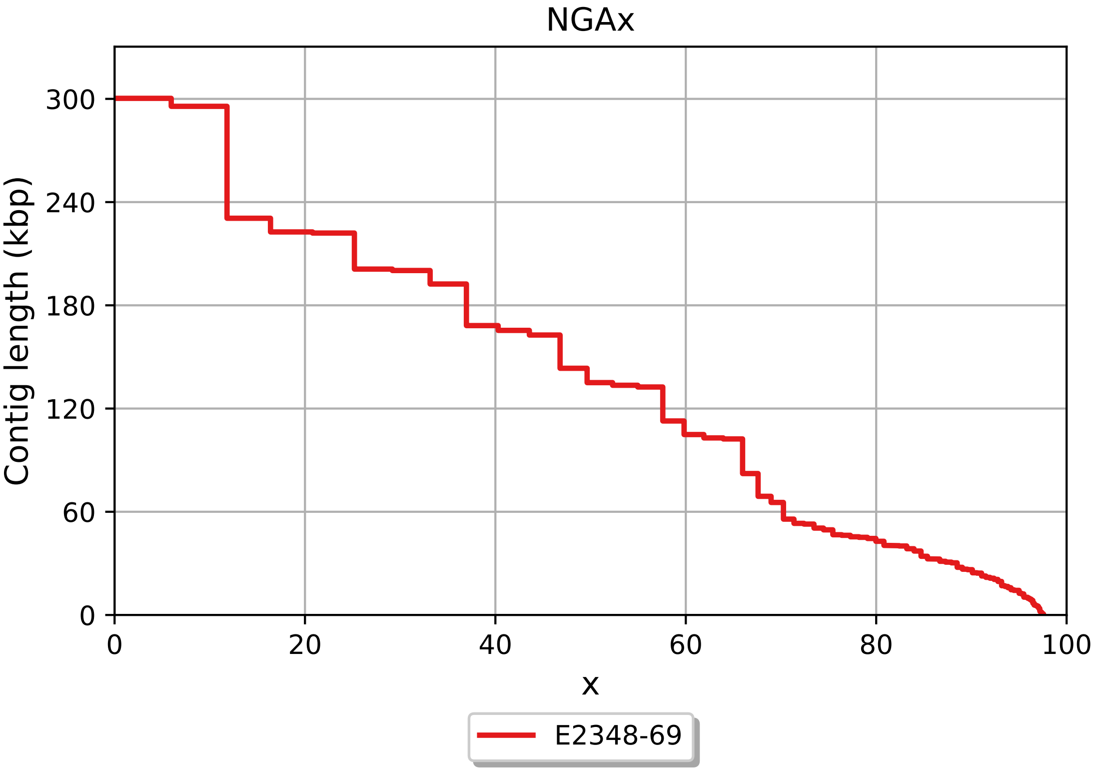

E2348-69 coverage histogram (bin size: 1x)
Total length (kbp)
0
500
1000
0
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
801
Coverage depth (x)
E2348-69


Misassemblies
5
4
3
2
1
0
E2348-69
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
E2348-69


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
20
40
60
80
Contig index
E2348-69
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
E2348-69


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
E2348-69