Report

	33_38.30
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	163613
Total length (>= 5000 bp)	115471
Total length (>= 10000 bp)	83631
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	30
Largest contig	18870
Total length	165907
Reference length	29835
GC (%)	37.69
Reference GC (%)	38.02
N50	10622
NG50	18870
N75	4527
NG75	13858
L50	6
LG50	1
L75	12
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.478
Duplication ratio	5.649
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.84
# indels per 100 kbp	40.86
Largest alignment	18870
Total aligned length	165885
NA50	10621
NGA50	18870
NA75	4526
NGA75	13857
LA50	6
LGA50	1
LA75	12
LGA75	2

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

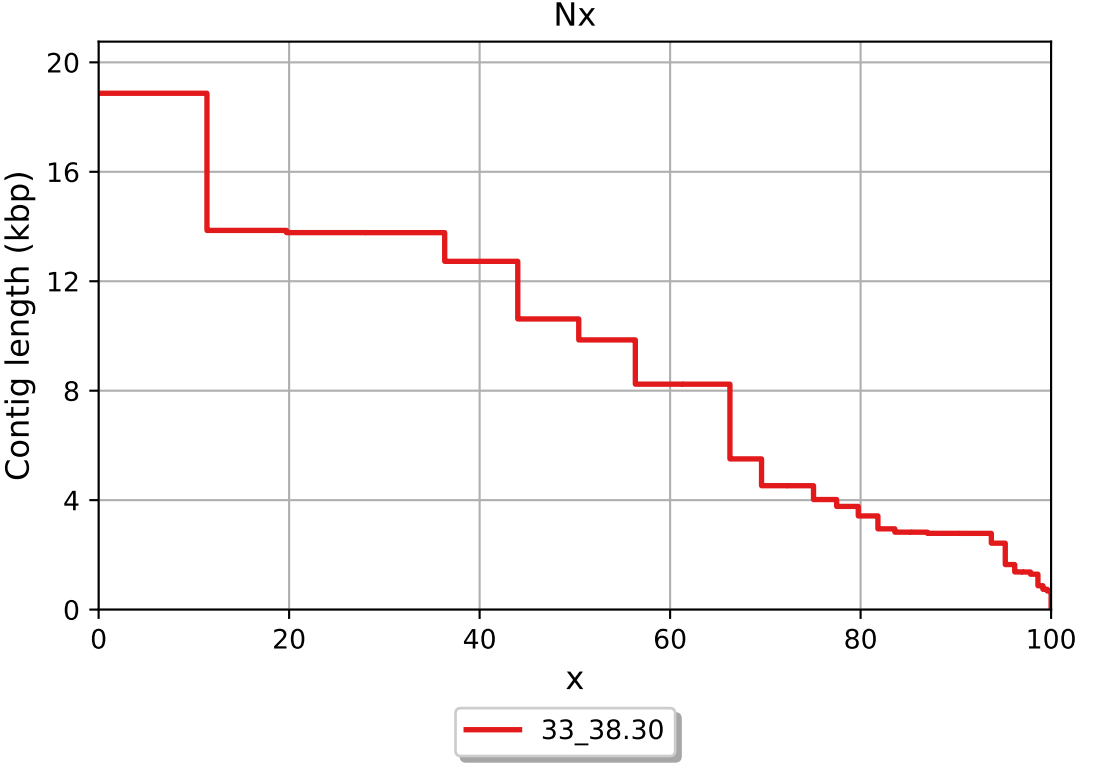
	33_38.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	7
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	12

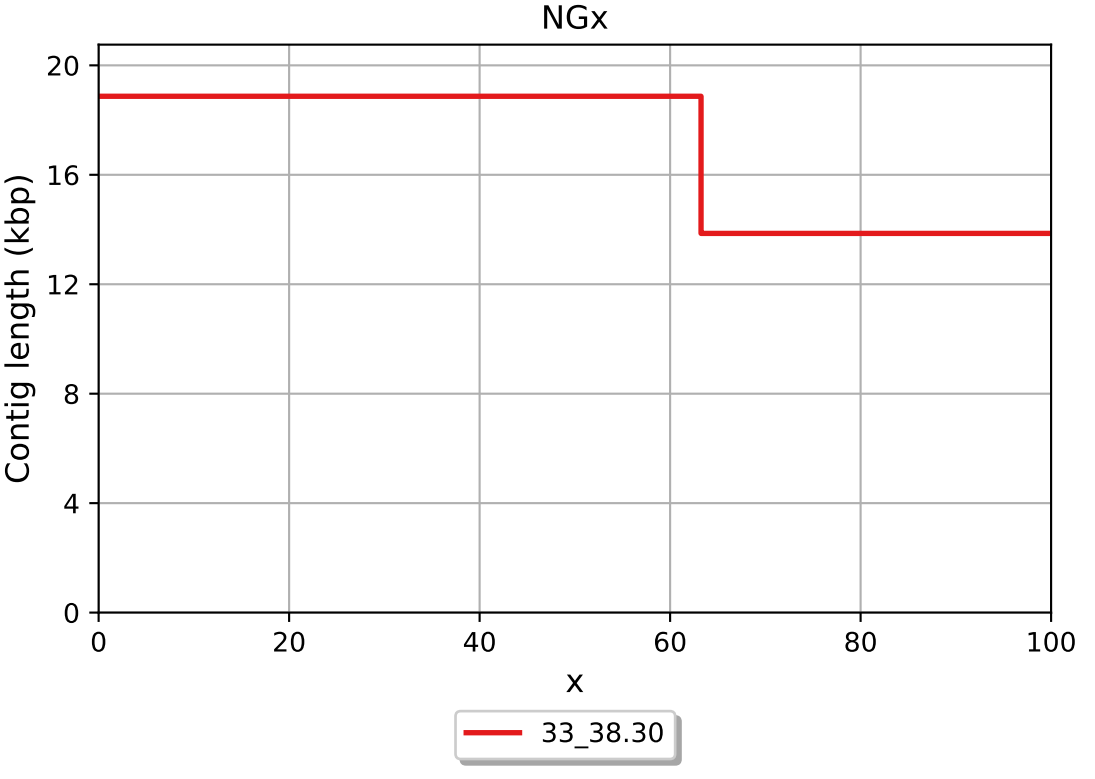
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

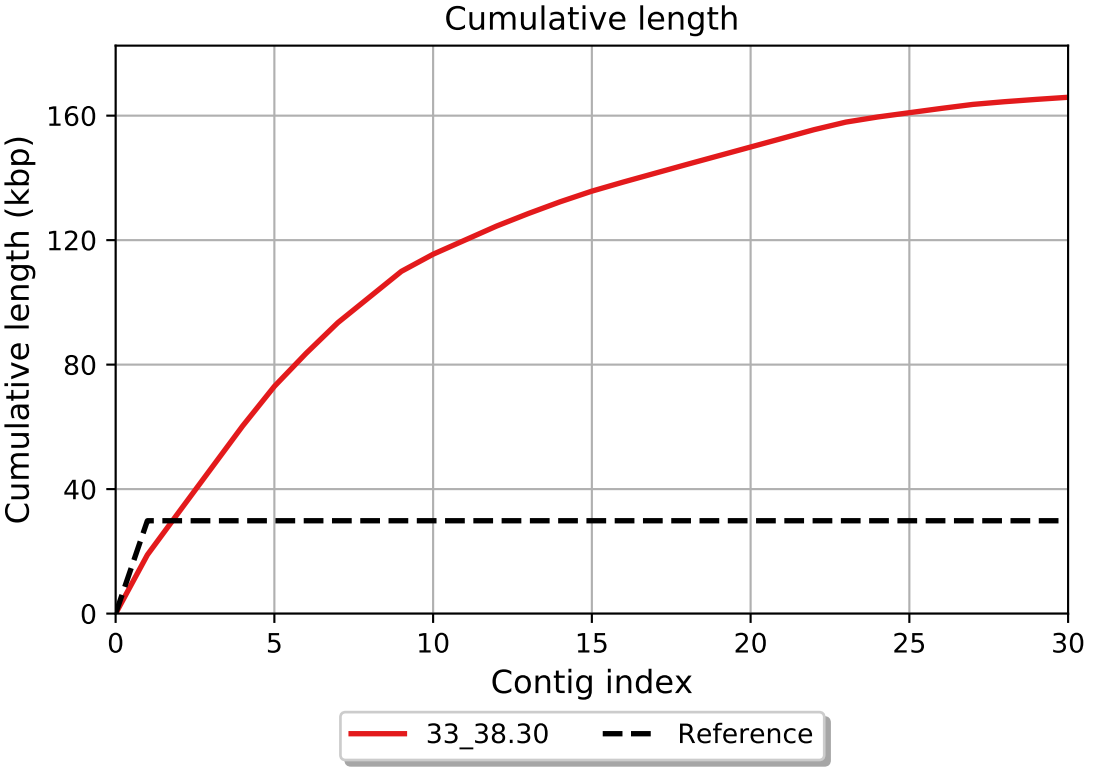
Unaligned report

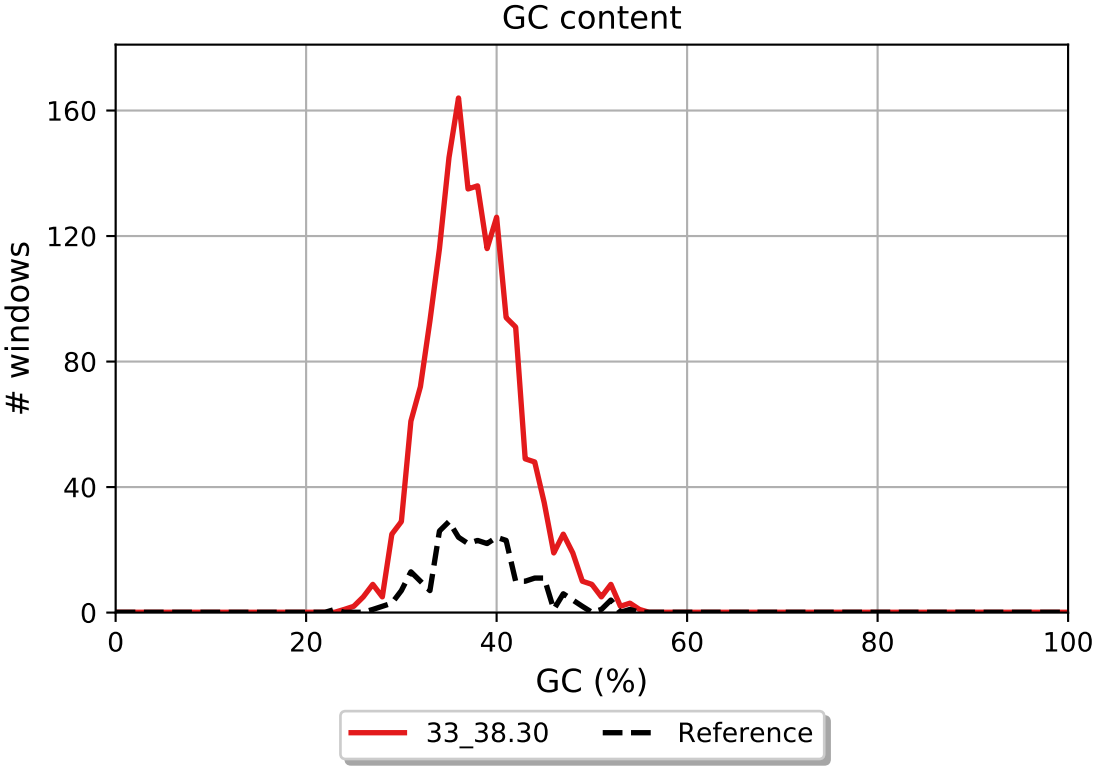
	33_38.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

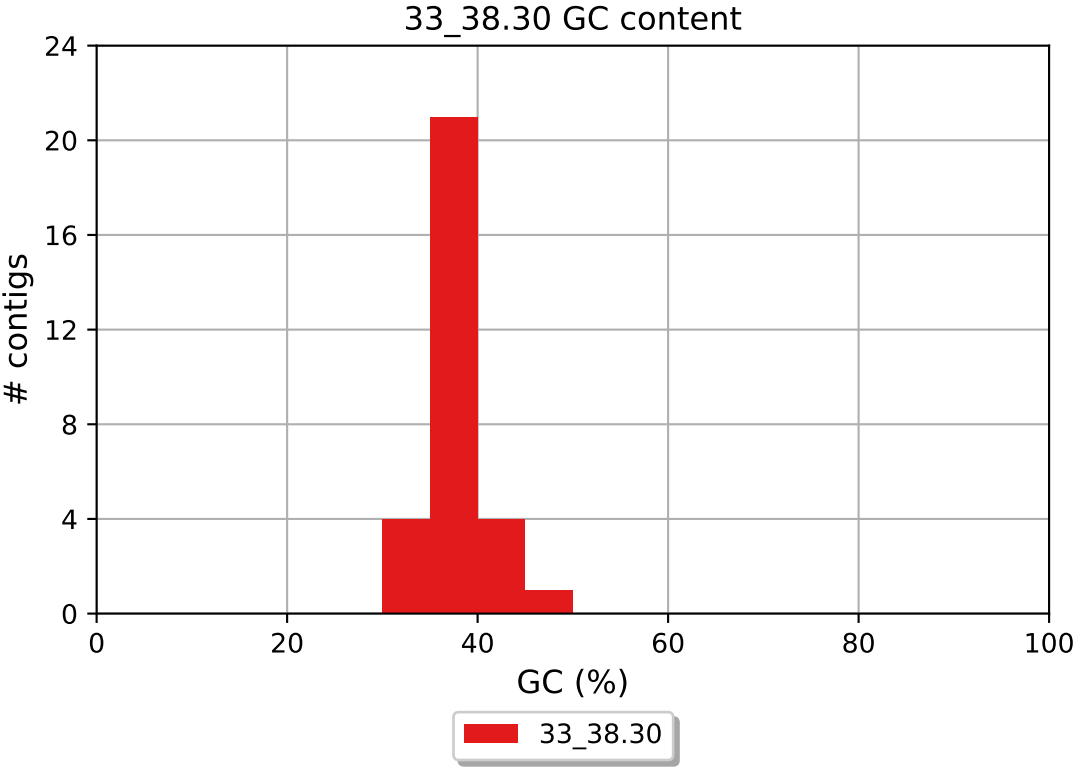
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

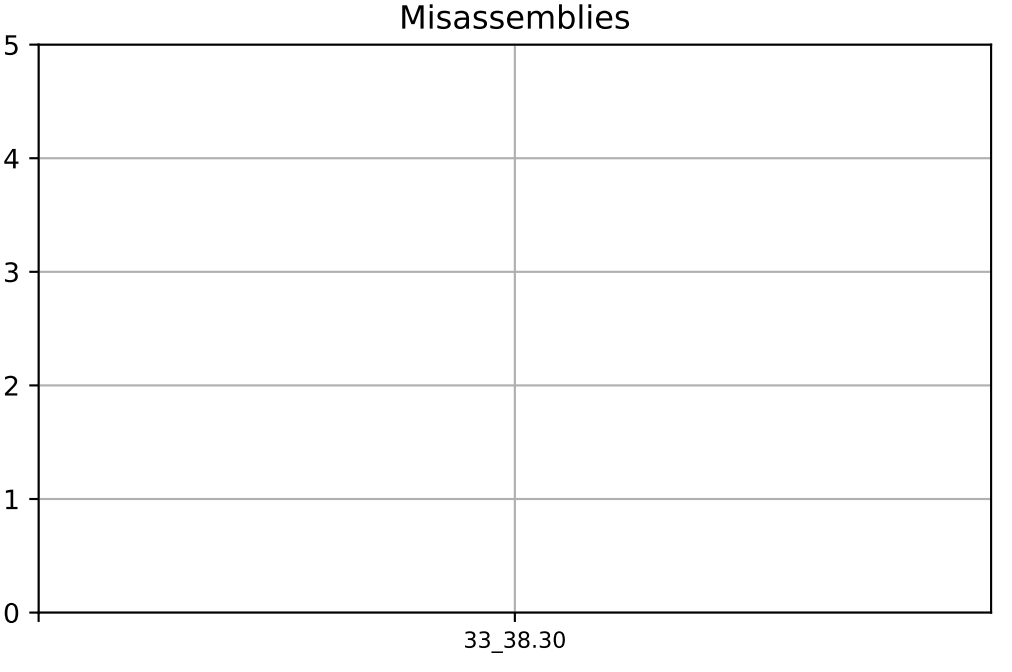

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
33_38.30

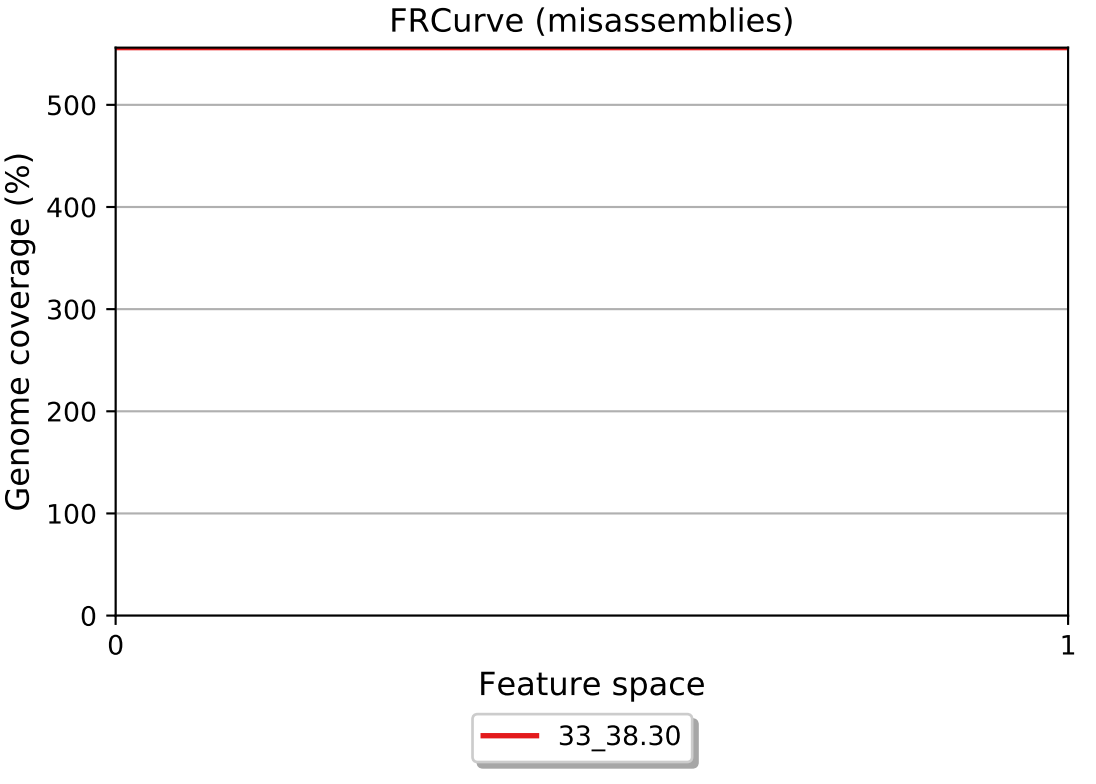

NGx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
33_38.30

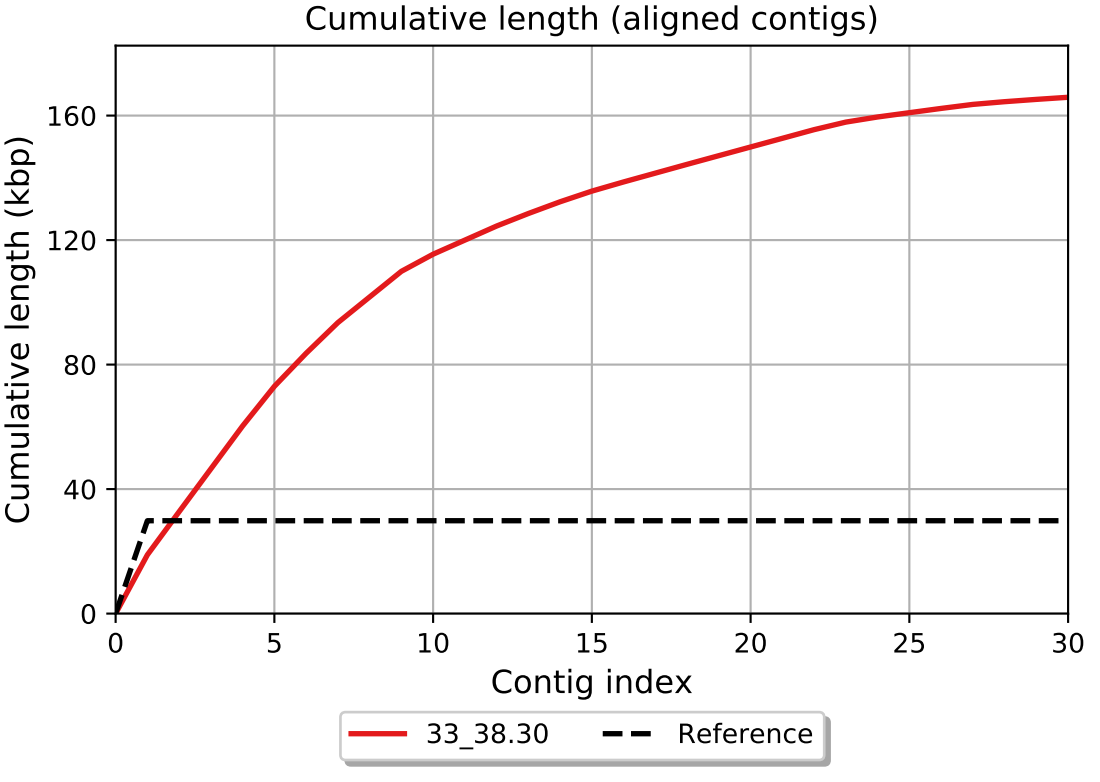

Cumulative length
Cumulative length (kbp)
0
40
80
120
160
0
5
10
15
20
25
30
Contig index
33_38.30
Reference

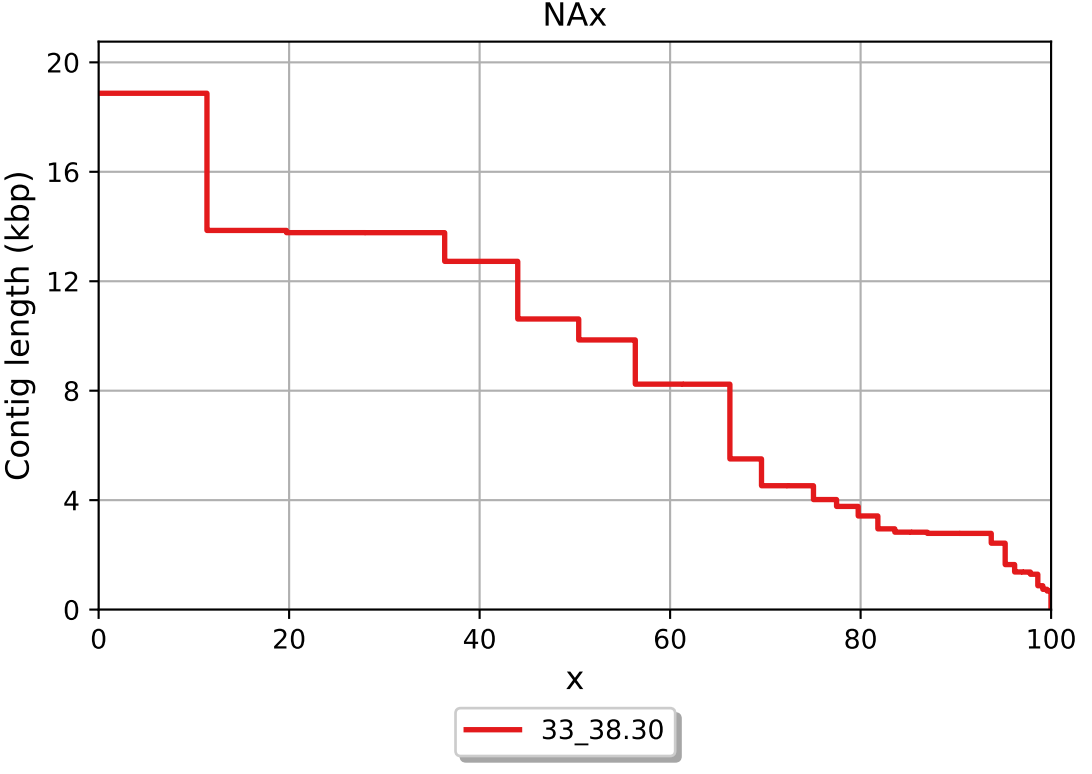

GC content
windows
GC (%)
0
40
80
120
160
0
20
40
60
80
100
33_38.30
Reference

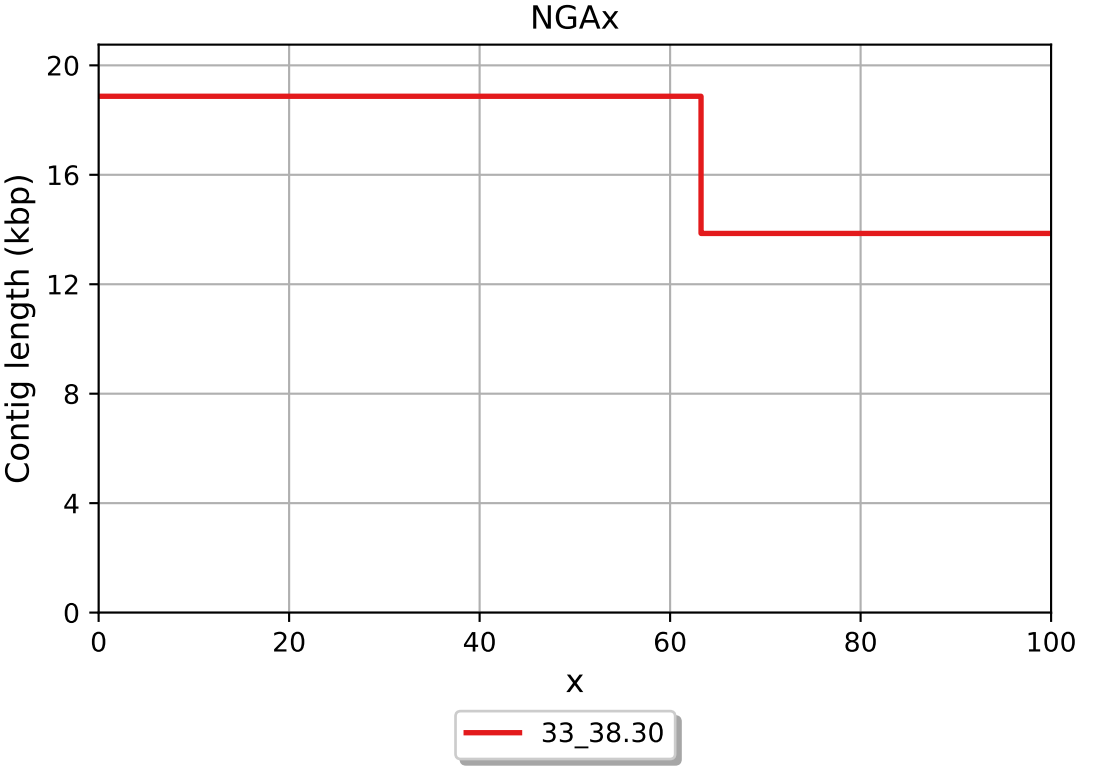

33_38.30 GC content
contigs
GC (%)
0
4
8
12
16
20
24
0
20
40
60
80
100
33_38.30


Misassemblies
5
4
3
2
1
0
33_38.30


FRCurve (misassemblies)
Genome coverage (%)
500
400
300
200
100
0
0
1
Feature space
33_38.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
40
80
120
160
0
5
10
15
20
25
30
Contig index
33_38.30
Reference


NAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
33_38.30


NGAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
33_38.30