Report

	33_0.30
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	96900
Total length (>= 5000 bp)	68306
Total length (>= 10000 bp)	44523
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	23
Largest contig	11289
Total length	99383
Reference length	29903
GC (%)	37.74
Reference GC (%)	37.97
N50	6577
NG50	11288
N75	2932
NG75	11288
L50	5
LG50	2
L75	10
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 (%)	97.820
Duplication ratio	3.398
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.54
# indels per 100 kbp	34.19
Largest alignment	11289
Total aligned length	99368
NA50	6576
NGA50	11288
NA75	2932
NGA75	11288
LA50	5
LGA50	2
LA75	10
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

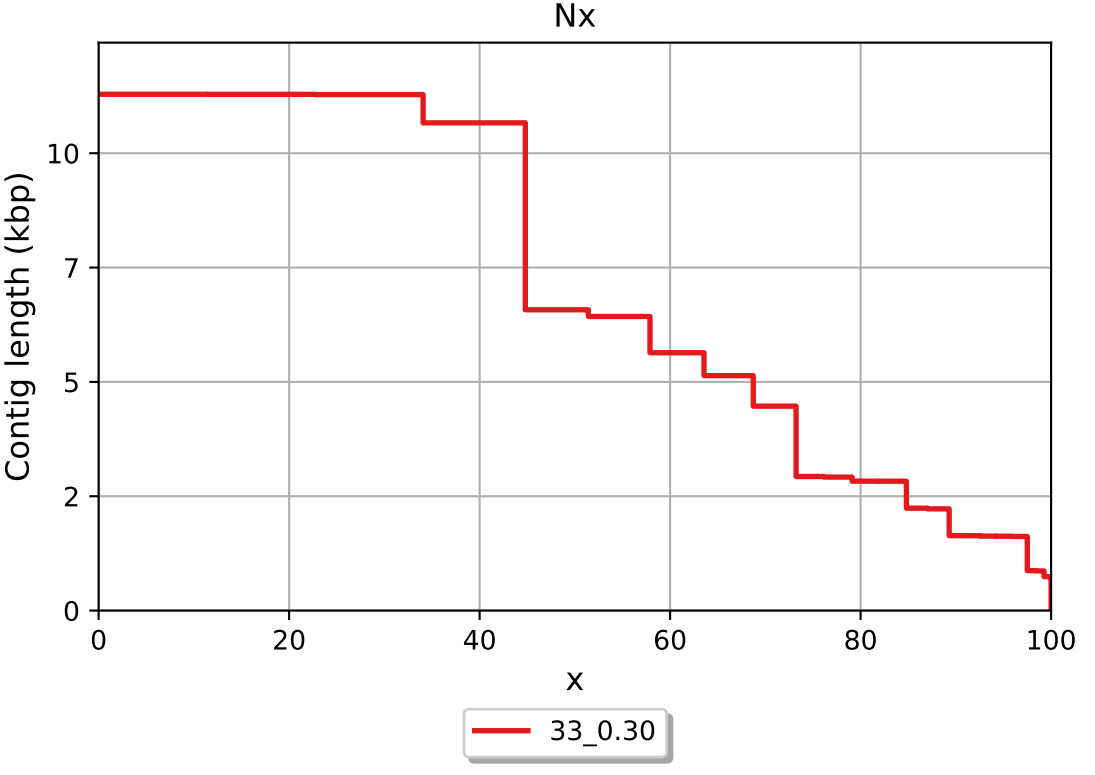
	33_0.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	18
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	10

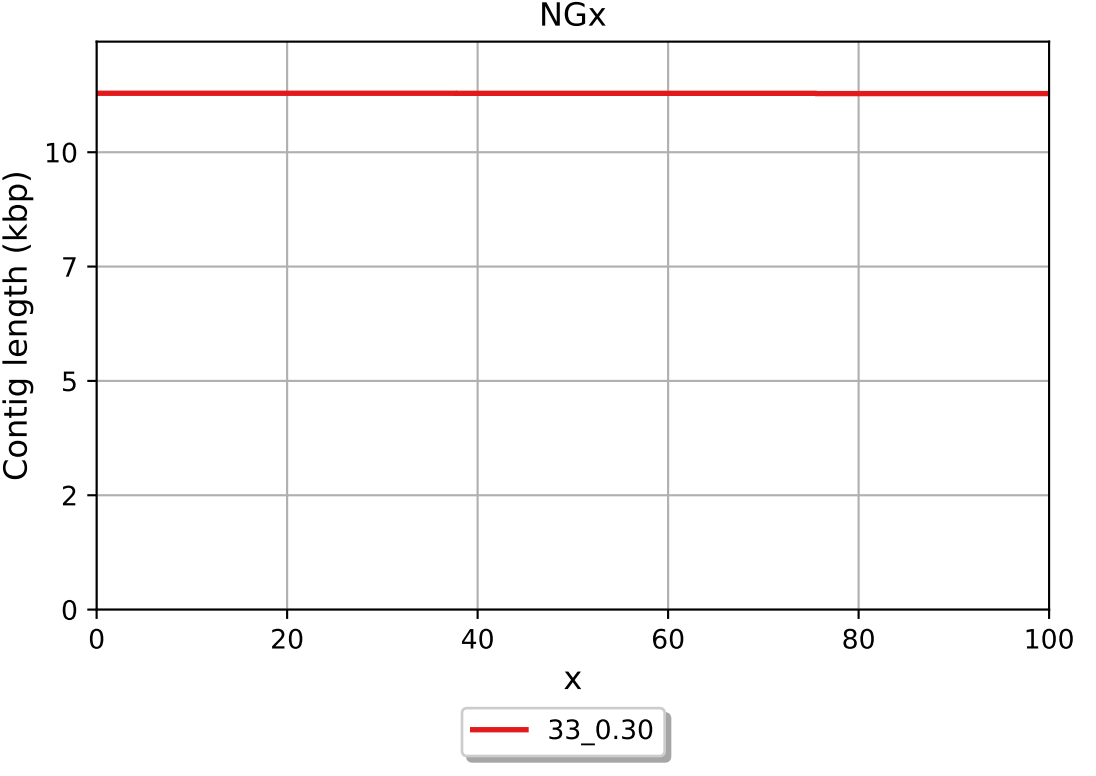
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

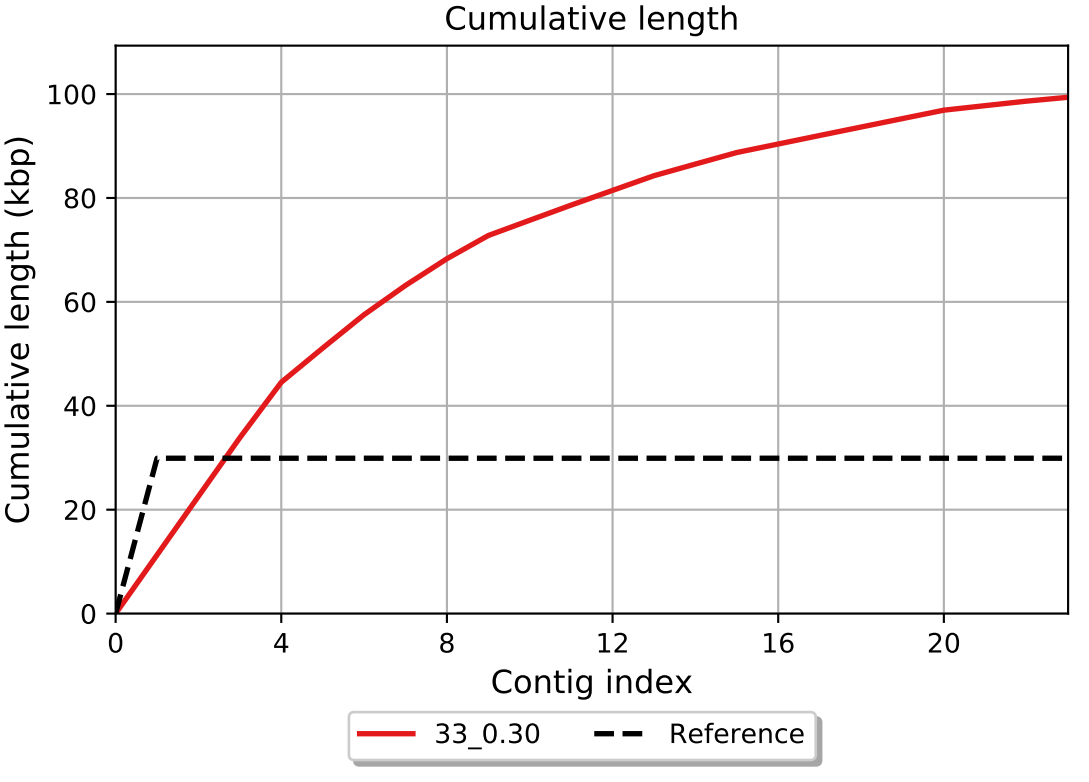
Unaligned report

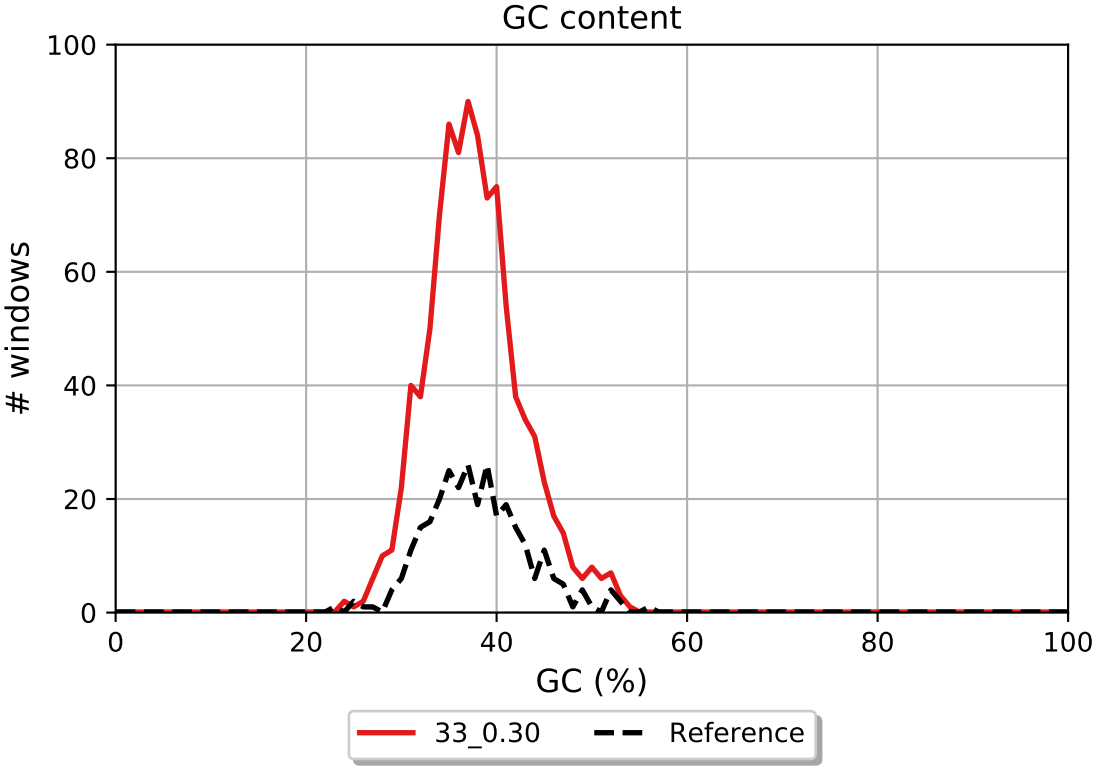
	33_0.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

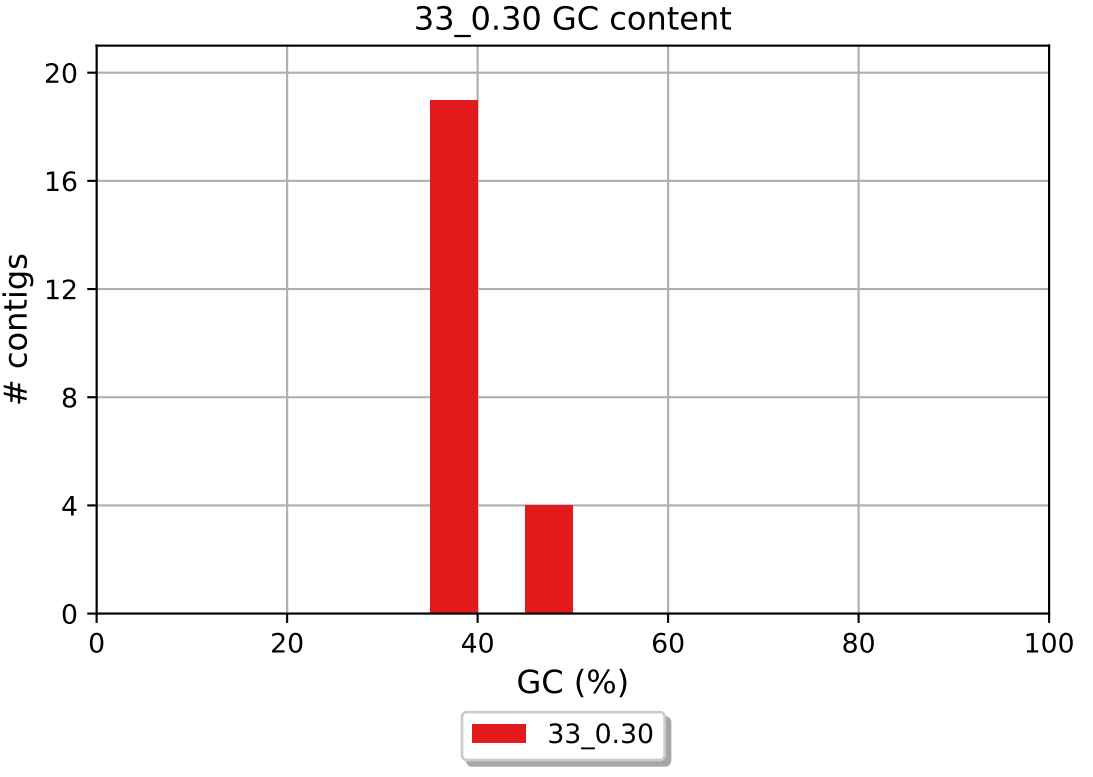
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

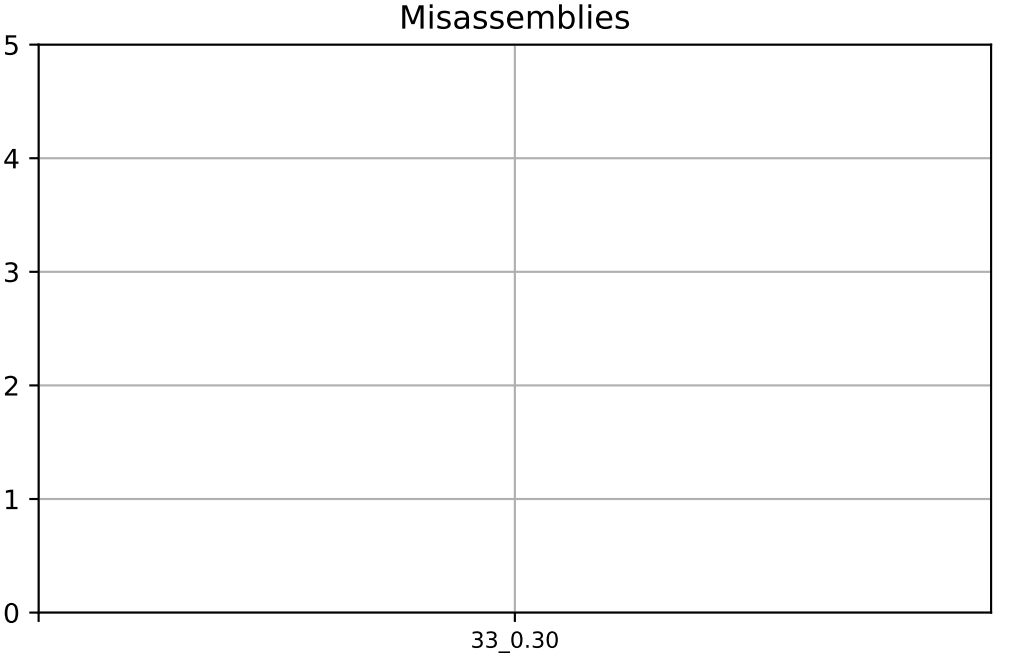

Nx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
33_0.30

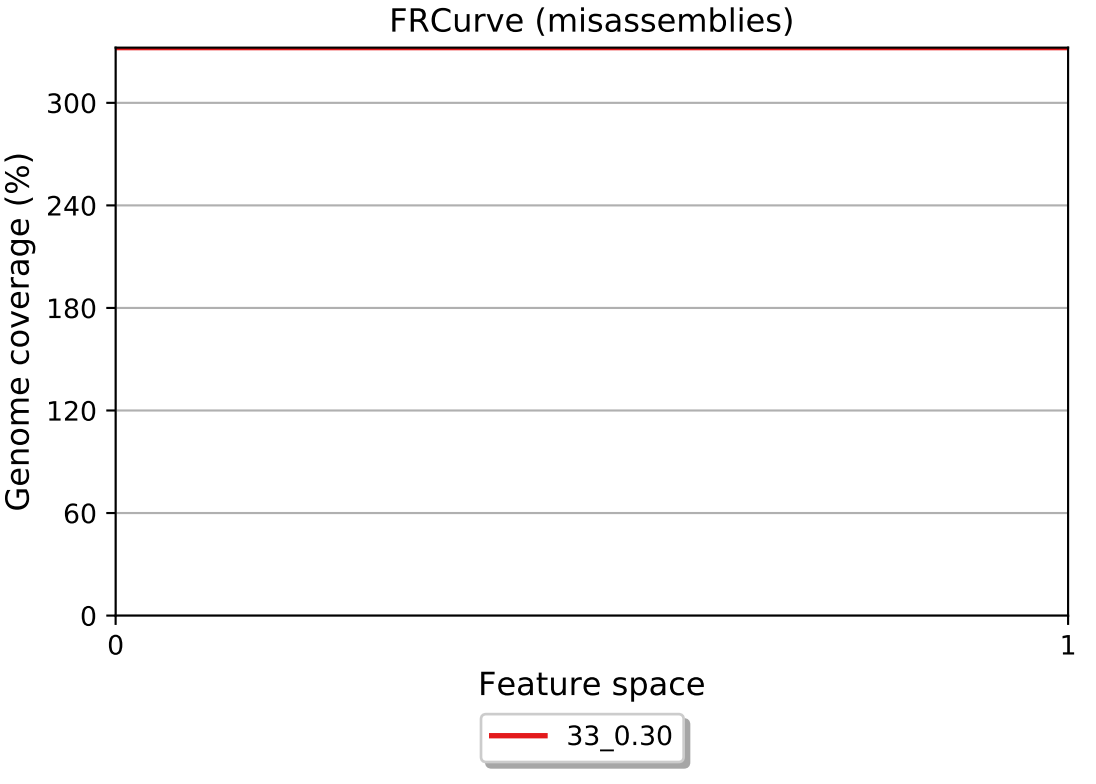

NGx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
33_0.30

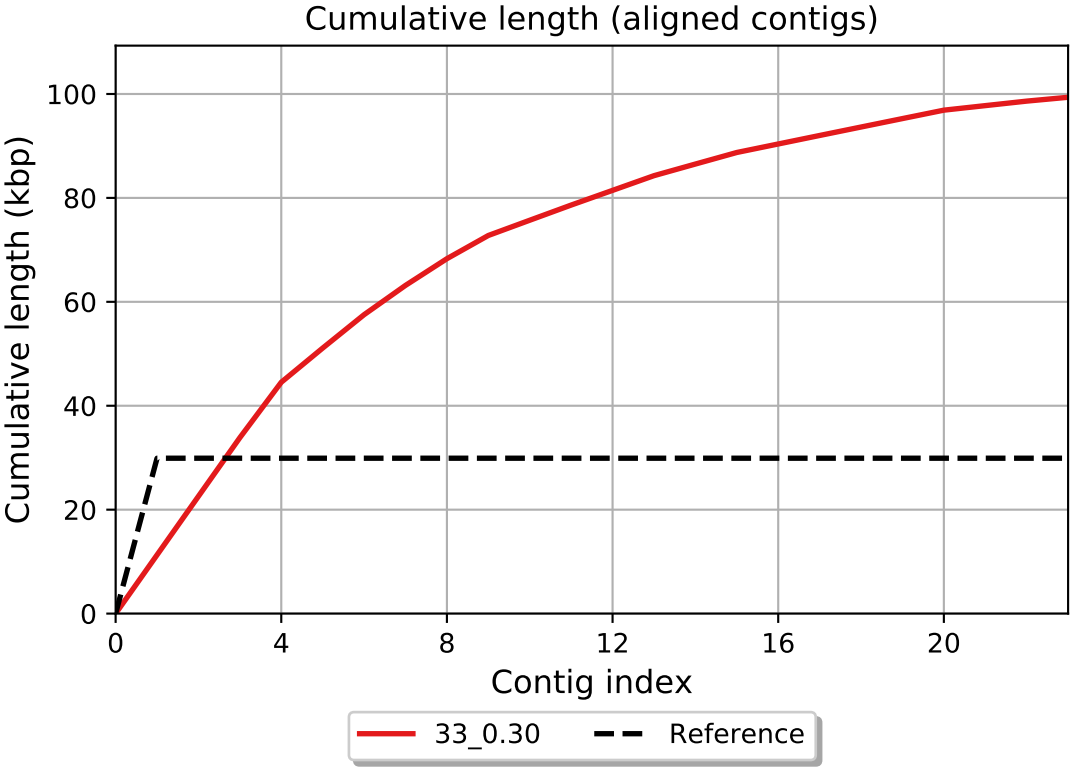

Cumulative length
Cumulative length (kbp)
100
80
60
40
20
0
0
4
8
12
16
20
Contig index
33_0.30
Reference

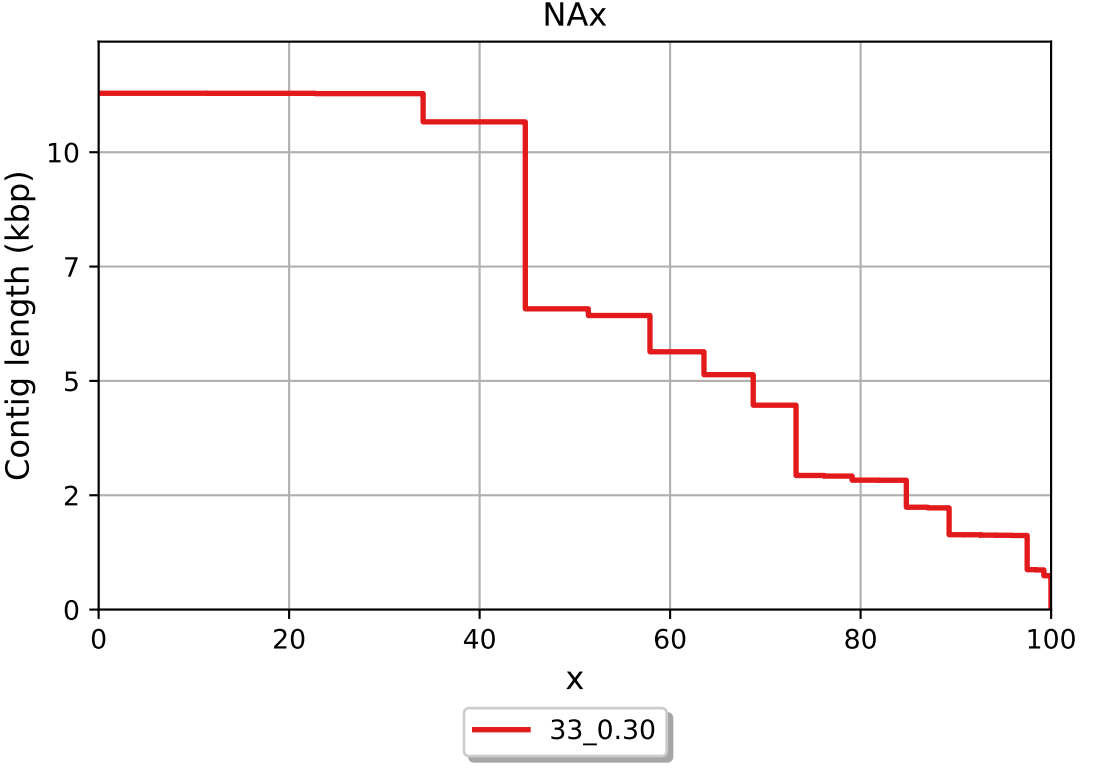

GC content
windows
GC (%)
0
20
40
60
80
100
33_0.30
Reference

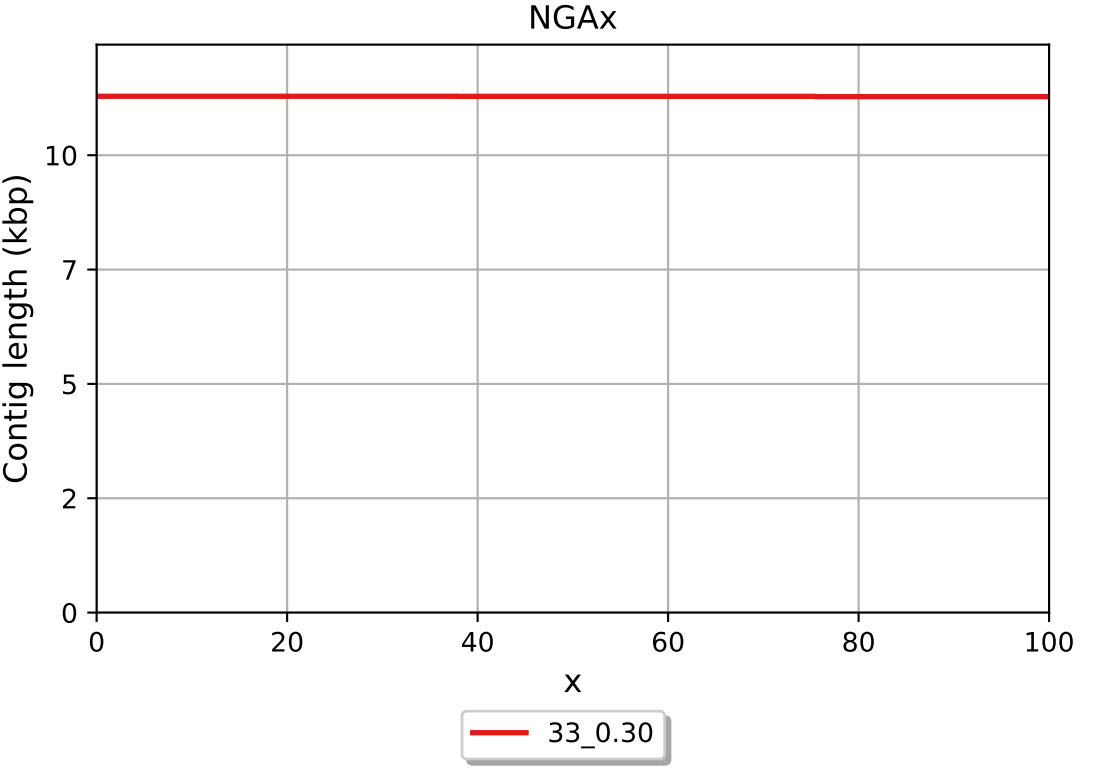

33_0.30 GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
33_0.30


Misassemblies
5
4
3
2
1
0
33_0.30


FRCurve (misassemblies)
Genome coverage (%)
300
240
180
120
60
0
0
1
Feature space
33_0.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
100
80
60
40
20
0
0
4
8
12
16
20
Contig index
33_0.30
Reference


NAx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
33_0.30


NGAx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
33_0.30