Report

	84_0.30
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	213228
Total length (>= 5000 bp)	180355
Total length (>= 10000 bp)	159671
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	28
Largest contig	22293
Total length	216609
Reference length	29863
GC (%)	37.85
Reference GC (%)	38.00
N50	11102
NG50	22293
N75	7501
NG75	22292
L50	7
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 (%)	99.326
Duplication ratio	7.311
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.63
# indels per 100 kbp	40.50
Largest alignment	22292
Total aligned length	216589
NA50	11101
NGA50	22292
NA75	7500
NGA75	22291
LA50	7
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

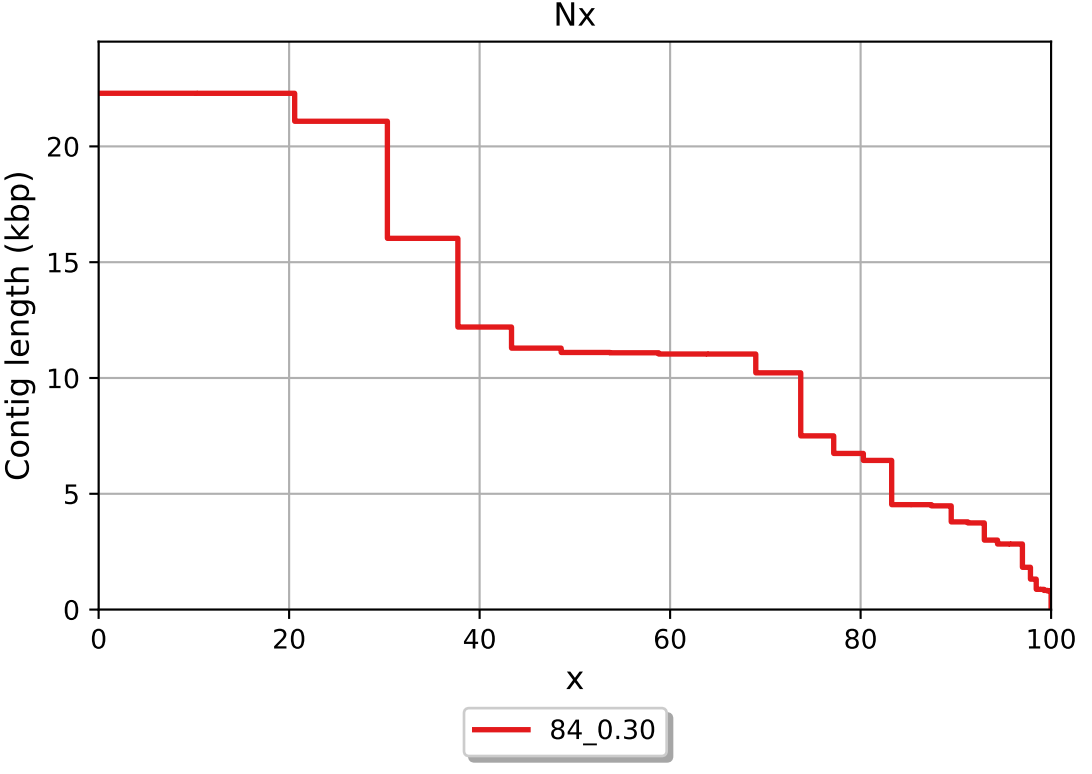
	84_0.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	7
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	12

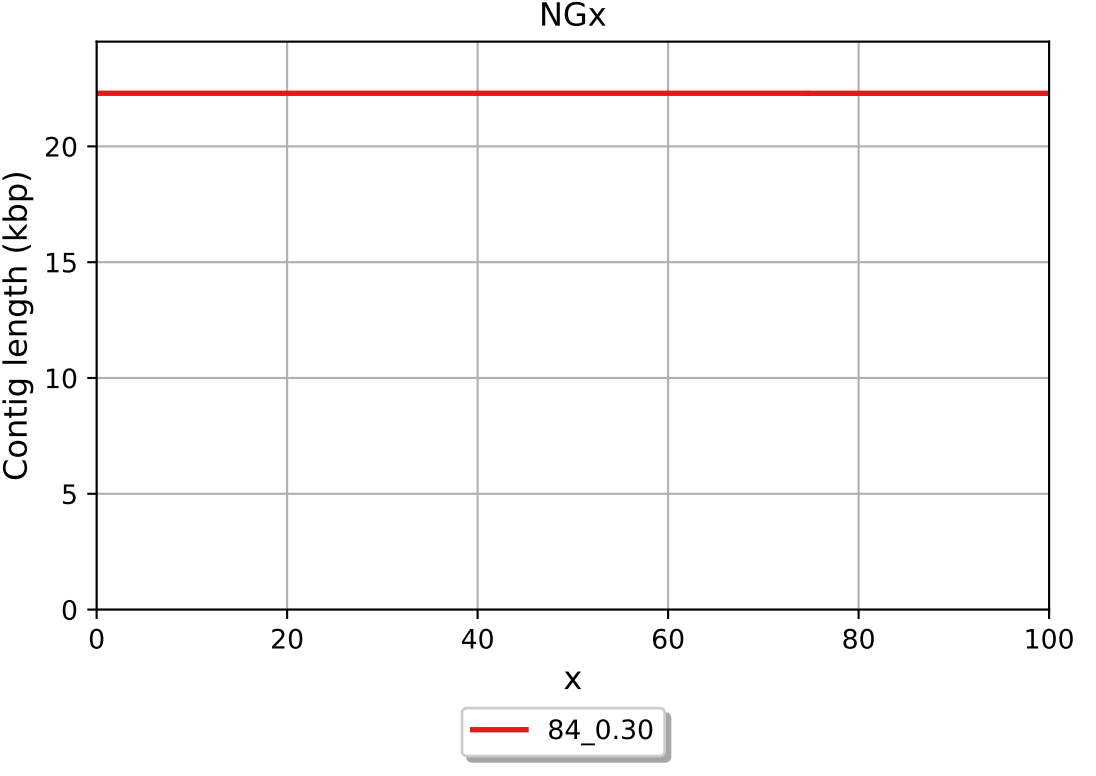
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

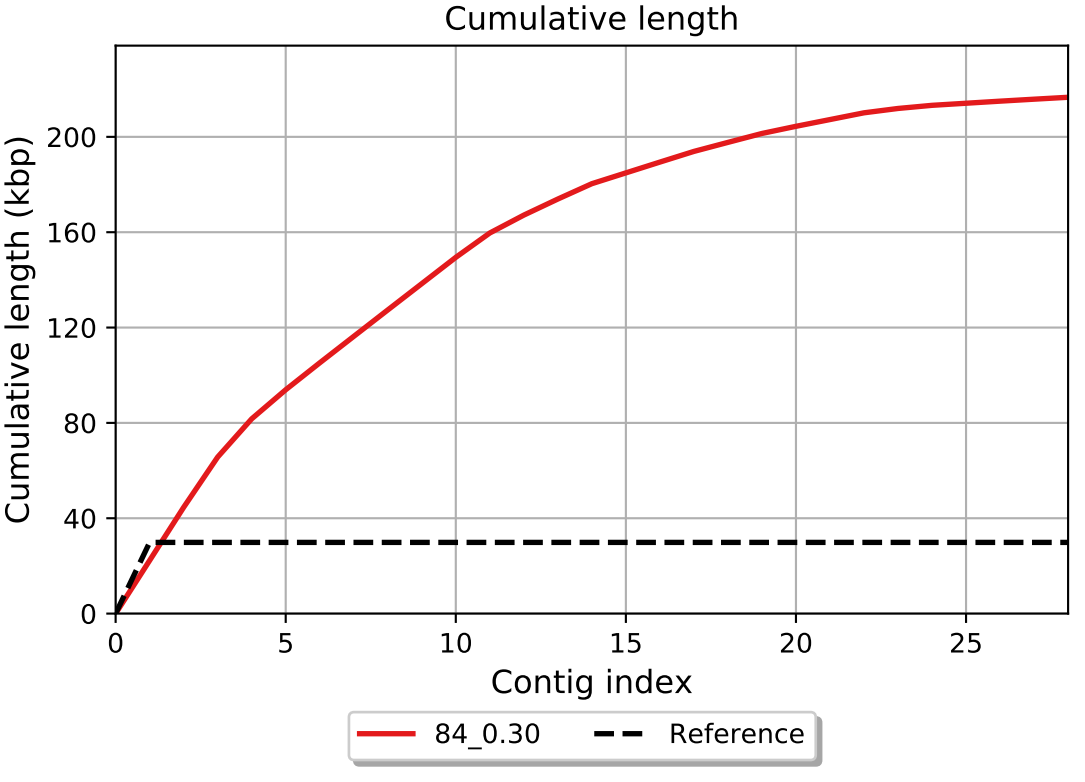
Unaligned report

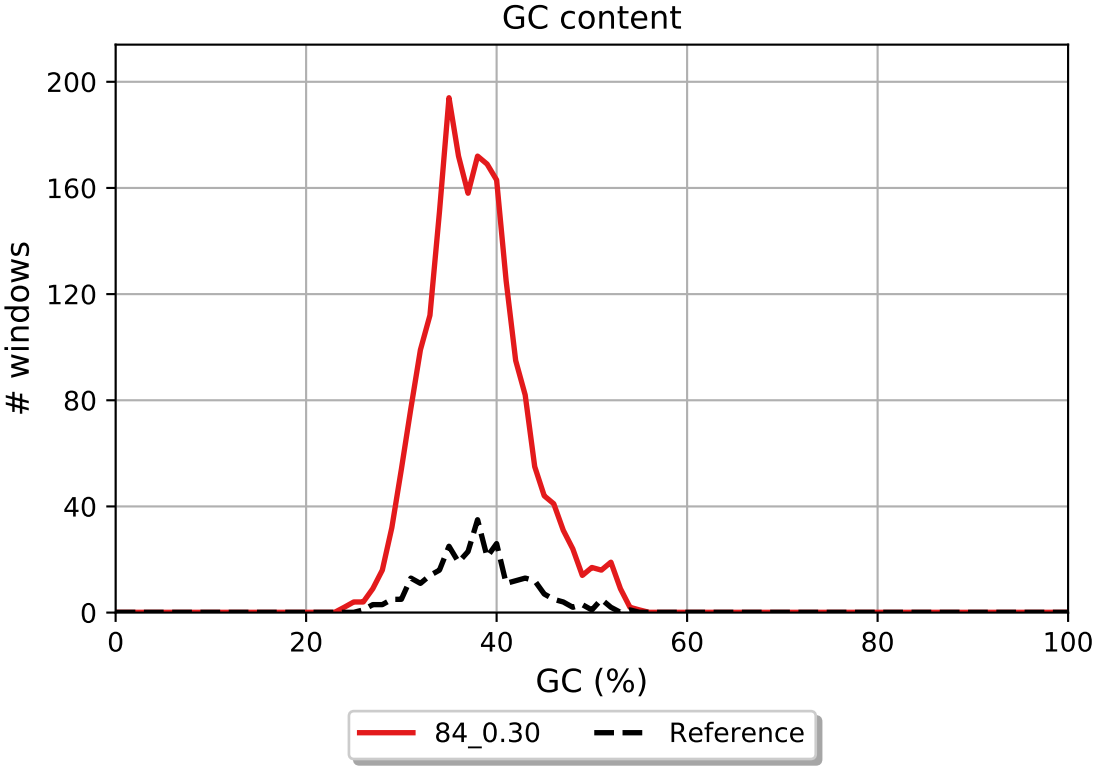
	84_0.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

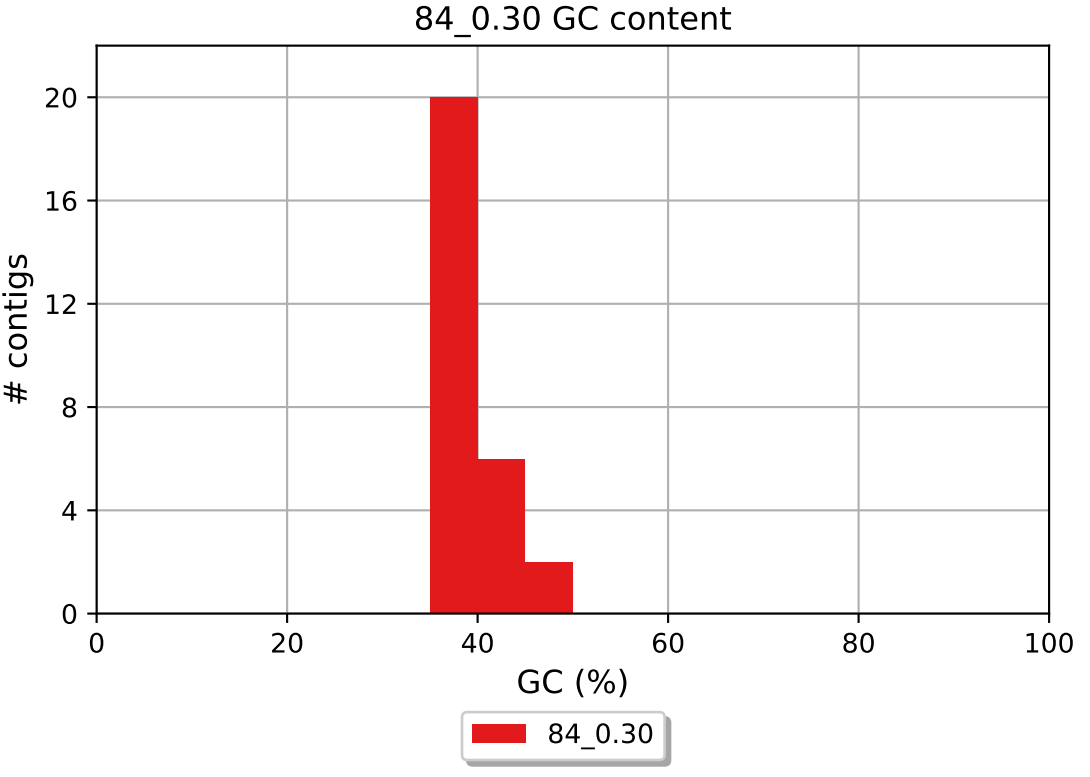
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

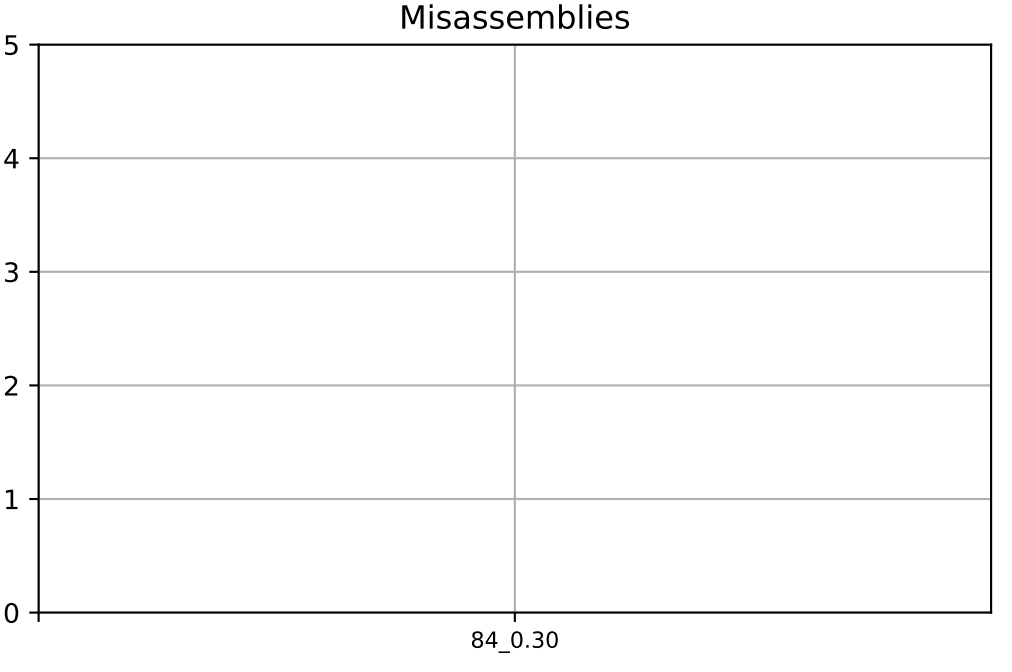

Nx
Contig length (kbp)
0
5
10
15
20
0
20
40
60
80
100
x
84_0.30

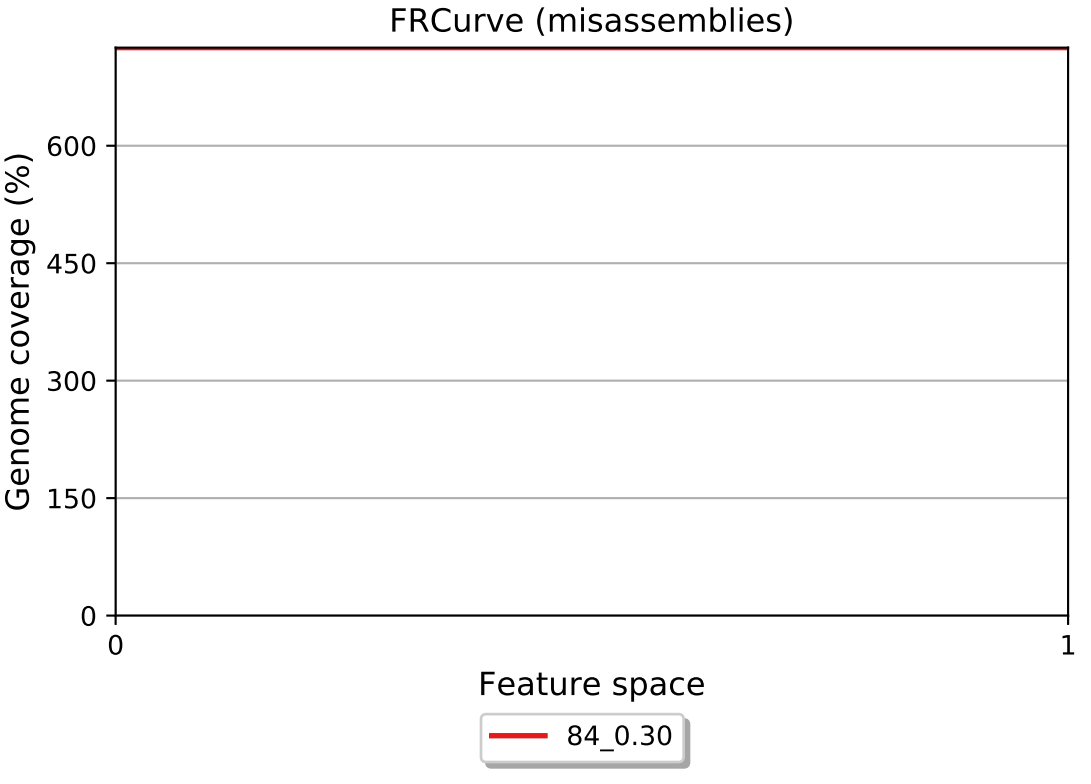

NGx
Contig length (kbp)
0
5
10
15
20
0
20
40
60
80
100
x
84_0.30

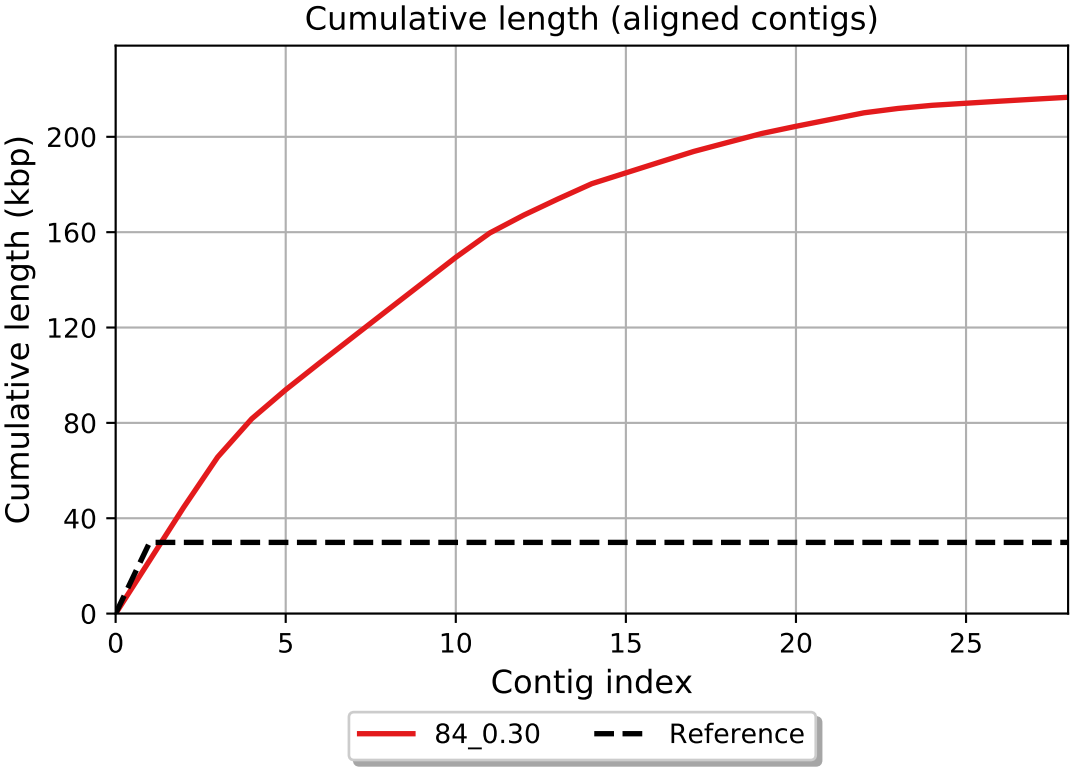

Cumulative length
Cumulative length (kbp)
0
40
80
120
160
200
0
5
10
15
20
25
Contig index
84_0.30
Reference

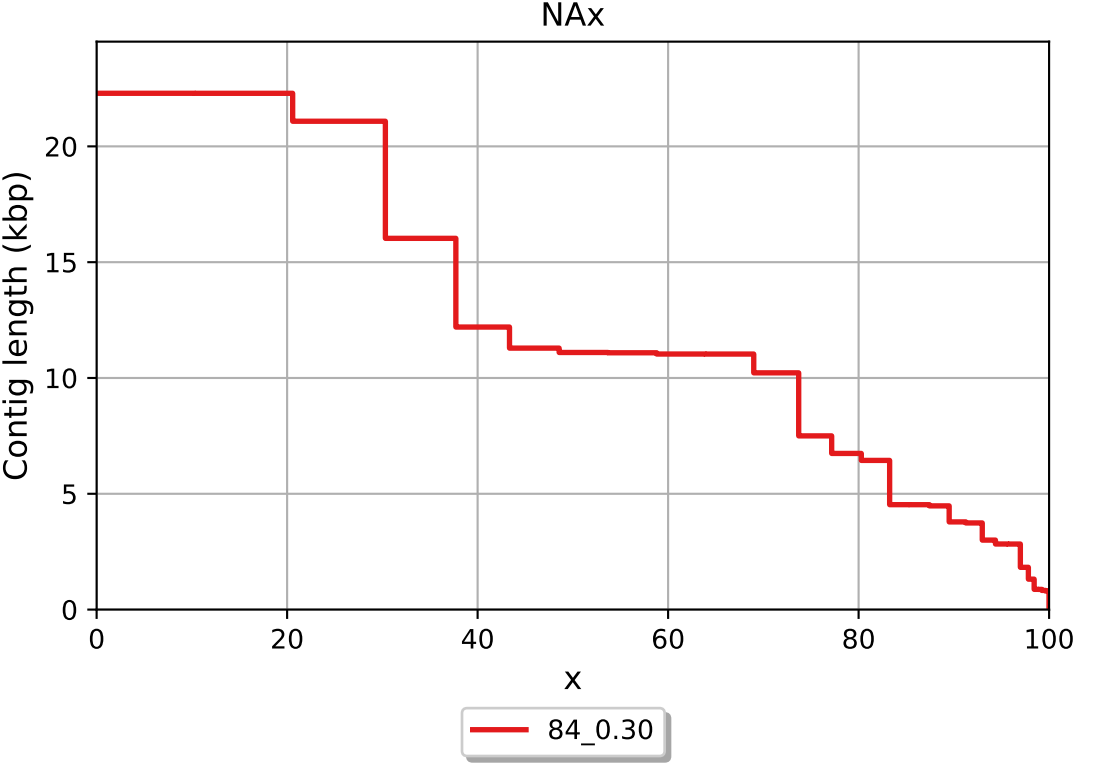

GC content
windows
200
160
120
80
40
0
0
20
40
60
80
100
GC (%)
84_0.30
Reference

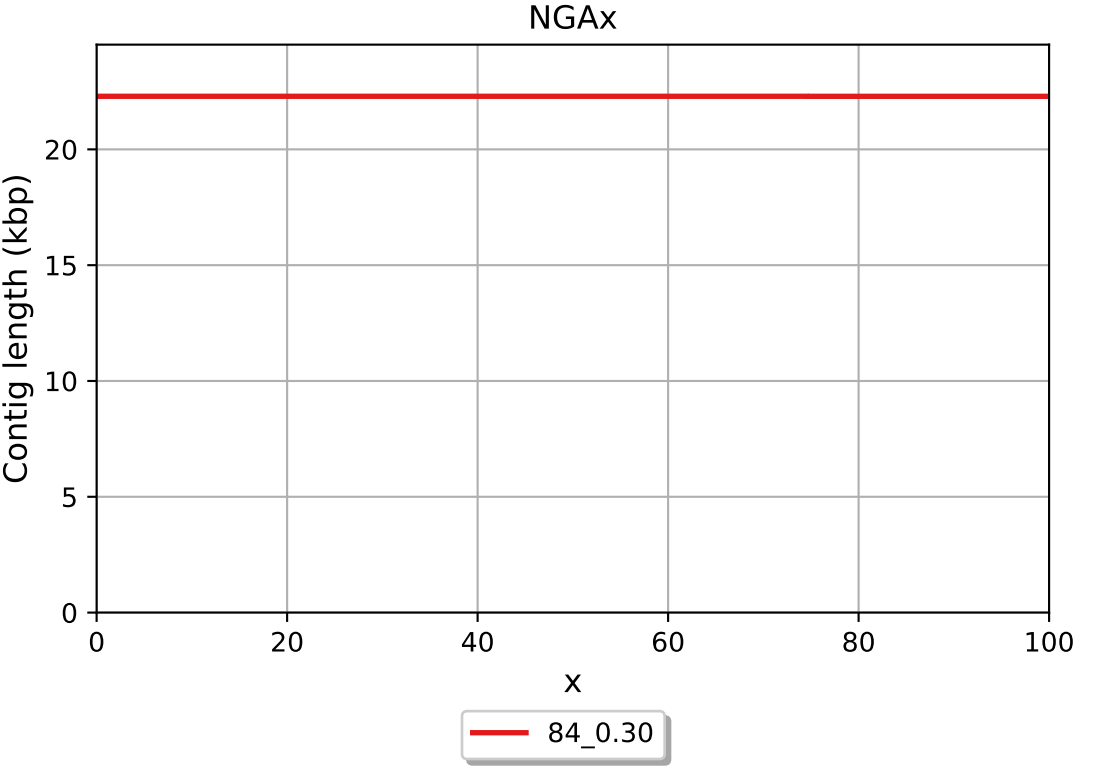

84_0.30 GC content
contigs
0
4
8
12
16
20
0
20
40
60
80
100
GC (%)
84_0.30


Misassemblies
5
4
3
2
1
0
84_0.30


FRCurve (misassemblies)
Genome coverage (%)
600
450
300
150
0
0
1
Feature space
84_0.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
40
80
120
160
200
0
5
10
15
20
25
Contig index
84_0.30
Reference


NAx
Contig length (kbp)
0
5
10
15
20
0
20
40
60
80
100
x
84_0.30


NGAx
Contig length (kbp)
0
5
10
15
20
0
20
40
60
80
100
x
84_0.30