Report

	84_38.30
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	131143
Total length (>= 5000 bp)	108992
Total length (>= 10000 bp)	42182
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	28
Largest contig	11036
Total length	133761
Reference length	29903
GC (%)	37.95
Reference GC (%)	37.97
N50	7271
NG50	11035
N75	5224
NG75	10056
L50	8
LG50	2
L75	13
LG75	3
# 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 (%)	98.866
Duplication ratio	4.524
# N's per 100 kbp	0.00
# mismatches per 100 kbp	186.04
# indels per 100 kbp	40.59
Largest alignment	11035
Total aligned length	133741
NA50	7270
NGA50	11034
NA75	5223
NGA75	10056
LA50	8
LGA50	2
LA75	13
LGA75	3

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

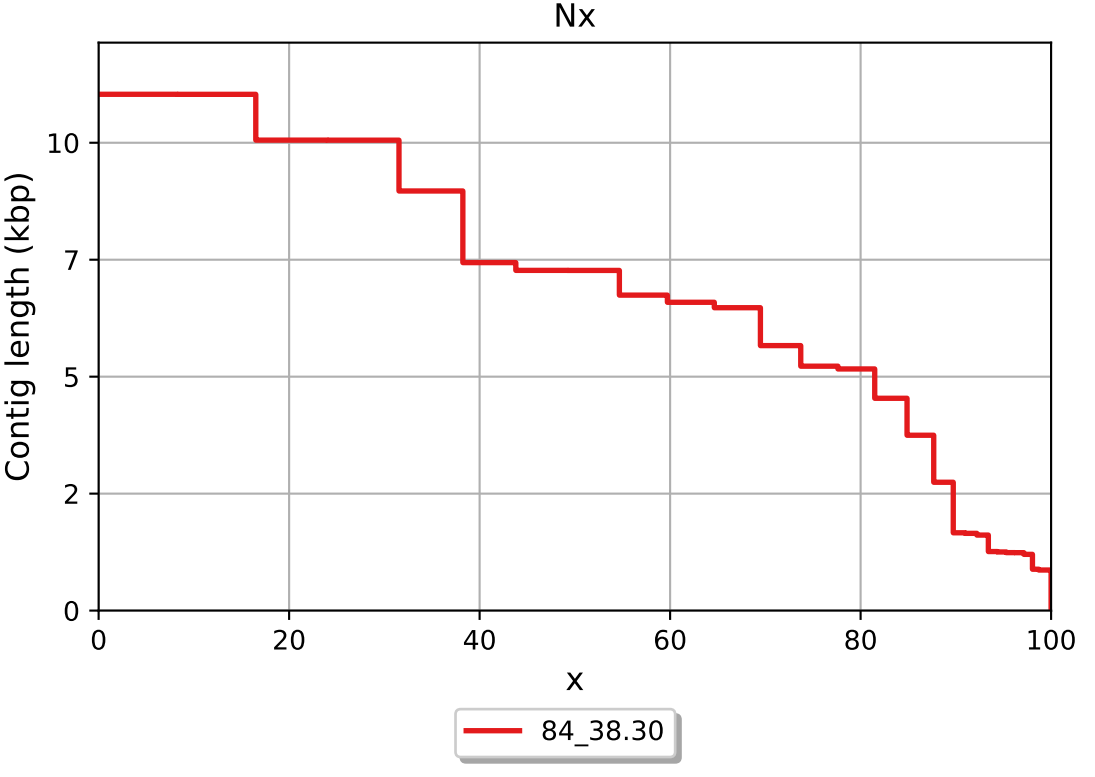
	84_38.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	55
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	12

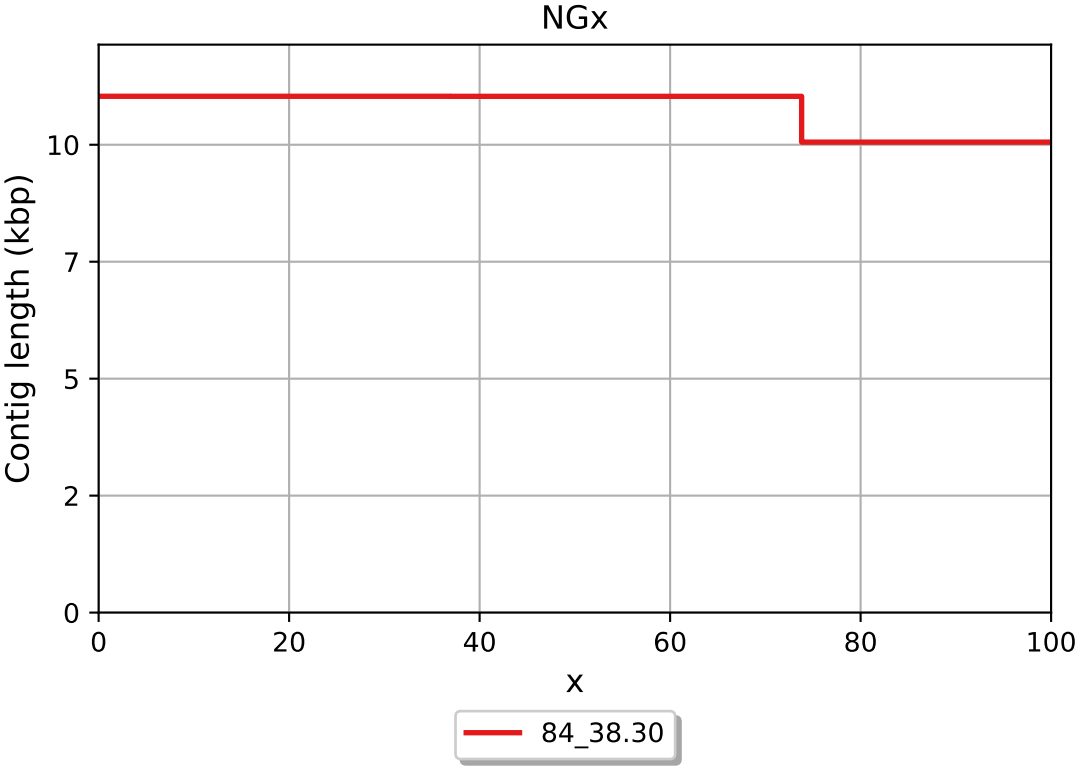
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

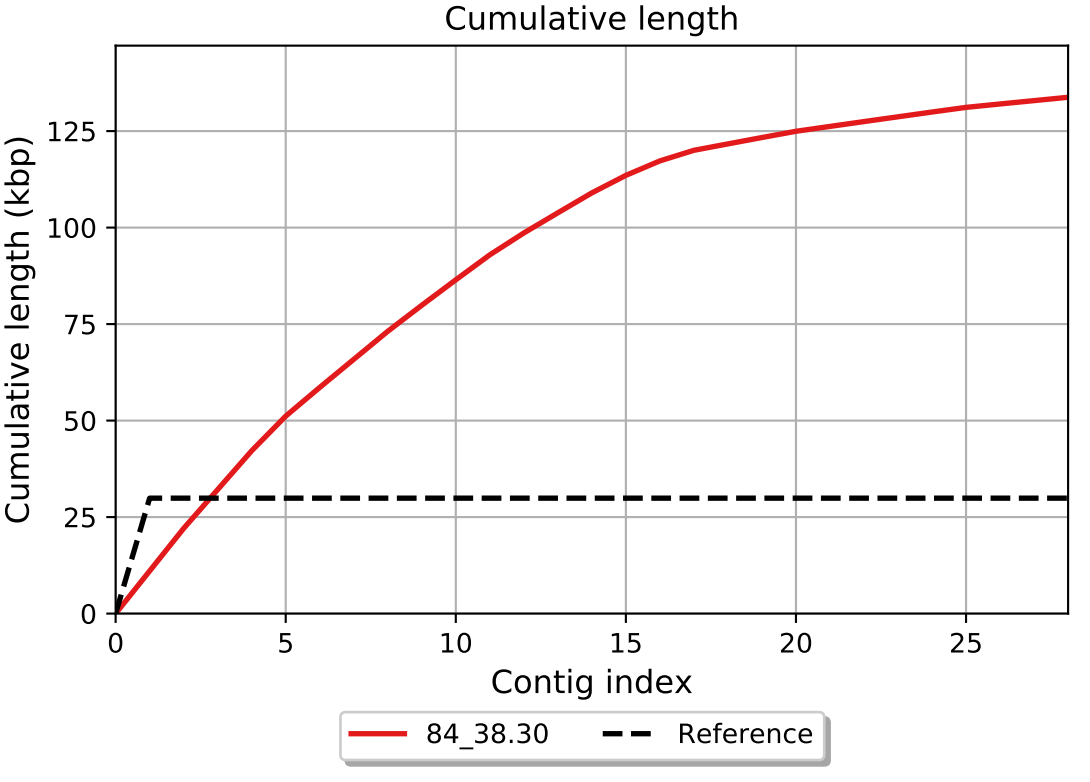
Unaligned report

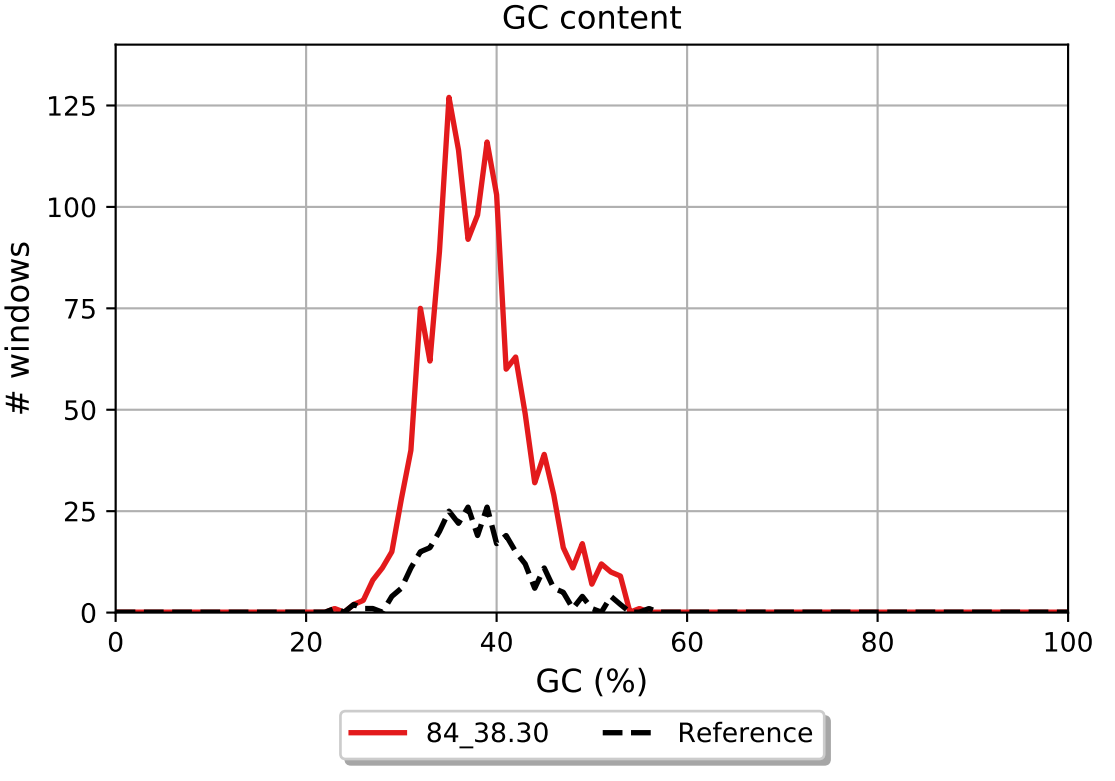
	84_38.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

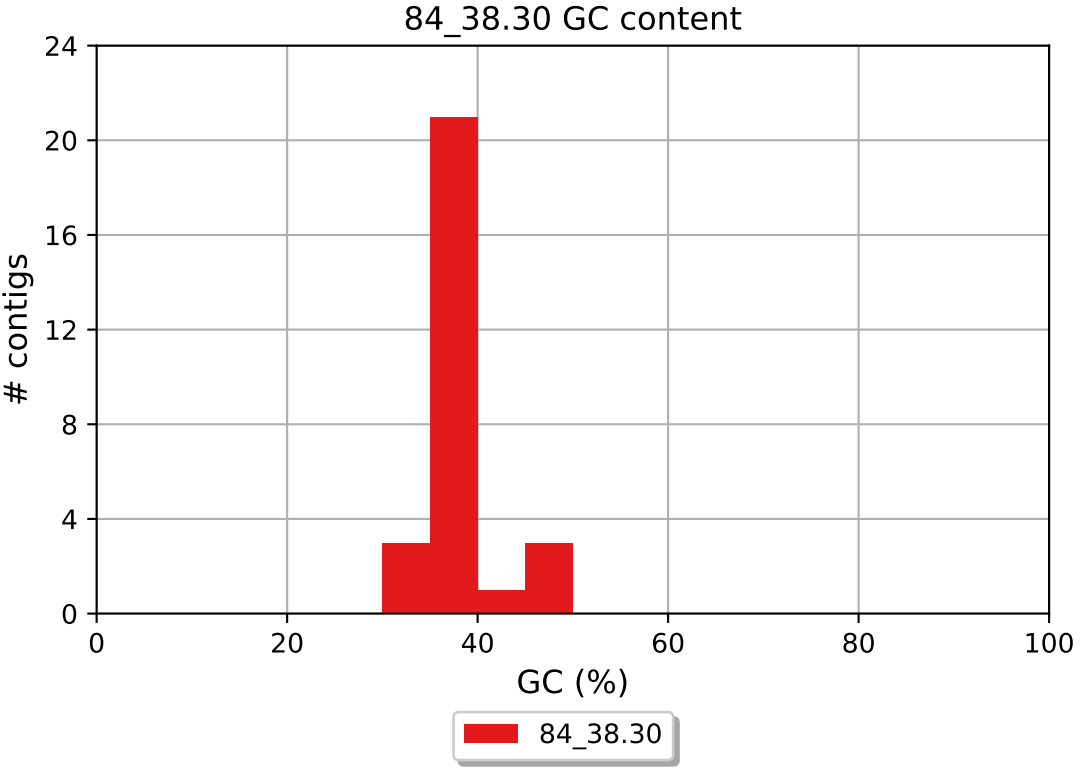
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

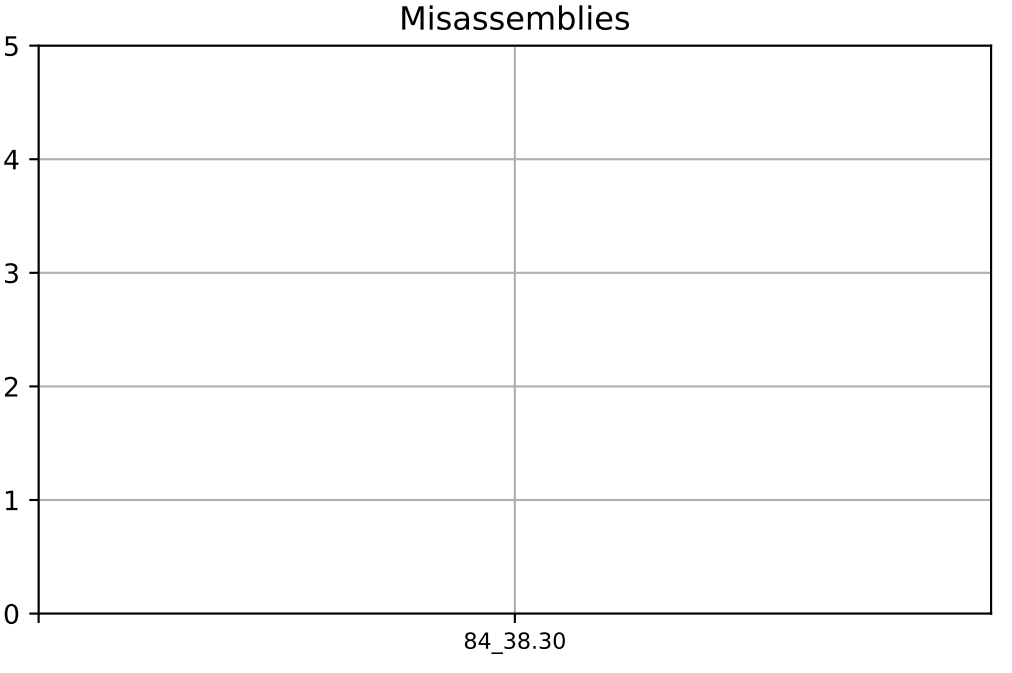

Nx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
84_38.30

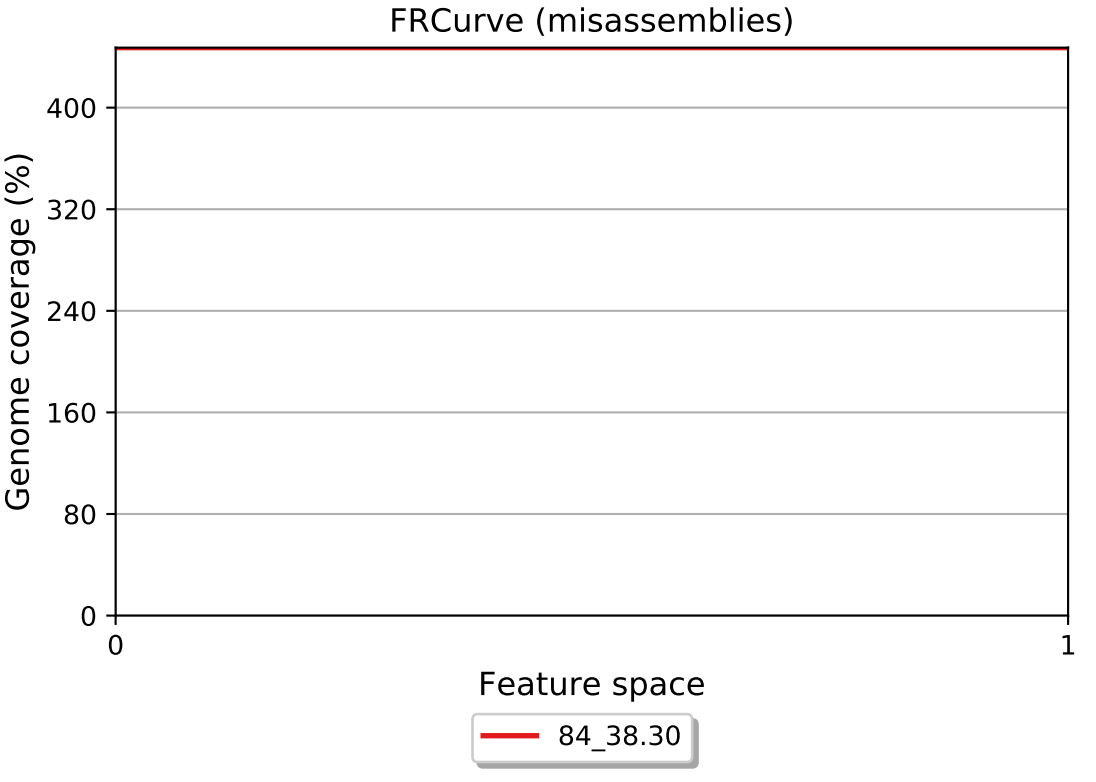

NGx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
84_38.30

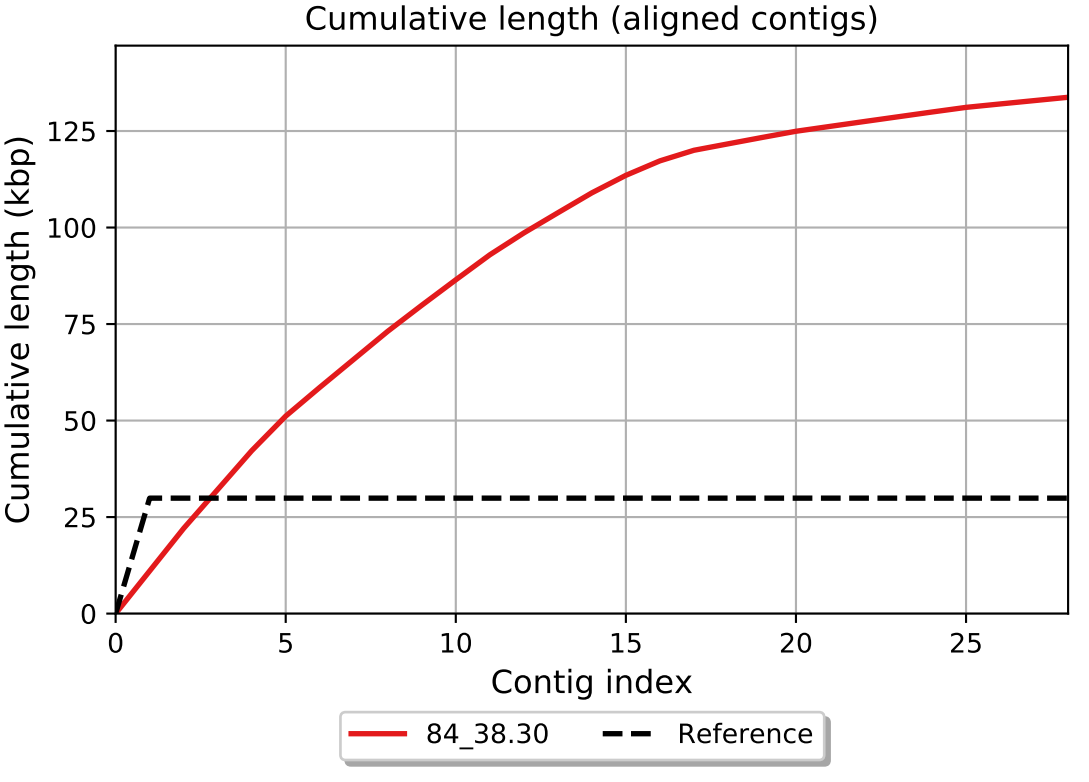

Cumulative length
Cumulative length (kbp)
0
25
50
75
100
125
0
5
10
15
20
25
Contig index
84_38.30
Reference

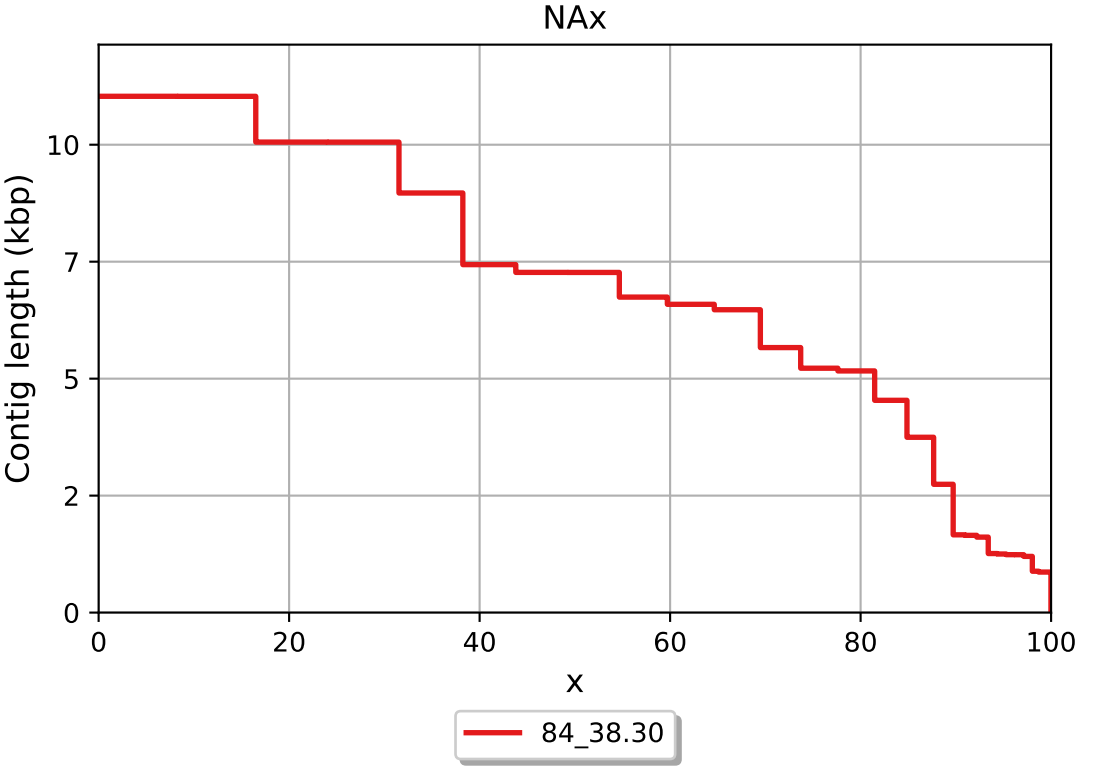

GC content
windows
125
100
75
50
25
0
0
20
40
60
80
100
GC (%)
84_38.30
Reference

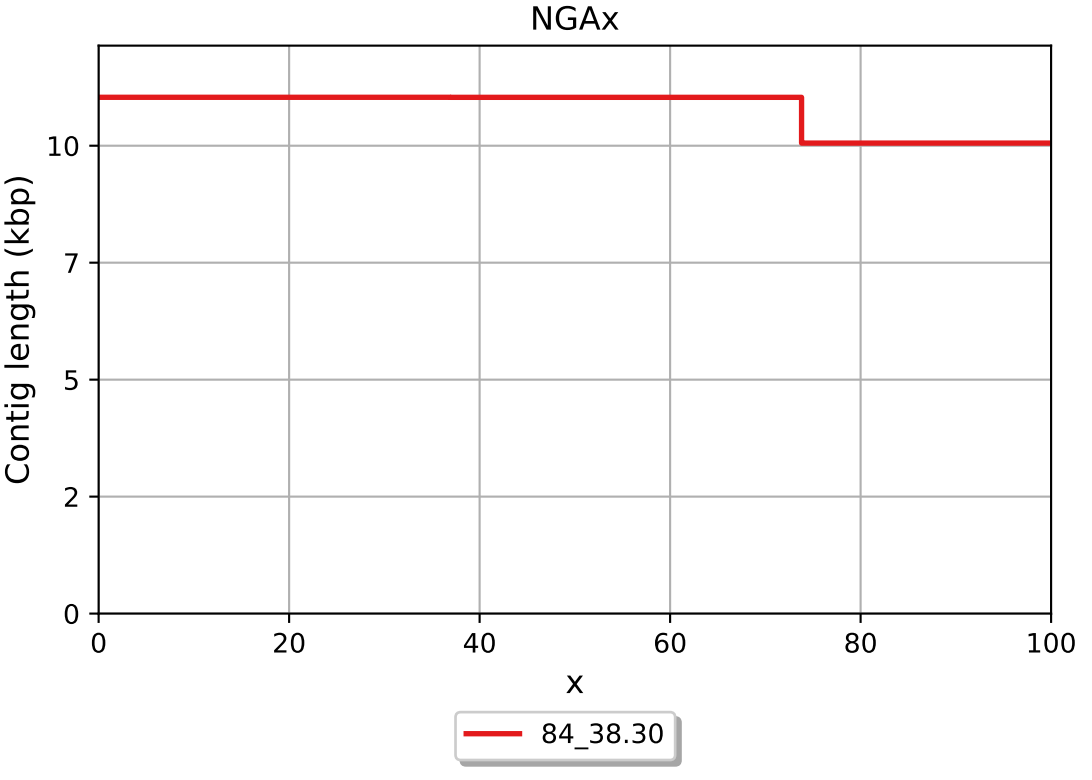

84_38.30 GC content
24
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
84_38.30


Misassemblies
5
4
3
2
1
0
84_38.30


FRCurve (misassemblies)
Genome coverage (%)
400
320
240
160
80
0
0
1
Feature space
84_38.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
25
50
75
100
125
0
5
10
15
20
25
Contig index
84_38.30
Reference


NAx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
84_38.30


NGAx
Contig length (kbp)
10
7
5
2
0
0
20
40
60
80
100
x
84_38.30