Report

	84_380.30
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	151032
Total length (>= 5000 bp)	103719
Total length (>= 10000 bp)	83015
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	26
Largest contig	15980
Total length	151877
Reference length	29903
GC (%)	37.90
Reference GC (%)	37.97
N50	10209
NG50	15980
N75	4452
NG75	12181
L50	7
LG50	1
L75	13
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 (%)	99.074
Duplication ratio	5.126
# N's per 100 kbp	0.00
# mismatches per 100 kbp	195.77
# indels per 100 kbp	40.50
Largest alignment	15979
Total aligned length	151855
NA50	10208
NGA50	15979
NA75	4451
NGA75	12181
LA50	7
LGA50	1
LA75	13
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

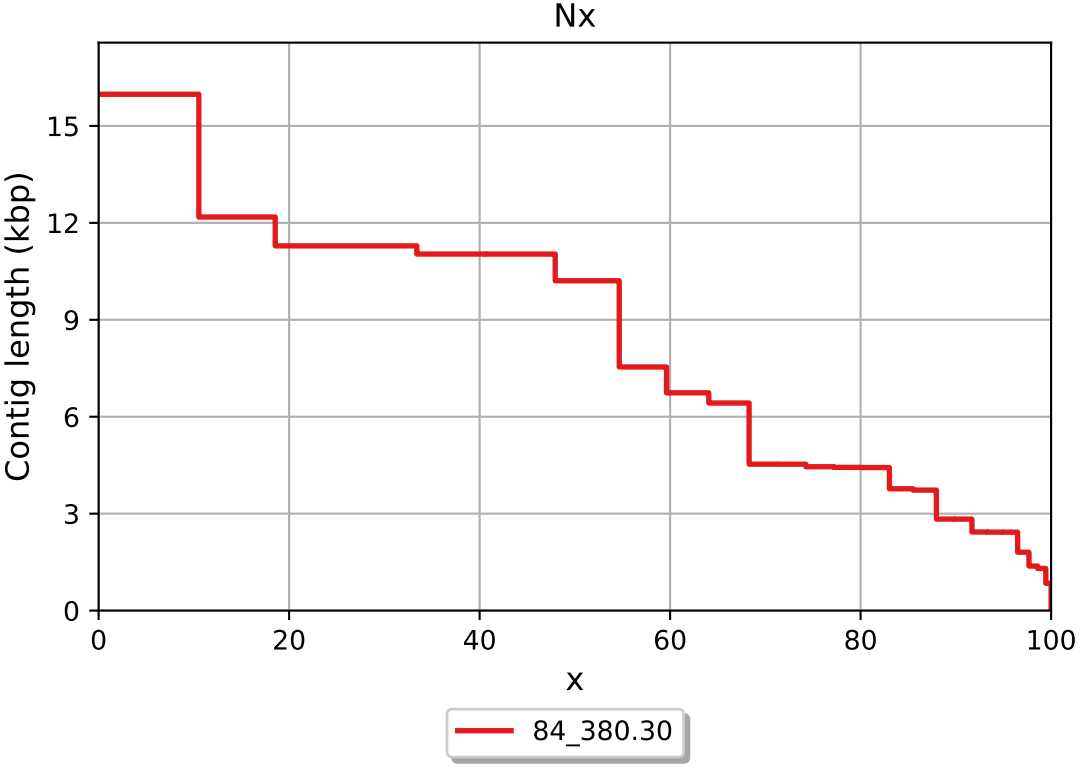
	84_380.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	58
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	12

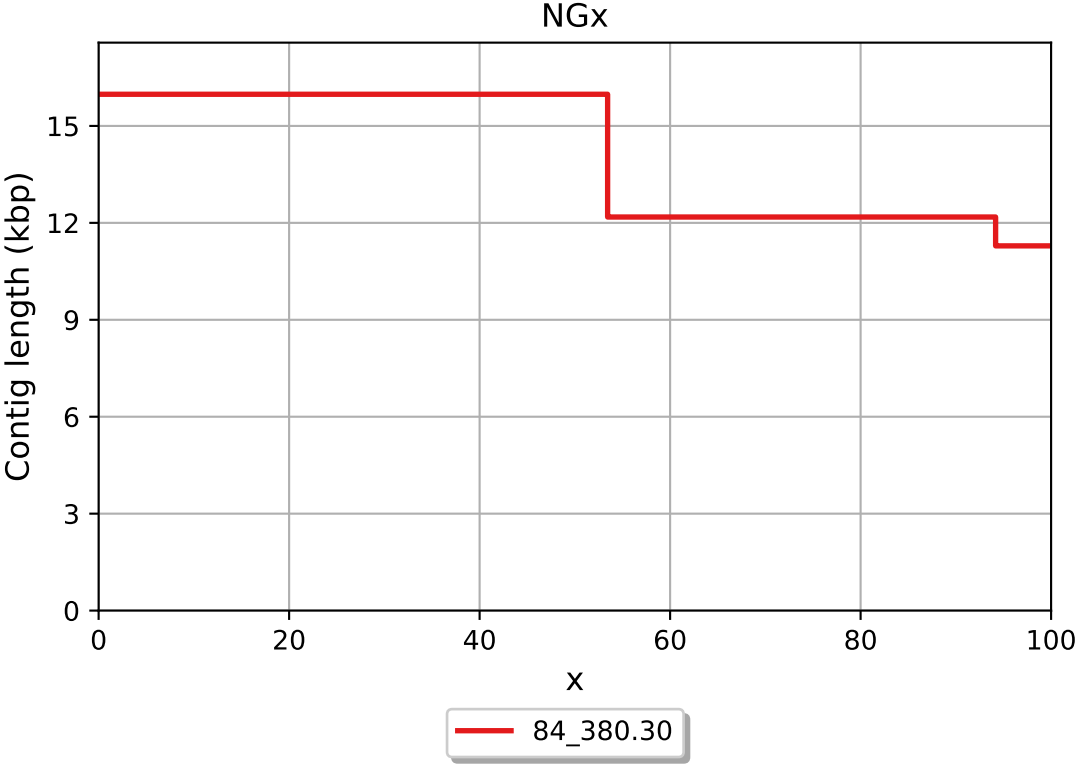
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

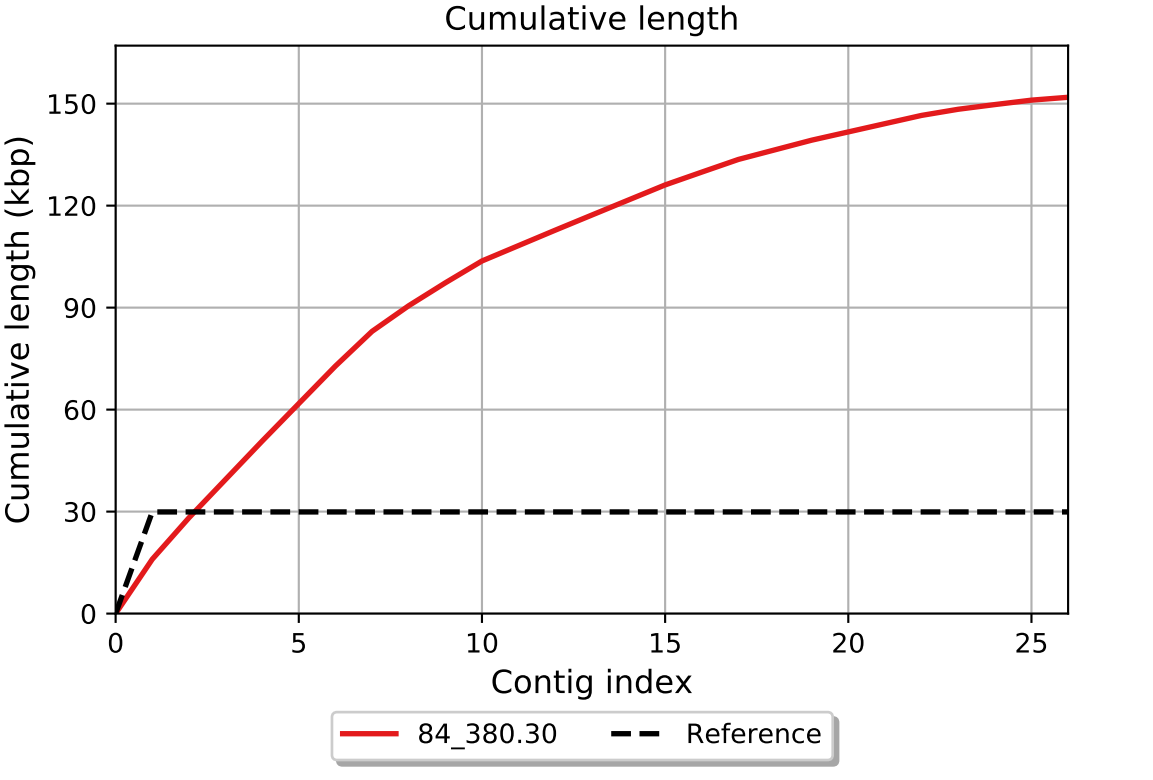
Unaligned report

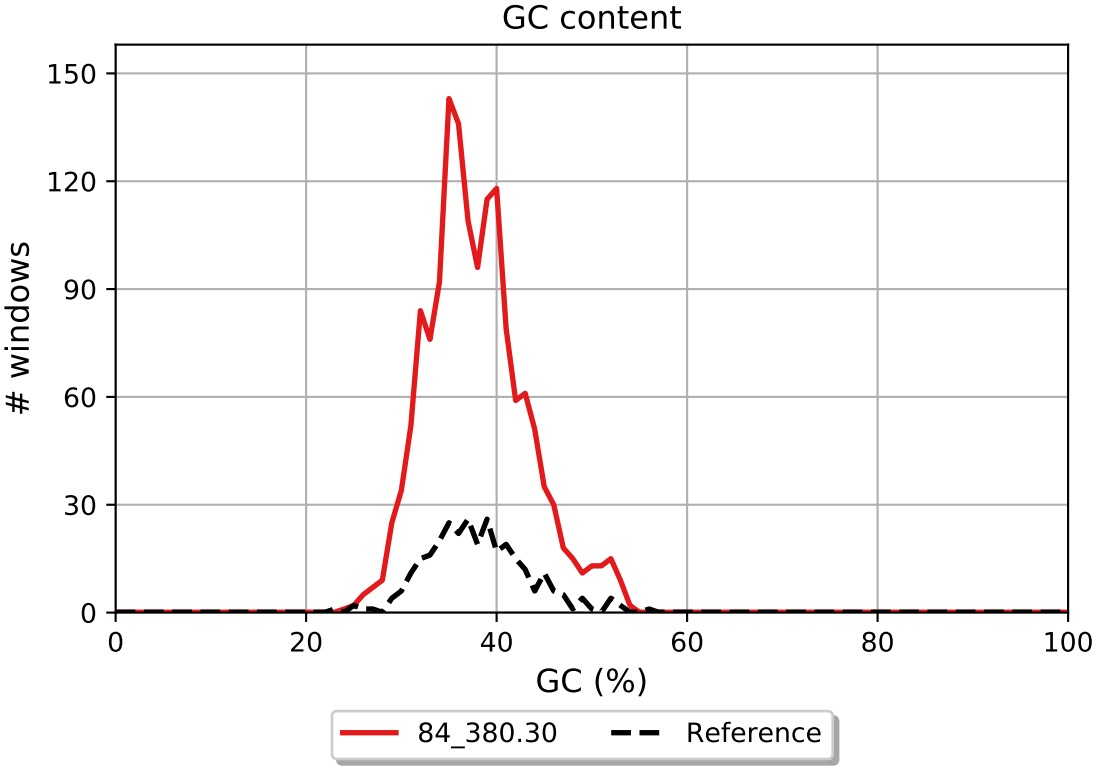
	84_380.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

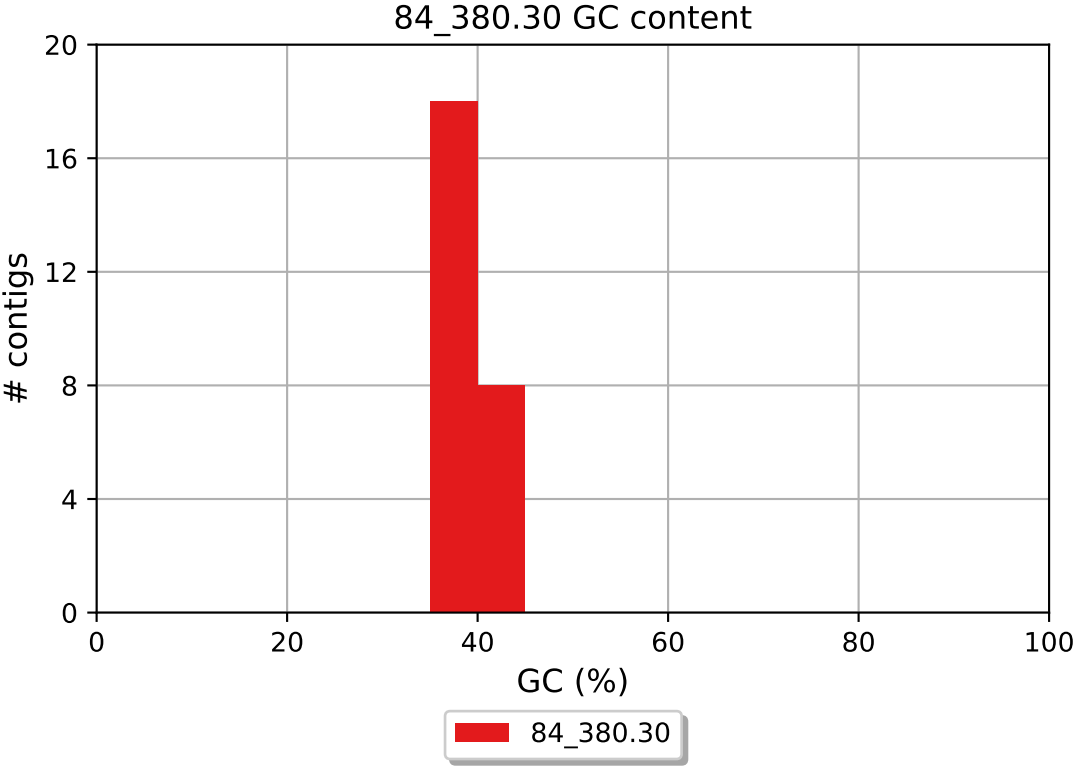
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

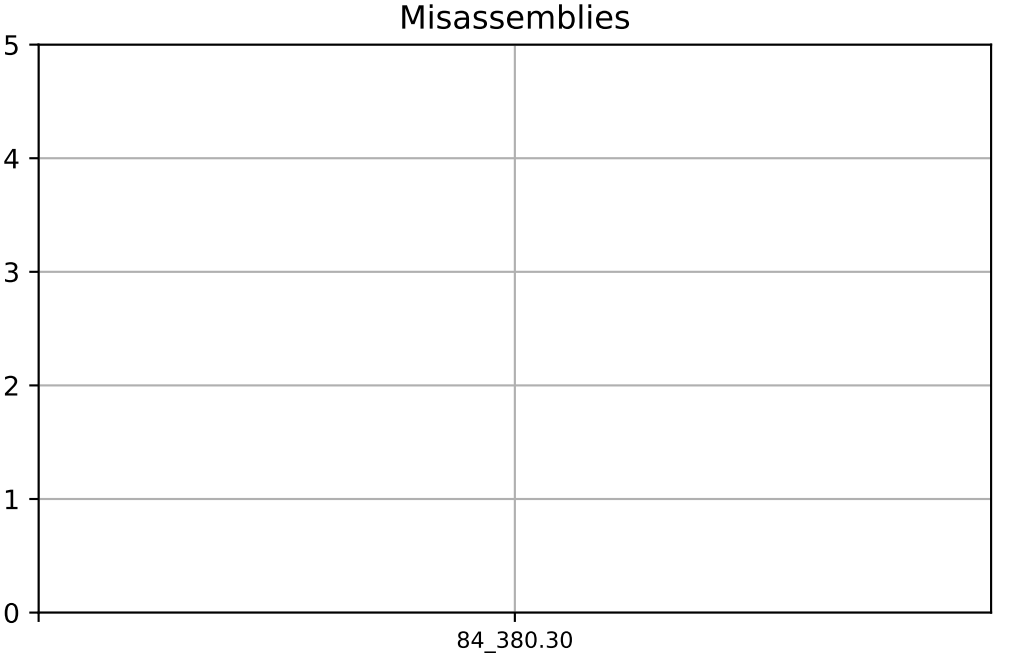

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
84_380.30

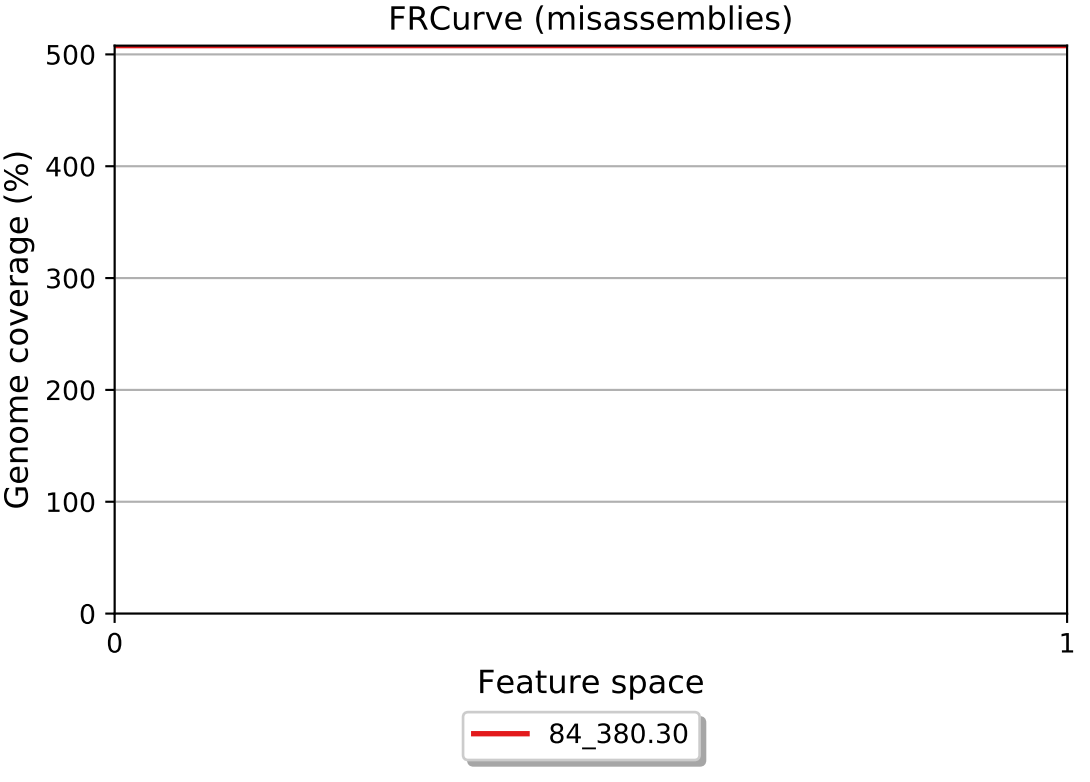

NGx
Contig length (kbp)
0
3
6
9
12
15
0
20
40
60
80
100
x
84_380.30

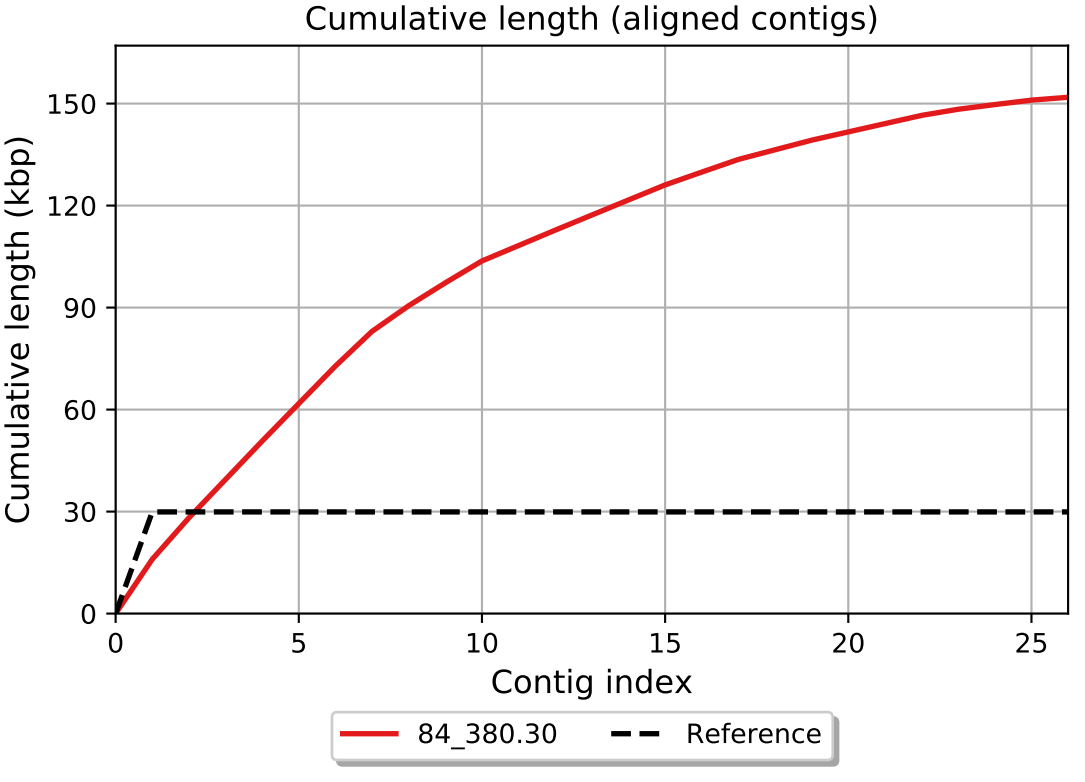

Cumulative length
Cumulative length (kbp)
150
120
90
60
30
0
0
5
10
15
20
25
Contig index
84_380.30
Reference

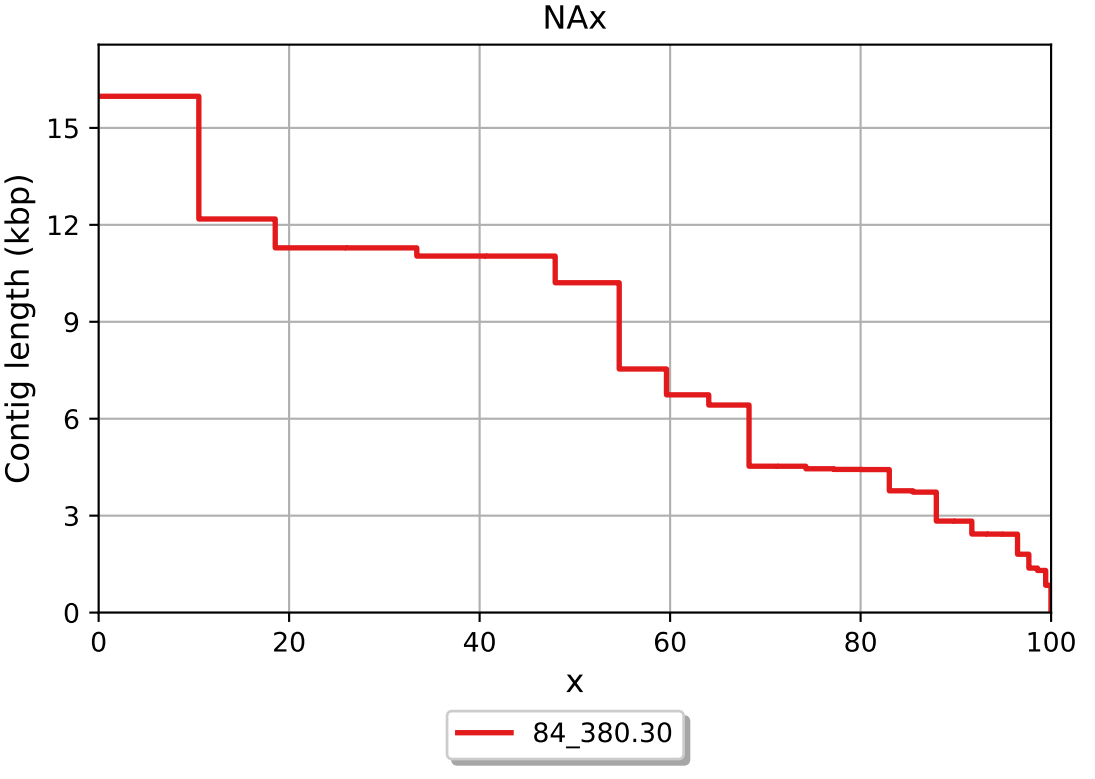

GC content
150
120
90
60
30
0
windows
0
20
40
60
80
100
GC (%)
84_380.30
Reference

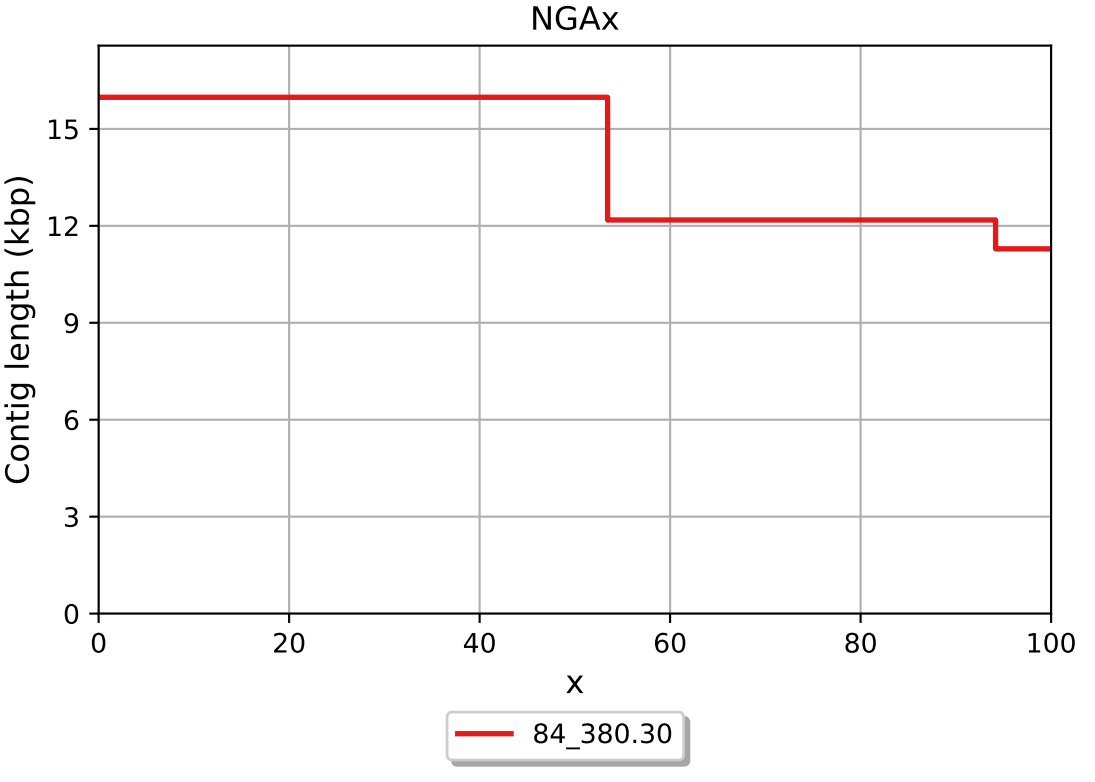

84_380.30 GC content
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
84_380.30


Misassemblies
5
4
3
2
1
0
84_380.30


FRCurve (misassemblies)
Genome coverage (%)
500
400
300
200
100
0
0
1
Feature space
84_380.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
150
120
90
60
30
0
0
5
10
15
20
25
Contig index
84_380.30
Reference


NAx
Contig length (kbp)
0
3
6
9
12
15
0
20
40
60
80
100
x
84_380.30


NGAx
Contig length (kbp)
0
3
6
9
12
15
0
20
40
60
80
100
x
84_380.30