Report

	assymbly_35
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1068
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2
Largest contig	934
Total length	1068
Reference length	1040
GC (%)	51.12
Reference GC (%)	51.25
N50	934
NG50	934
N90	134
NG90	134
auN	833.6
auNG	856.1
L50	1
LG50	1
L90	2
LG90	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 (%)	100.000
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	934
Total aligned length	1068
NA50	934
NGA50	934
NA90	134
NGA90	134
auNA	833.6
auNGA	856.1
LA50	1
LGA50	1
LA90	2
LGA90	2

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

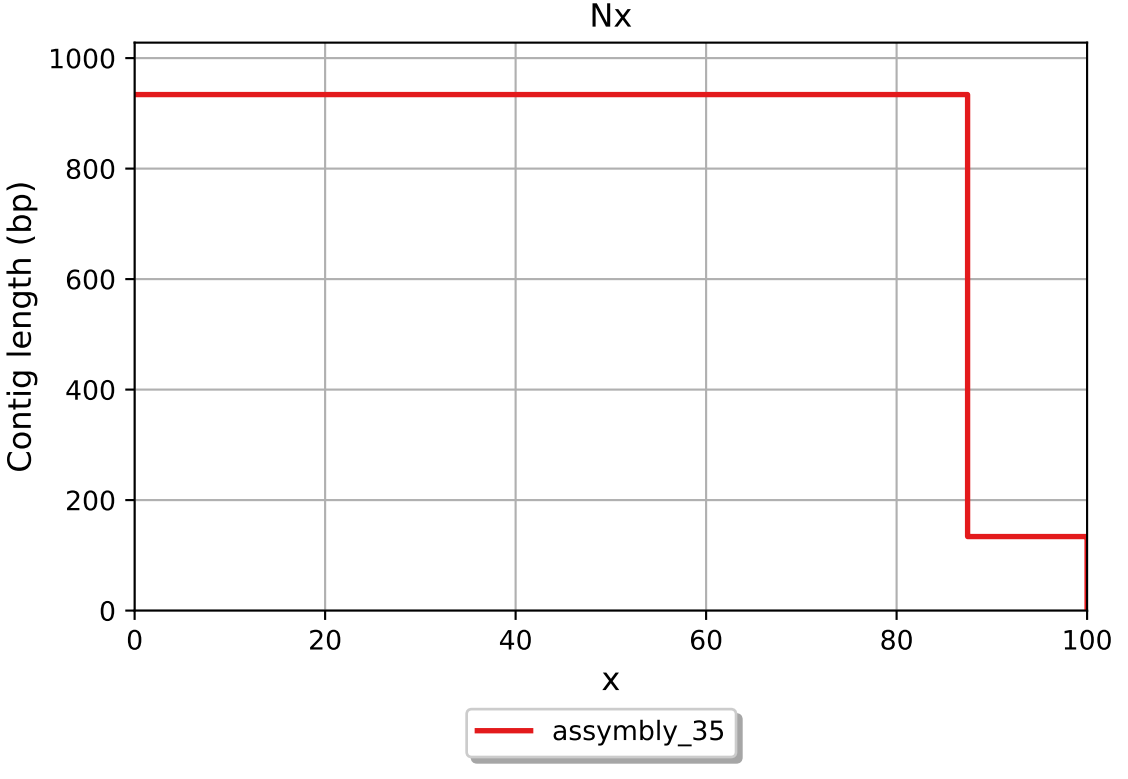
	assymbly_35
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

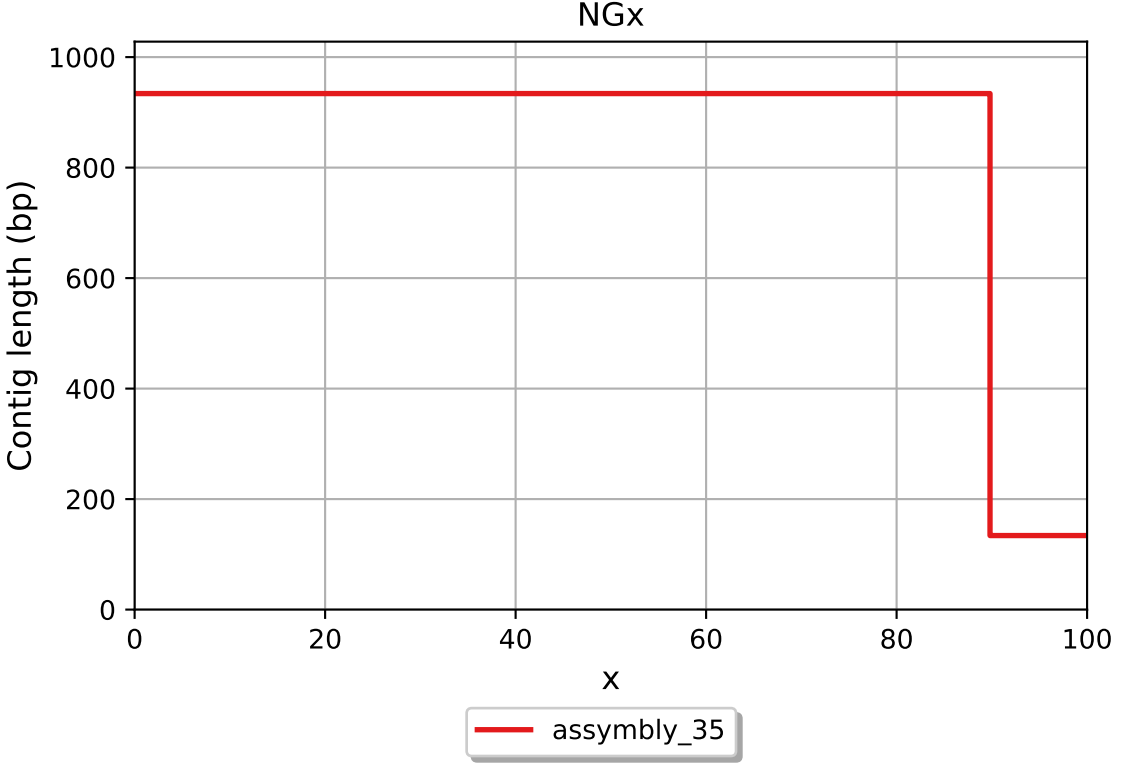
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

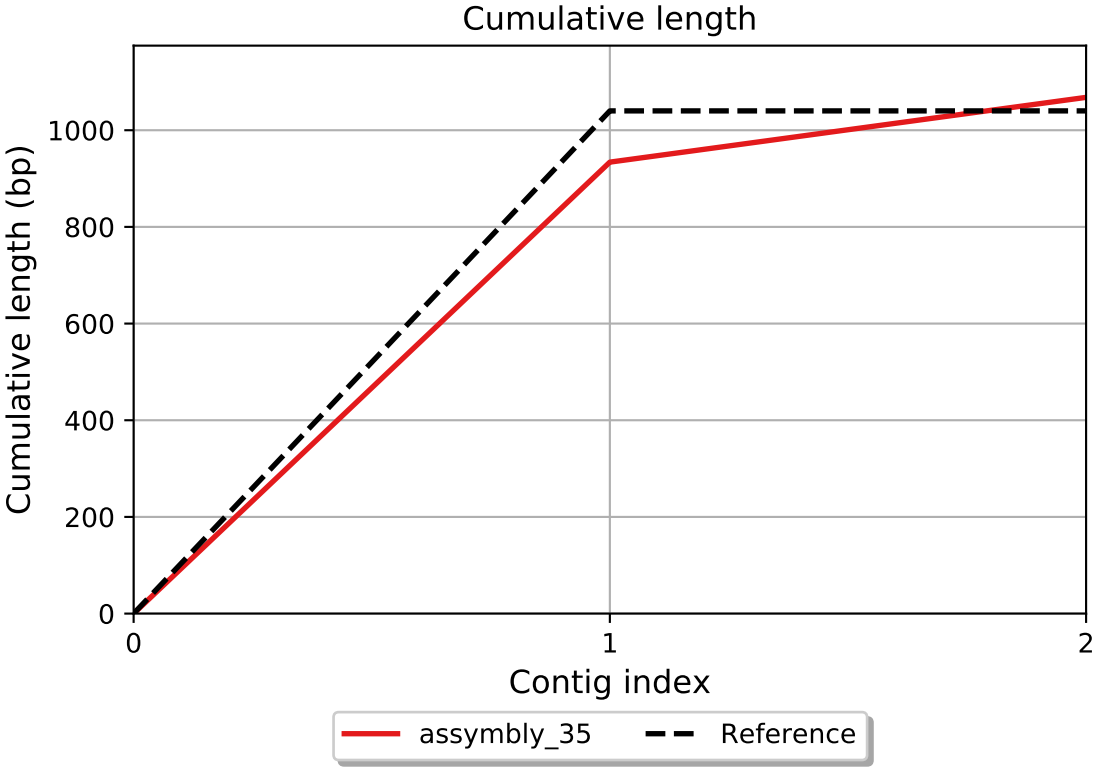
Unaligned report

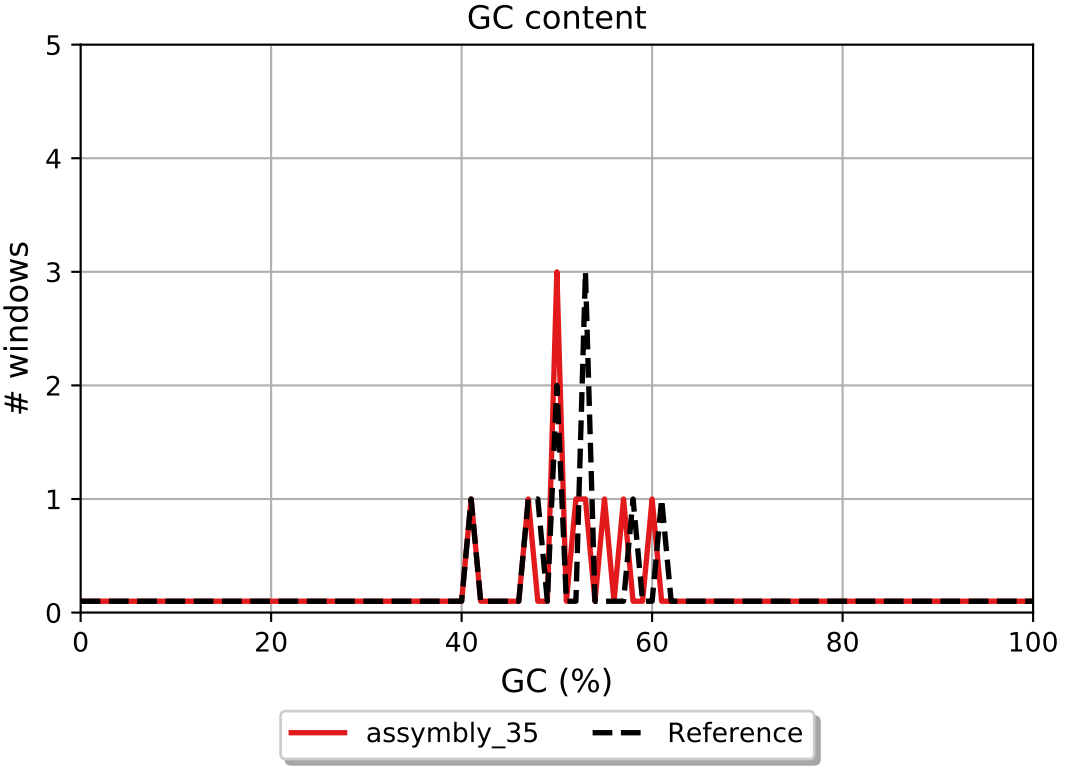
	assymbly_35
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

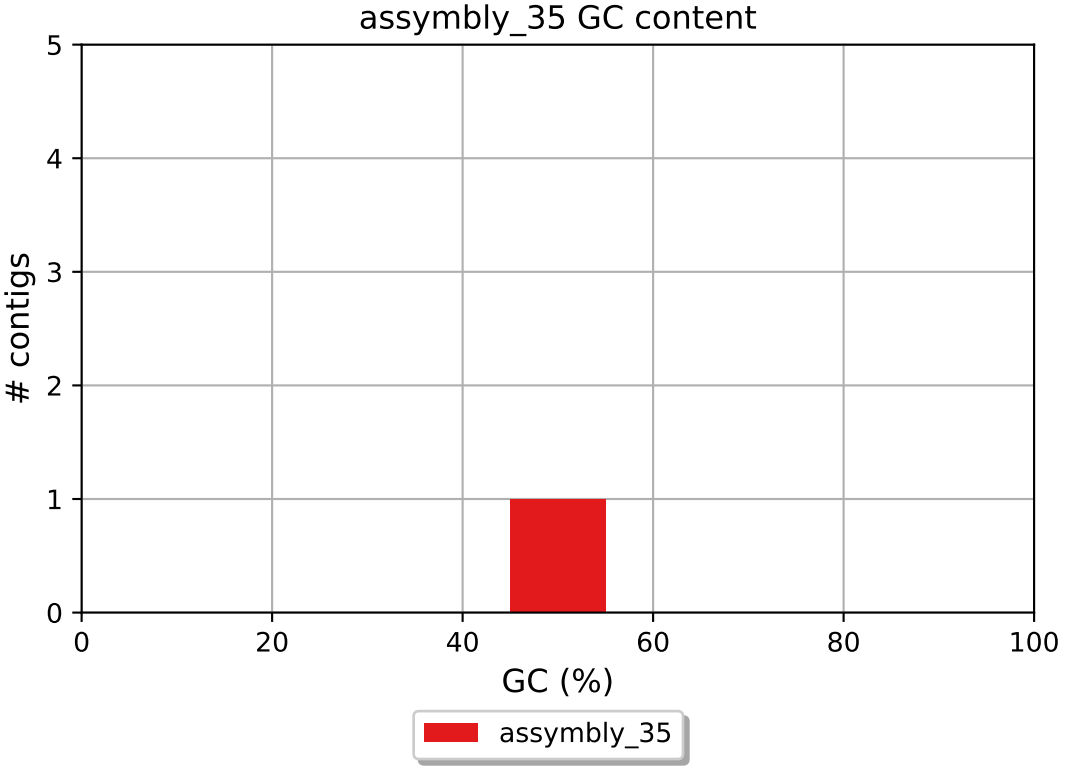
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

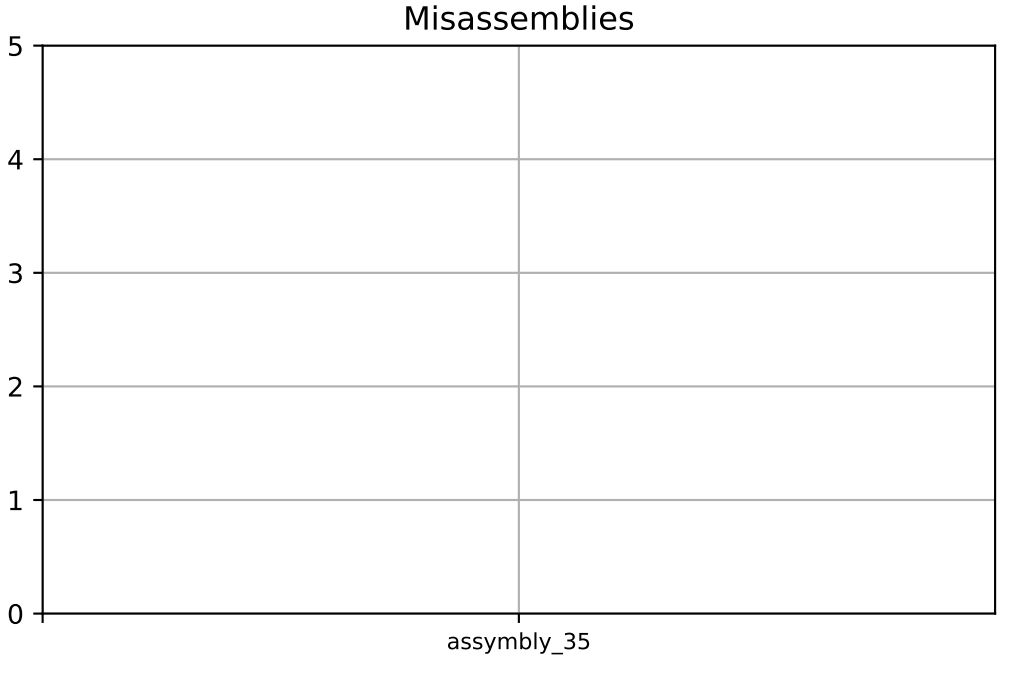

Nx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
assymbly_35

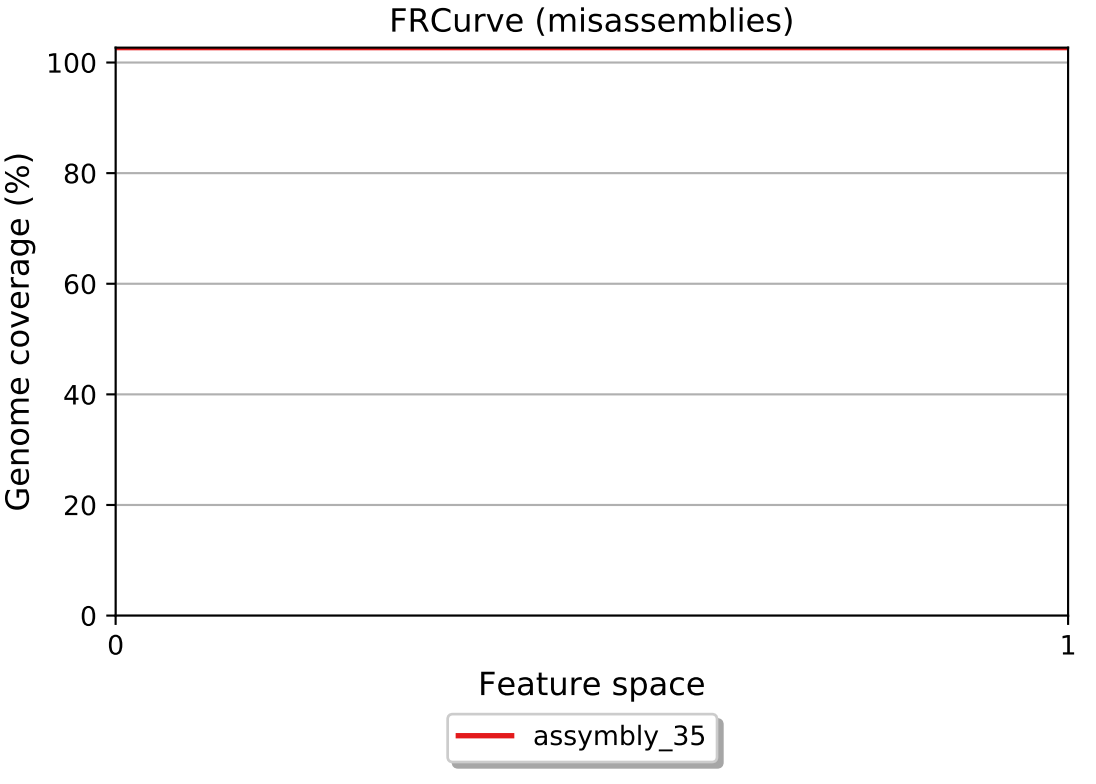

NGx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
assymbly_35

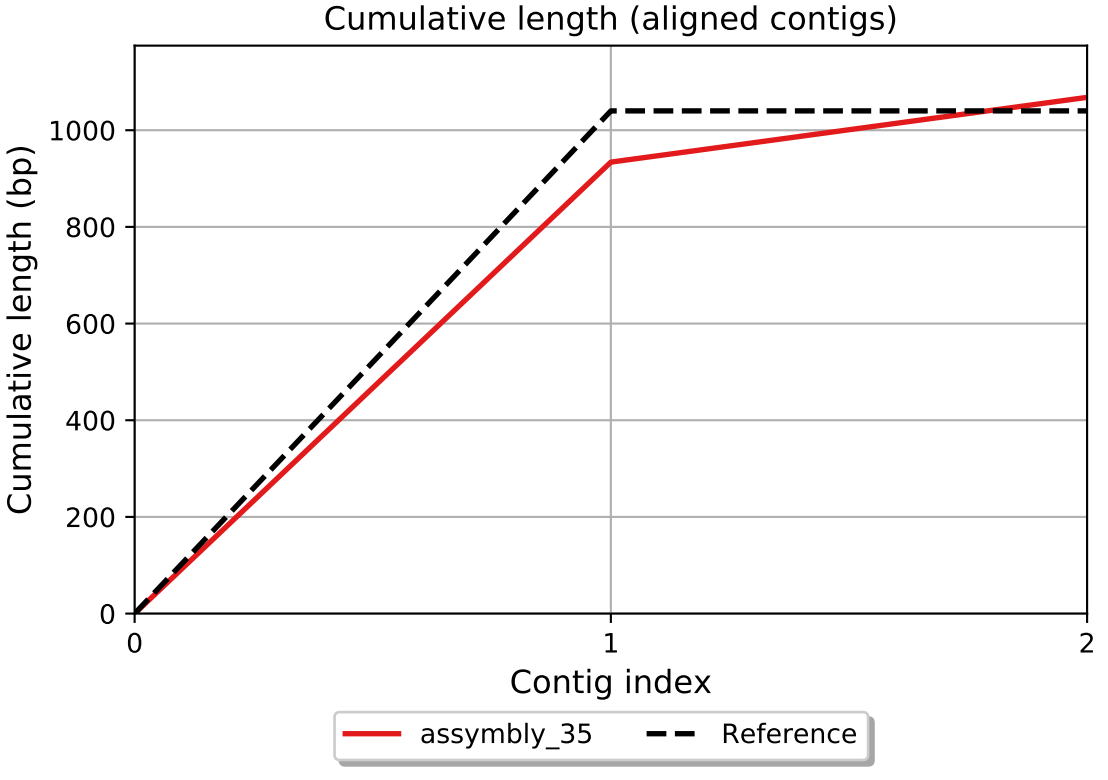

Cumulative length
Cumulative length (bp)
1000
800
600
400
200
0
0
1
2
Contig index
assymbly_35
Reference

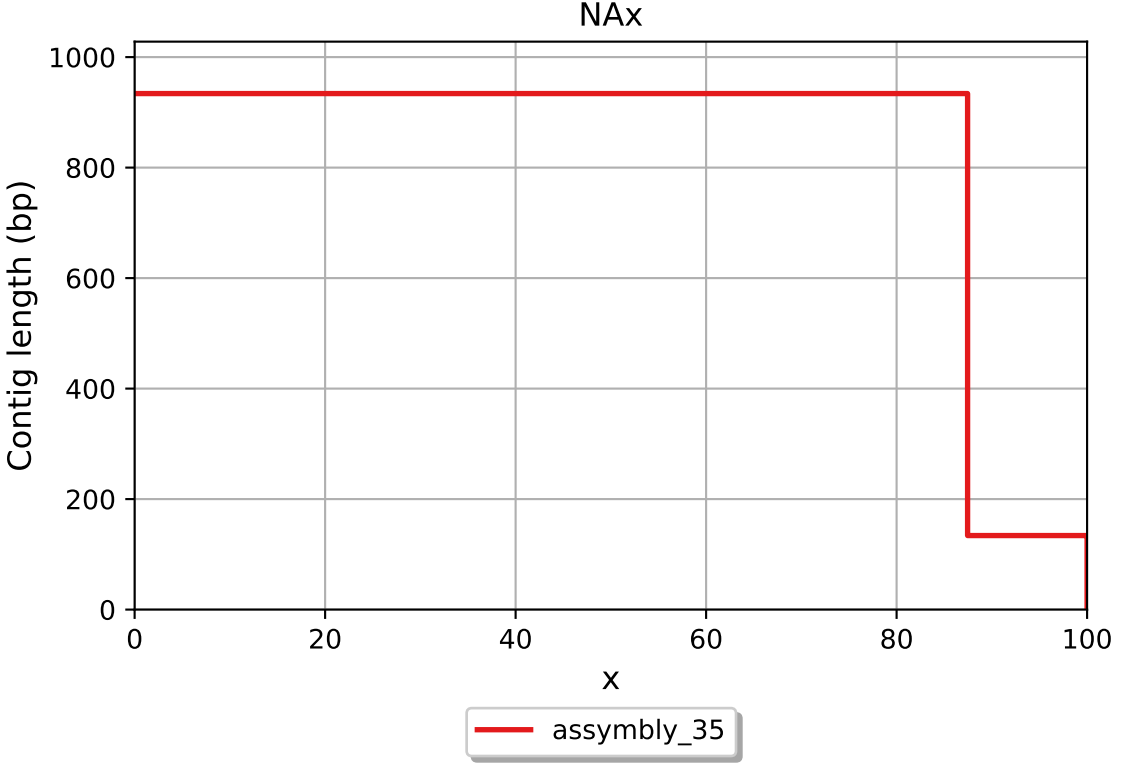

GC content
windows
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assymbly_35
Reference

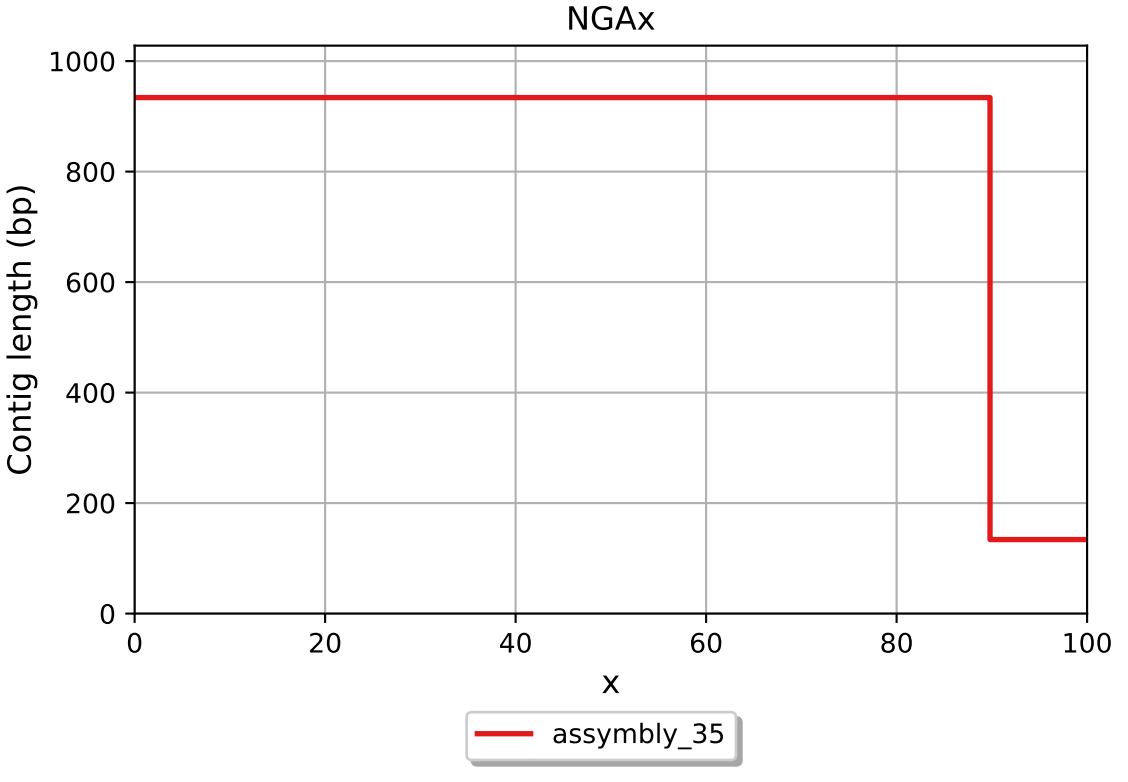

assymbly_35 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assymbly_35


Misassemblies
5
4
3
2
1
0
assymbly_35


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
assymbly_35


Cumulative length (aligned contigs)
Cumulative length (bp)
0
200
400
600
800
1000
0
1
2
Contig index
assymbly_35
Reference


NAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
assymbly_35


NGAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
assymbly_35