Report	assembly
# contigs (>= 0 bp)	21
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	12119410
Total length (>= 1000 bp)	12119410
Total length (>= 5000 bp)	12117316
Total length (>= 10000 bp)	12117316
Total length (>= 25000 bp)	12083761
Total length (>= 50000 bp)	12052444
# contigs	21
Largest contig	1499554
Total length	12119410
Reference length	12157105
GC (%)	38.30
Reference GC (%)	38.15
N50	809074
NG50	809074
N90	430059
NG90	430059
auN	854376.4
auNG	851727.2
L50	6
LG50	6
L90	14
LG90	14
# misassemblies	89
# misassembled contigs	18
Misassembled contigs length	12083761
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 15 part
Unaligned length	85785
Genome fraction (%)	97.266
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	211.62
# indels per 100 kbp	21.74
Largest alignment	843303
Total aligned length	12030510
NA50	284119
NGA50	284119
NA90	109892
NGA90	107862
auNA	373426.9
auNGA	372269.1
LA50	12
LGA50	12
LA90	40
LGA90	41

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

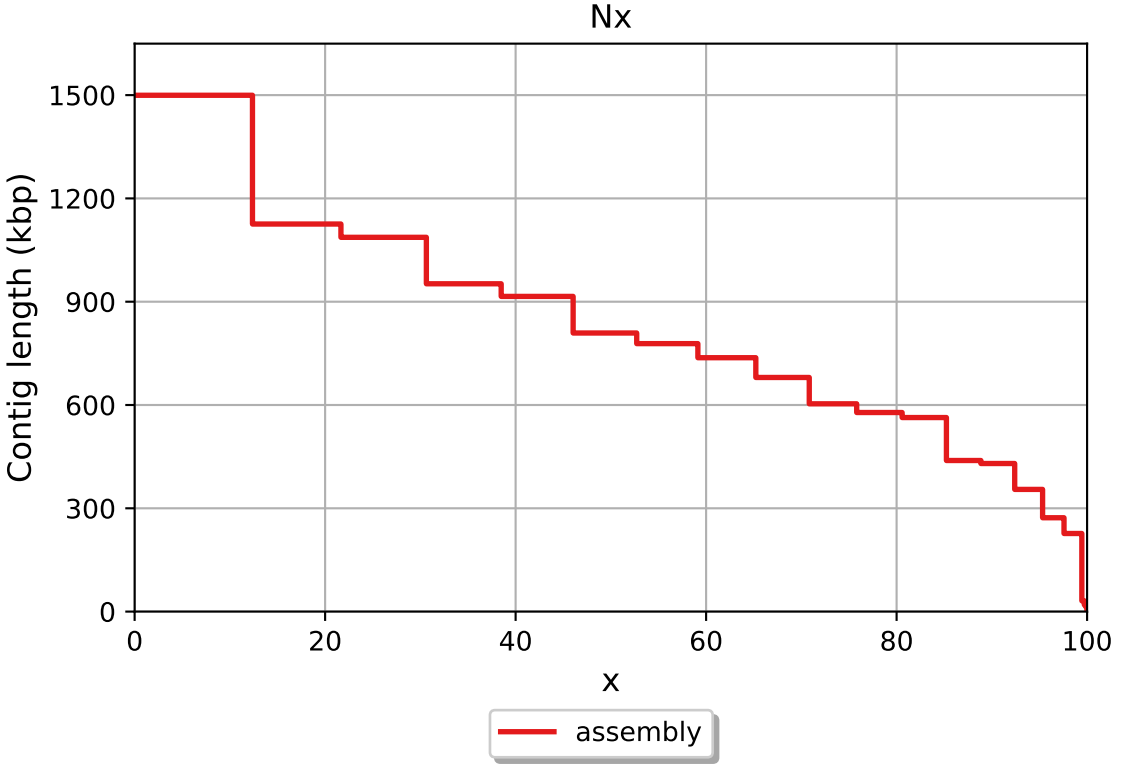
	assembly
# misassemblies	89
# contig misassemblies	89
# c. relocations	32
# c. translocations	57
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	18
Misassembled contigs length	12083761
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	25459
# indels	2616
# indels (<= 5 bp)	2230
# indels (> 5 bp)	386
Indels length	14429

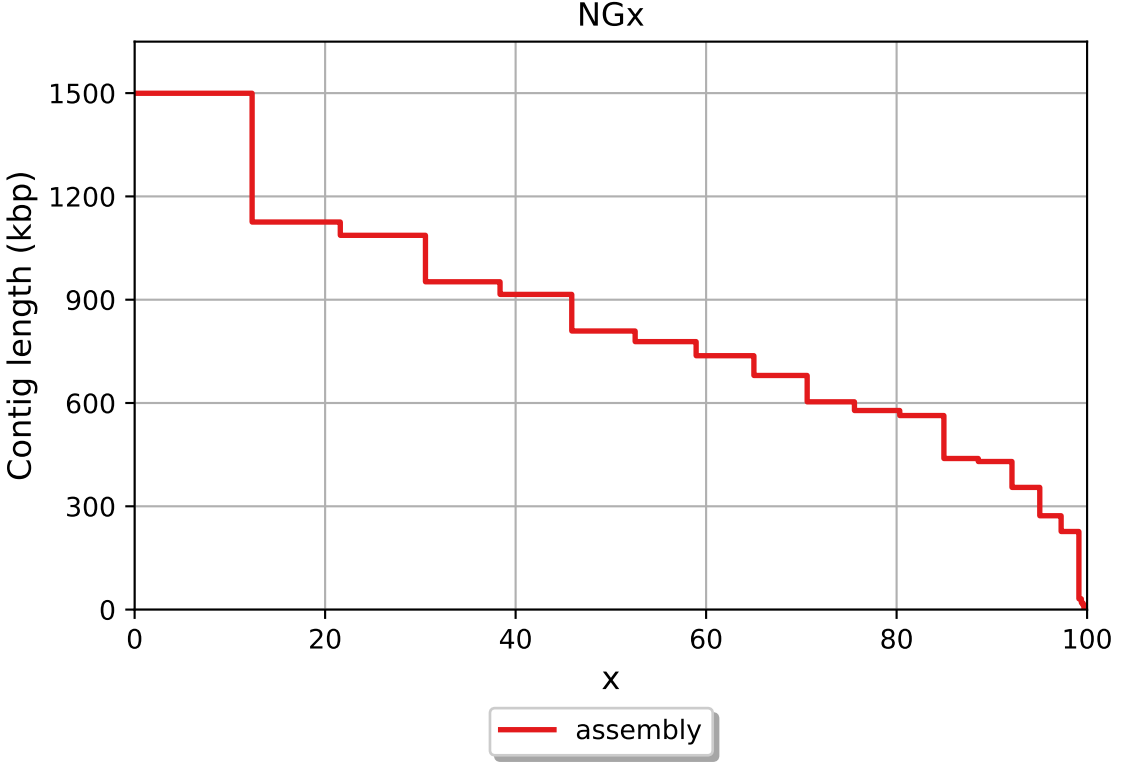
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

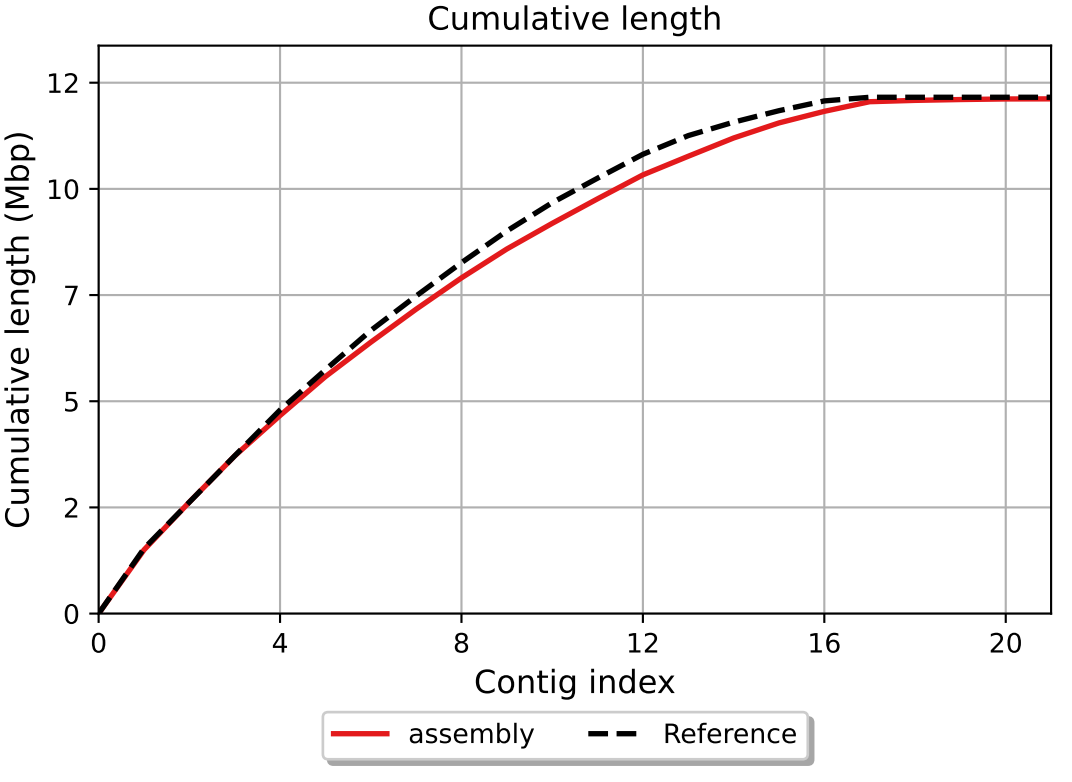
Unaligned report

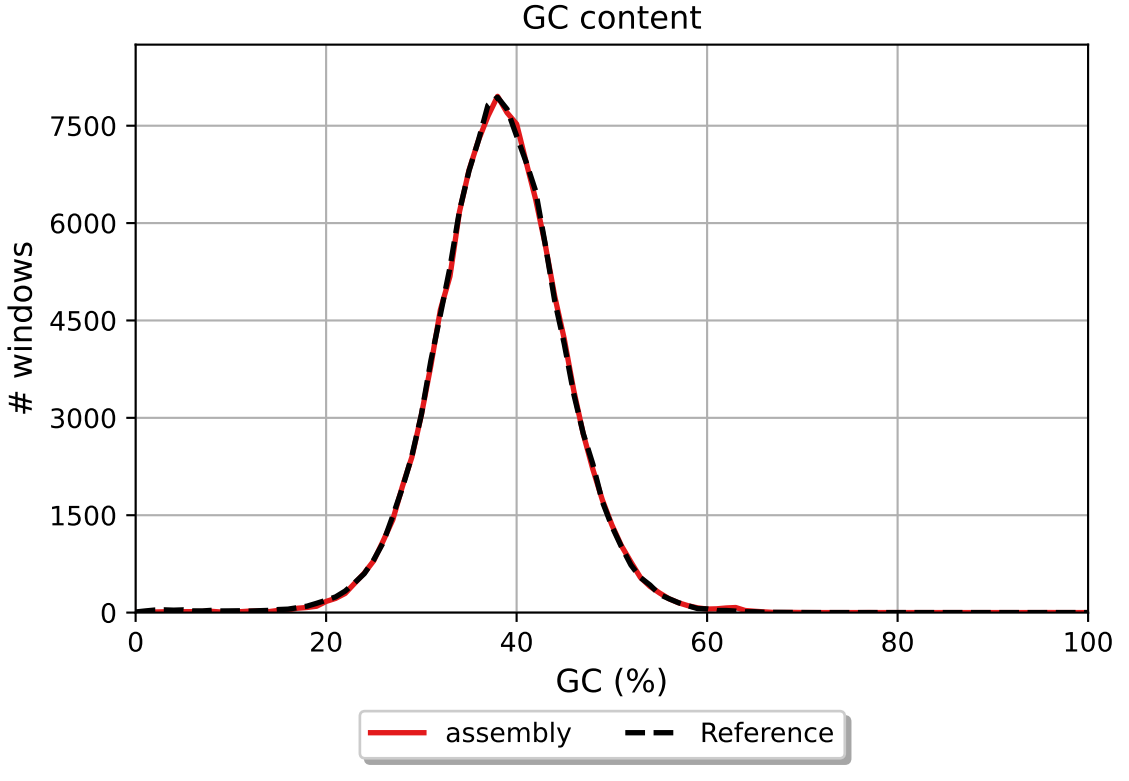
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	85785
# N's	0

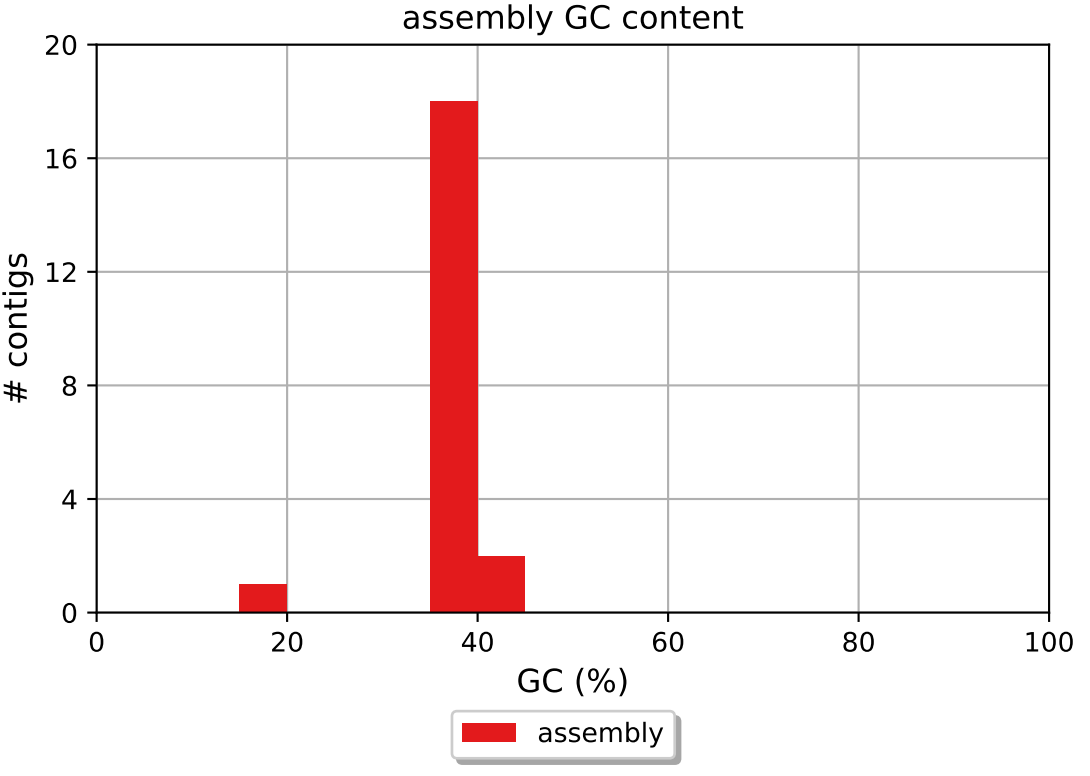
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

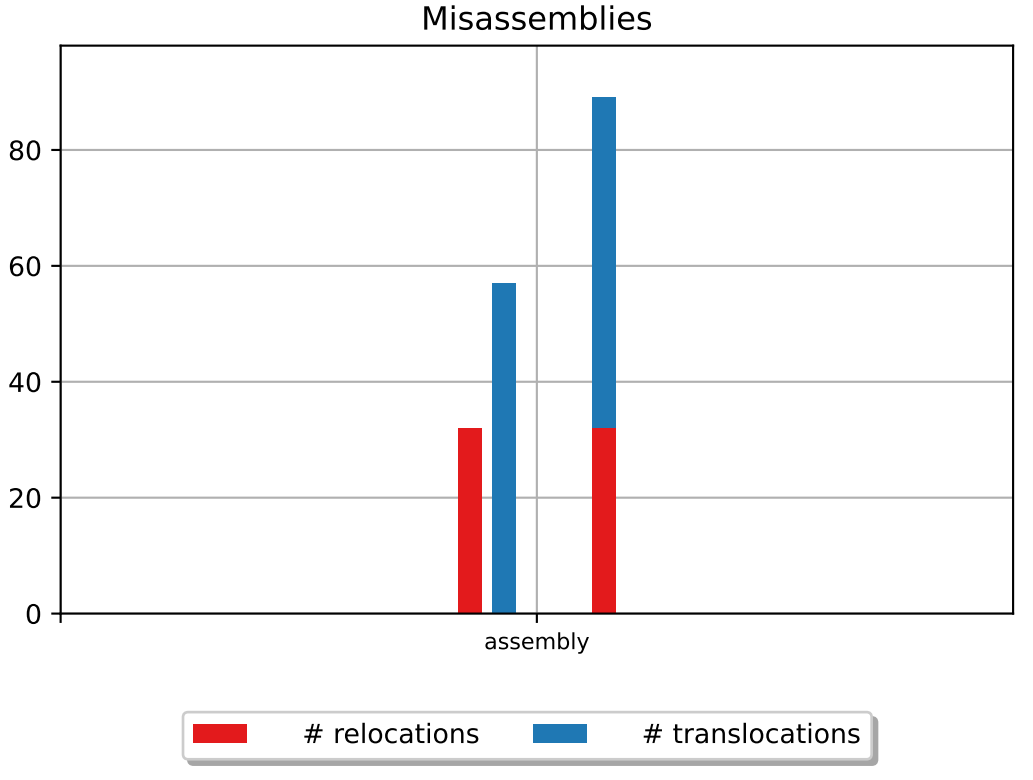

Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
assembly

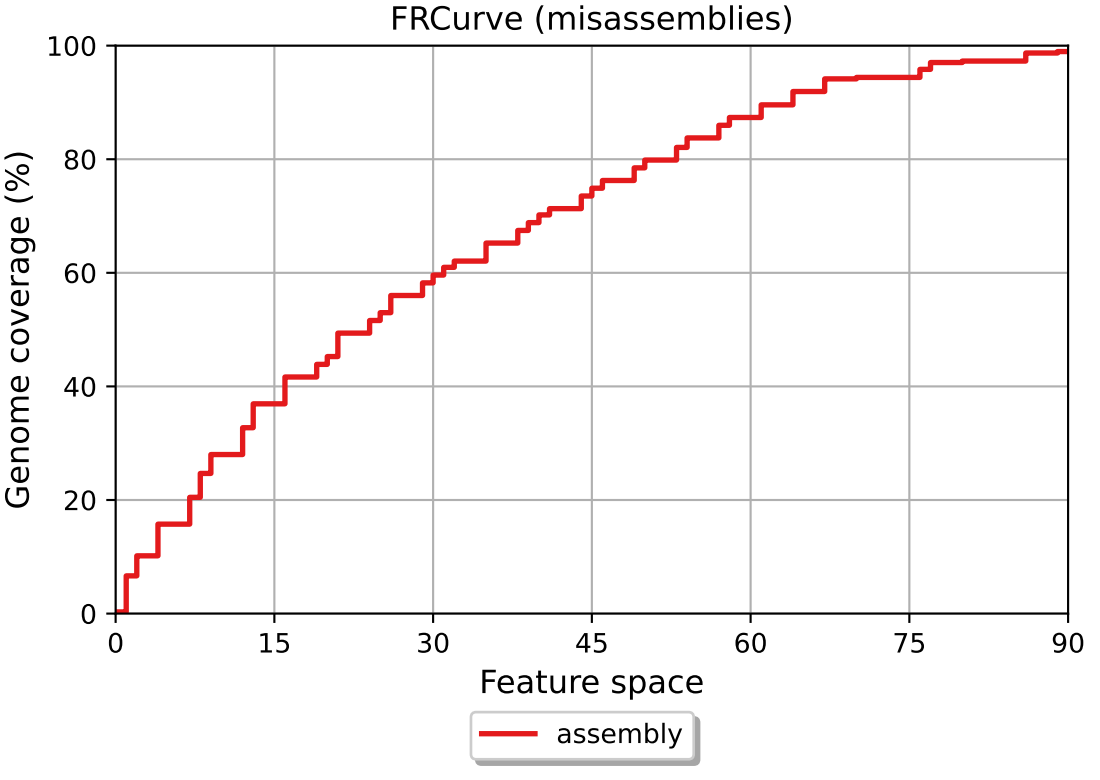

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
assembly

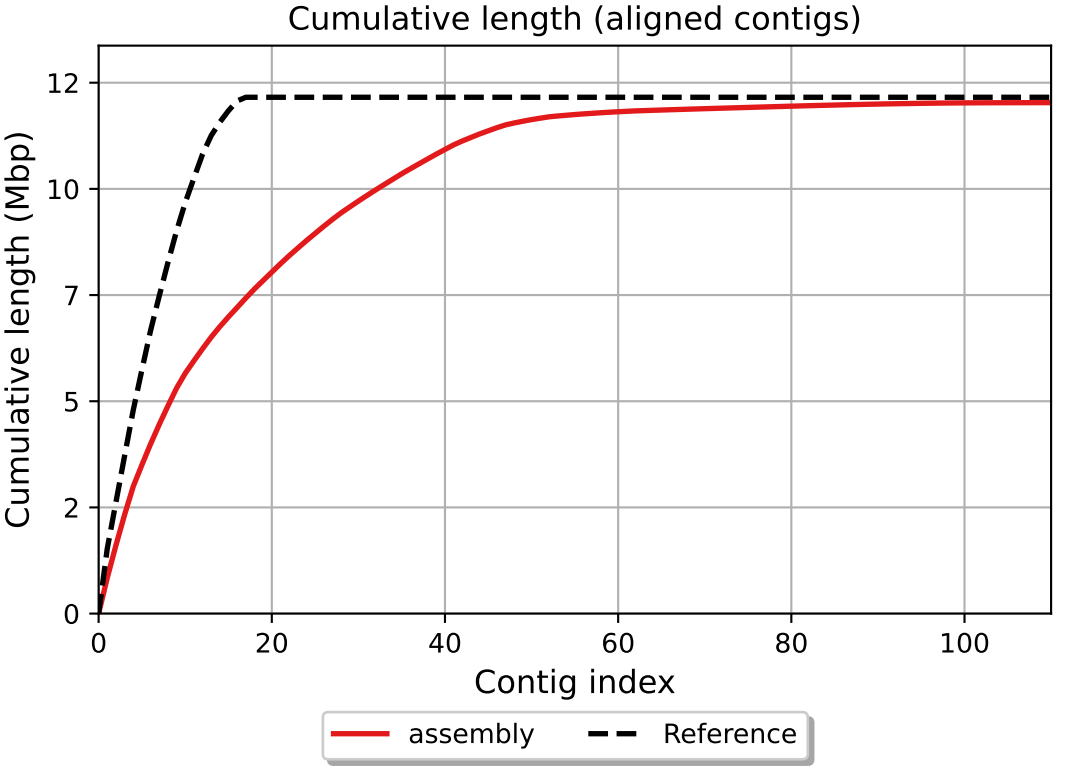

Cumulative length
Cumulative length (Mbp)
0
2
5
7
10
12
0
4
8
12
16
20
Contig index
assembly
Reference

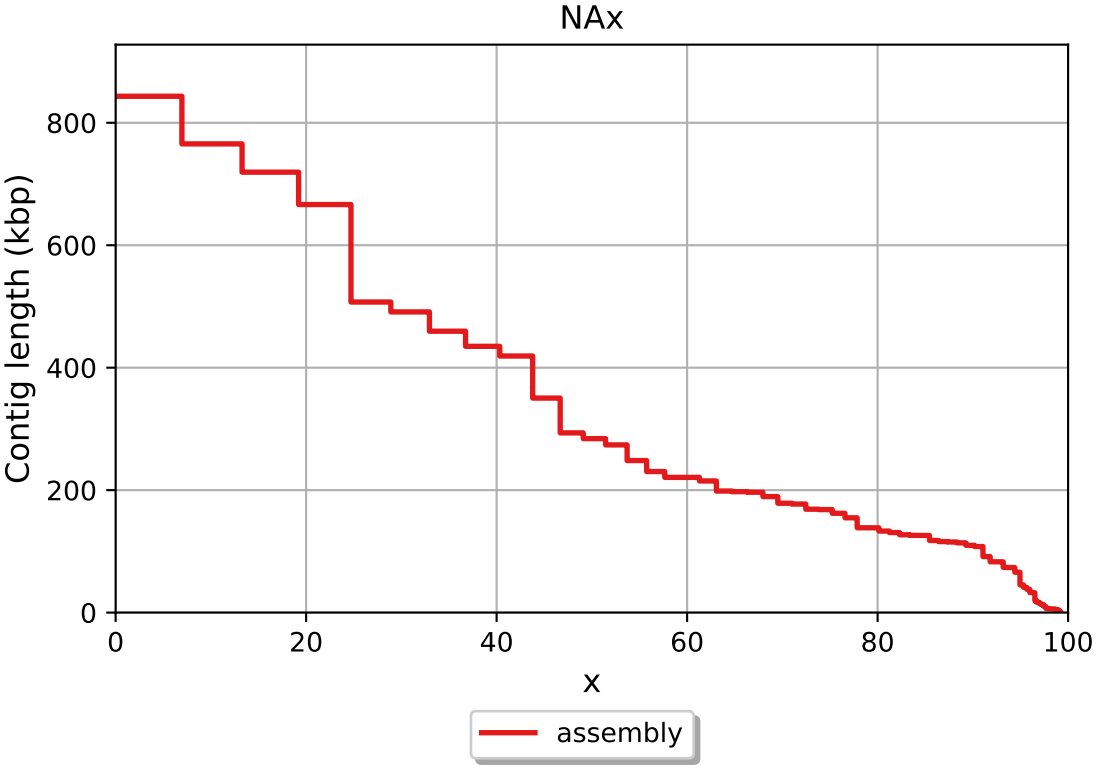

GC content
windows
7500
6000
4500
3000
1500
0
0
20
40
60
80
100
GC (%)
assembly
Reference

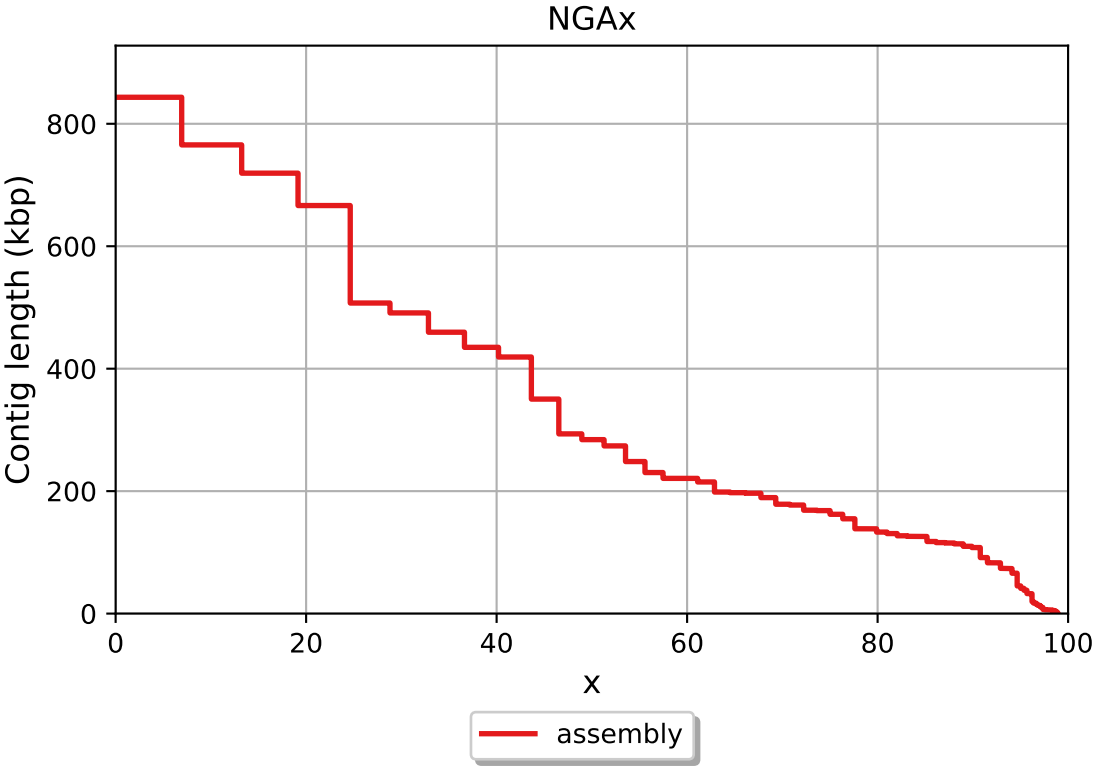

assembly GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
assembly


Misassemblies
80
60
40
20
0
assembly
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
75
90
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
Contig index
assembly
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
assembly


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
assembly