Report

	assembly
# contigs (>= 0 bp)	93
# contigs (>= 1000 bp)	93
# contigs (>= 5000 bp)	92
# contigs (>= 10000 bp)	91
# contigs (>= 25000 bp)	69
# contigs (>= 50000 bp)	36
Total length (>= 0 bp)	4333634
Total length (>= 1000 bp)	4333634
Total length (>= 5000 bp)	4329652
Total length (>= 10000 bp)	4321011
Total length (>= 25000 bp)	3898840
Total length (>= 50000 bp)	2810496
# contigs	93
Largest contig	155648
Total length	4333634
Reference length	4639675
GC (%)	50.62
Reference GC (%)	50.79
N50	61597
NG50	60121
N75	34871
NG75	30767
L50	25
LG50	28
L75	47
LG75	54
# misassemblies	16
# misassembled contigs	10
Misassembled contigs length	586450
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 47 part
Unaligned length	143387
Genome fraction (%)	88.312
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.85
# indels per 100 kbp	552.43
Largest alignment	154705
Total aligned length	4186218
NA50	56579
NGA50	55056
NA75	30502
NGA75	27296
LA50	26
LGA50	29
LA75	53
LGA75	61

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

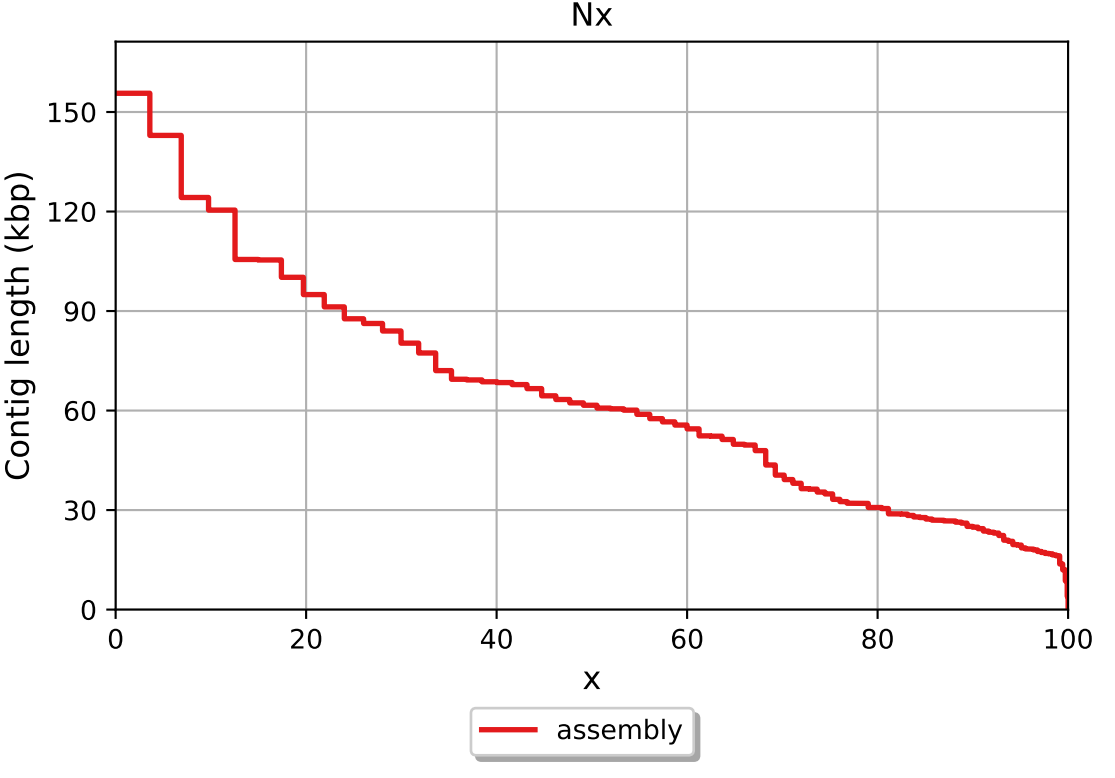
	assembly
# misassemblies	16
# contig misassemblies	16
# c. relocations	13
# c. translocations	0
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	586450
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1633
# indels	22635
# indels (<= 5 bp)	22617
# indels (> 5 bp)	18
Indels length	24116

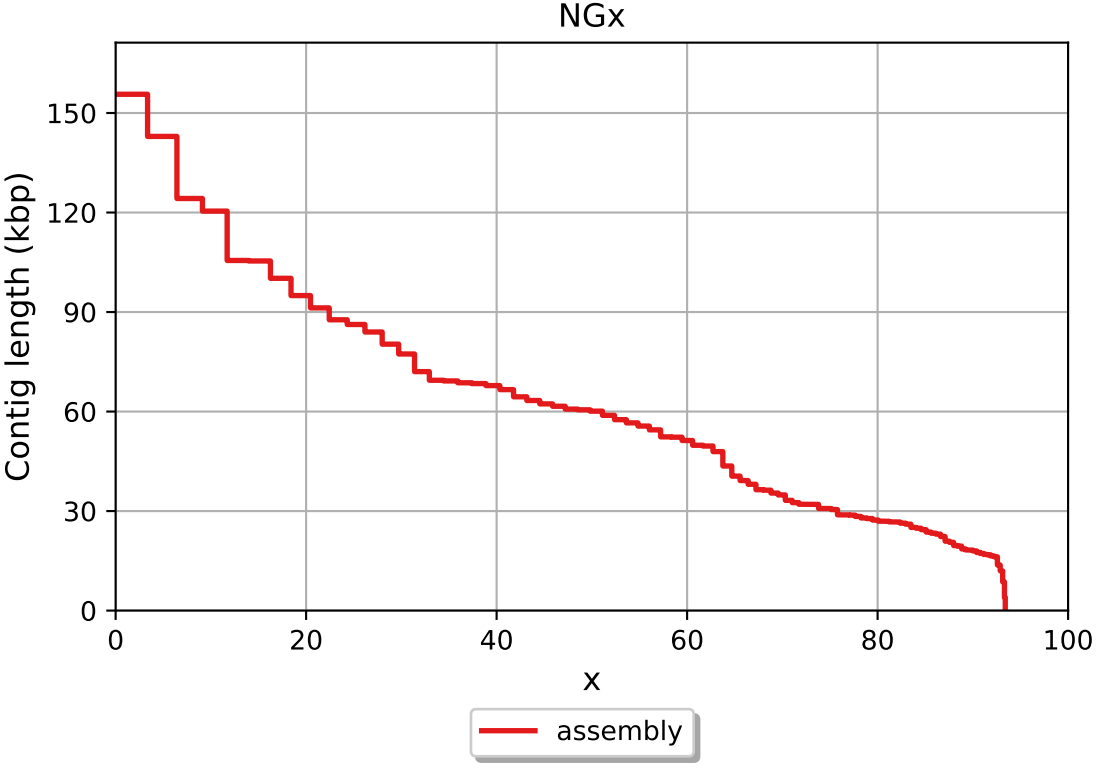
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

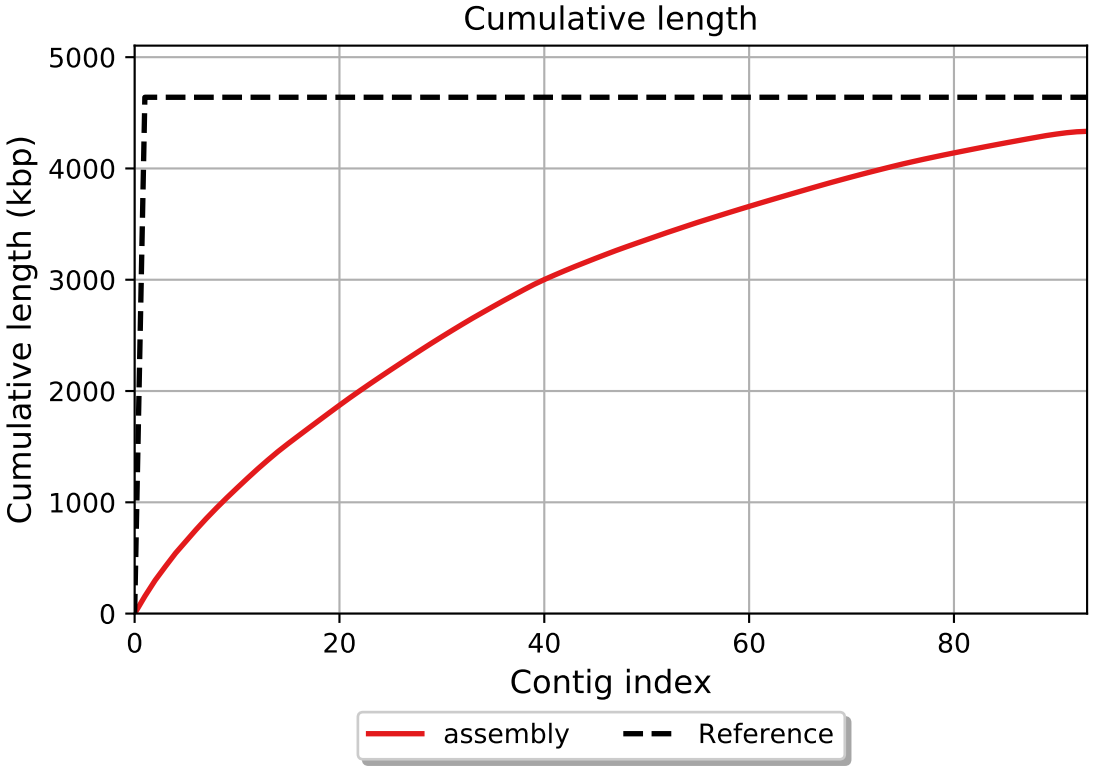
Unaligned report

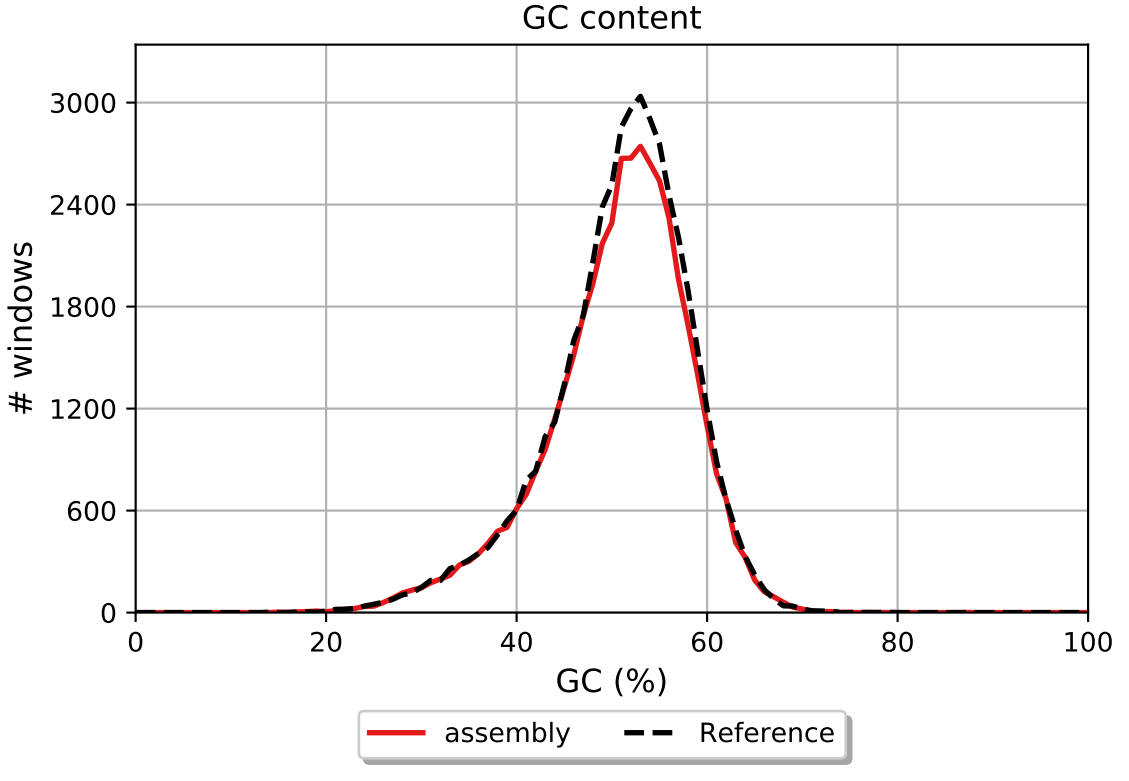
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	47
Partially unaligned length	143387
# N's	0

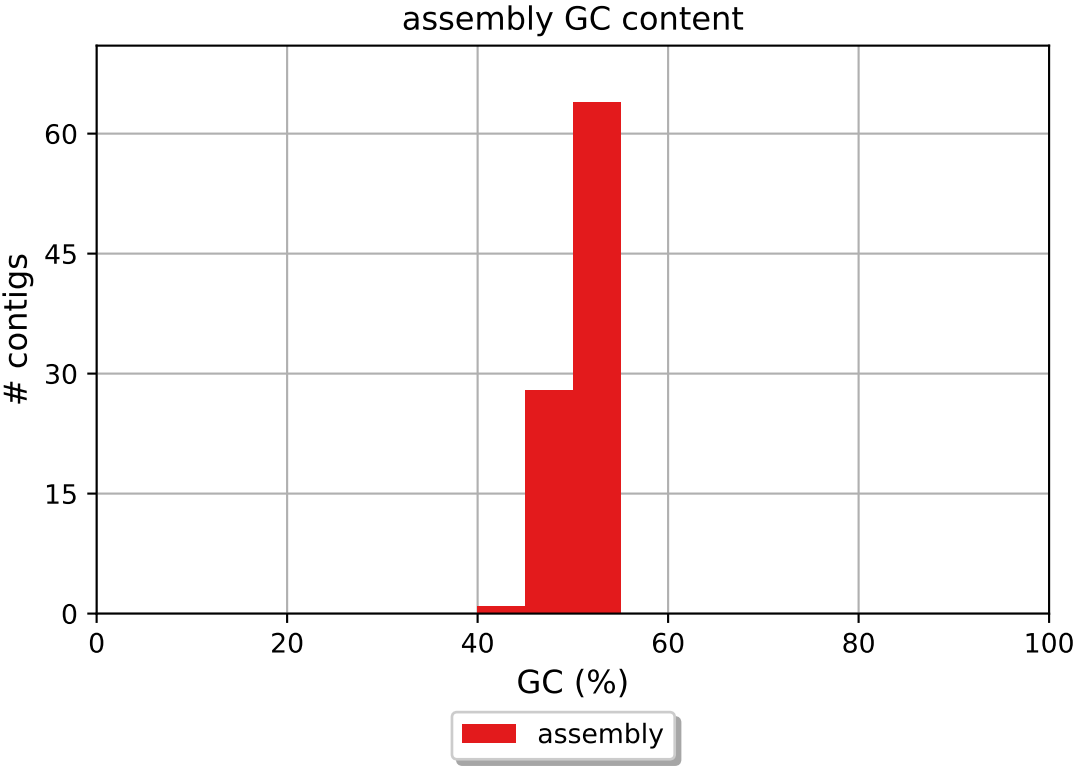
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

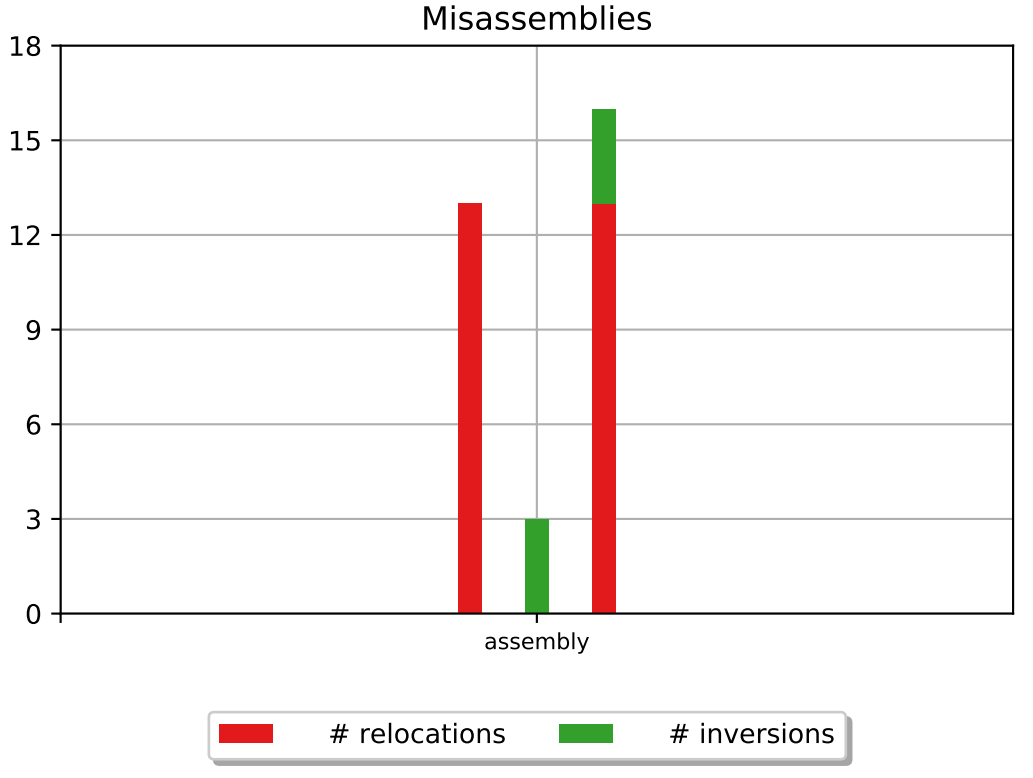

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
assembly

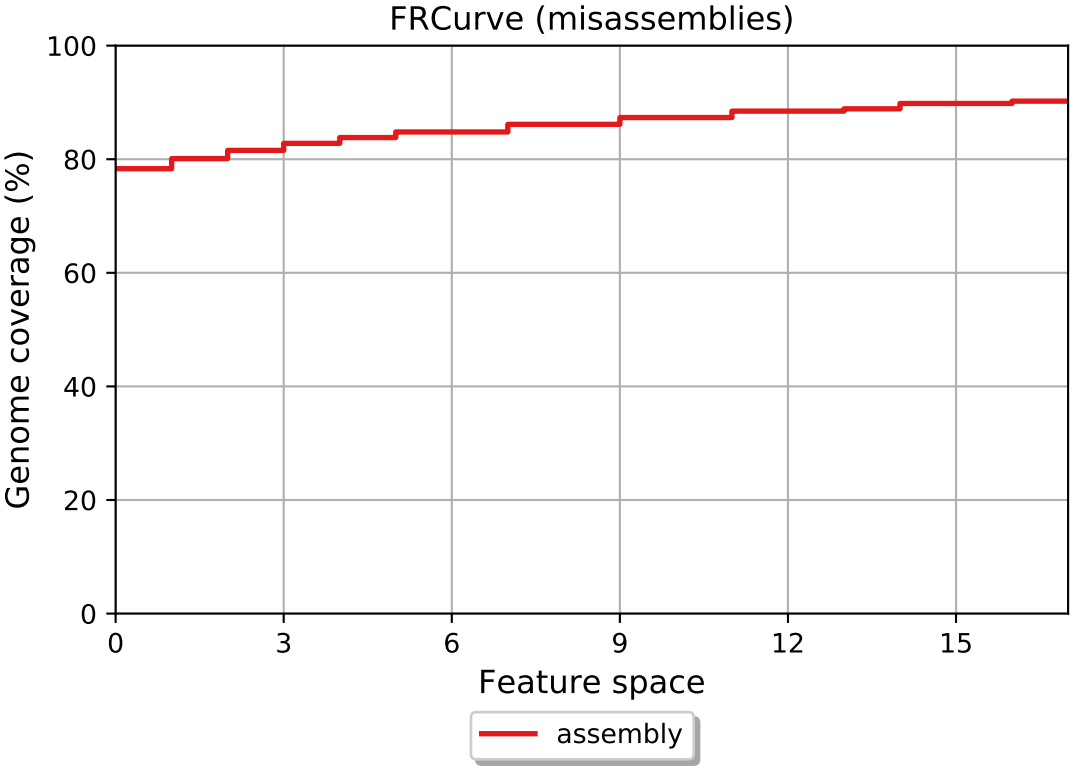

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
assembly

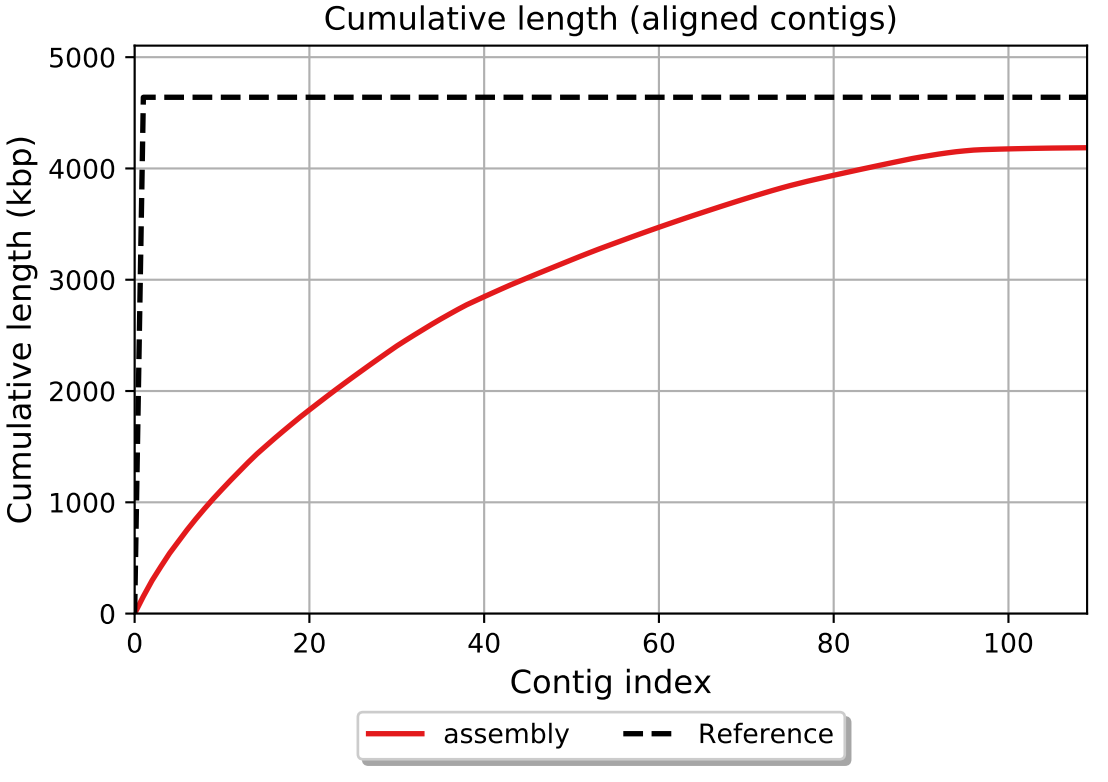

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
assembly
Reference

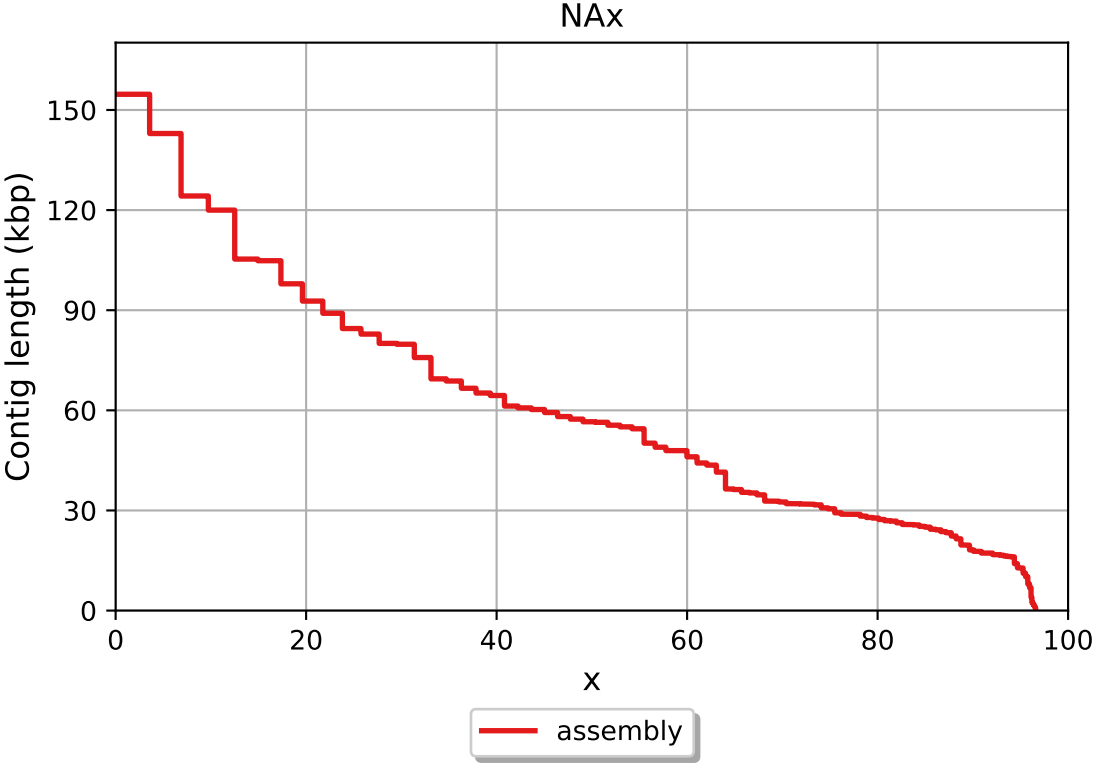

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
assembly
Reference

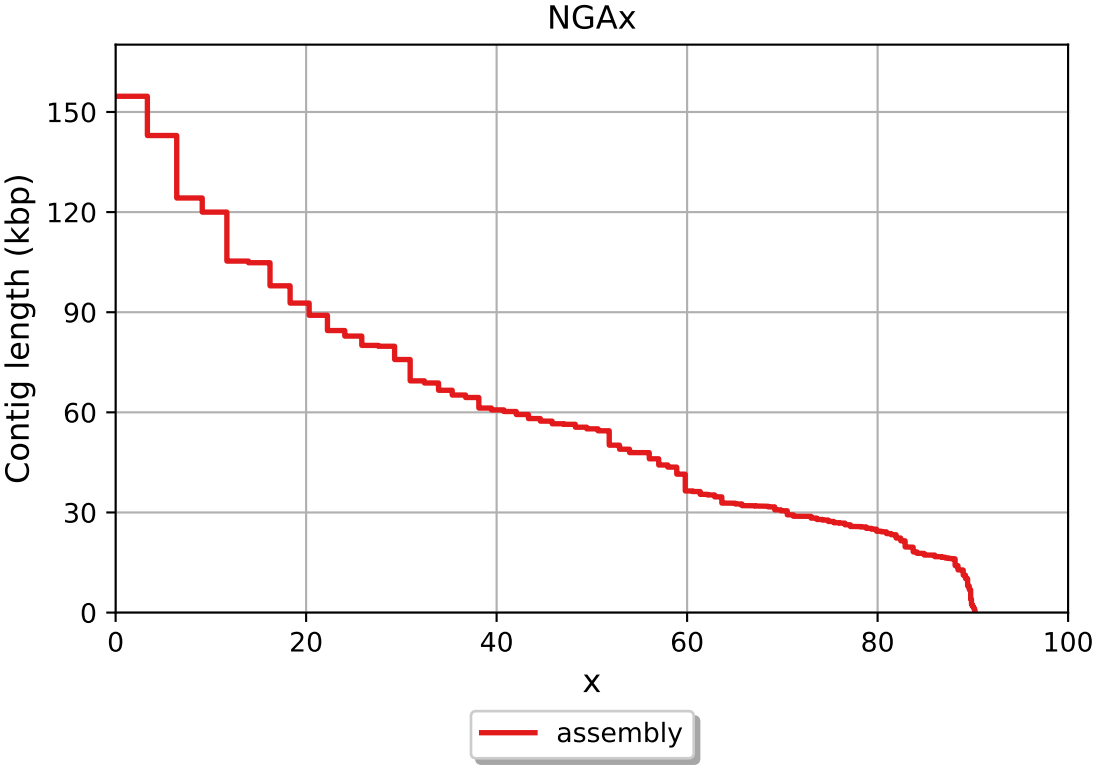

assembly GC content
contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
assembly


Misassemblies
18
15
12
9
6
3
0
assembly
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
assembly
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
assembly


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
assembly