Report

	soap_assembly
# contigs (>= 0 bp)	1860740
# contigs (>= 1000 bp)	976
# contigs (>= 5000 bp)	185
# contigs (>= 10000 bp)	35
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	144429265
Total length (>= 1000 bp)	3481709
Total length (>= 5000 bp)	1519455
Total length (>= 10000 bp)	474977
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1860740
Largest contig	23413
Total length	144429265
Reference length	3990777
GC (%)	43.23
Reference GC (%)	36.99
N50	68
NG50	3893
N75	52
NG75	1963
L50	507130
LG50	293
L75	1144776
LG75	648
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	8441
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	1848491 + 0 part
Unaligned length	139416614
Genome fraction (%)	99.541
Duplication ratio	1.283
# N's per 100 kbp	0.00
# mismatches per 100 kbp	642.01
# indels per 100 kbp	66.89
Largest alignment	23413
Total aligned length	4831633
NGA50	3888
NGA75	1957
LGA50	294
LGA75	649

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

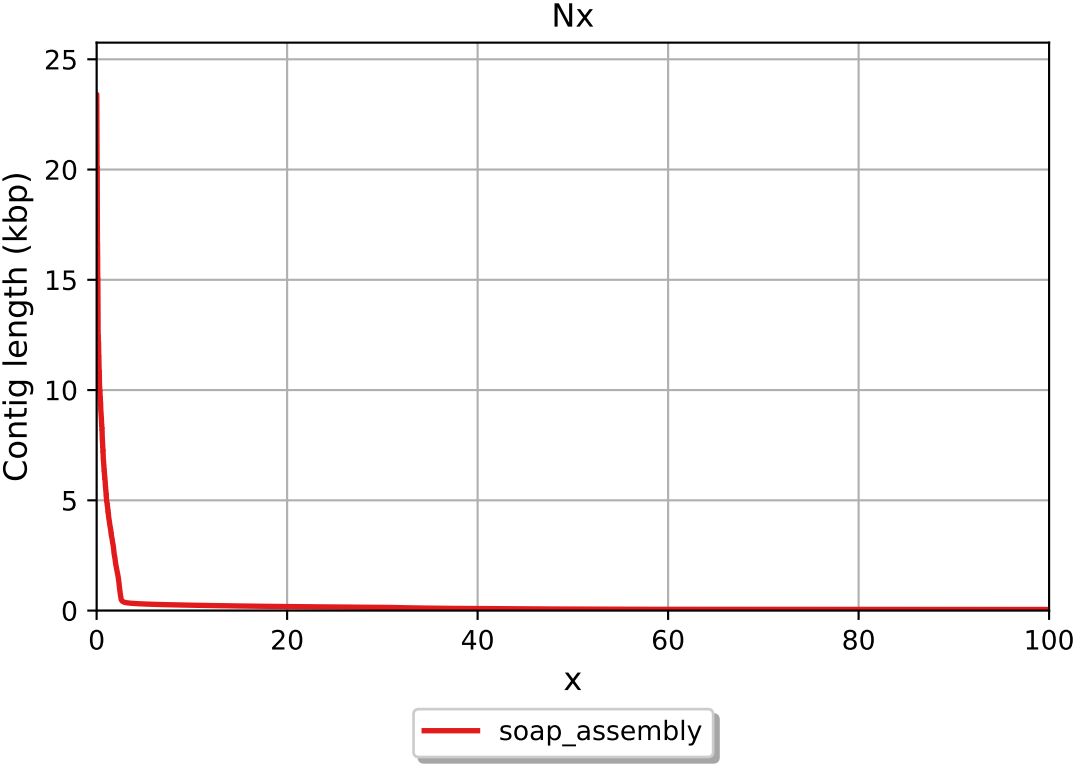
	soap_assembly
# misassemblies	5
# contig misassemblies	5
# c. relocations	5
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	8441
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	25080
# indels	2613
# indels (<= 5 bp)	2592
# indels (> 5 bp)	21
Indels length	4243

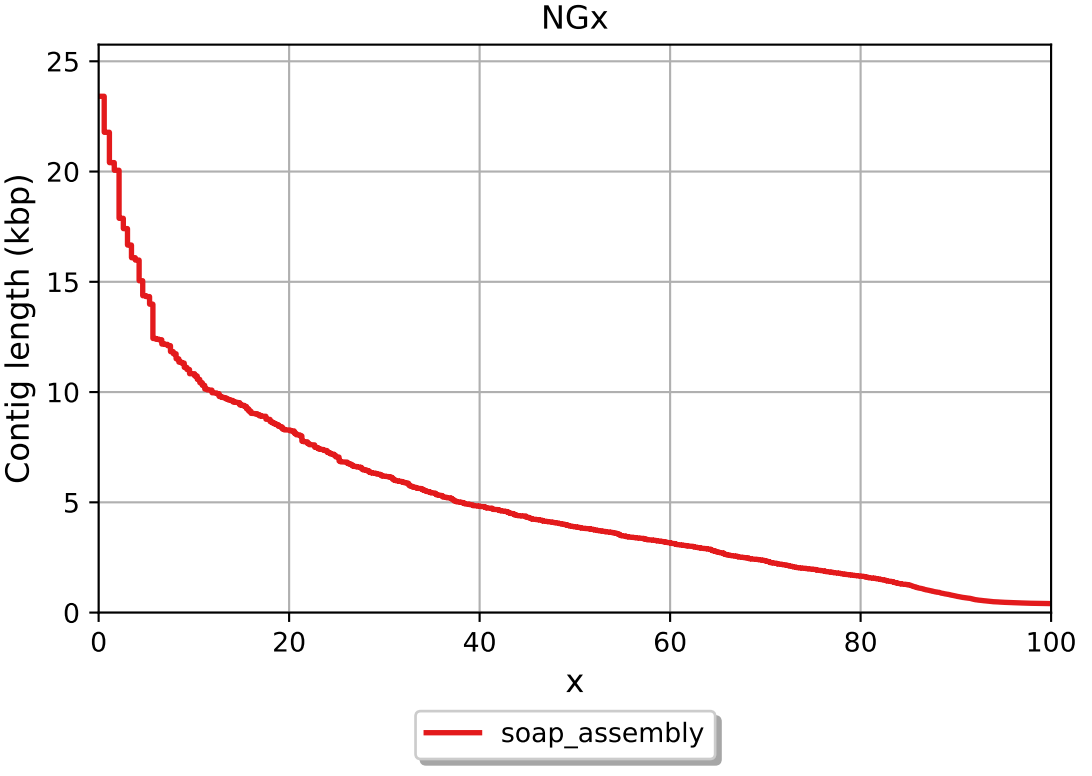
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

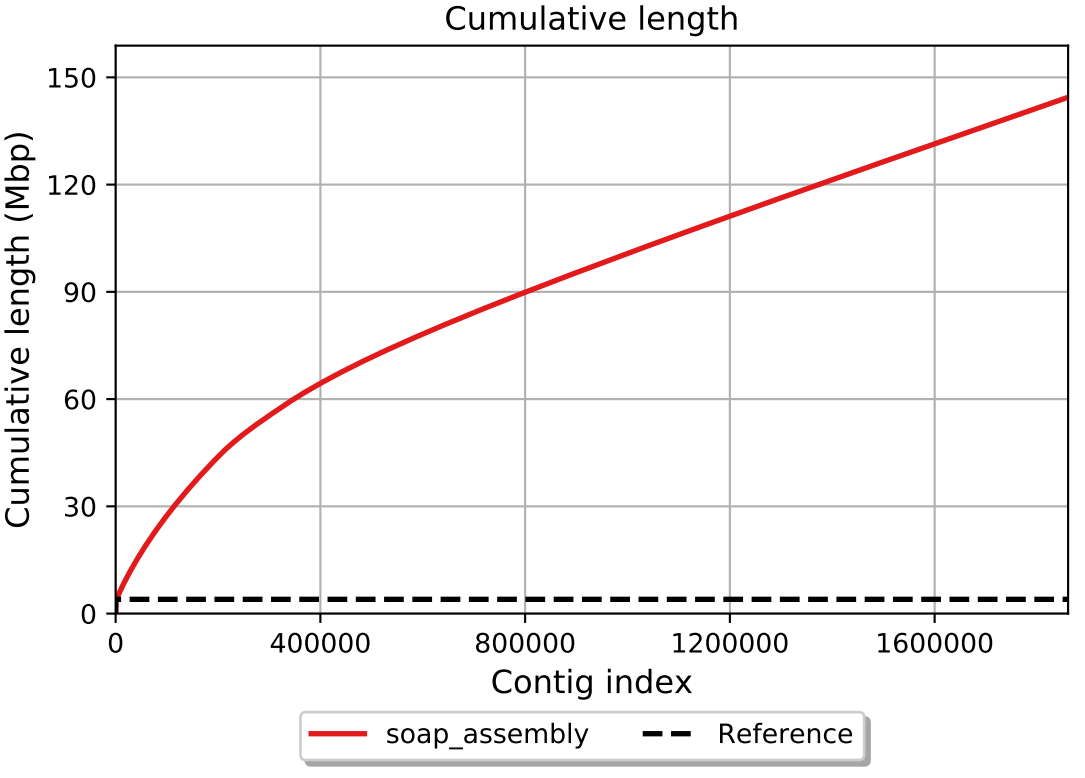
Unaligned report

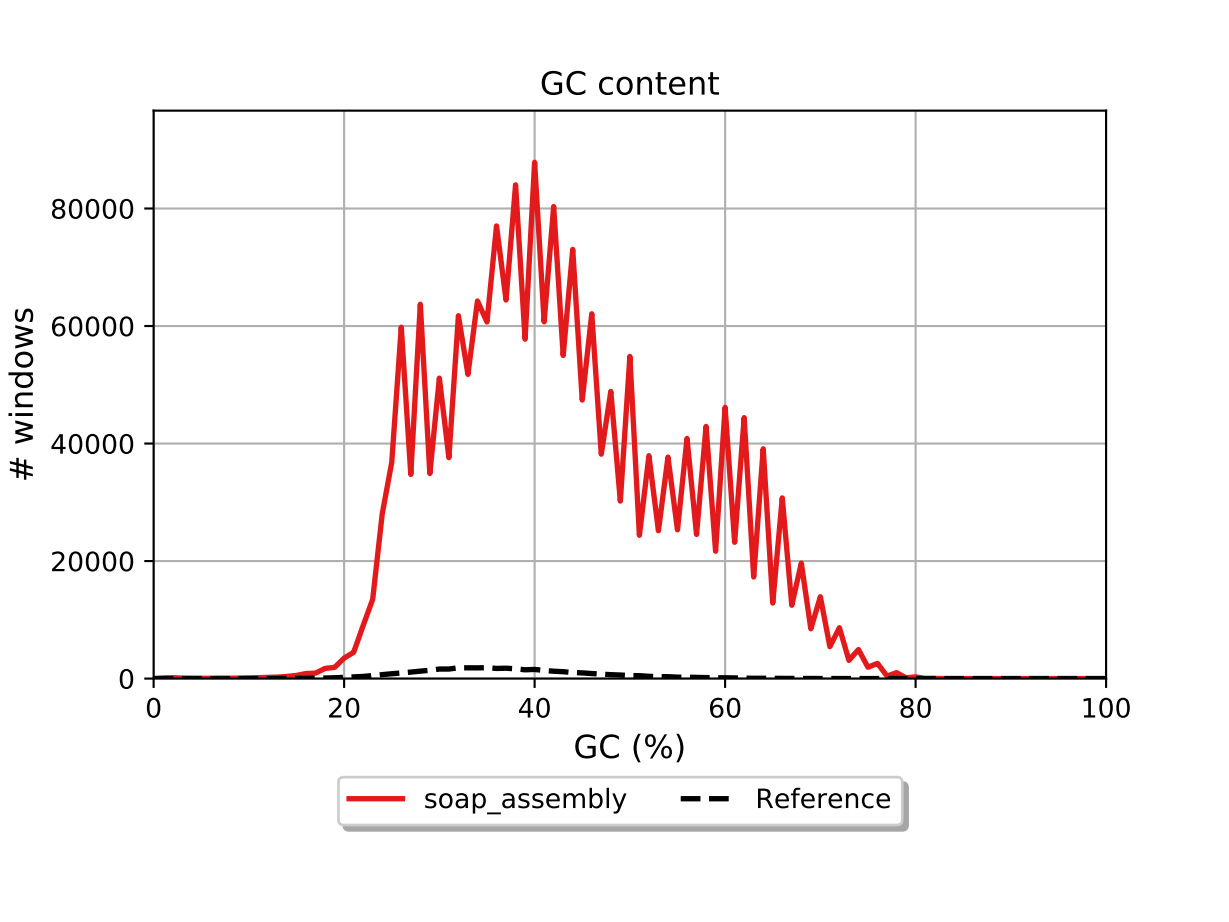
	soap_assembly
# fully unaligned contigs	1848491
Fully unaligned length	139416614
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

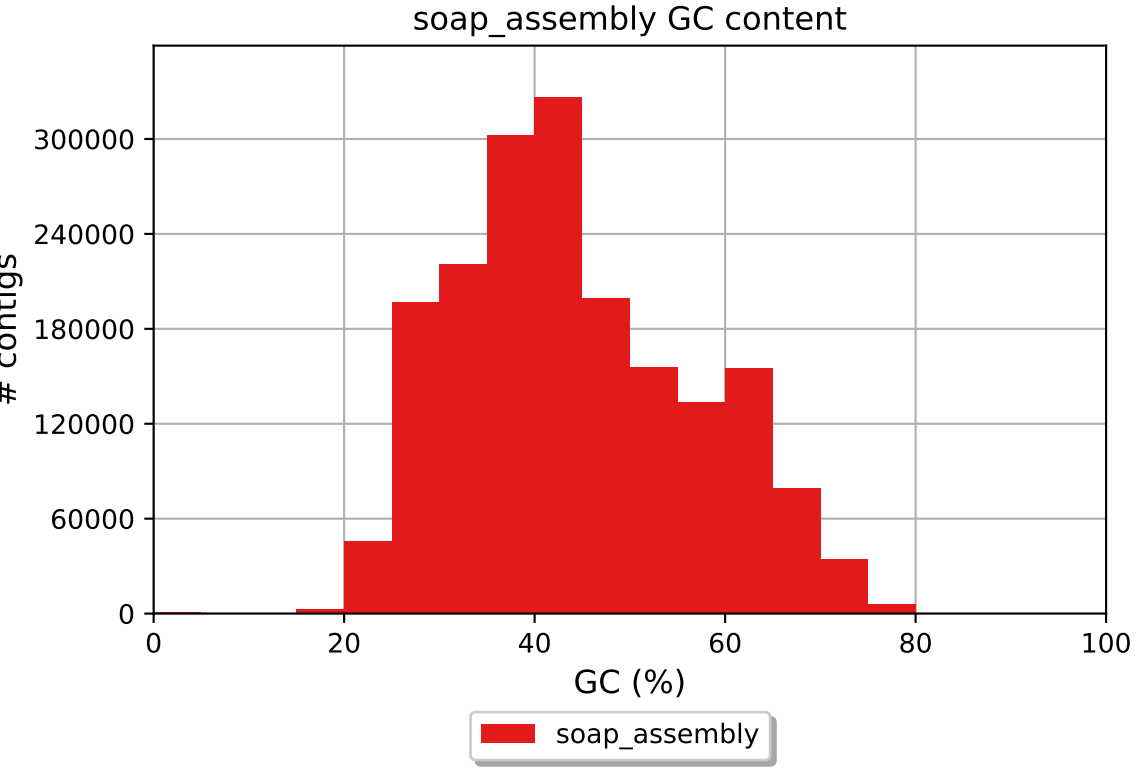
All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

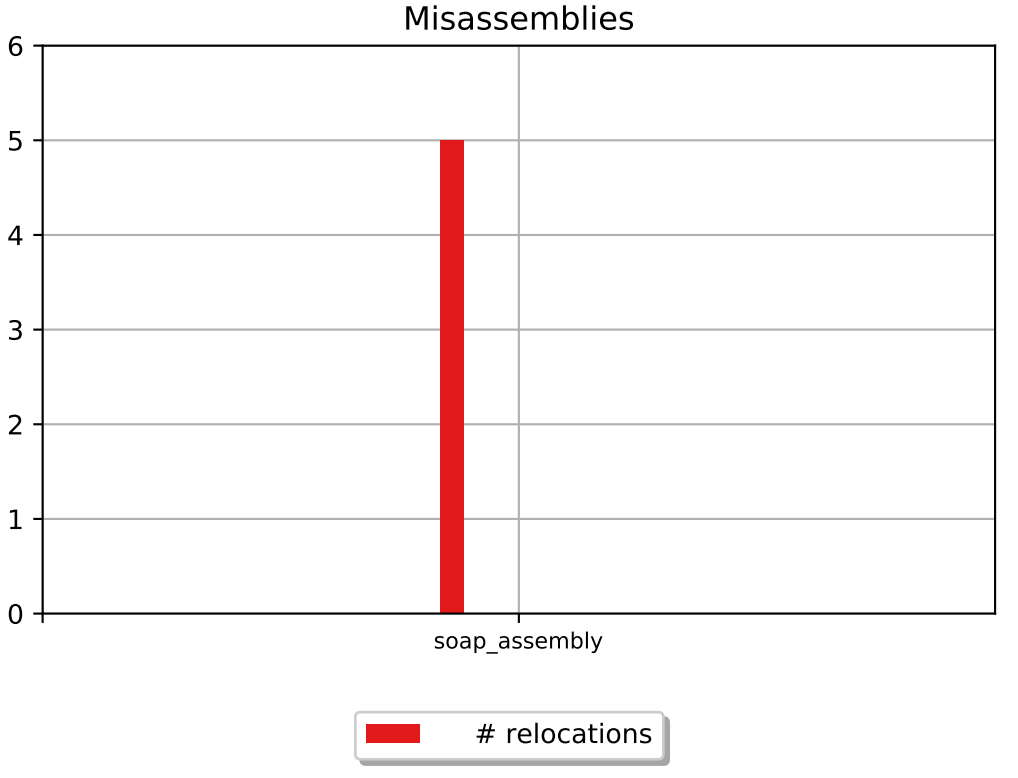

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
soap_assembly

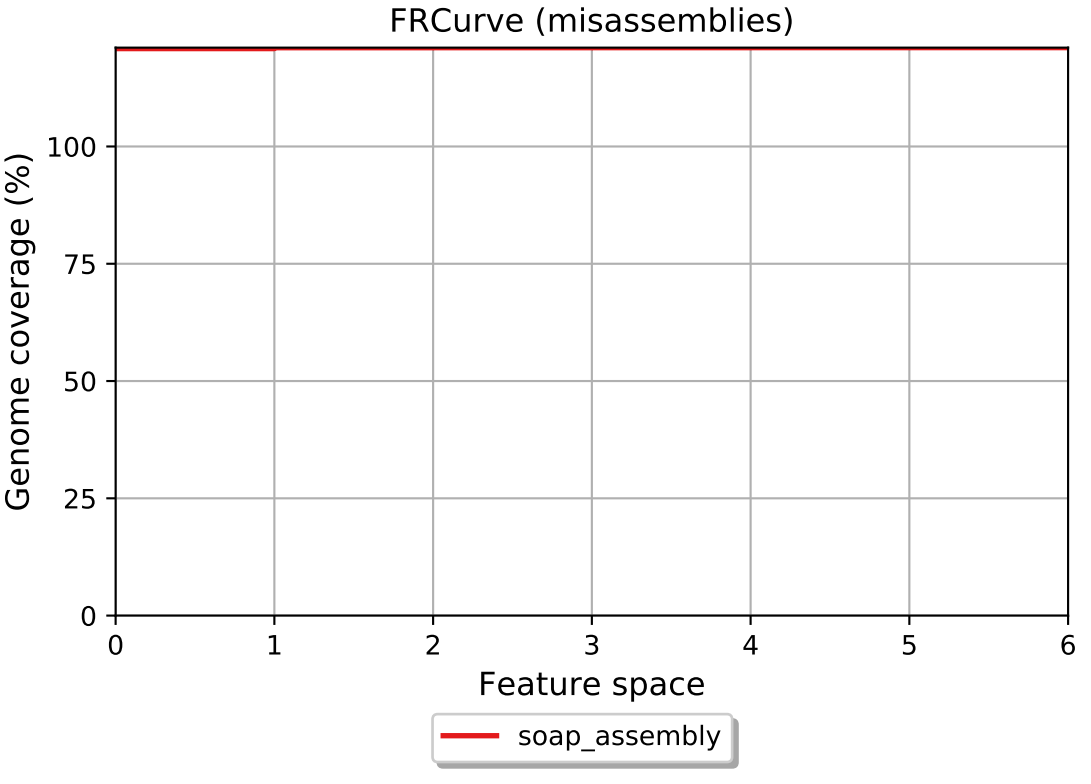

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
soap_assembly

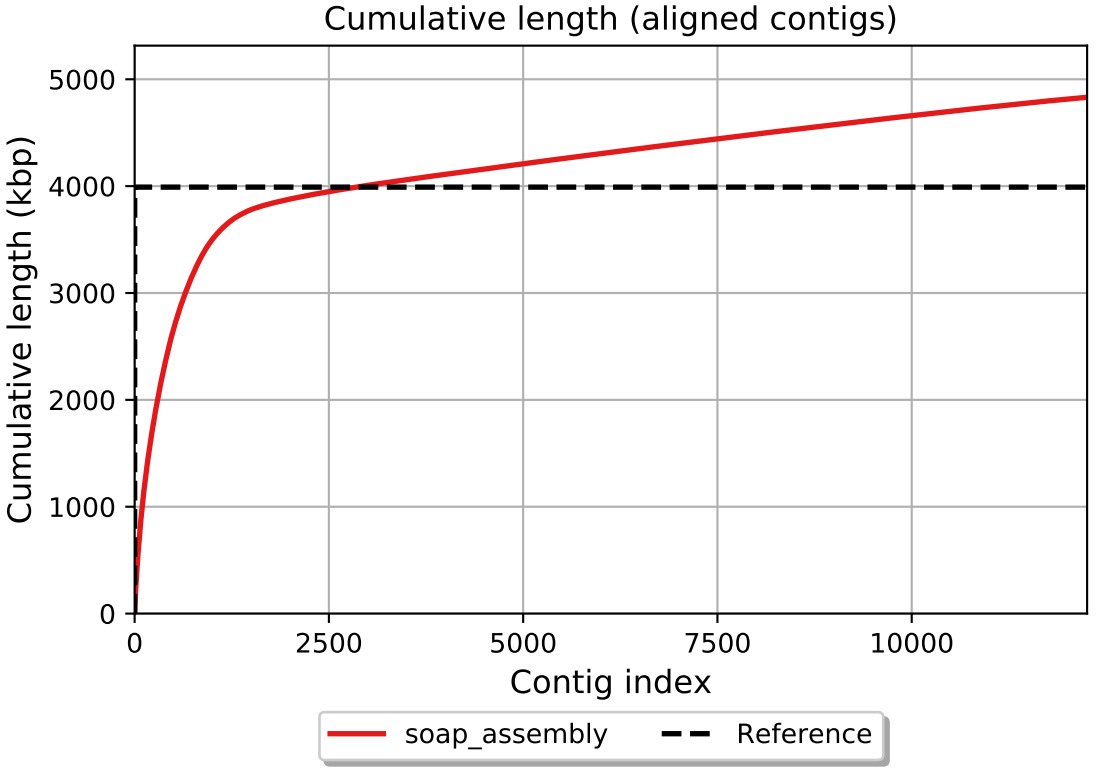

Cumulative length
Cumulative length (Mbp)
150
120
90
60
30
0
0
400000
800000
1200000
1600000
Contig index
soap_assembly
Reference

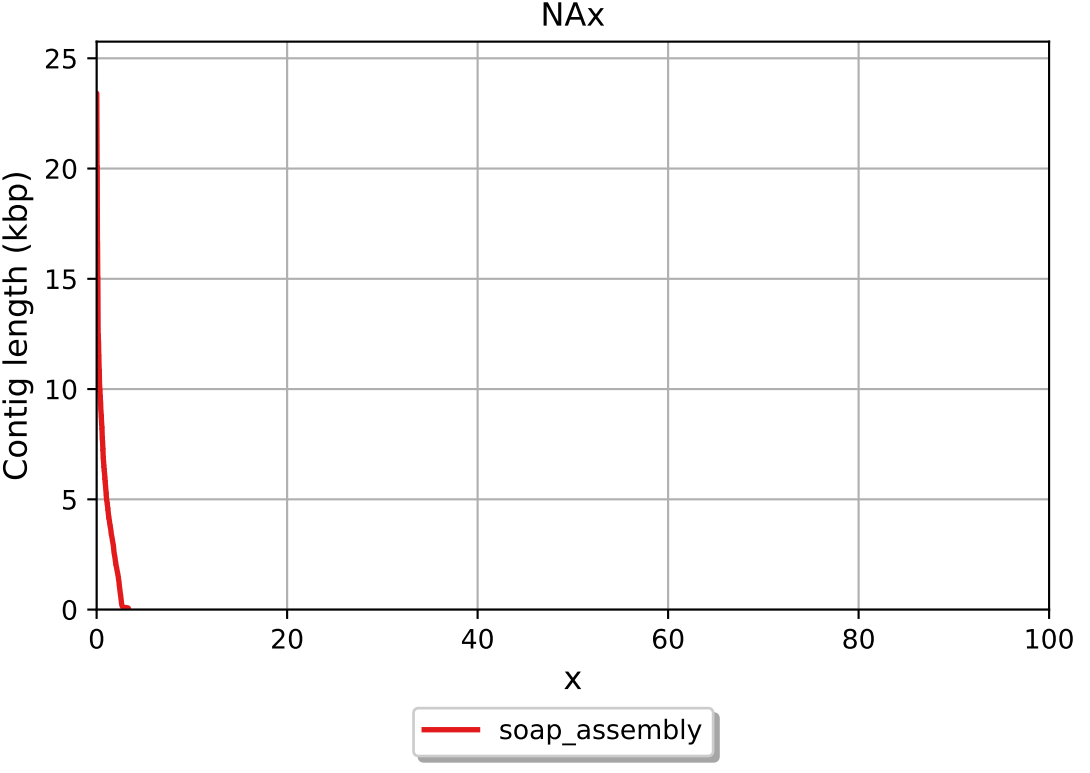

GC content
windows
80000
60000
40000
20000
0
0
20
40
60
80
100
GC (%)
soap_assembly
Reference

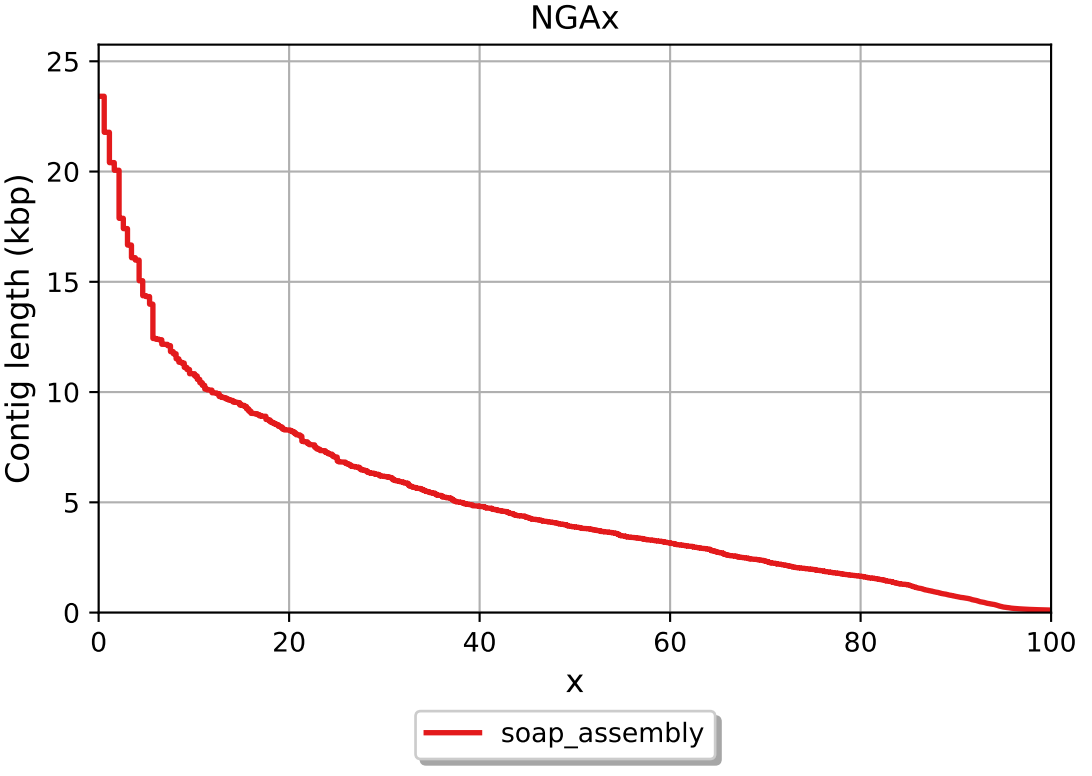

soap_assembly GC content
contigs
300000
240000
180000
120000
60000
0
0
20
40
60
80
100
GC (%)
soap_assembly


Misassemblies
6
5
4
3
2
1
0
soap_assembly
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
75
50
25
0
0
1
2
3
4
5
6
Feature space
soap_assembly


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2500
5000
7500
10000
Contig index
soap_assembly
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
soap_assembly


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
soap_assembly