Report

	TARA_SOC_RAW
# contigs (>= 1000 bp)	167
# contigs (>= 5000 bp)	23
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	741143
Total length (>= 5000 bp)	440718
Total length (>= 10000 bp)	378718
Total length (>= 25000 bp)	278308
Total length (>= 50000 bp)	122423
# contigs	167
Largest contig	63887
Total length	741143
Reference length	7658814
GC (%)	37.52
Reference GC (%)	63.29
N50	10153
N75	2879
L50	13
L75	54
# 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	3
# unaligned contigs	5 + 162 part
Unaligned length	727283
Genome fraction (%)	0.058
Duplication ratio	3.094
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6184.42
# indels per 100 kbp	22.33
Largest alignment	298
Total aligned length	13860
NGA50	-

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

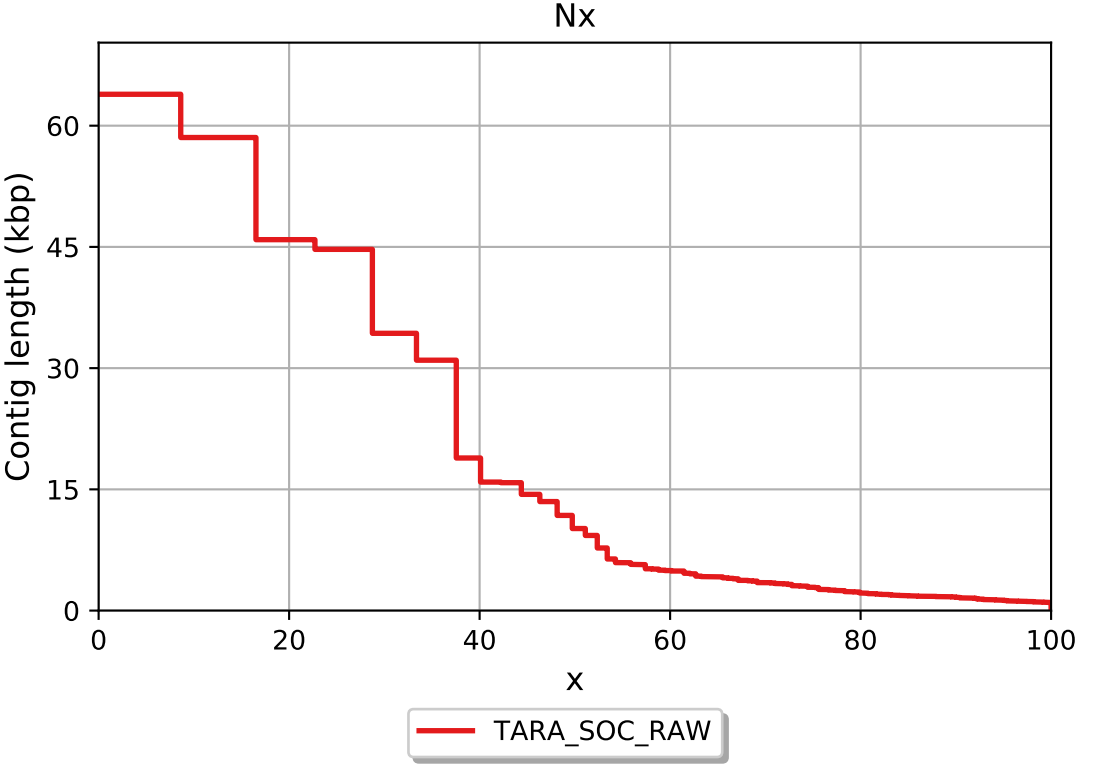
	TARA_SOC_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	162
# possible misassemblies	192
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	277
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	3

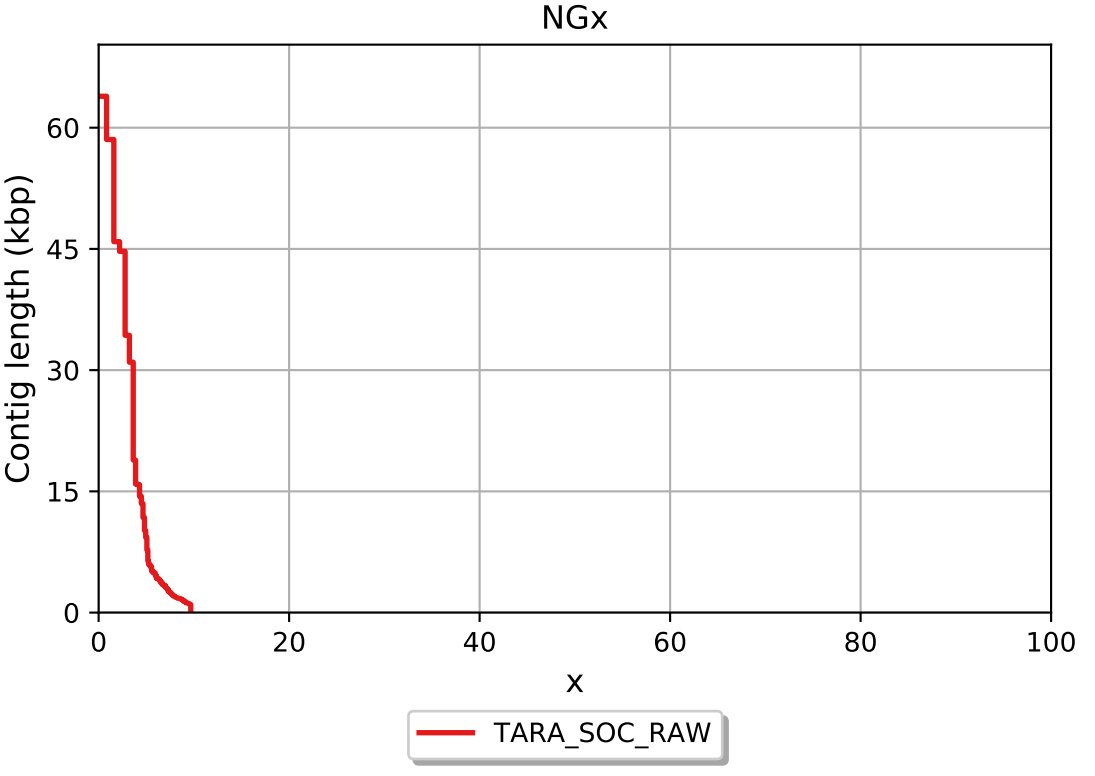
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

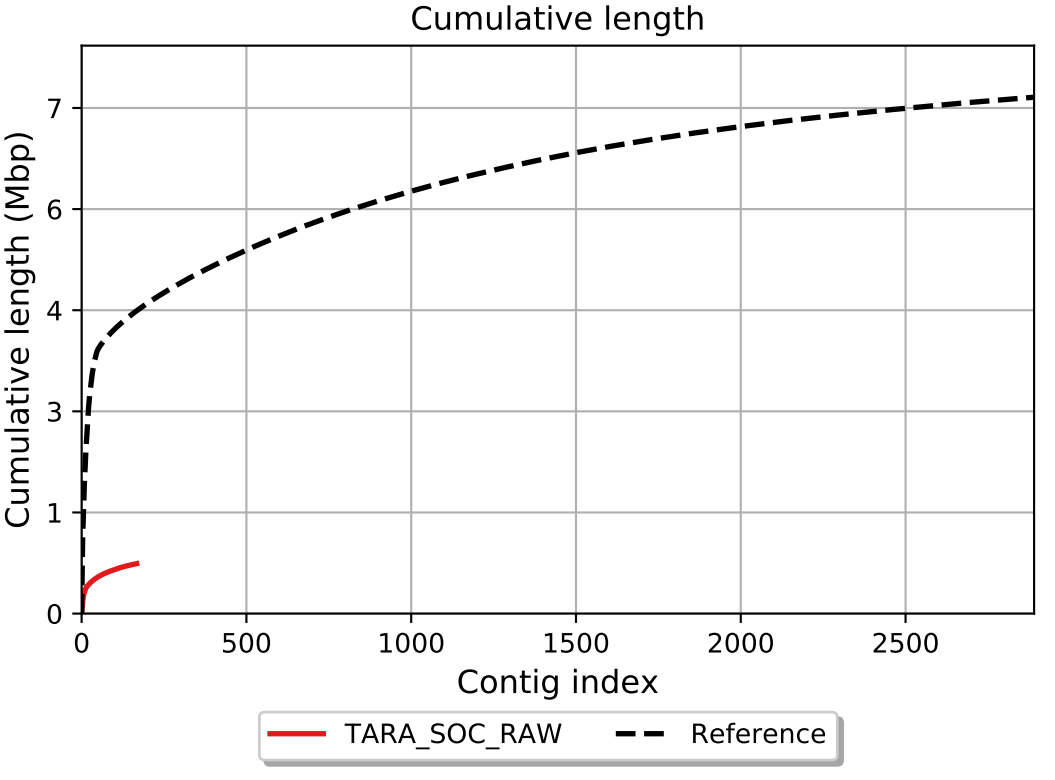
Unaligned report

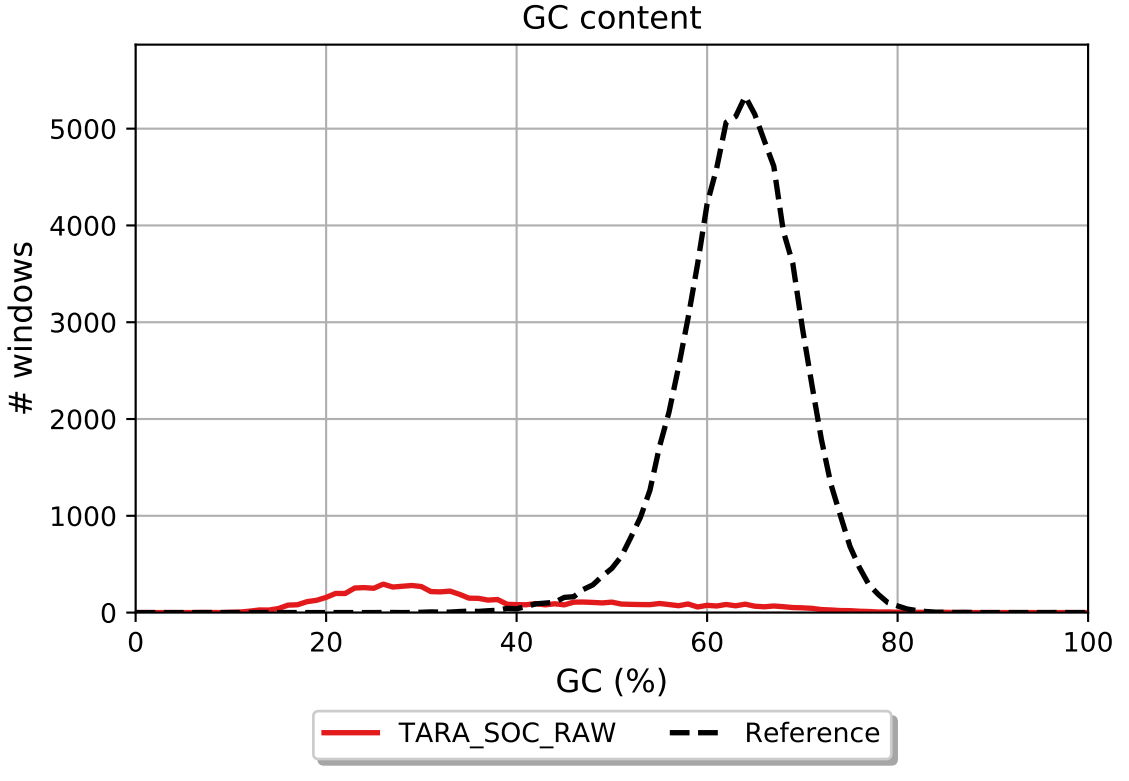
	TARA_SOC_RAW
# fully unaligned contigs	5
Fully unaligned length	16592
# partially unaligned contigs	162
Partially unaligned length	710691
# N's	0

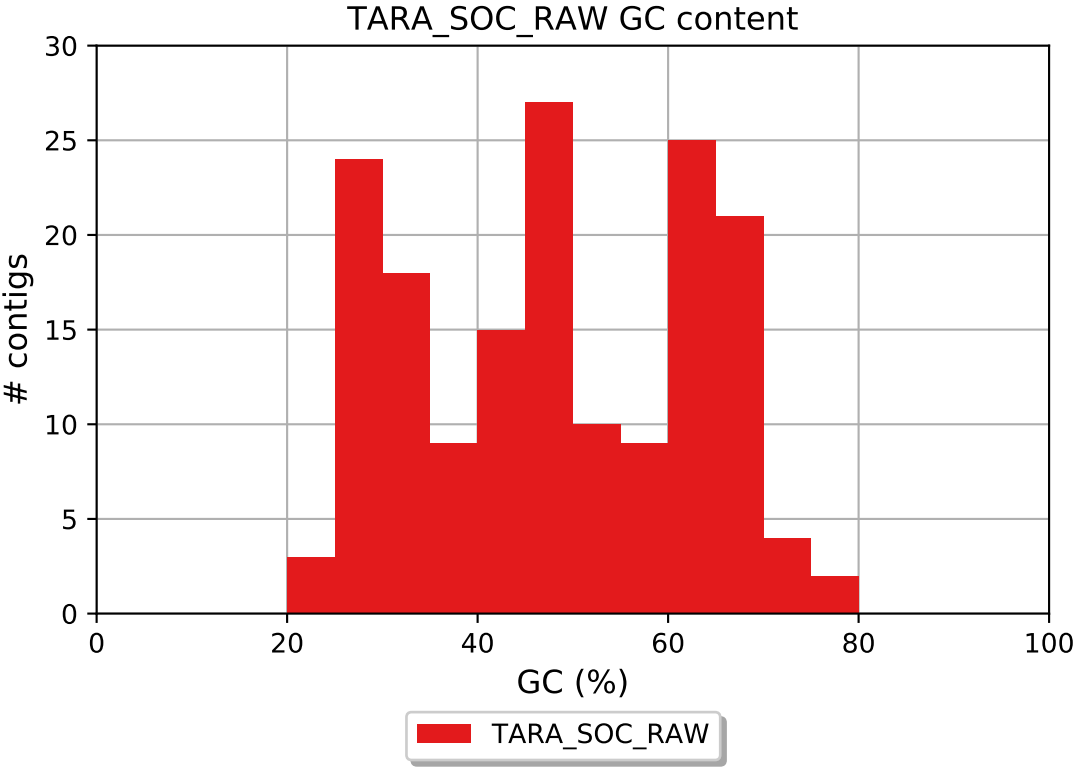
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

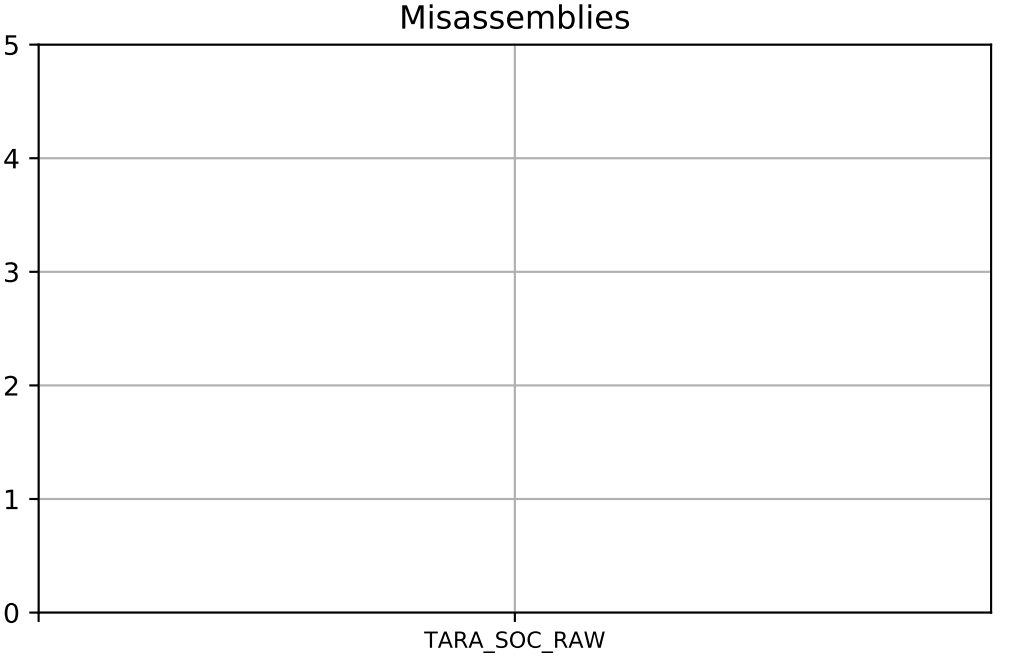

Nx
Contig length (kbp)
0
15
30
45
60
0
20
40
60
80
100
x
TARA_SOC_RAW

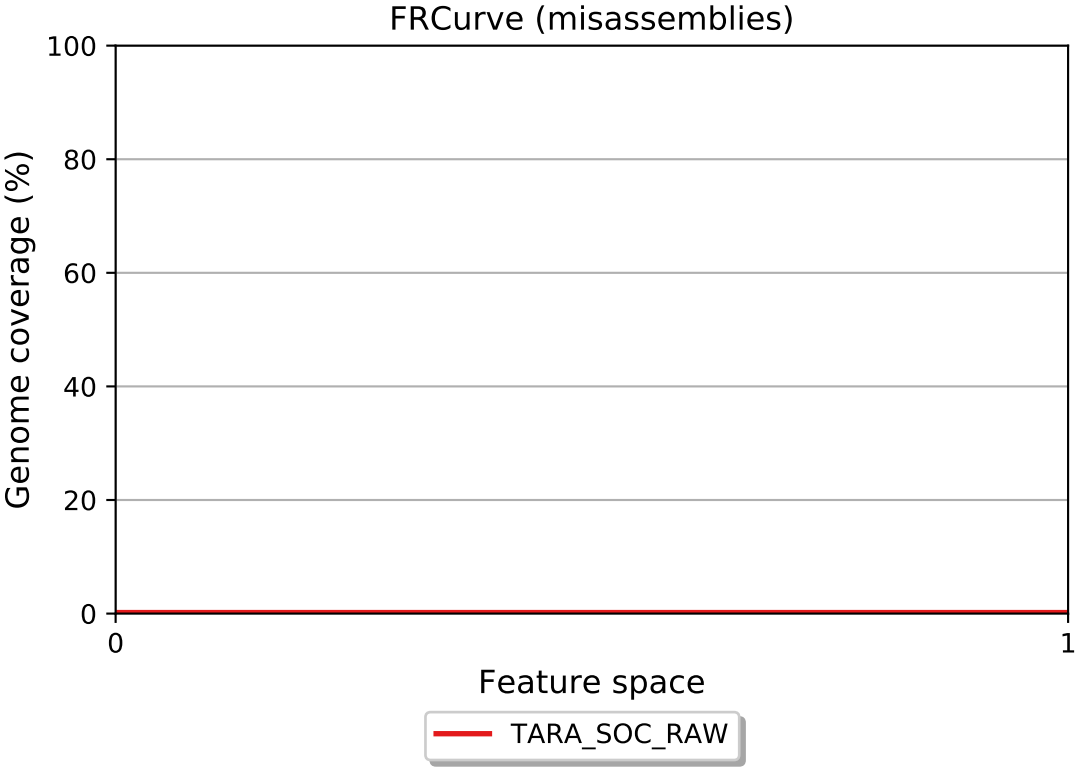

NGx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
TARA_SOC_RAW

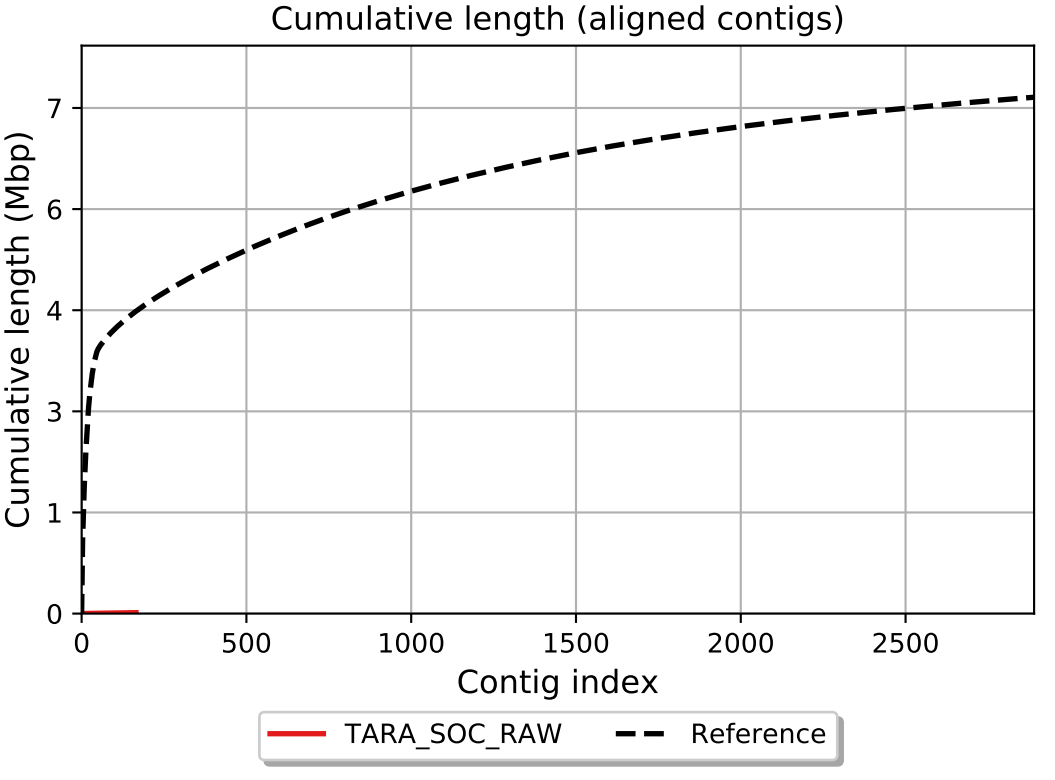

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
7
0
500
1000
1500
2000
2500
Contig index
TARA_SOC_RAW
Reference

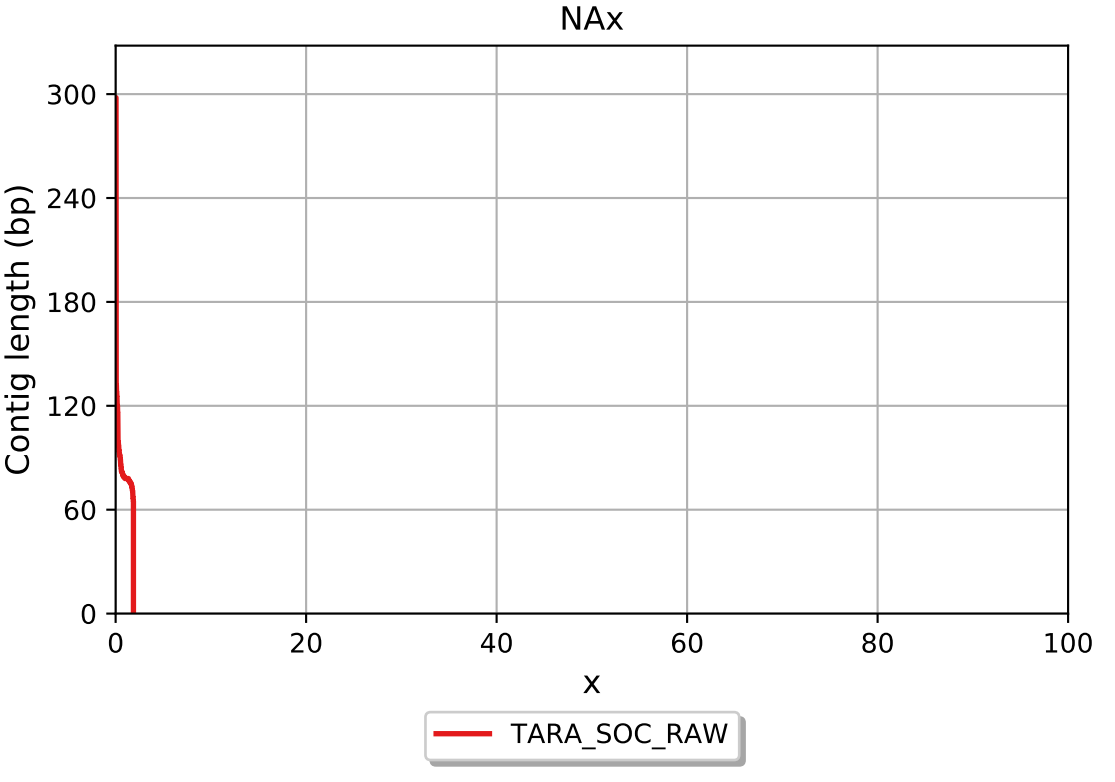

GC content
windows
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
GC (%)
TARA_SOC_RAW
Reference

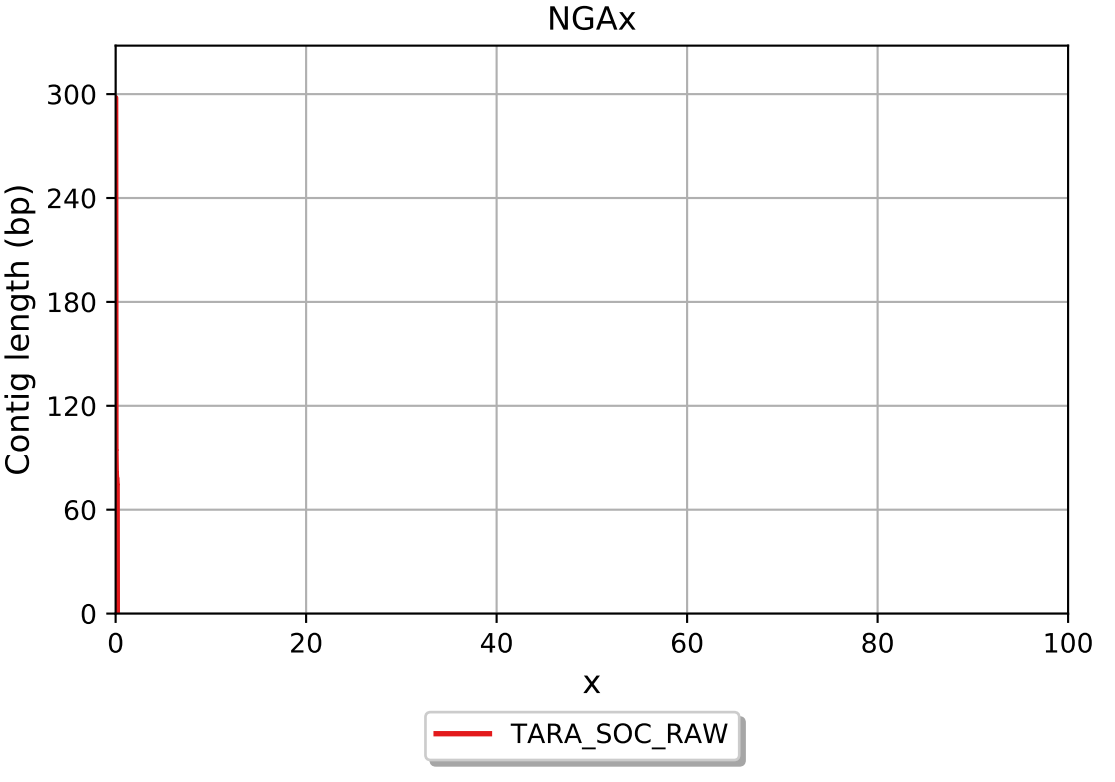

TARA_SOC_RAW GC content
contigs
GC (%)
0
5
10
15
20
25
30
0
20
40
60
80
100
TARA_SOC_RAW


Misassemblies
5
4
3
2
1
0
TARA_SOC_RAW


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
7
0
500
1000
1500
2000
2500
Contig index
TARA_SOC_RAW
Reference


NAx
Contig length (bp)
300
240
180
120
60
0
0
20
40
60
80
100
x
TARA_SOC_RAW


NGAx
Contig length (bp)
300
240
180
120
60
0
0
20
40
60
80
100
x
TARA_SOC_RAW