Report

	TARA_SOC_RAW
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	62238
Total length (>= 5000 bp)	5563
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	27
Largest contig	5563
Total length	62238
Reference length	4234461
GC (%)	46.05
Reference GC (%)	41.03
N50	2487
N75	1818
L50	9
L75	17
# 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	8 + 19 part
Unaligned length	60408
Genome fraction (%)	0.015
Duplication ratio	2.961
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9061.49
# indels per 100 kbp	161.81
Largest alignment	201
Total aligned length	1830
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

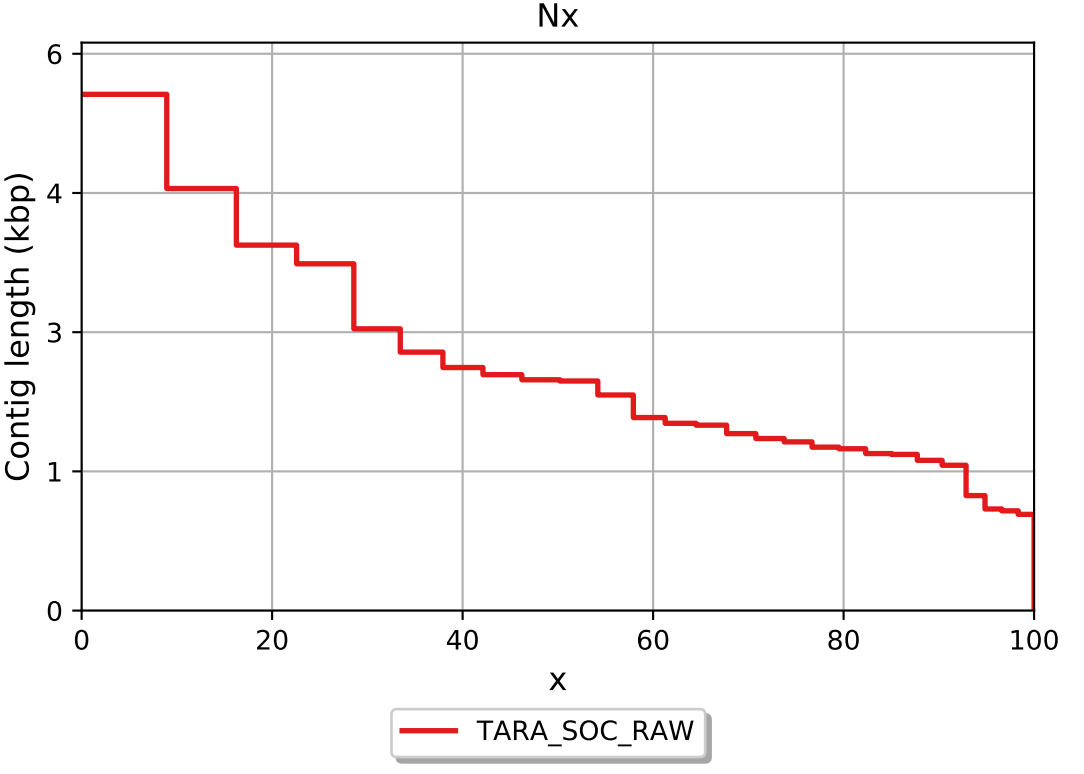
	TARA_SOC_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	25
# possible misassemblies	30
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	56
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

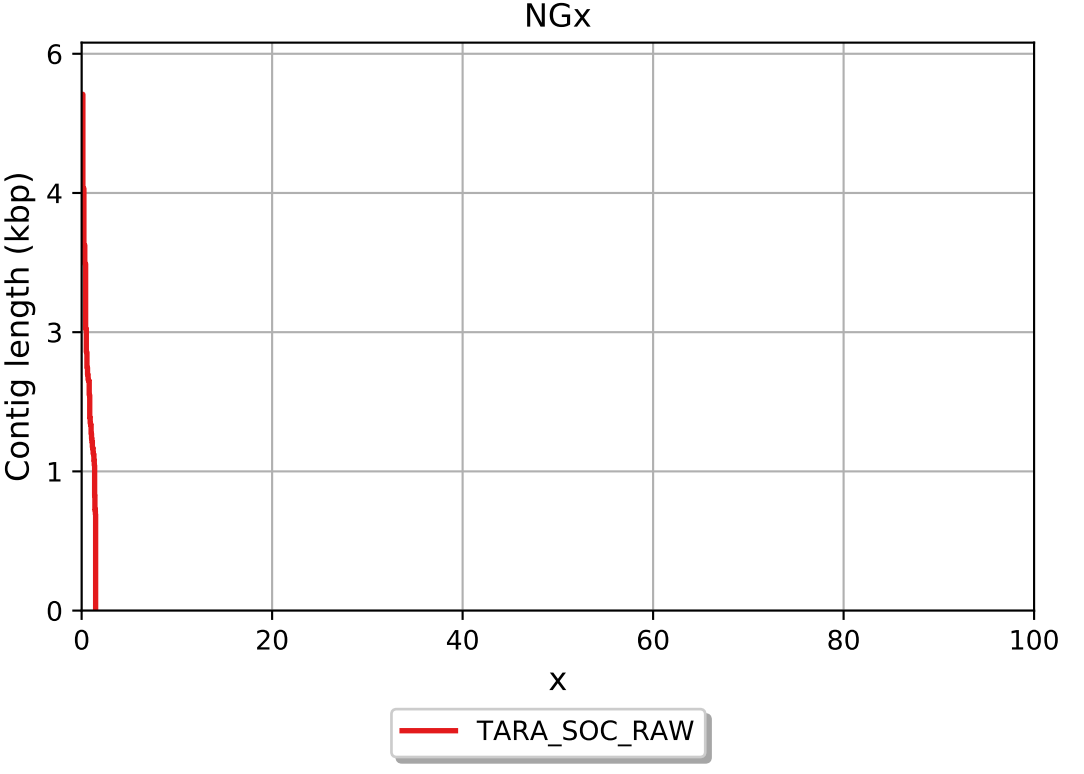
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

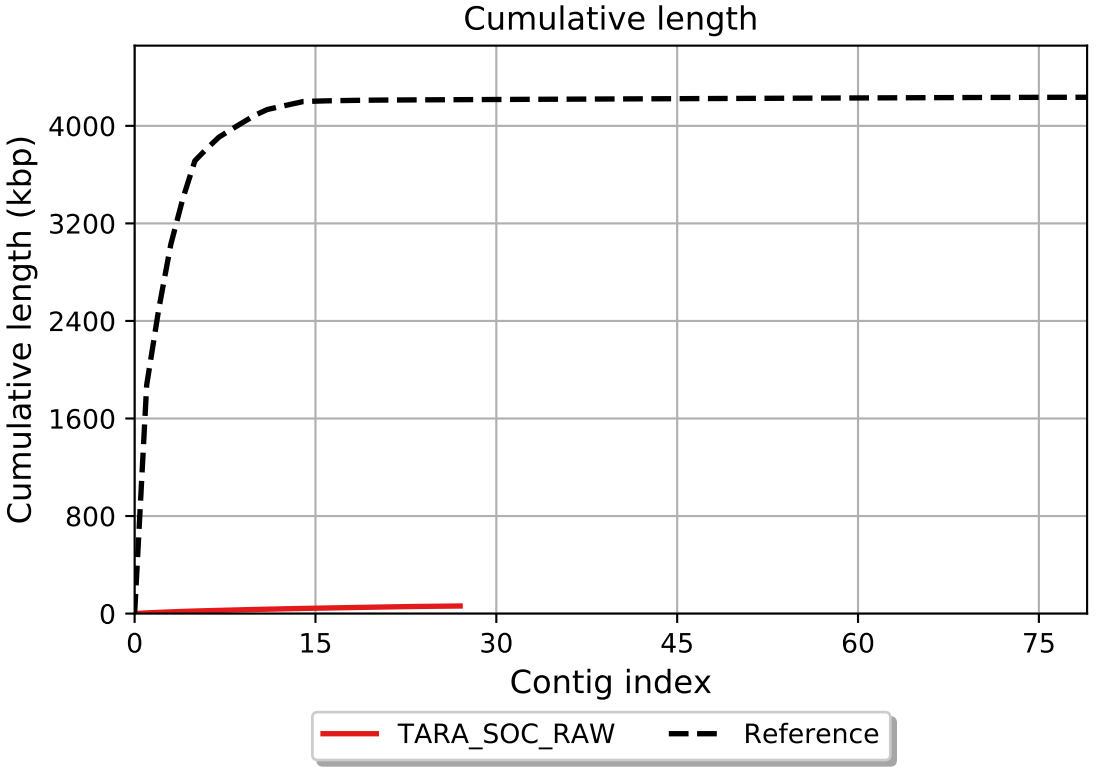
Unaligned report

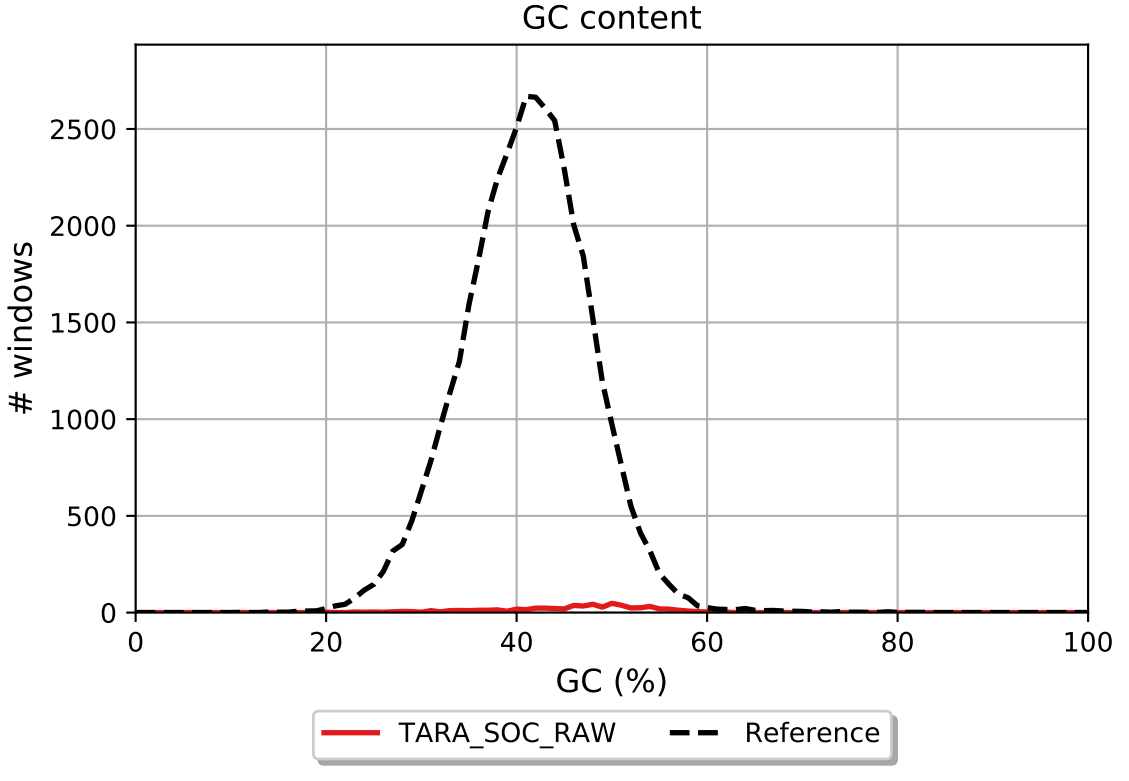
	TARA_SOC_RAW
# fully unaligned contigs	8
Fully unaligned length	14087
# partially unaligned contigs	19
Partially unaligned length	46321
# N's	0

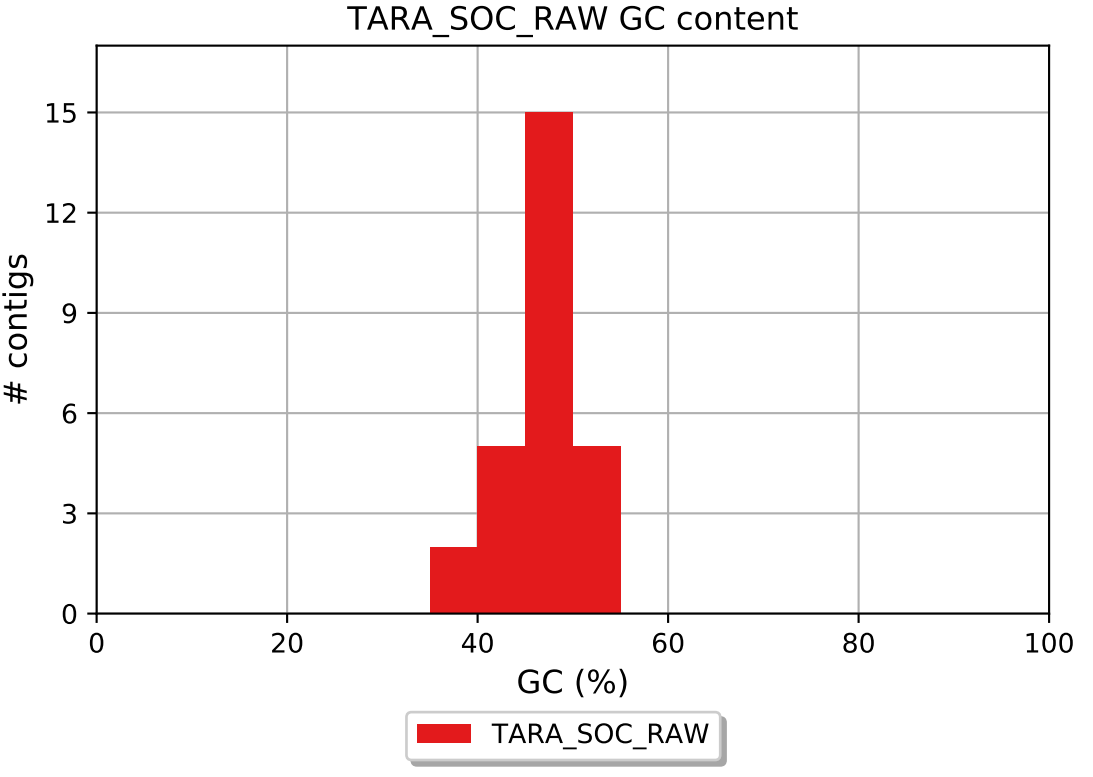
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

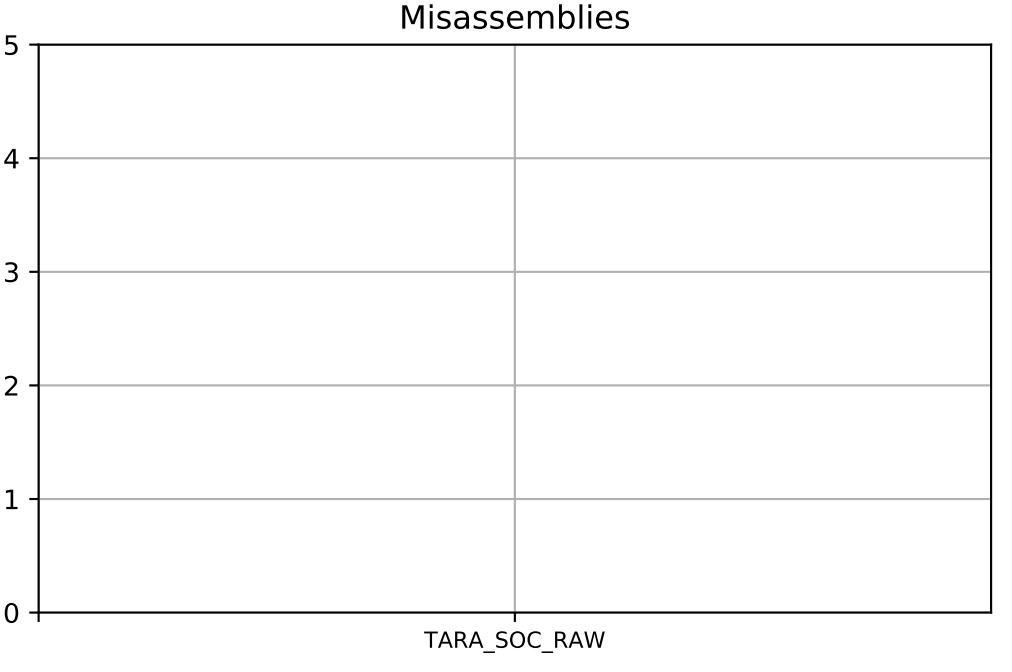

Nx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
TARA_SOC_RAW

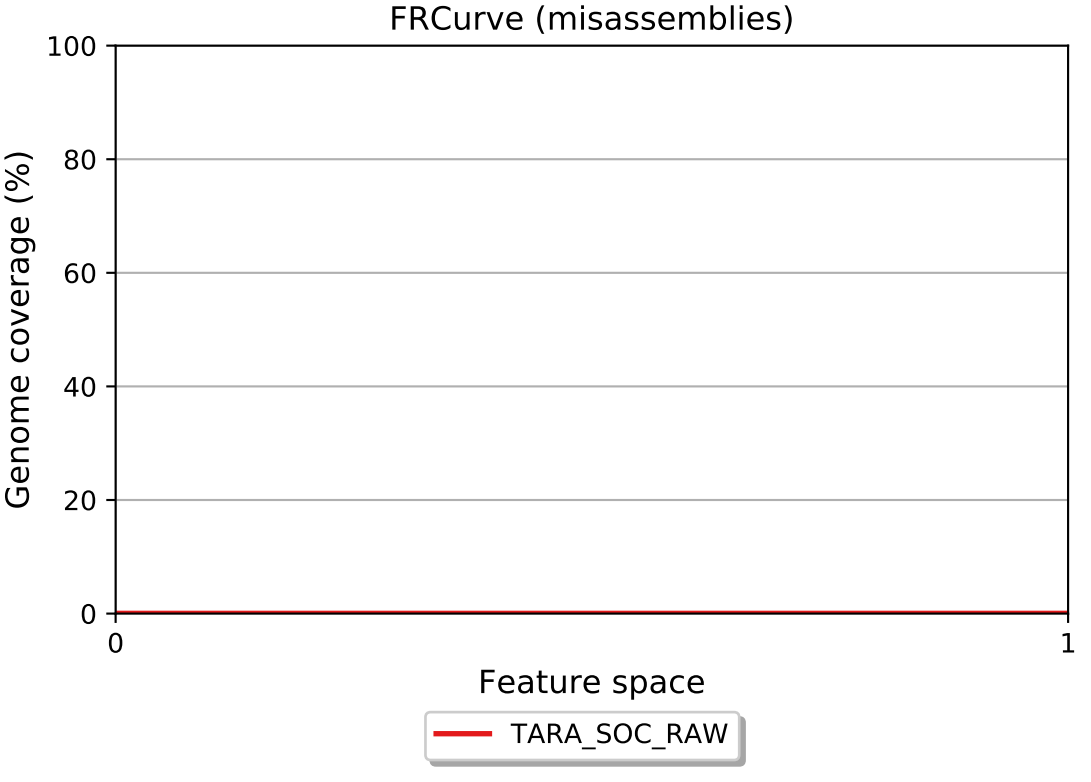

NGx
Contig length (kbp)
6
4
3
1
0
0
20
40
60
80
100
x
TARA_SOC_RAW

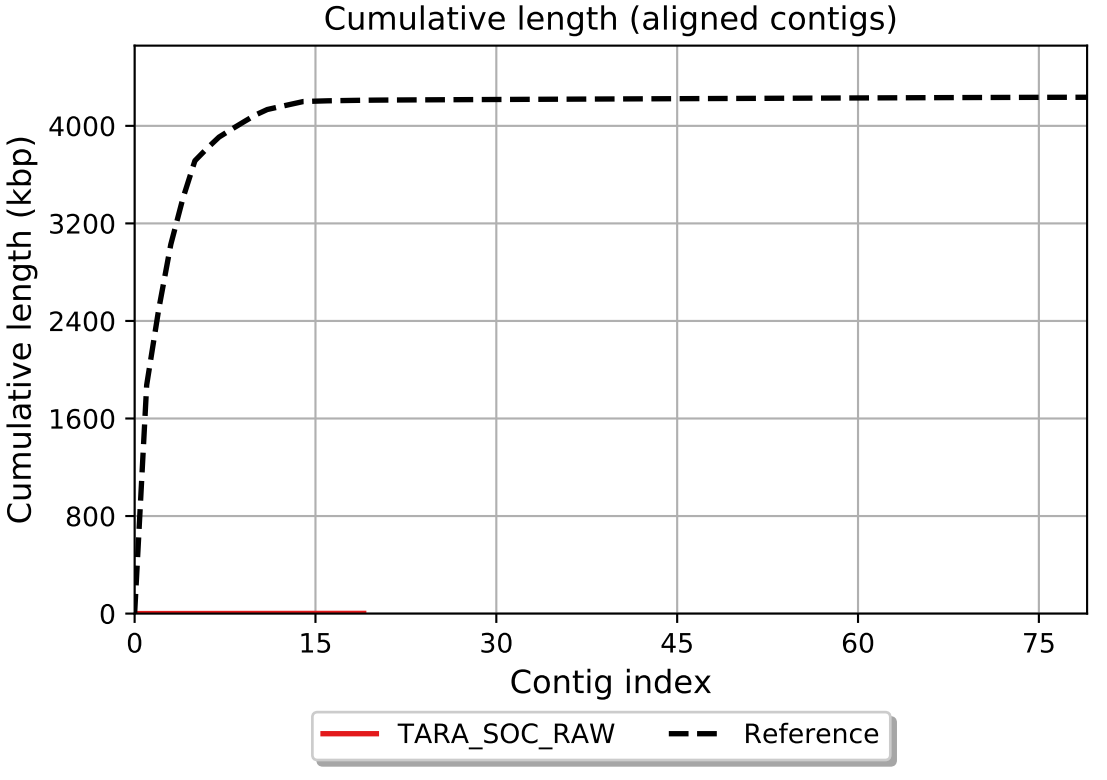

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
15
30
45
60
75
Contig index
TARA_SOC_RAW
Reference

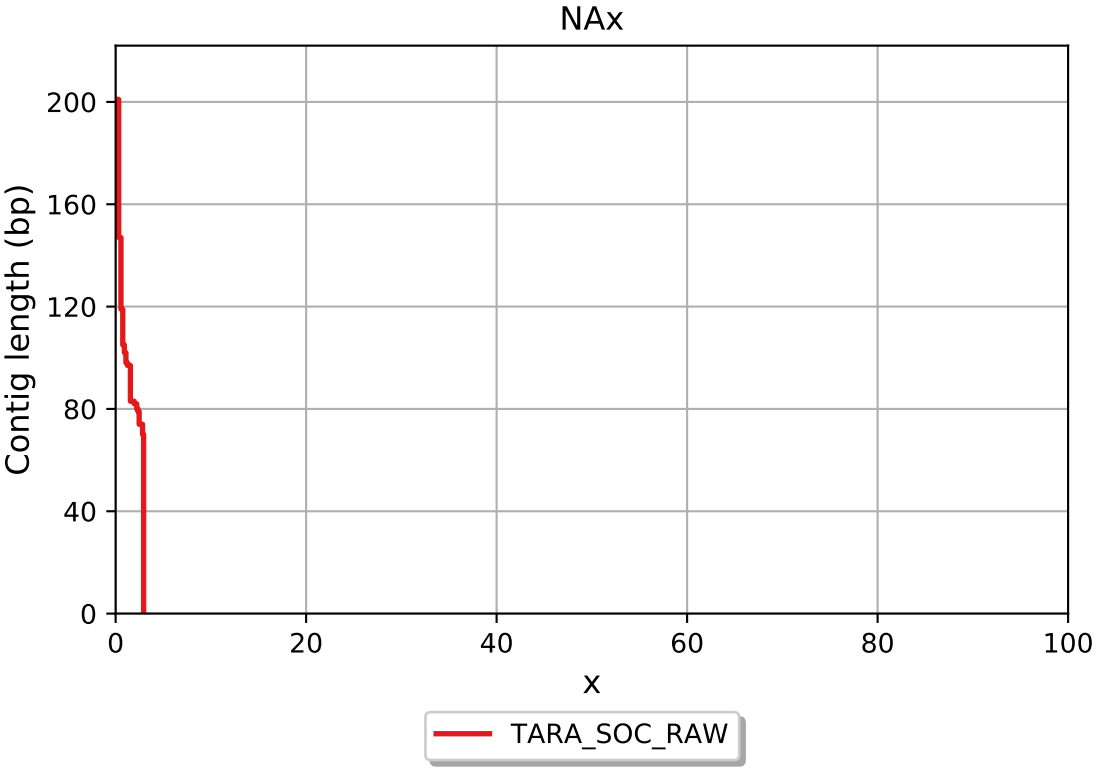

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
TARA_SOC_RAW
Reference

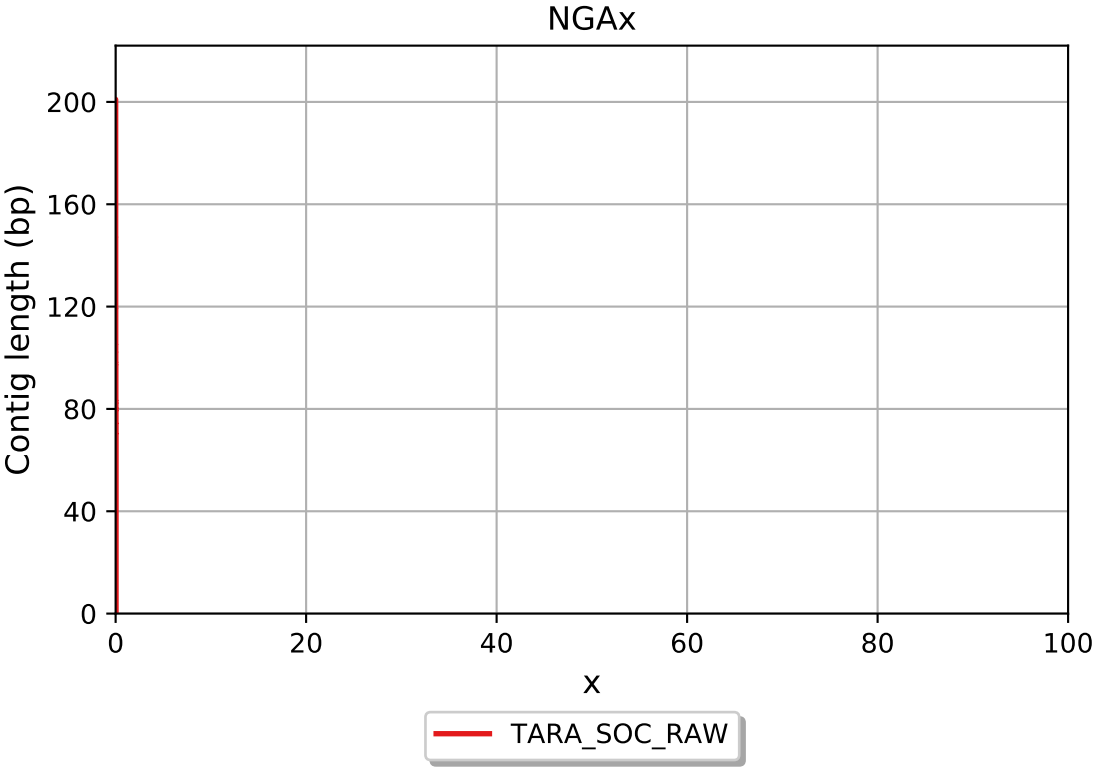

TARA_SOC_RAW GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
TARA_SOC_RAW


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 (kbp)
4000
3200
2400
1600
800
0
0
15
30
45
60
75
Contig index
TARA_SOC_RAW
Reference


NAx
Contig length (bp)
200
160
120
80
40
0
0
20
40
60
80
100
x
TARA_SOC_RAW


NGAx
Contig length (bp)
200
160
120
80
40
0
0
20
40
60
80
100
x
TARA_SOC_RAW