Report

	TARA_ION_RAW
# contigs (>= 1000 bp)	383
# contigs (>= 5000 bp)	57
# contigs (>= 10000 bp)	30
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	1942203
Total length (>= 5000 bp)	1282191
Total length (>= 10000 bp)	1102192
Total length (>= 25000 bp)	798696
Total length (>= 50000 bp)	622831
# contigs	383
Largest contig	154464
Total length	1942203
Reference length	7658814
GC (%)	46.95
Reference GC (%)	63.29
N50	13494
N75	3293
L50	19
L75	102
# 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	2
# unaligned contigs	8 + 374 part
Unaligned length	1910879
Genome fraction (%)	0.057
Duplication ratio	7.211
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12430.94
# indels per 100 kbp	92.08
Largest alignment	159
Total aligned length	30385
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

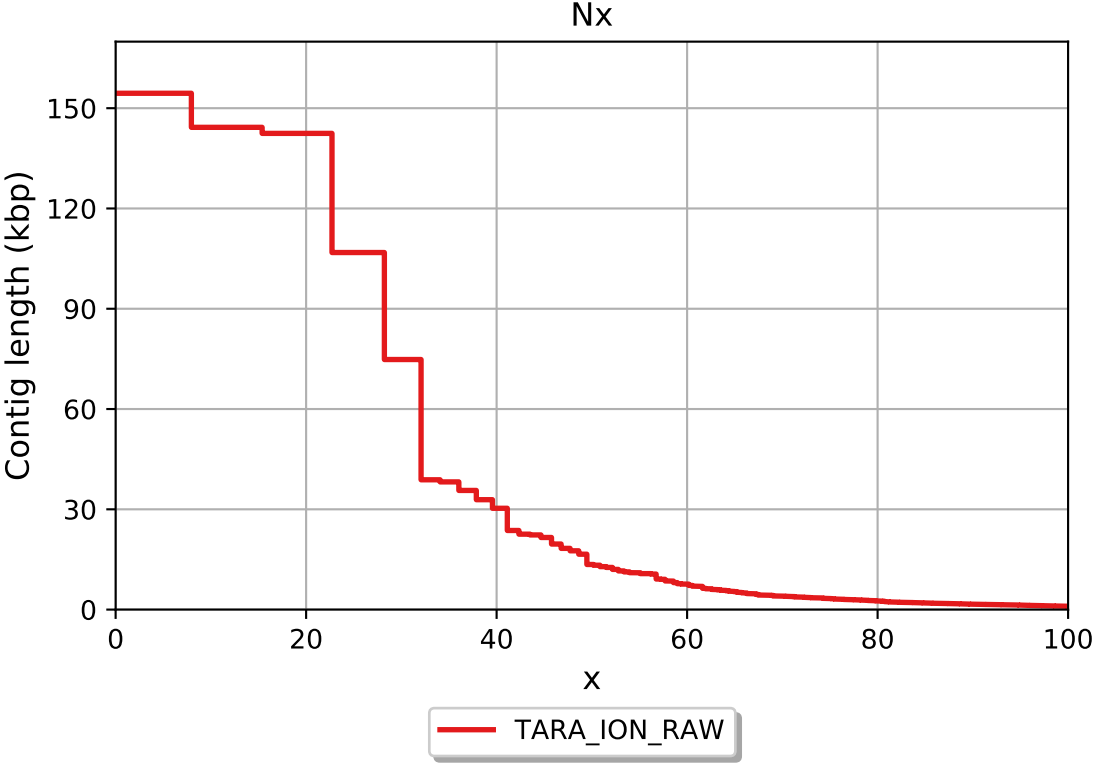
	TARA_ION_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	378
# possible misassemblies	457
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	540
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	7

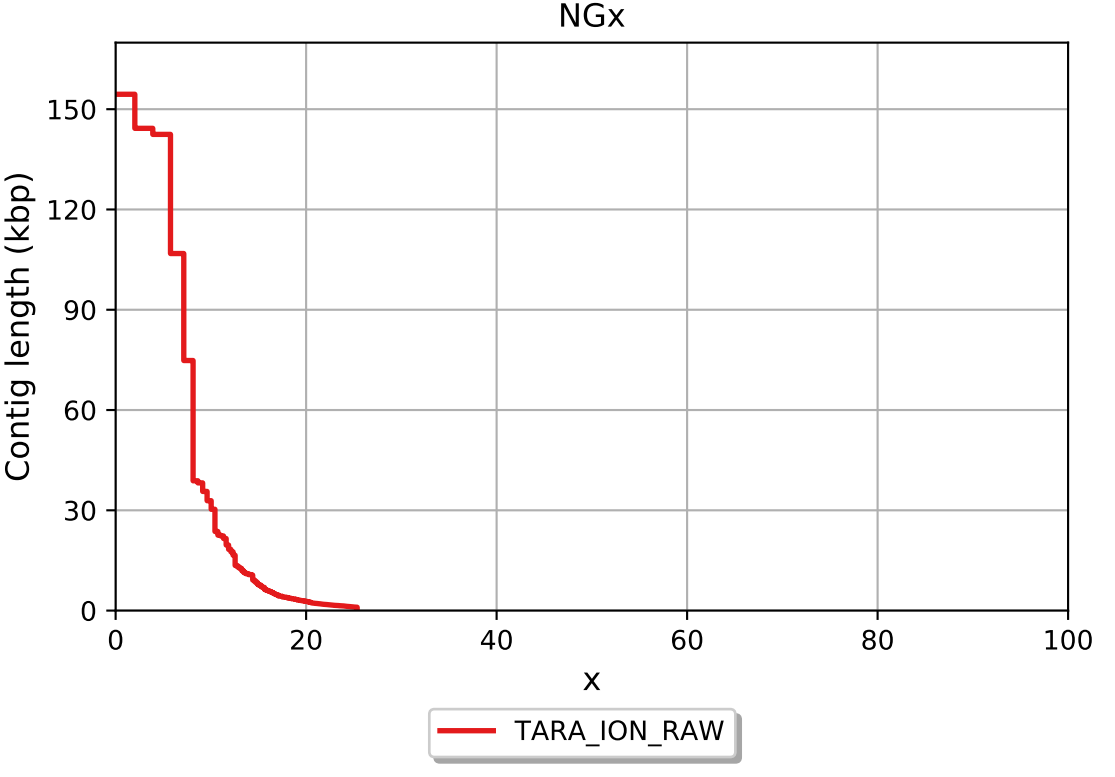
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

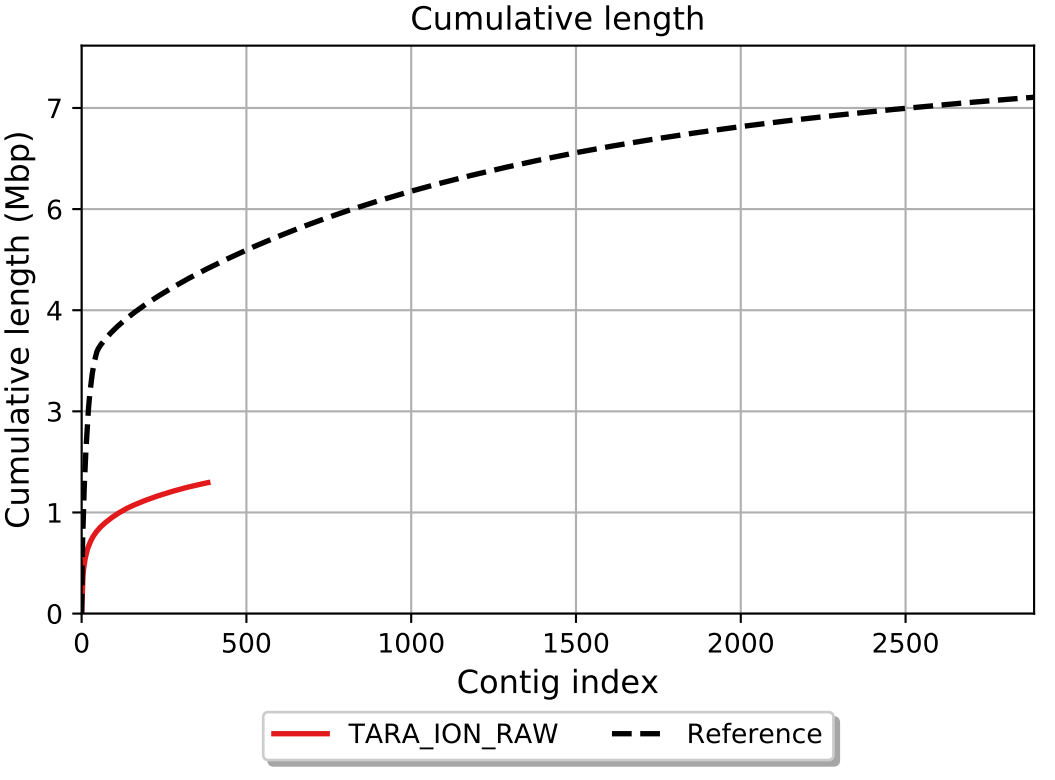
Unaligned report

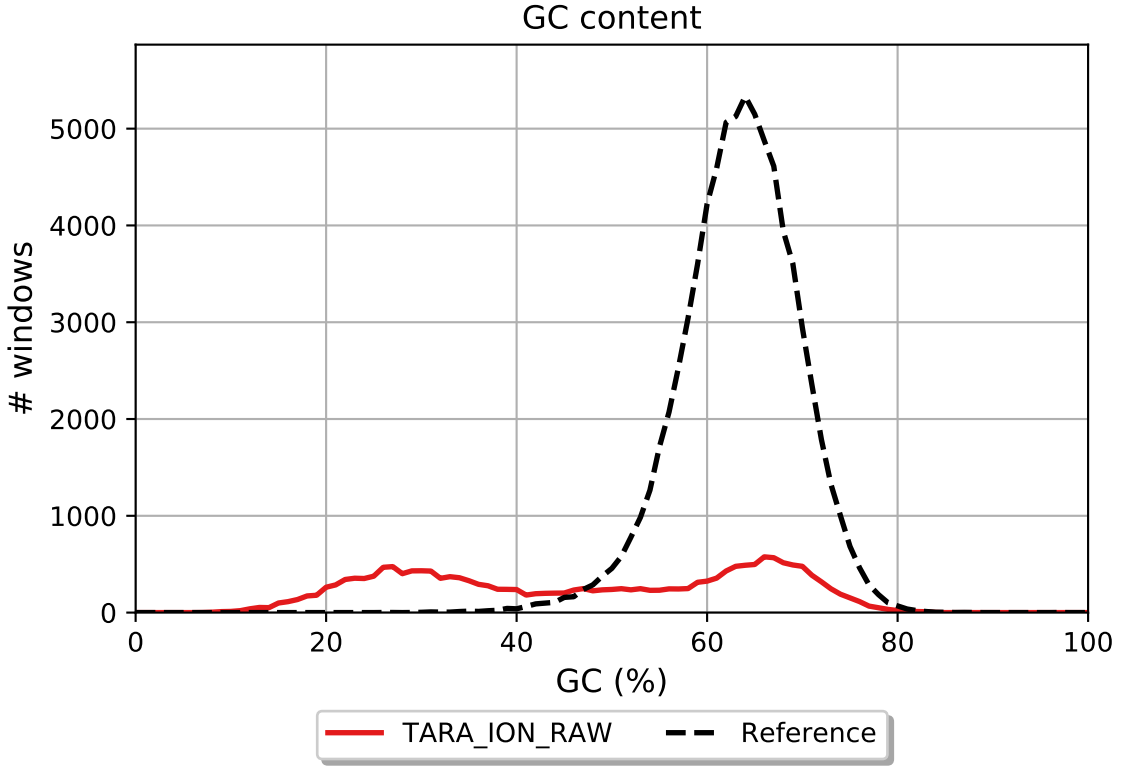
	TARA_ION_RAW
# fully unaligned contigs	8
Fully unaligned length	73094
# partially unaligned contigs	374
Partially unaligned length	1837785
# N's	0

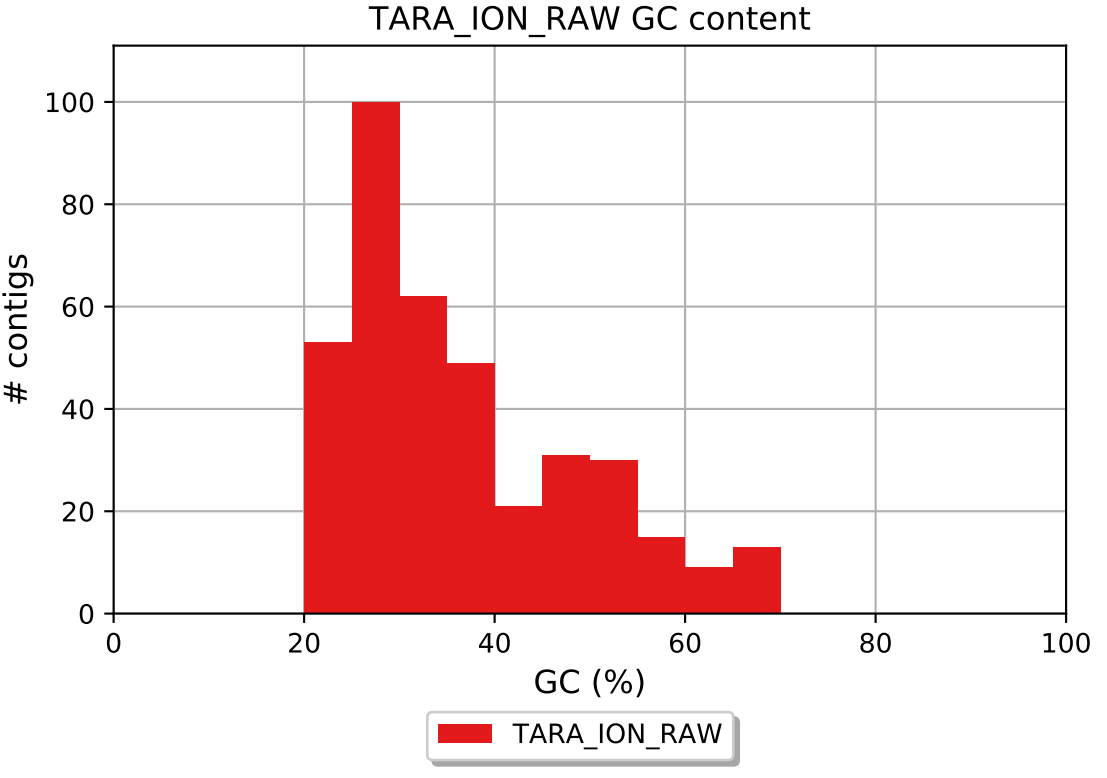
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

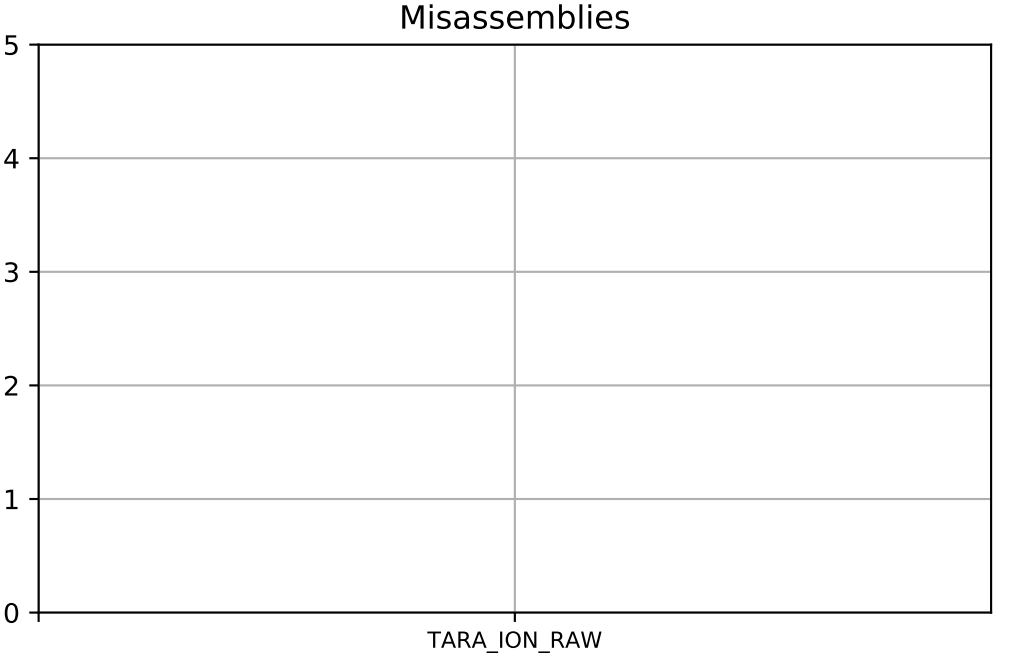

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
TARA_ION_RAW

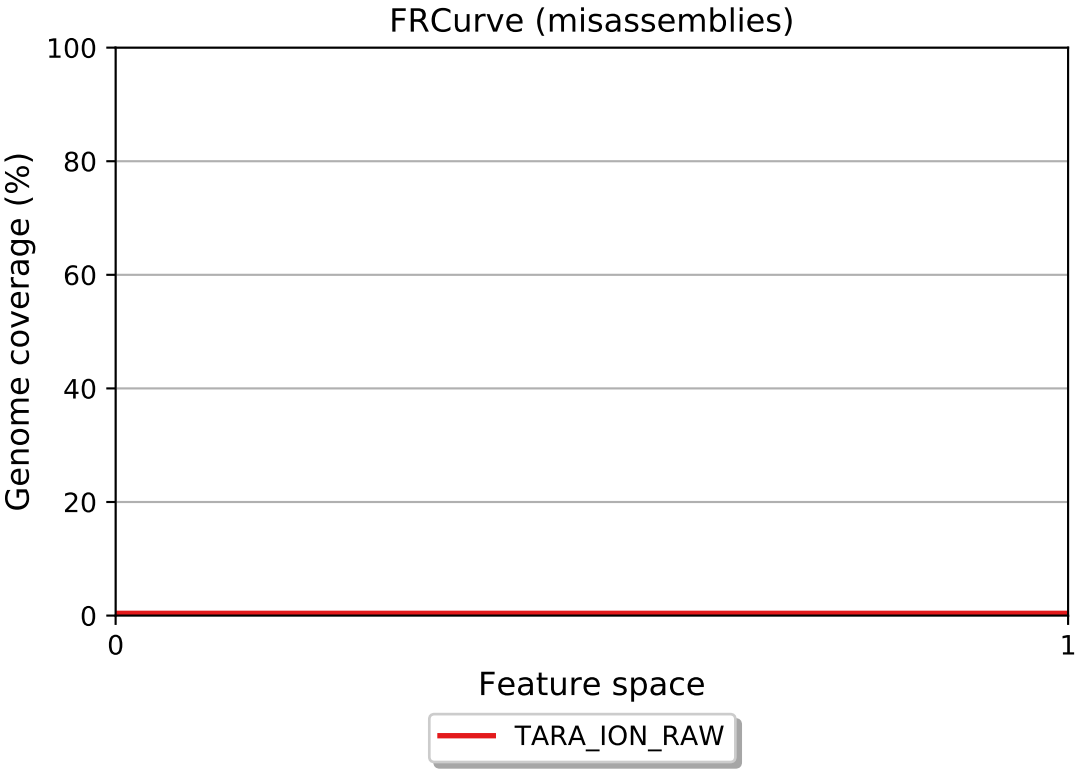

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
TARA_ION_RAW

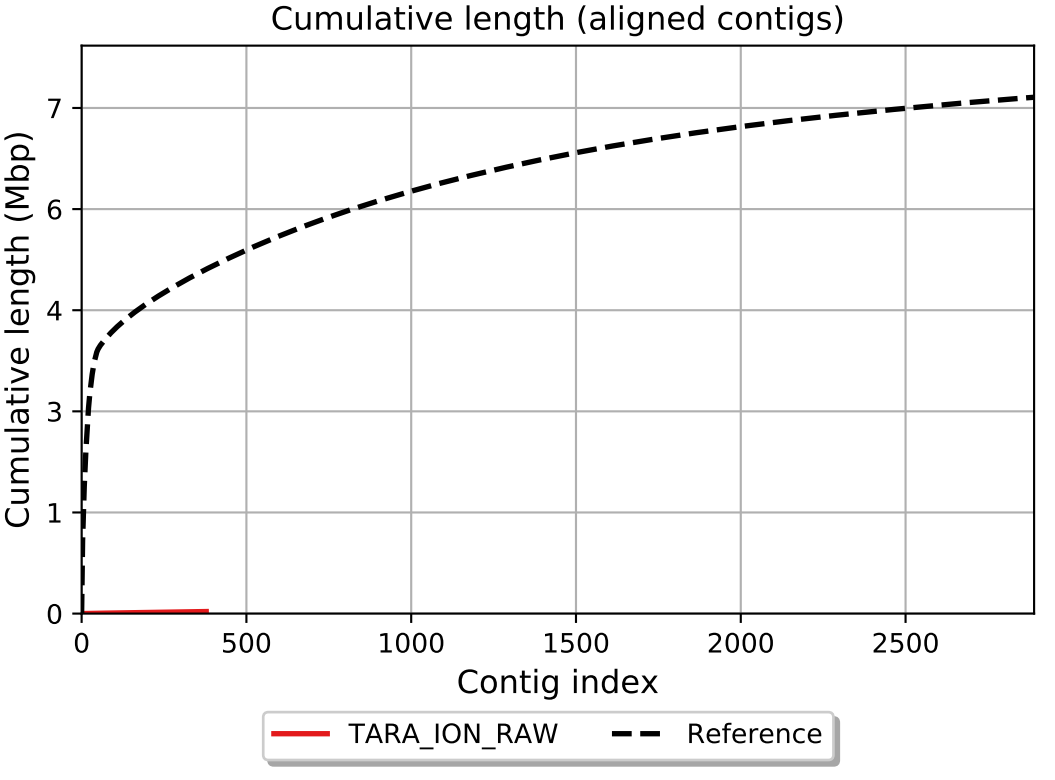

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
7
0
500
1000
1500
2000
2500
Contig index
TARA_ION_RAW
Reference

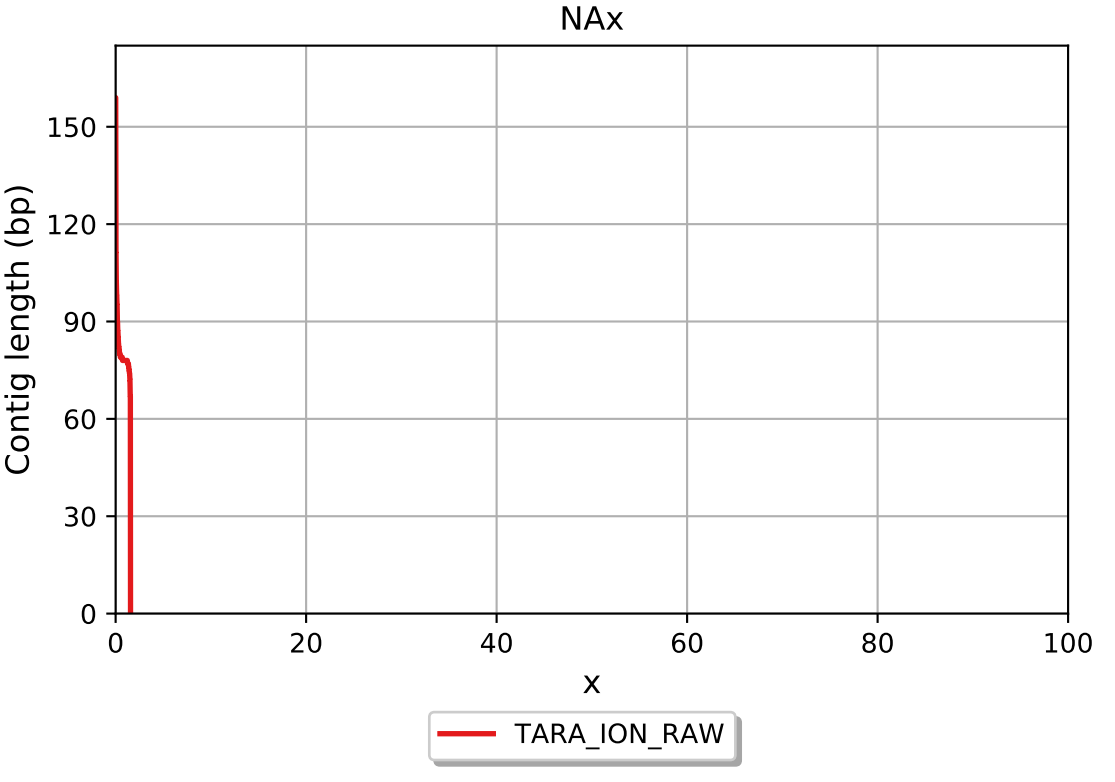

GC content
windows
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
GC (%)
TARA_ION_RAW
Reference

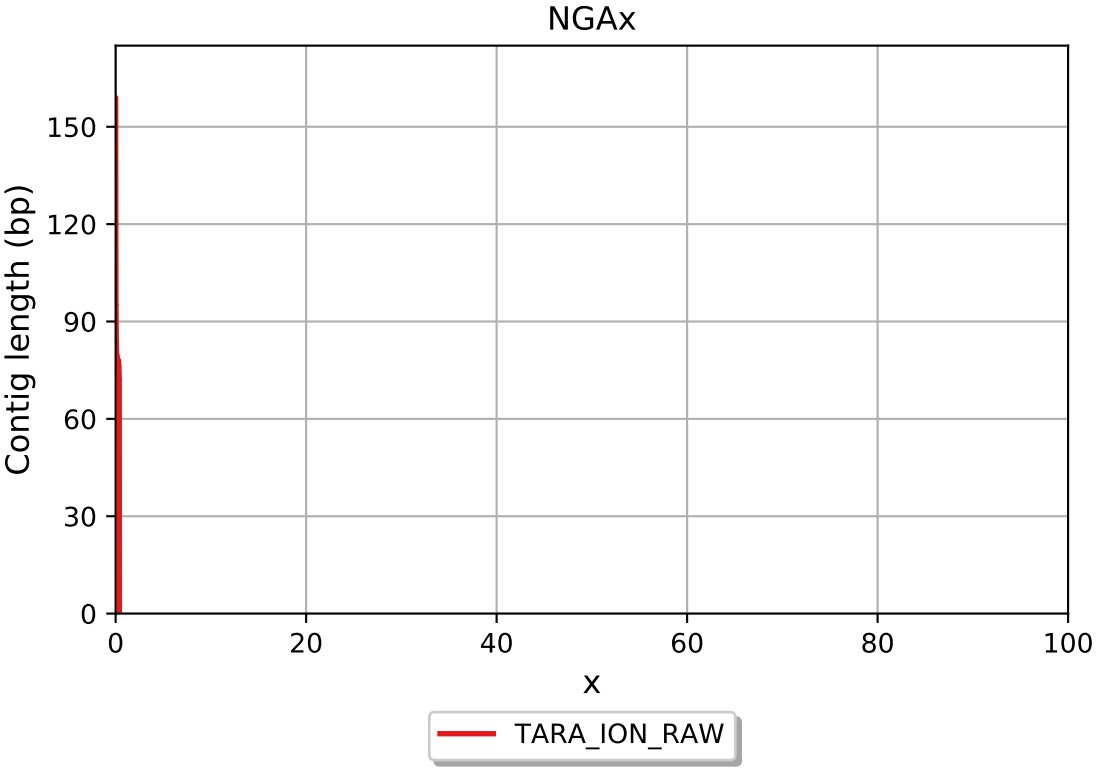

TARA_ION_RAW GC content
contigs
GC (%)
0
20
40
60
80
100
TARA_ION_RAW


Misassemblies
5
4
3
2
1
0
TARA_ION_RAW


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


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


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


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