Report

	TARA_ASW_RAW
# contigs (>= 1000 bp)	171
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	688495
Total length (>= 5000 bp)	395329
Total length (>= 10000 bp)	339559
Total length (>= 25000 bp)	247066
Total length (>= 50000 bp)	217934
# contigs	171
Largest contig	91009
Total length	688495
Reference length	5854900
GC (%)	45.76
Reference GC (%)	63.53
N50	9457
N75	2296
L50	11
L75	57
# 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	4 + 166 part
Unaligned length	673804
Genome fraction (%)	0.058
Duplication ratio	4.301
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7903.98
# indels per 100 kbp	87.82
Largest alignment	306
Total aligned length	14022
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

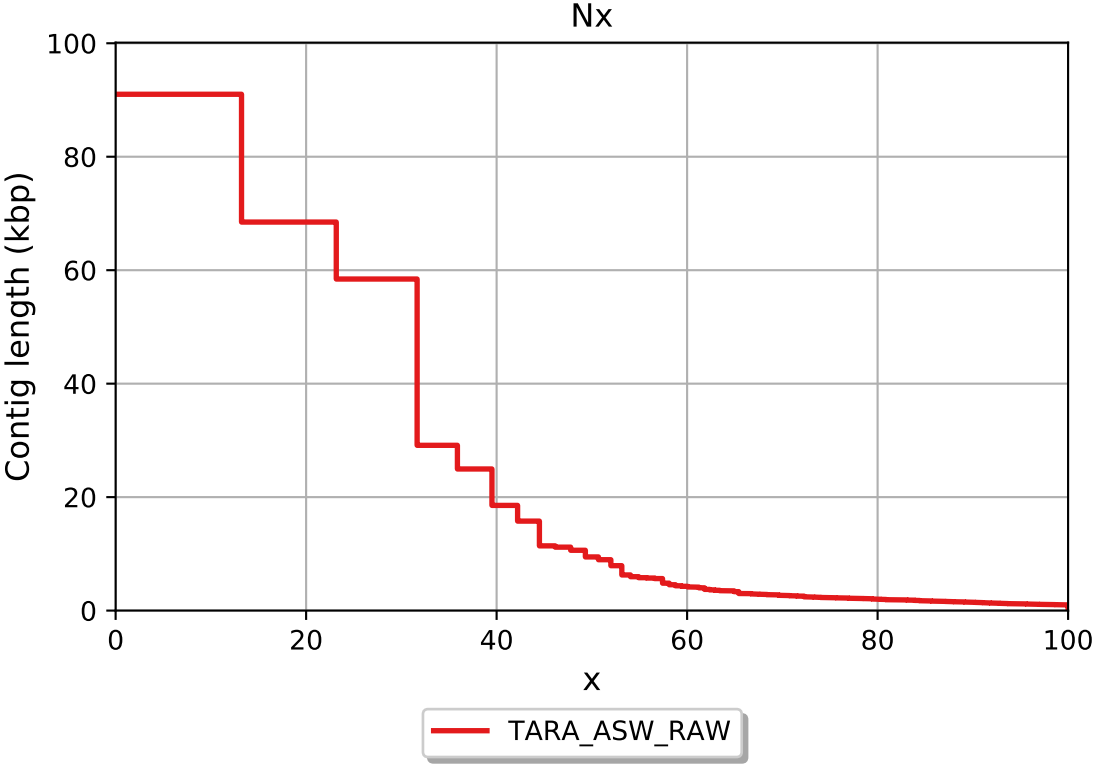
	TARA_ASW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	169
# possible misassemblies	209
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	270
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

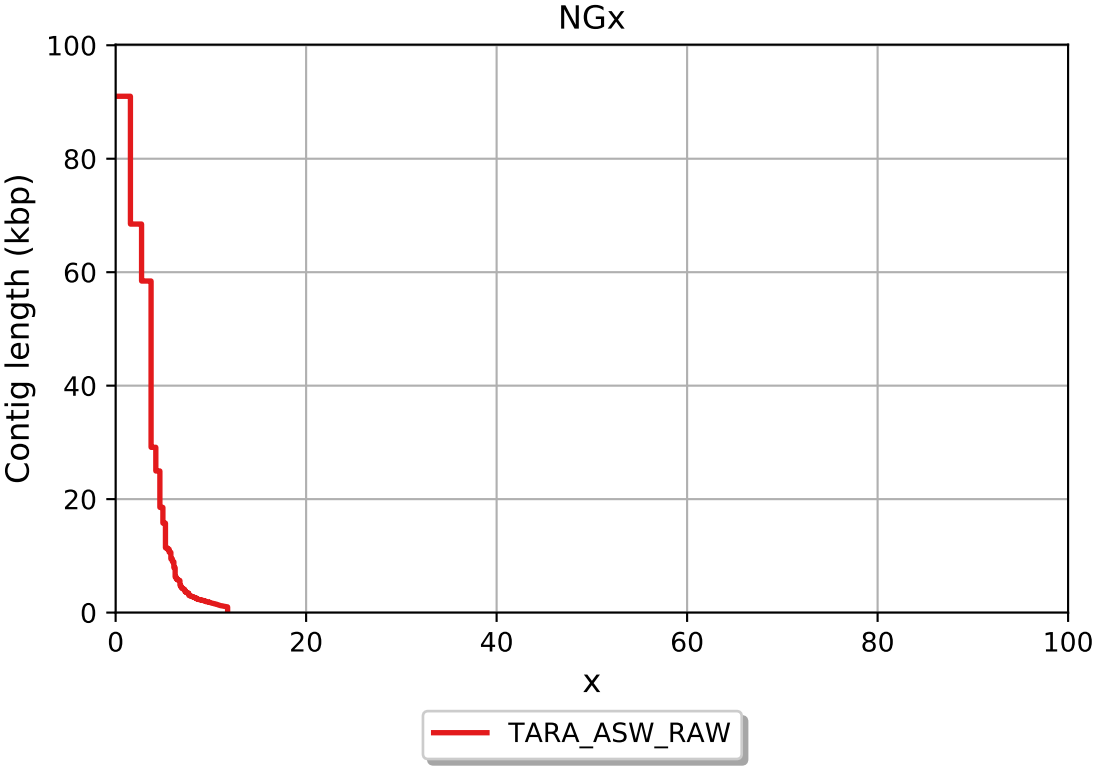
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

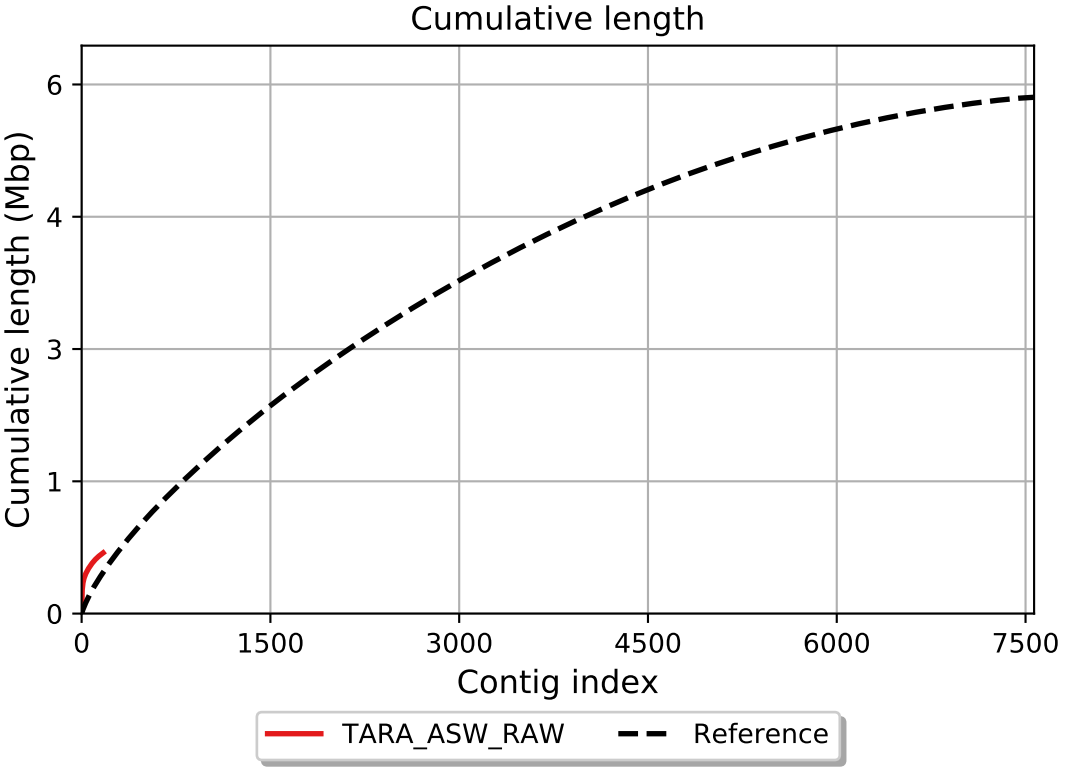
Unaligned report

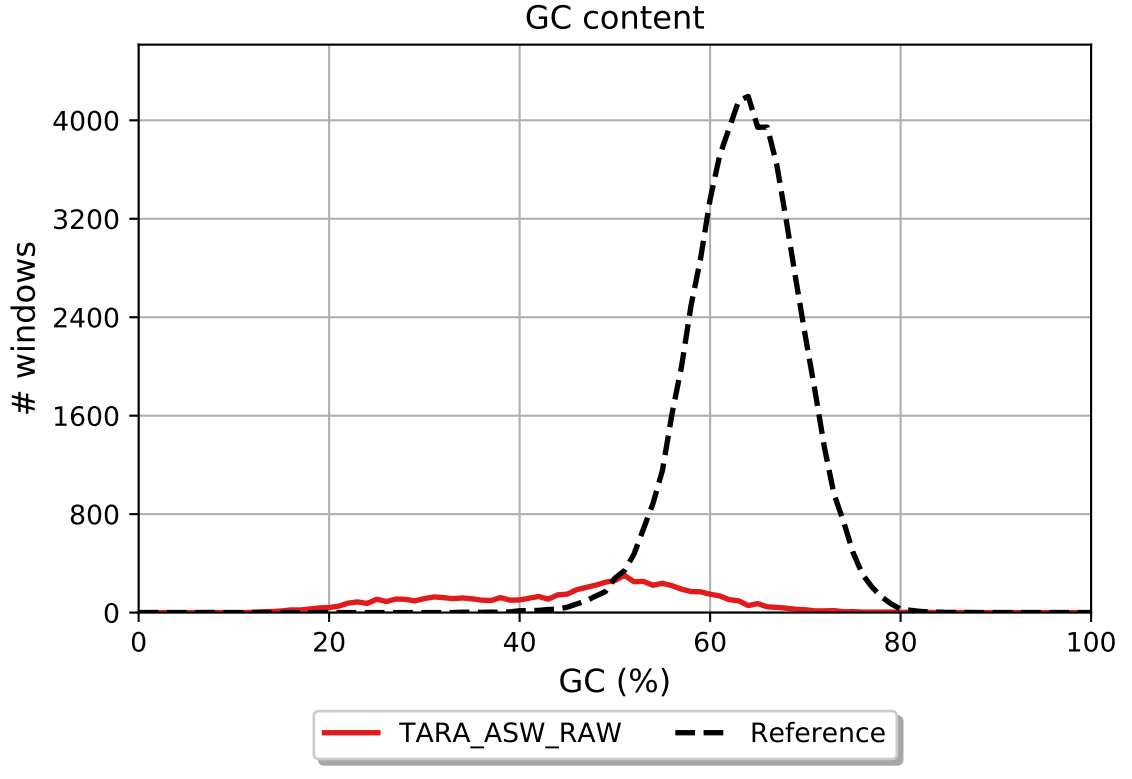
	TARA_ASW_RAW
# fully unaligned contigs	4
Fully unaligned length	9459
# partially unaligned contigs	166
Partially unaligned length	664345
# N's	0

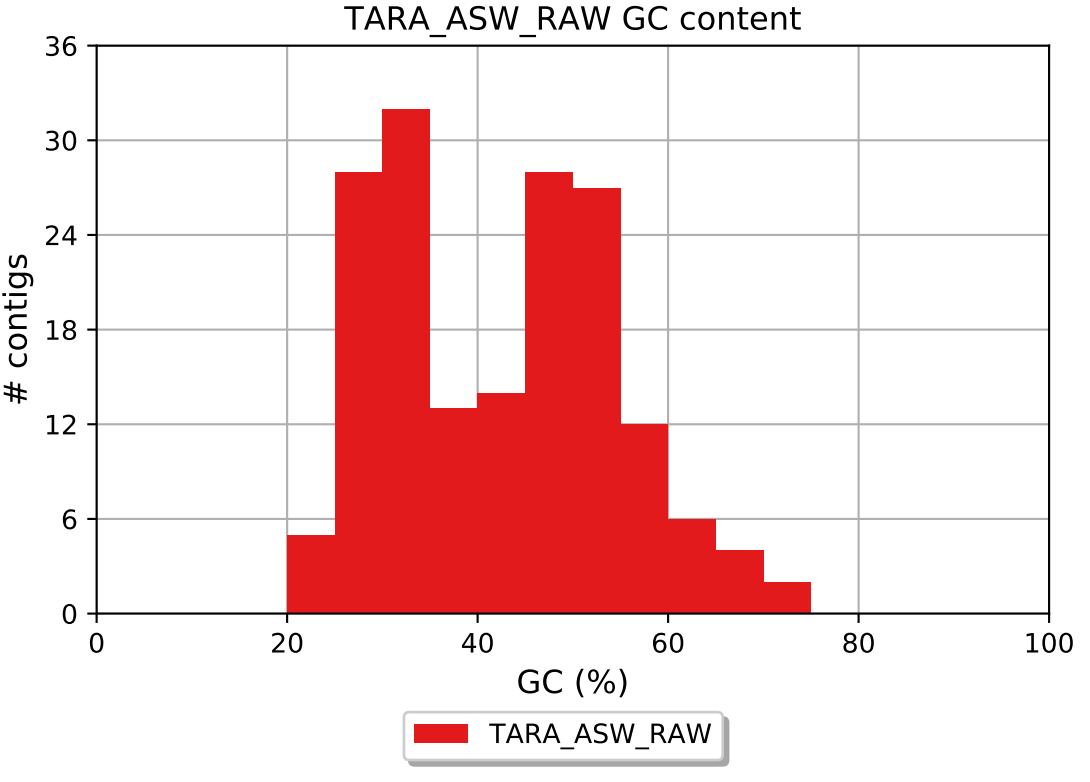
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

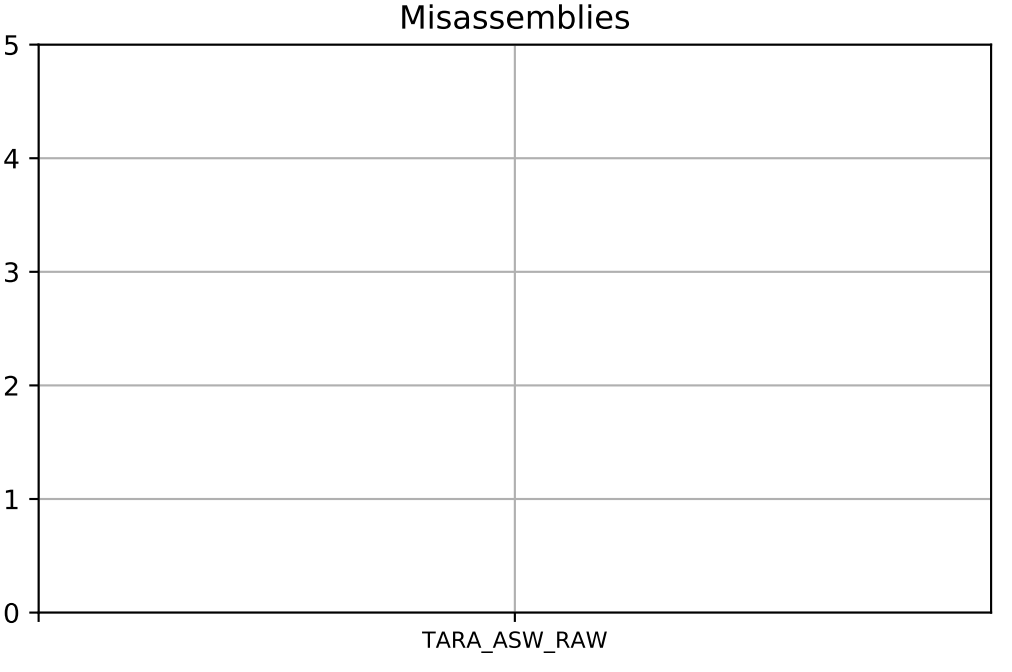

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
TARA_ASW_RAW

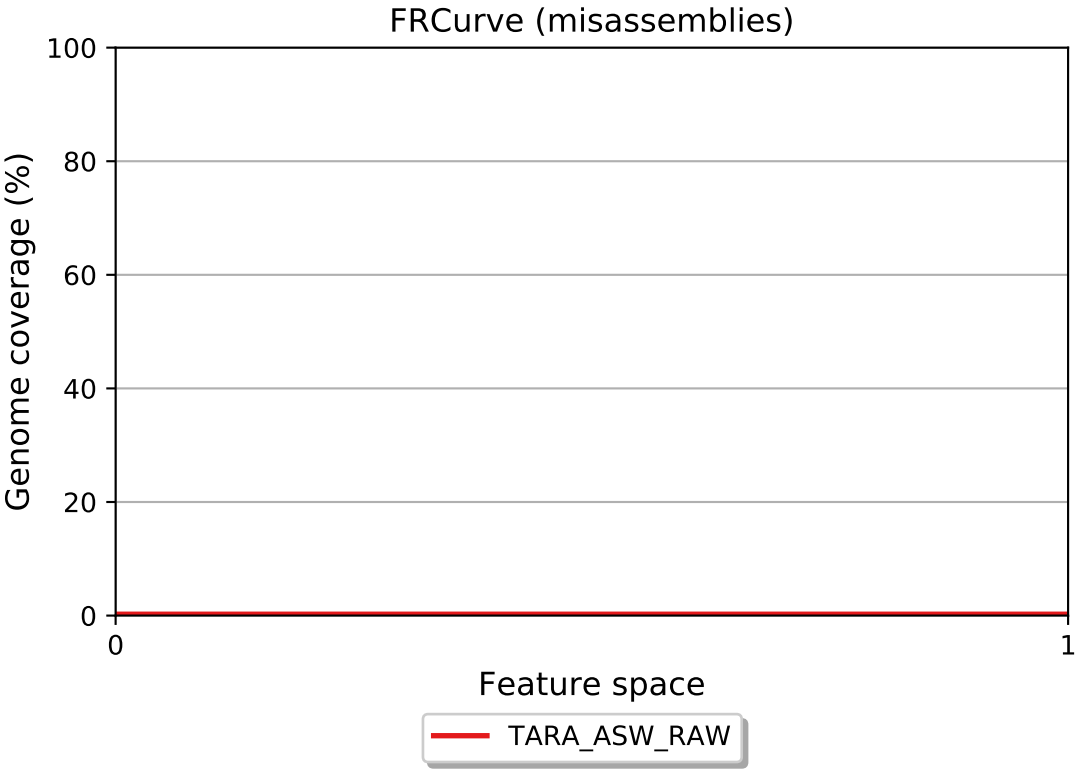

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
TARA_ASW_RAW

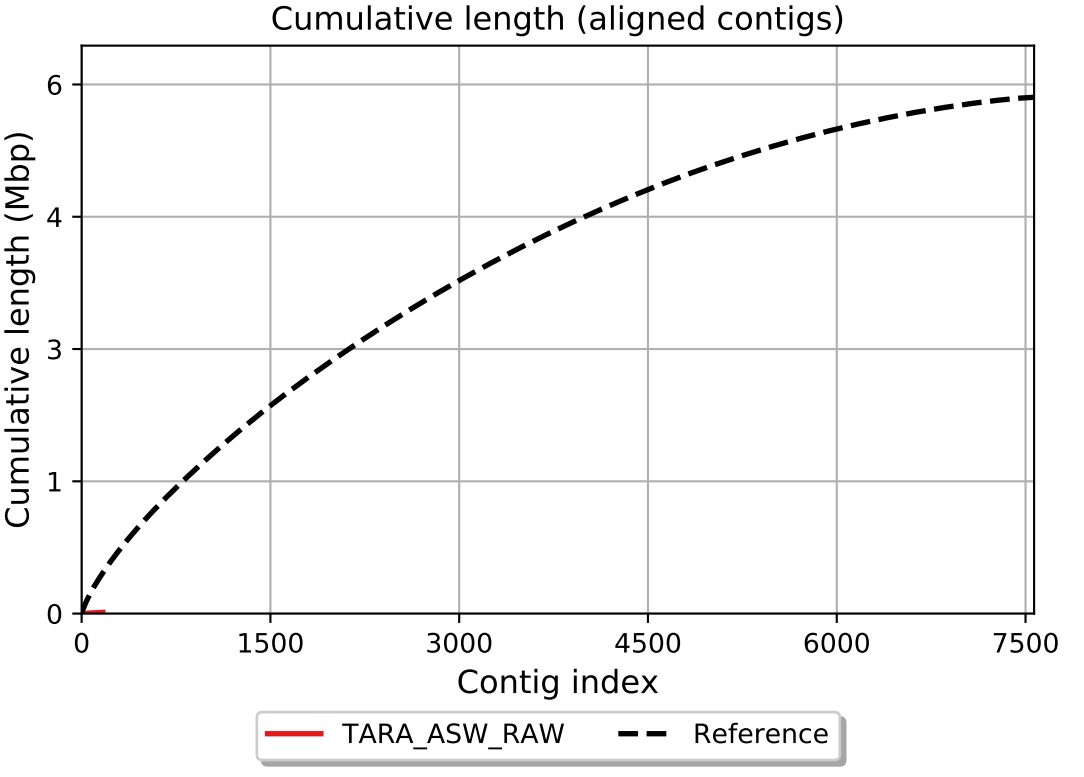

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
1500
3000
4500
6000
7500
Contig index
TARA_ASW_RAW
Reference

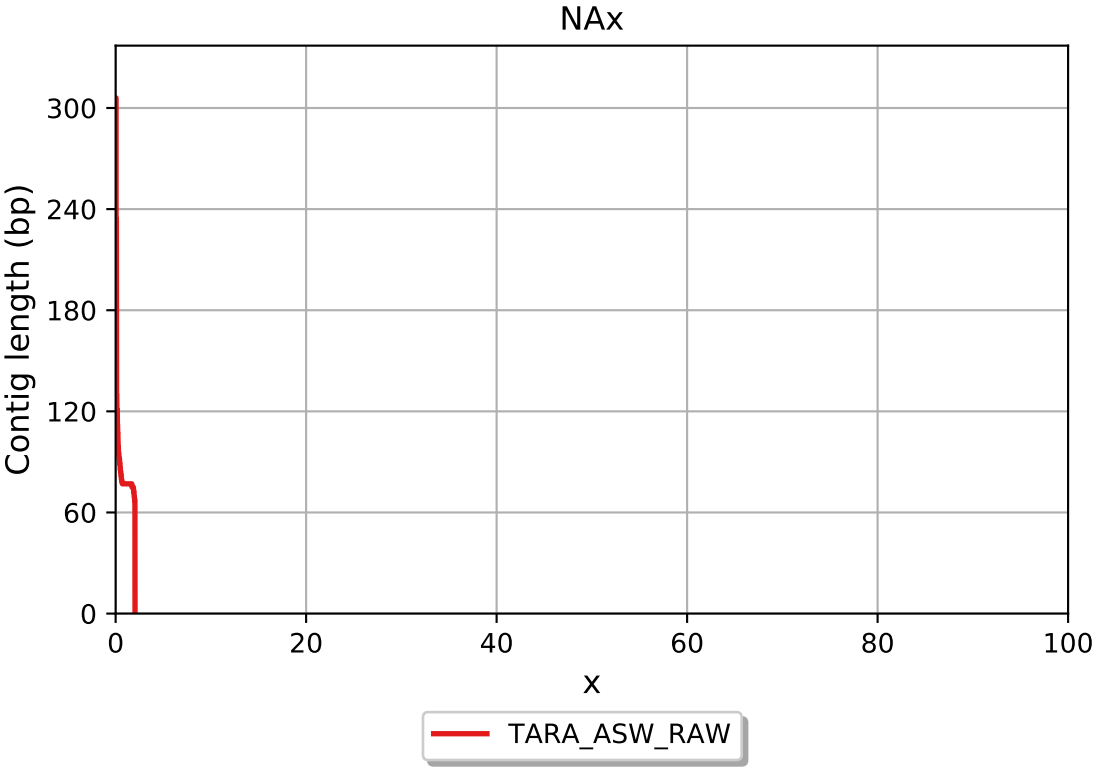

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
TARA_ASW_RAW
Reference

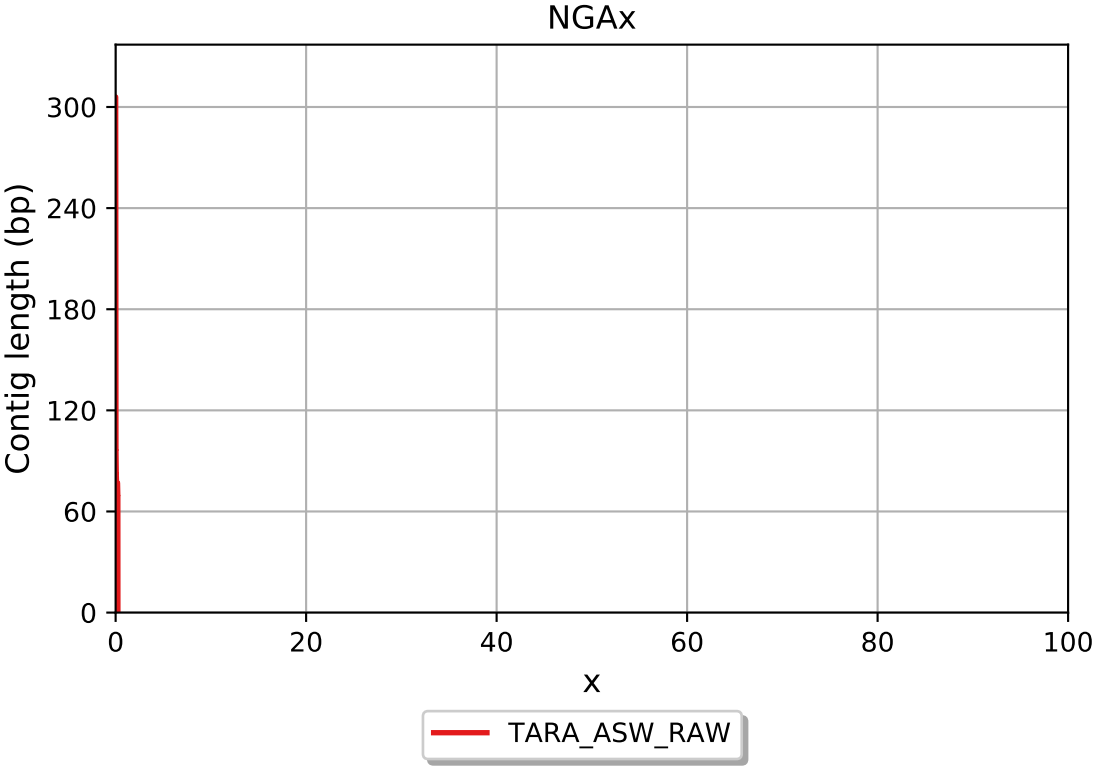

TARA_ASW_RAW GC content
contigs
GC (%)
0
6
12
18
24
30
36
0
20
40
60
80
100
TARA_ASW_RAW


Misassemblies
5
4
3
2
1
0
TARA_ASW_RAW


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
1500
3000
4500
6000
7500
Contig index
TARA_ASW_RAW
Reference


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


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