Report

	TARA_ASW_RAW
# contigs (>= 0 bp)	989154
# contigs (>= 1000 bp)	989154
# contigs (>= 5000 bp)	38869
# contigs (>= 10000 bp)	9877
# contigs (>= 25000 bp)	1638
# contigs (>= 50000 bp)	333
Total length (>= 0 bp)	1970794888
Total length (>= 1000 bp)	1970794888
Total length (>= 5000 bp)	382484797
Total length (>= 10000 bp)	189227956
Total length (>= 25000 bp)	69982681
Total length (>= 50000 bp)	26580787
# contigs	989154
Largest contig	414653
Total length	1970794888
Reference length	7658814
N50	1994
N75	1336
L50	250870
L75	558634
# 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	8
# unaligned contigs	988899 + 253 part
Unaligned length	1970771177
Genome fraction (%)	0.068
Duplication ratio	30.160
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26241.13
# indels per 100 kbp	1495.11
Largest alignment	234
Total aligned length	21999

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

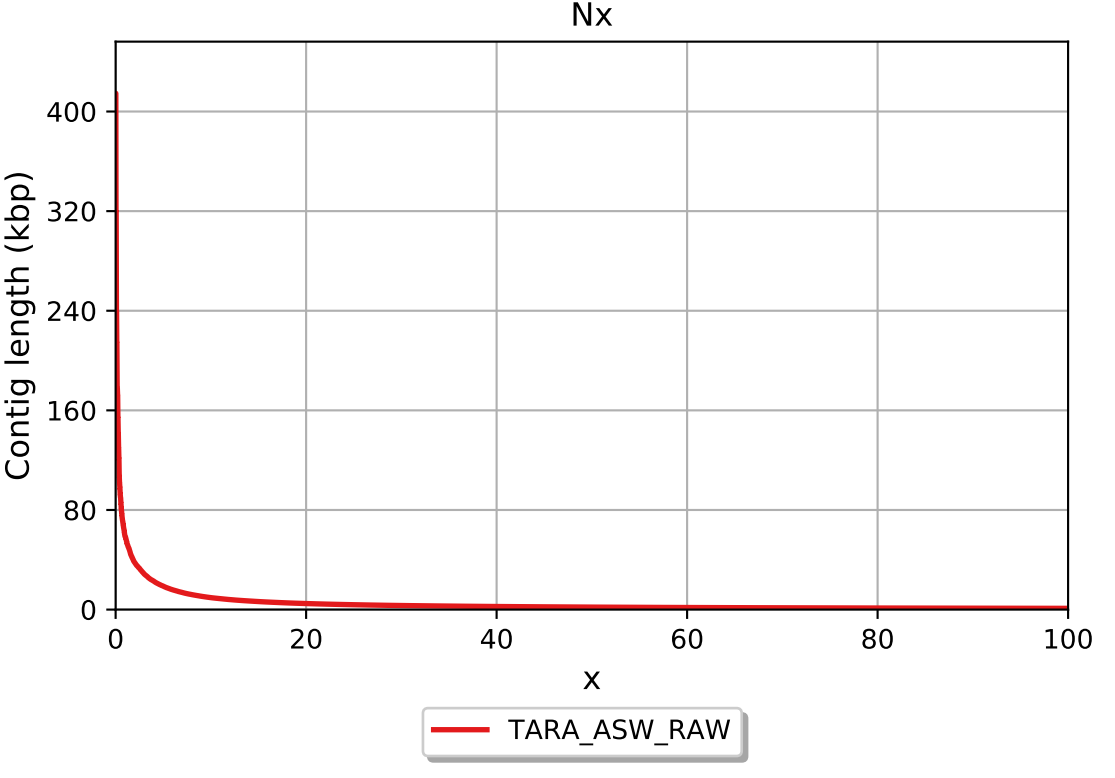
	TARA_ASW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	246
# possible misassemblies	294
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	1369
# indels	78
# indels (<= 5 bp)	78
# indels (> 5 bp)	0
Indels length	148

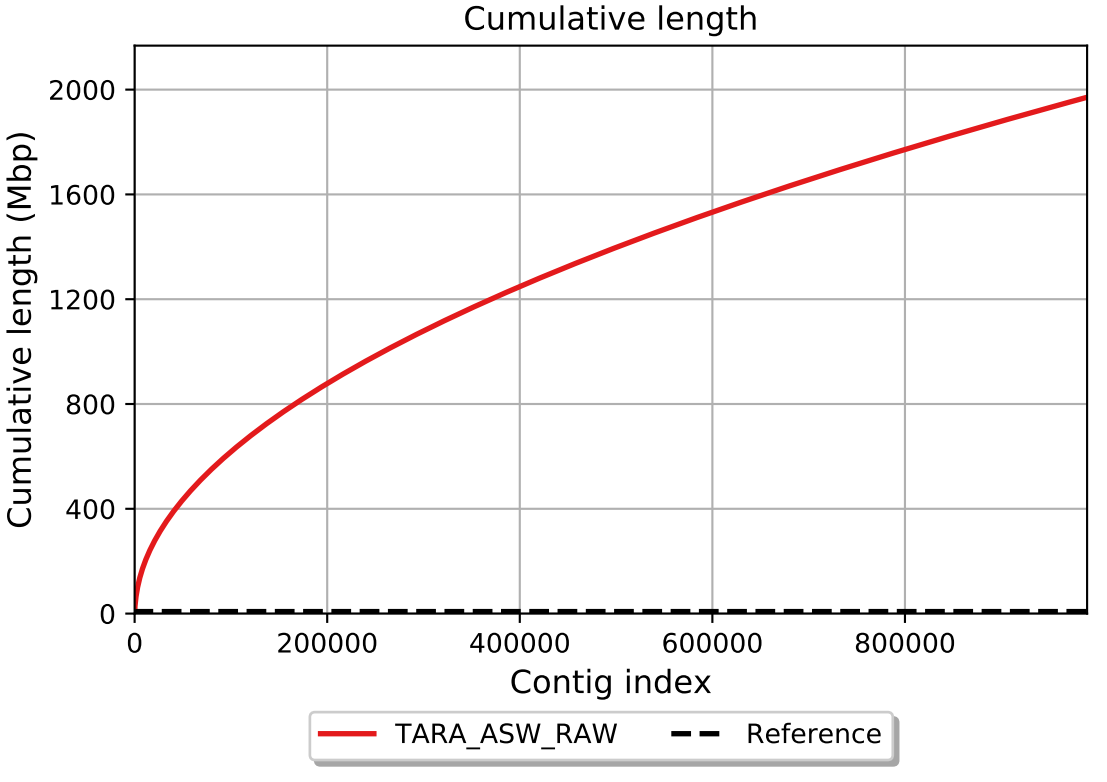
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

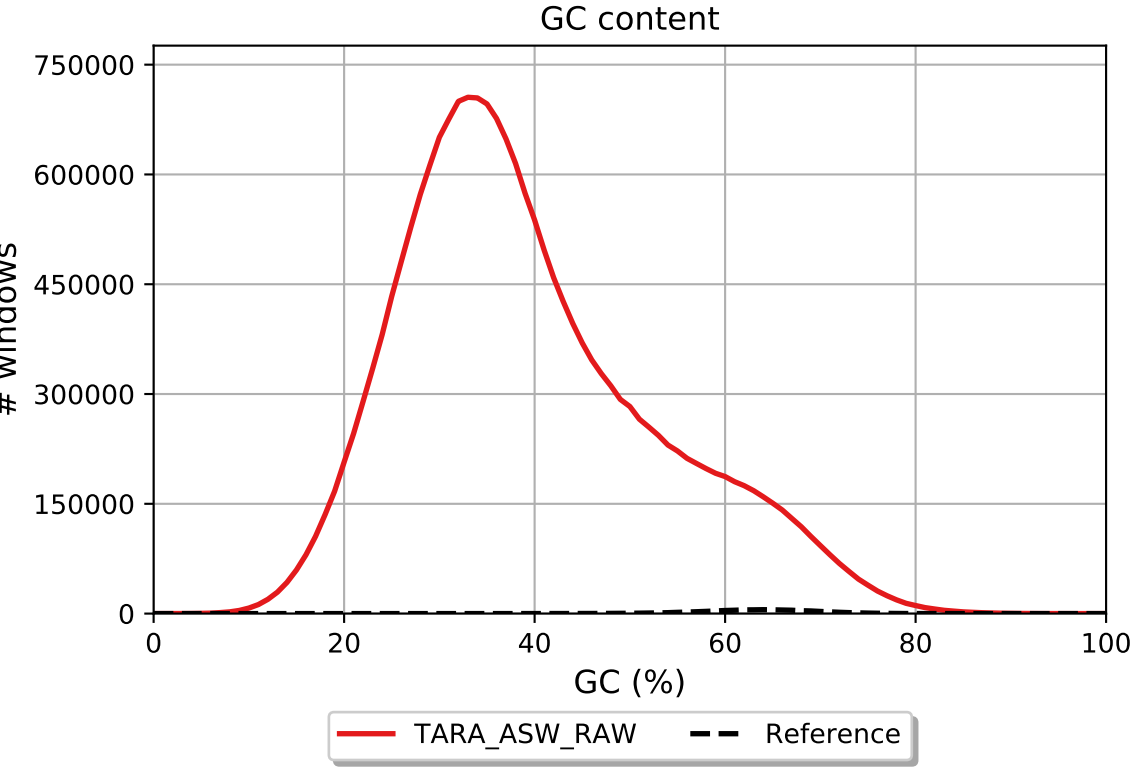
Unaligned report

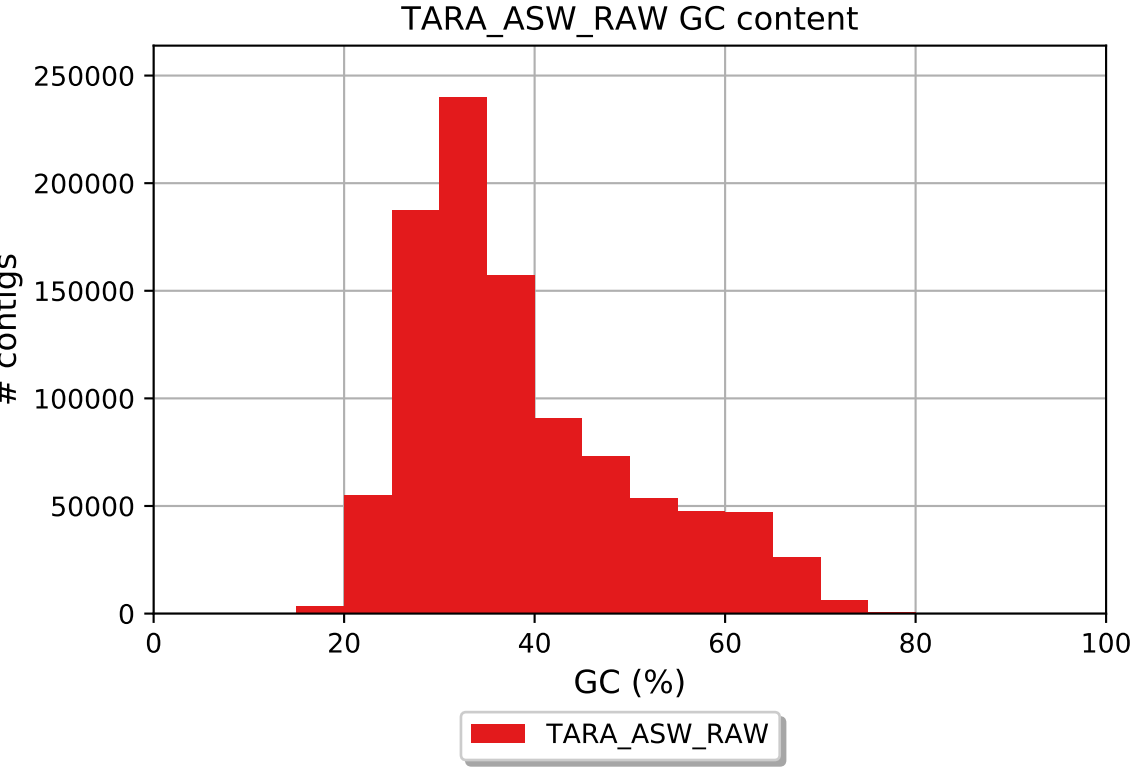
	TARA_ASW_RAW
# fully unaligned contigs	988899
Fully unaligned length	1969779547
# partially unaligned contigs	253
Partially unaligned length	991630
# N's	0

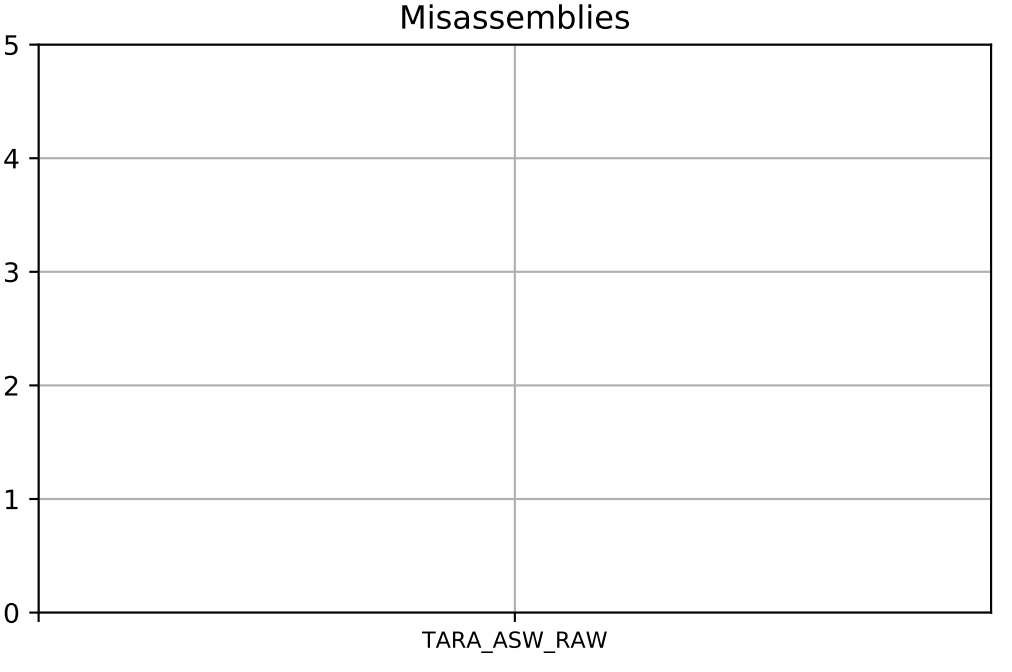
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

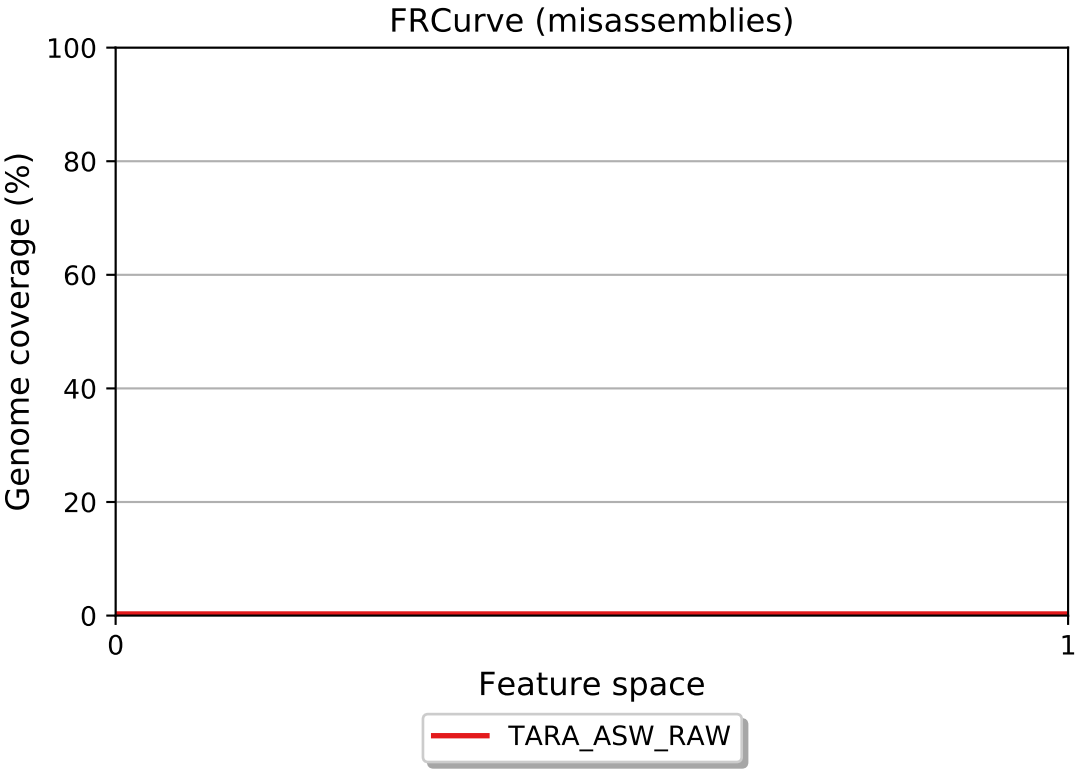

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
TARA_ASW_RAW

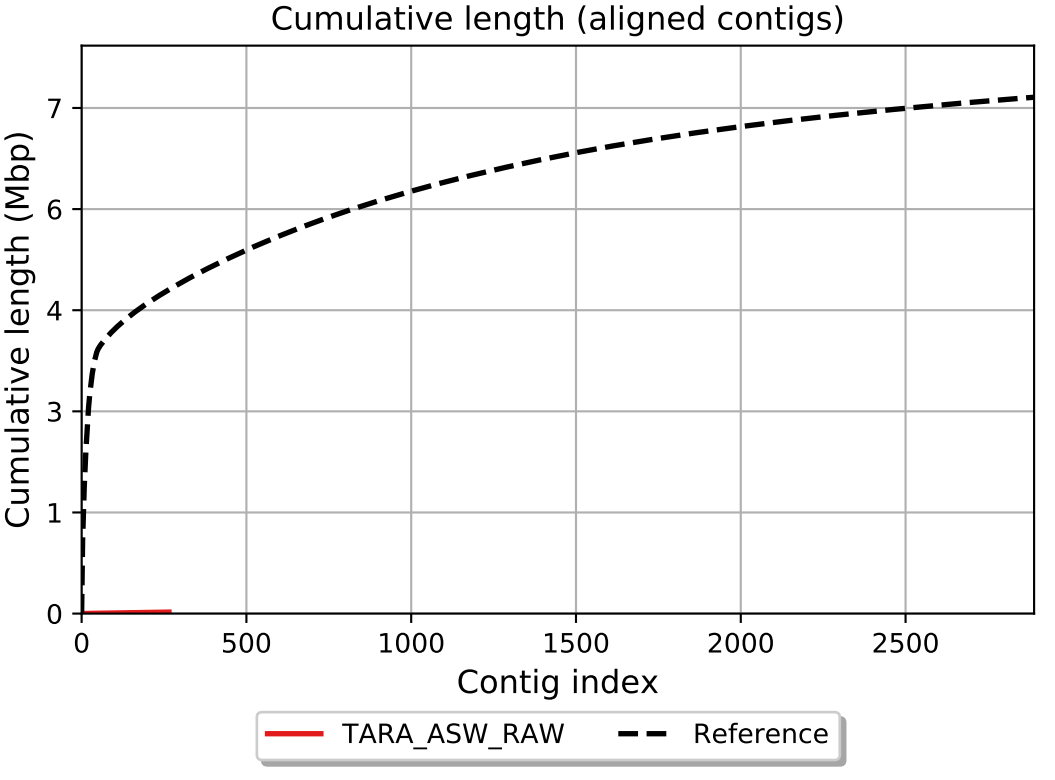

Cumulative length
Cumulative length (Mbp)
2000
1600
1200
800
400
0
0
200000
400000
600000
800000
Contig index
TARA_ASW_RAW
Reference

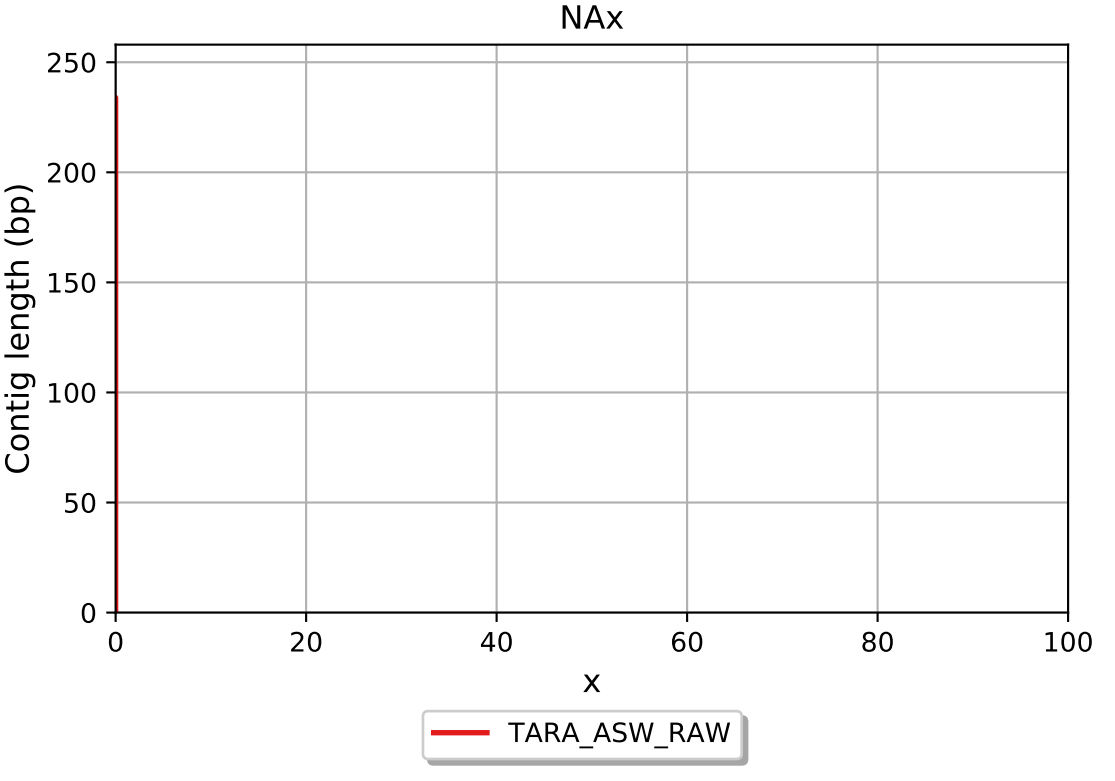

GC content
750000
600000
450000
300000
150000
0
windows
0
20
40
60
80
100
GC (%)
TARA_ASW_RAW
Reference


TARA_ASW_RAW GC content
250000
200000
150000
100000
50000
0
contigs
0
20
40
60
80
100
GC (%)
TARA_ASW_RAW


Misassemblies
5
4
3
2
1
0
TARA_ASW_RAW


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


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


NAx
Contig length (bp)
250
200
150
100
50
0
0
20
40
60
80
100
x
TARA_ASW_RAW