Report

	TARA_ASE_RAW
# contigs (>= 0 bp)	766472
# contigs (>= 1000 bp)	766472
# contigs (>= 5000 bp)	23509
# contigs (>= 10000 bp)	5257
# contigs (>= 25000 bp)	699
# contigs (>= 50000 bp)	146
Total length (>= 0 bp)	1430179911
Total length (>= 1000 bp)	1430179911
Total length (>= 5000 bp)	214871738
Total length (>= 10000 bp)	94359835
Total length (>= 25000 bp)	29656132
Total length (>= 50000 bp)	11639915
# contigs	766472
Largest contig	387648
Total length	1430179911
Reference length	7658814
N50	1830
N75	1291
L50	212842
L75	449143
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	5552
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	766326 + 146 part
Unaligned length	1430164816
Genome fraction (%)	0.086
Duplication ratio	2.503
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5268.74
# indels per 100 kbp	30.28
Largest alignment	1719
Total aligned length	15095

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

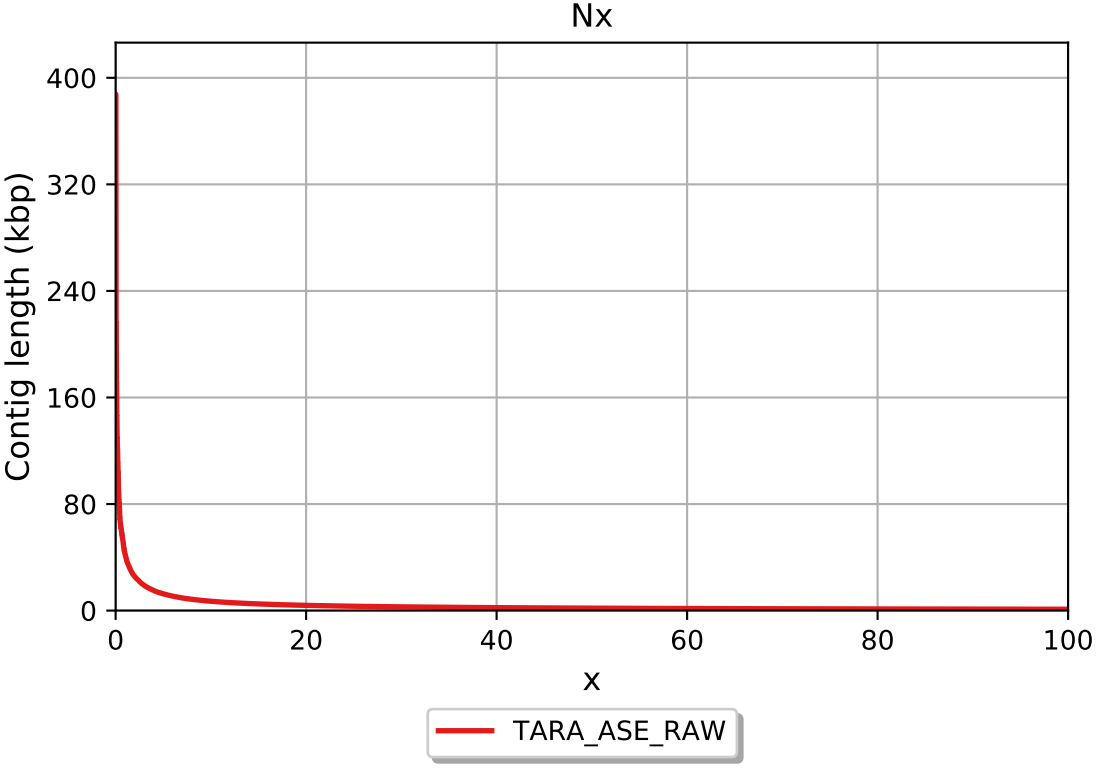
	TARA_ASE_RAW
# misassemblies	2
# contig misassemblies	2
# c. relocations	0
# c. translocations	2
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	1
Misassembled contigs length	5552
# possibly misassembled contigs	141
# possible misassemblies	158
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	348
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	4

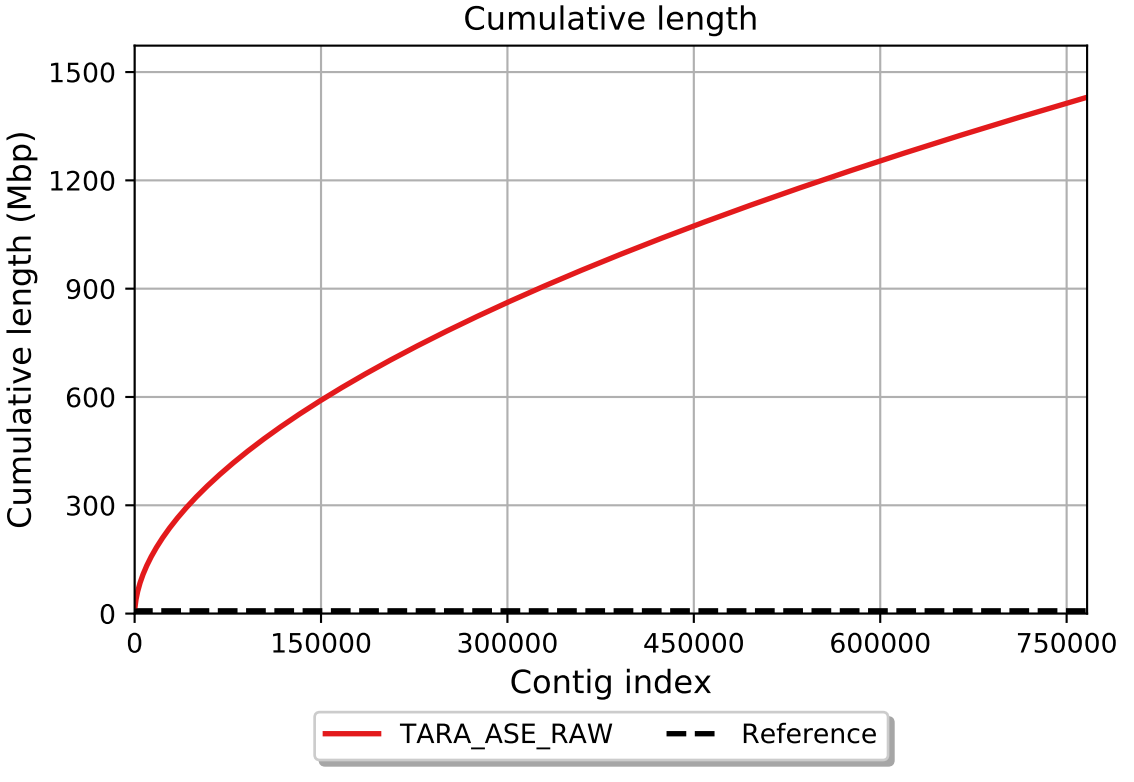
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

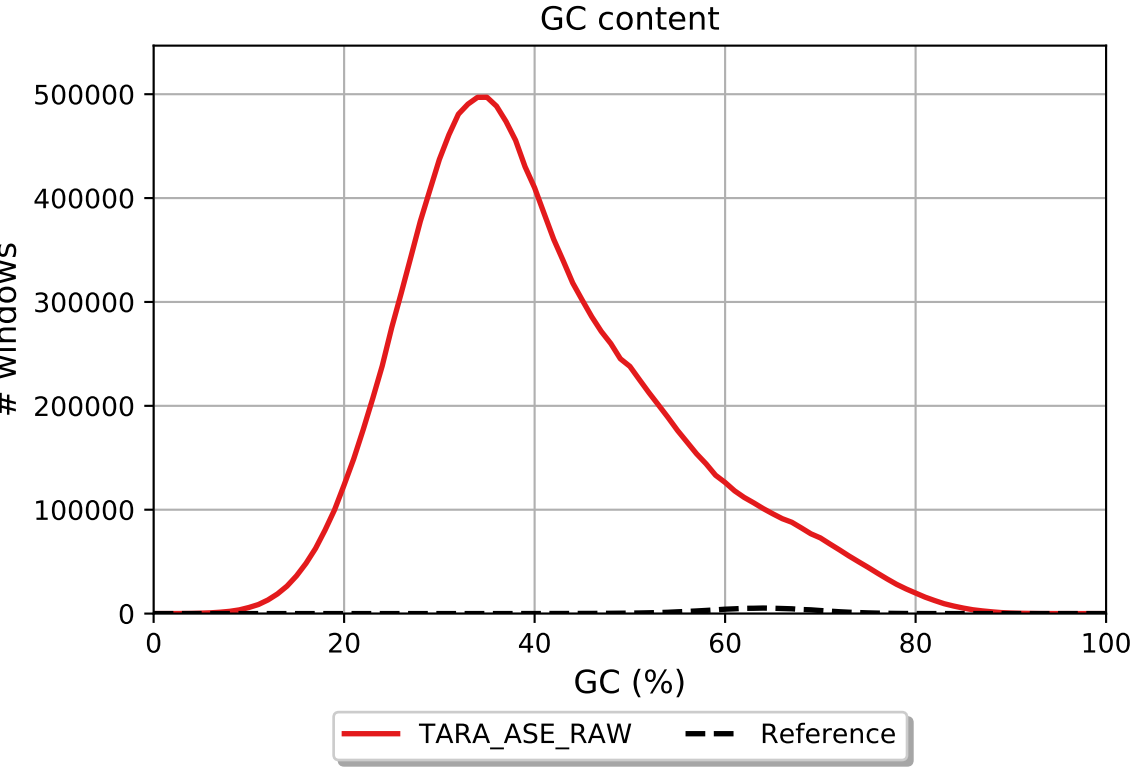
Unaligned report

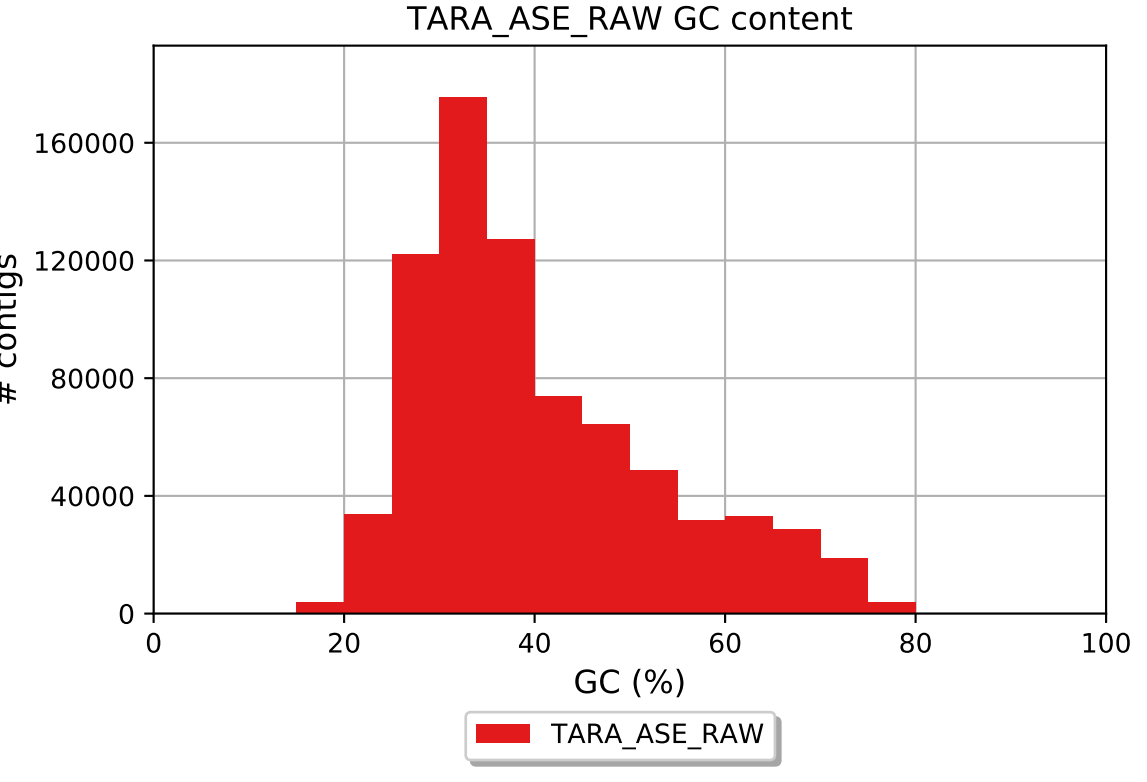
	TARA_ASE_RAW
# fully unaligned contigs	766326
Fully unaligned length	1429853246
# partially unaligned contigs	146
Partially unaligned length	311570
# N's	0

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).

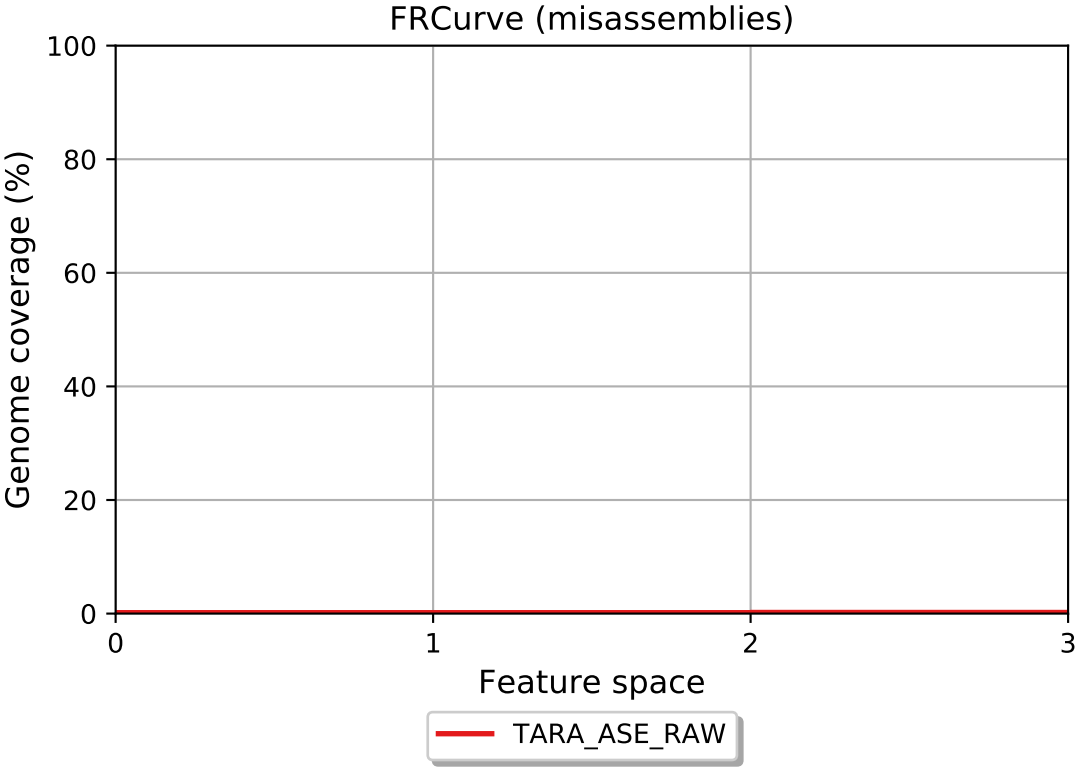

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
TARA_ASE_RAW

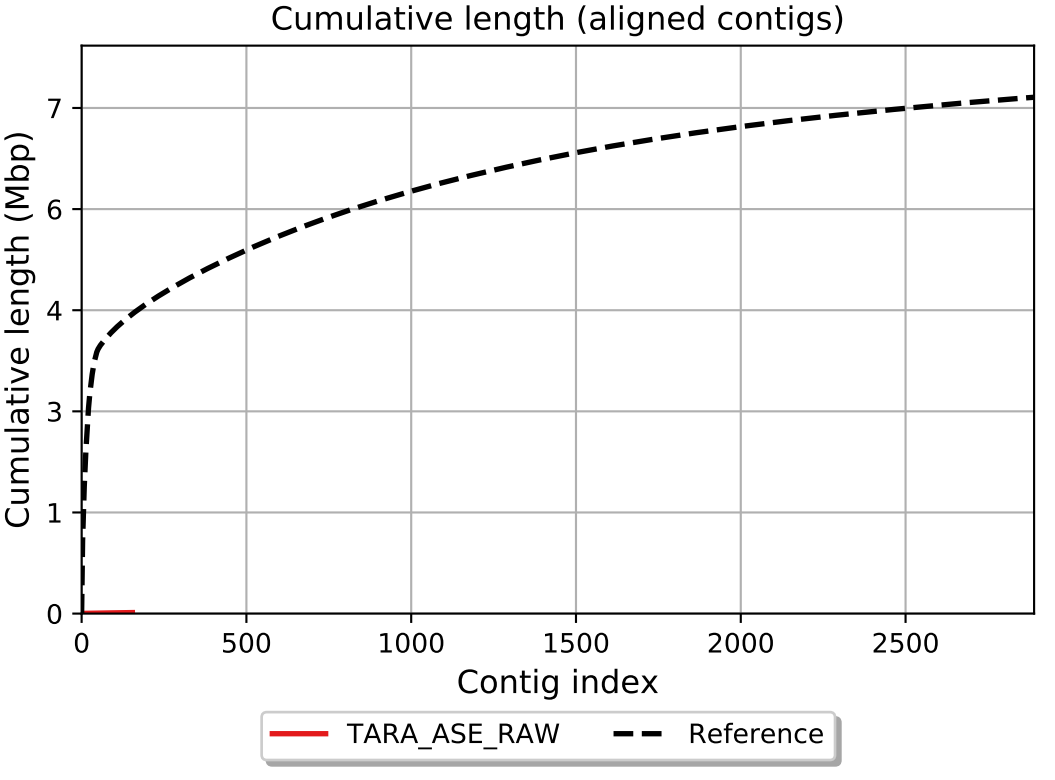

Cumulative length
Cumulative length (Mbp)
1500
1200
900
600
300
0
0
150000
300000
450000
600000
750000
Contig index
TARA_ASE_RAW
Reference

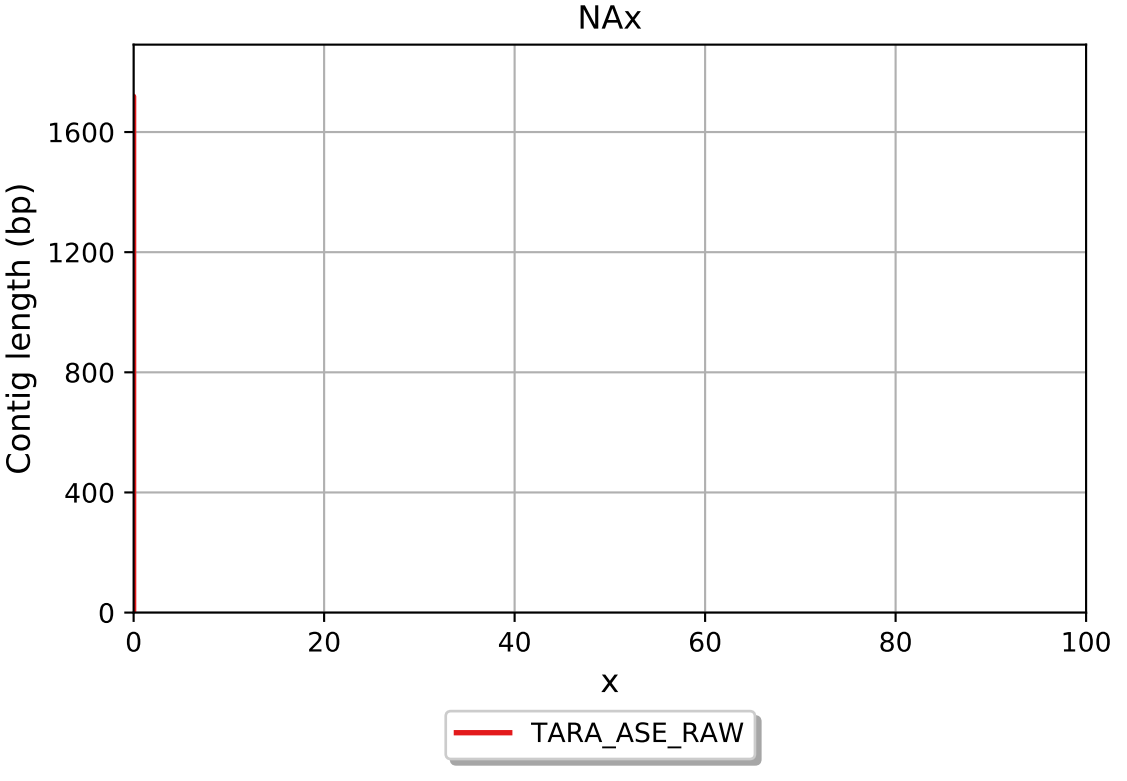

GC content
500000
400000
300000
200000
100000
0
windows
0
20
40
60
80
100
GC (%)
TARA_ASE_RAW
Reference


TARA_ASE_RAW GC content
contigs
160000
120000
80000
40000
0
0
20
40
60
80
100
GC (%)
TARA_ASE_RAW

Misassemblies
5
4
3
2
1
0
TARA_ASE_RAW
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
TARA_ASE_RAW


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


NAx
Contig length (bp)
1600
1200
800
400
0
0
20
40
60
80
100
x
TARA_ASE_RAW