Report

	TARA_ANW_RAW
# contigs (>= 0 bp)	1267057
# contigs (>= 1000 bp)	1267057
# contigs (>= 5000 bp)	59397
# contigs (>= 10000 bp)	15465
# contigs (>= 25000 bp)	2423
# contigs (>= 50000 bp)	529
Total length (>= 0 bp)	2648602495
Total length (>= 1000 bp)	2648602495
Total length (>= 5000 bp)	593369101
Total length (>= 10000 bp)	299298940
Total length (>= 25000 bp)	113445149
Total length (>= 50000 bp)	50720126
# contigs	1267057
Largest contig	1019813
Total length	2648602495
Reference length	4234461
N50	2138
N75	1378
L50	302257
L75	696663
# 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	3
# unaligned contigs	1267002 + 55 part
Unaligned length	2648597147
Genome fraction (%)	0.032
Duplication ratio	4.088
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13002.19
# indels per 100 kbp	73.05
Largest alignment	201
Total aligned length	5348

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

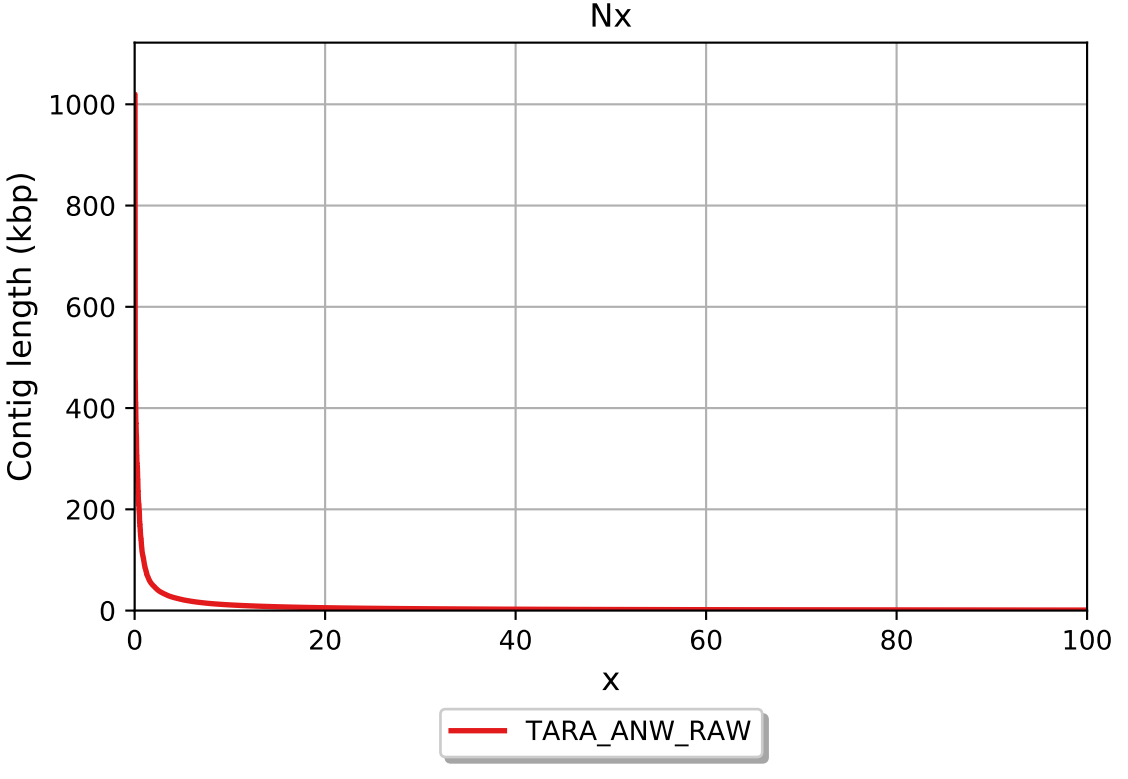
	TARA_ANW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	52
# possible misassemblies	59
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	178
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

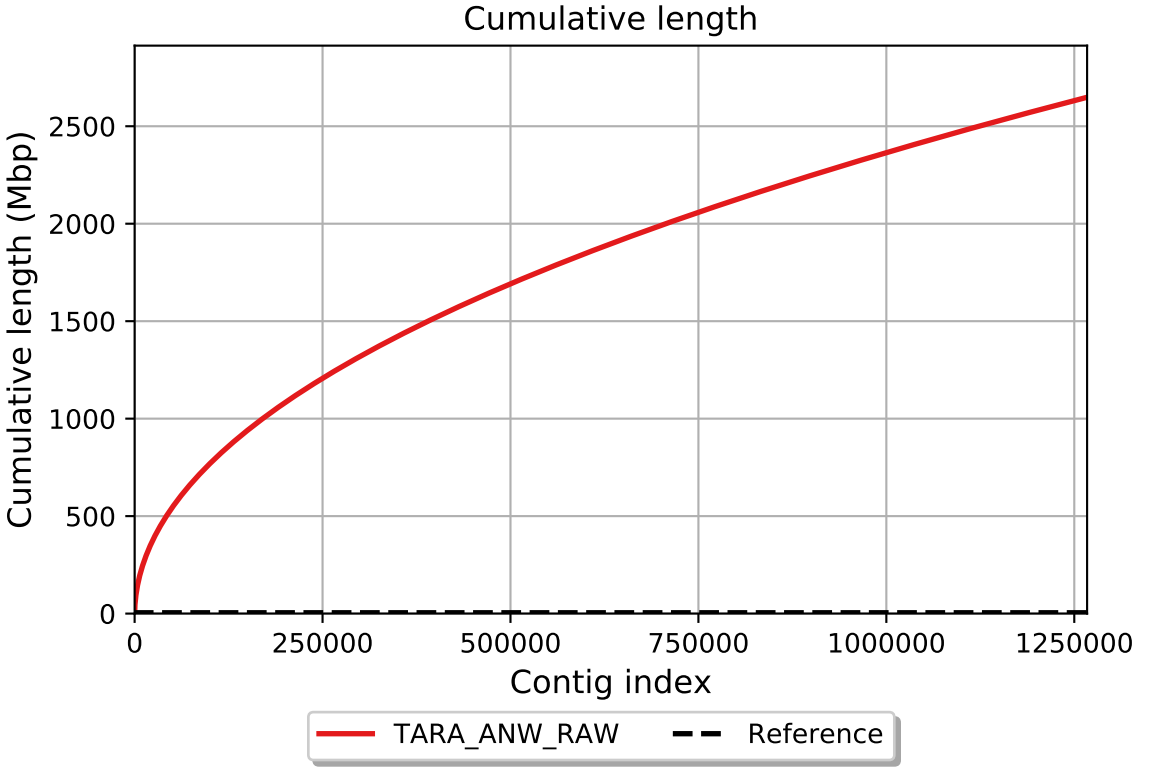
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

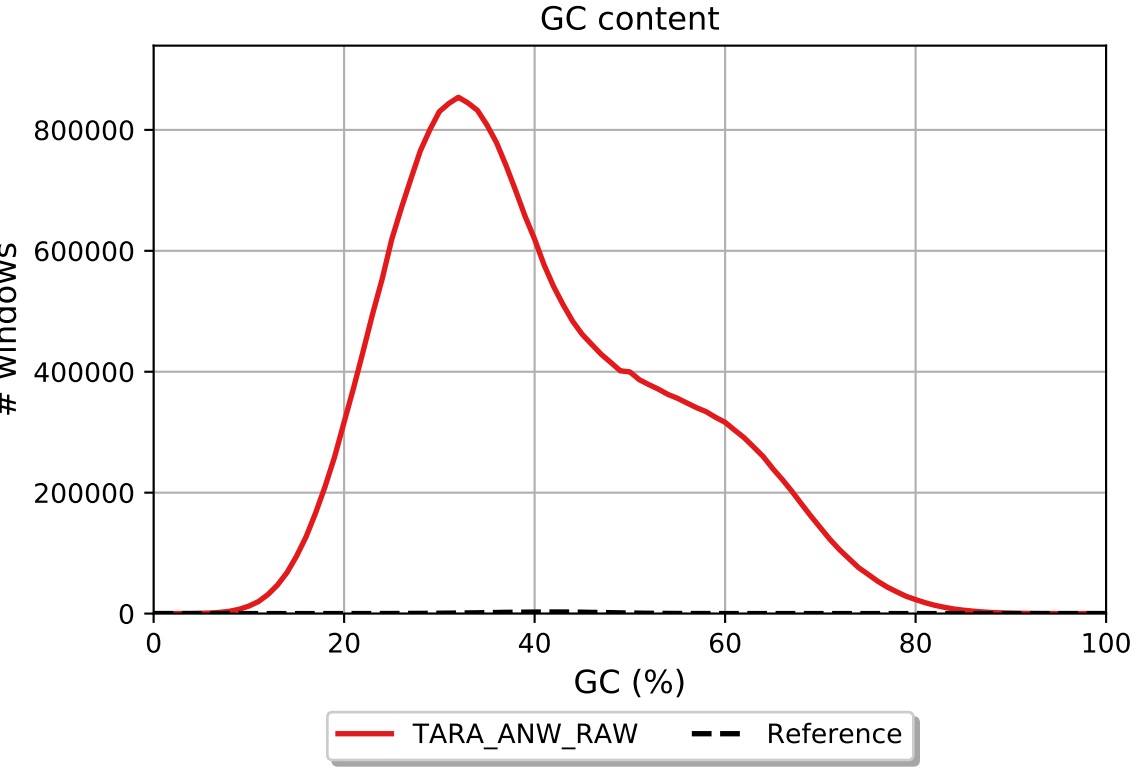
Unaligned report

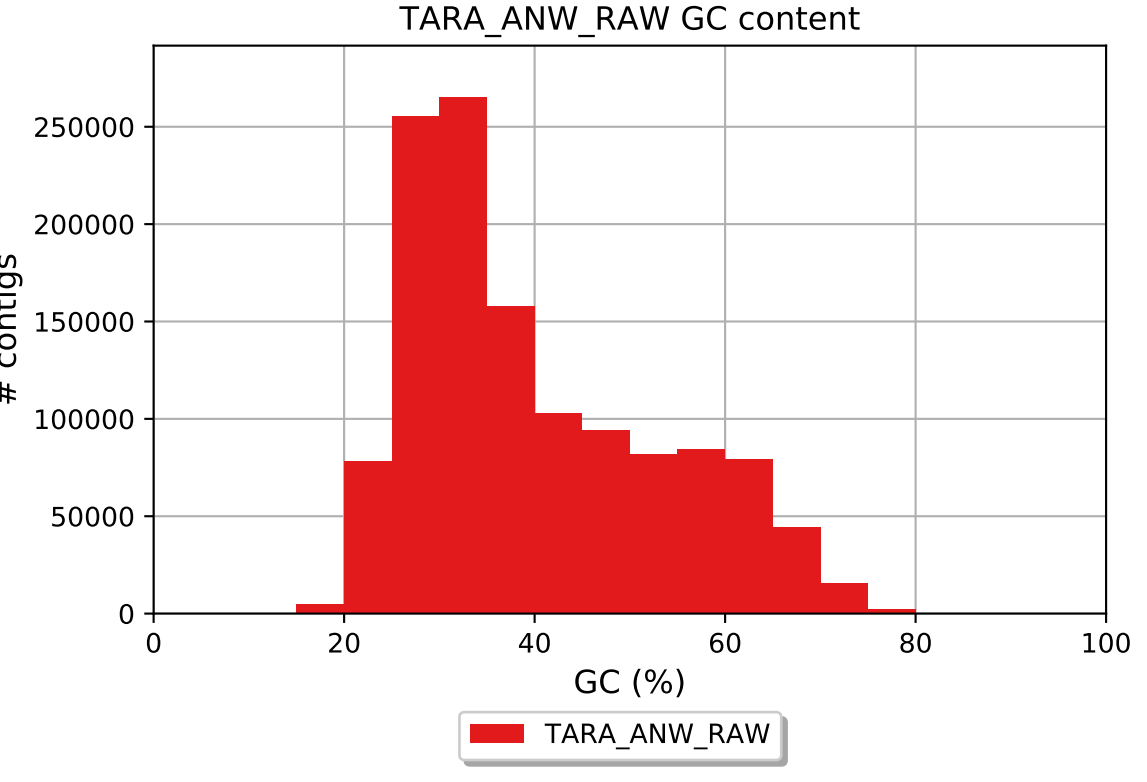
	TARA_ANW_RAW
# fully unaligned contigs	1267002
Fully unaligned length	2648395133
# partially unaligned contigs	55
Partially unaligned length	202014
# N's	0

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).

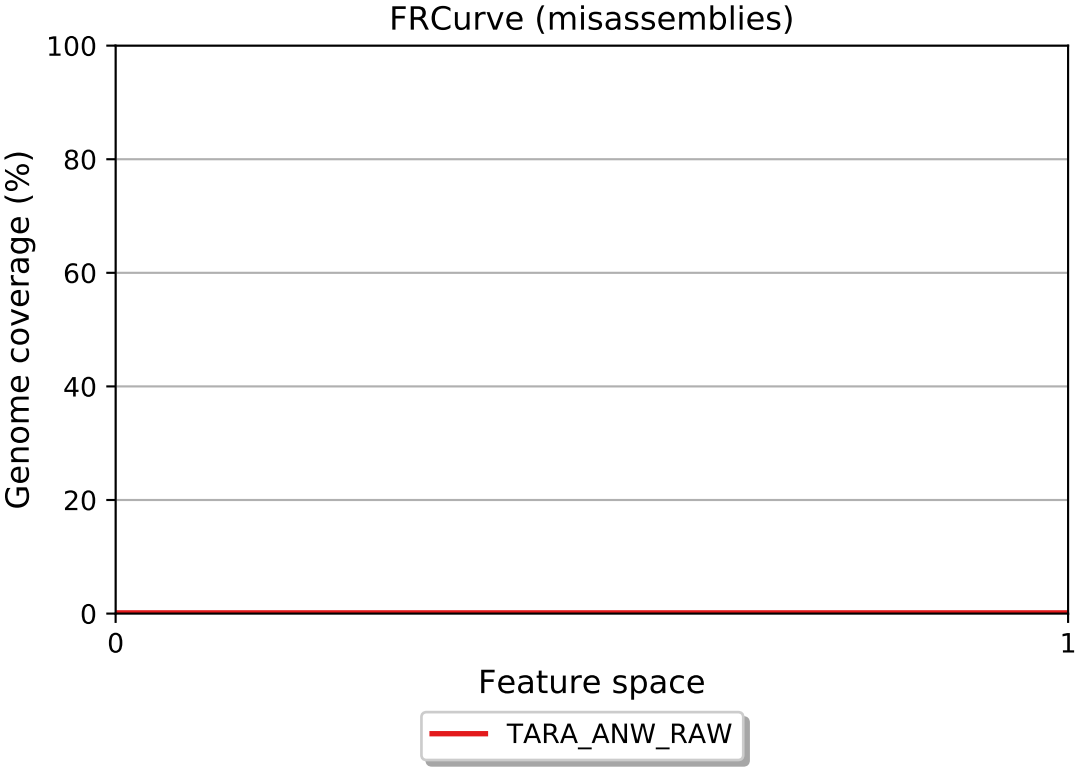

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
TARA_ANW_RAW

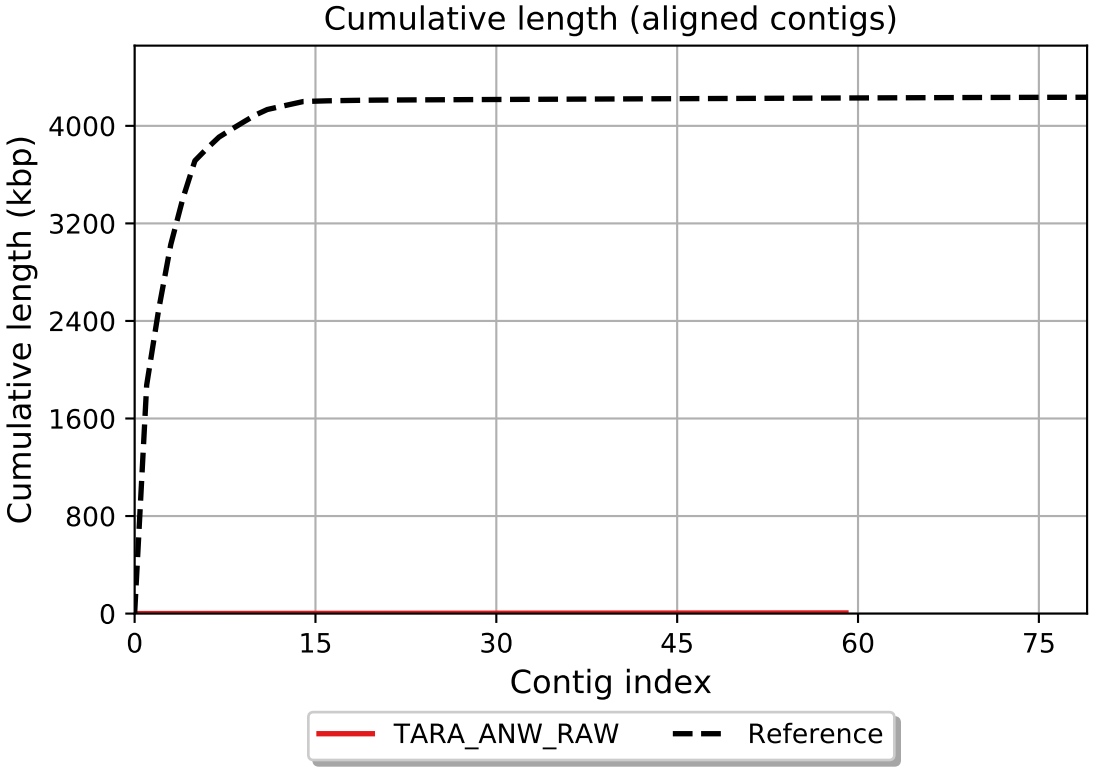

Cumulative length
Cumulative length (Mbp)
2500
2000
1500
1000
500
0
0
250000
500000
750000
1000000
1250000
Contig index
TARA_ANW_RAW
Reference

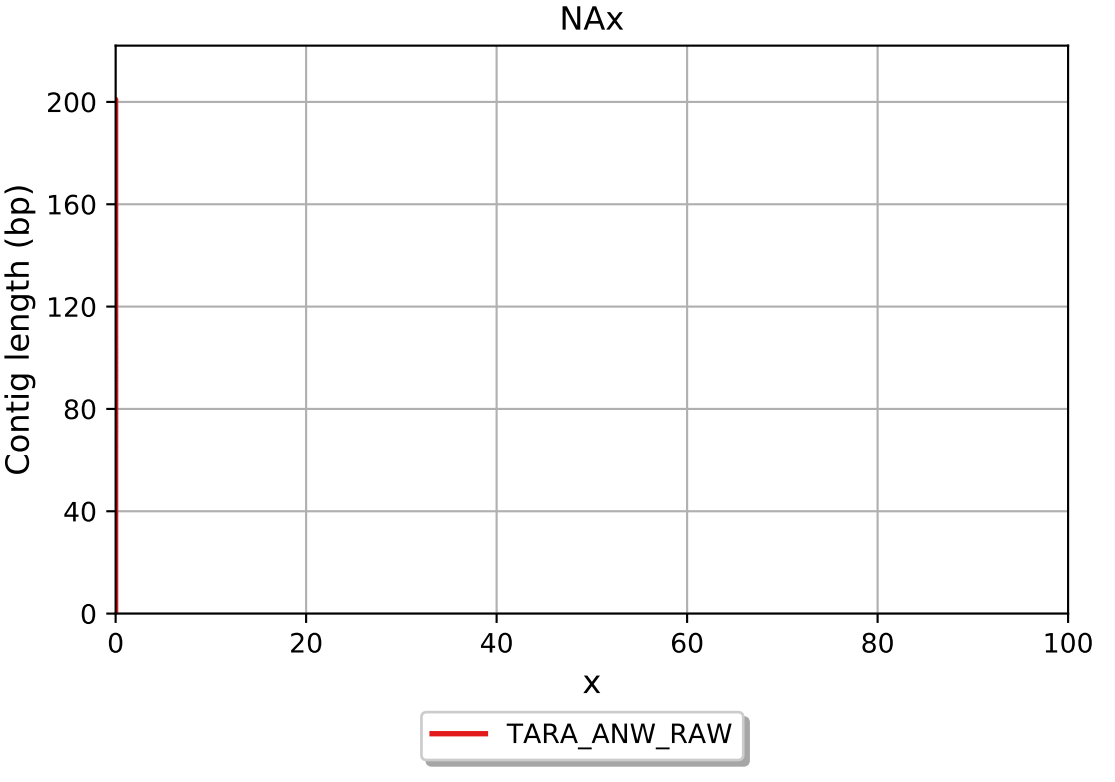

GC content
800000
600000
400000
200000
0
windows
0
20
40
60
80
100
GC (%)
TARA_ANW_RAW
Reference


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

Misassemblies
5
4
3
2
1
0
TARA_ANW_RAW


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


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


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