Report

	TARA_ANE_RAW
# contigs (>= 1000 bp)	37
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	110348
Total length (>= 5000 bp)	43563
Total length (>= 10000 bp)	43563
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	37
Largest contig	24659
Total length	110348
Reference length	3561038
GC (%)	47.52
Reference GC (%)	41.87
N50	3076
N75	2142
L50	6
L75	16
# 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	7 + 30 part
Unaligned length	107366
Genome fraction (%)	0.020
Duplication ratio	4.102
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12379.64
# indels per 100 kbp	0.00
Largest alignment	120
Total aligned length	2982
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

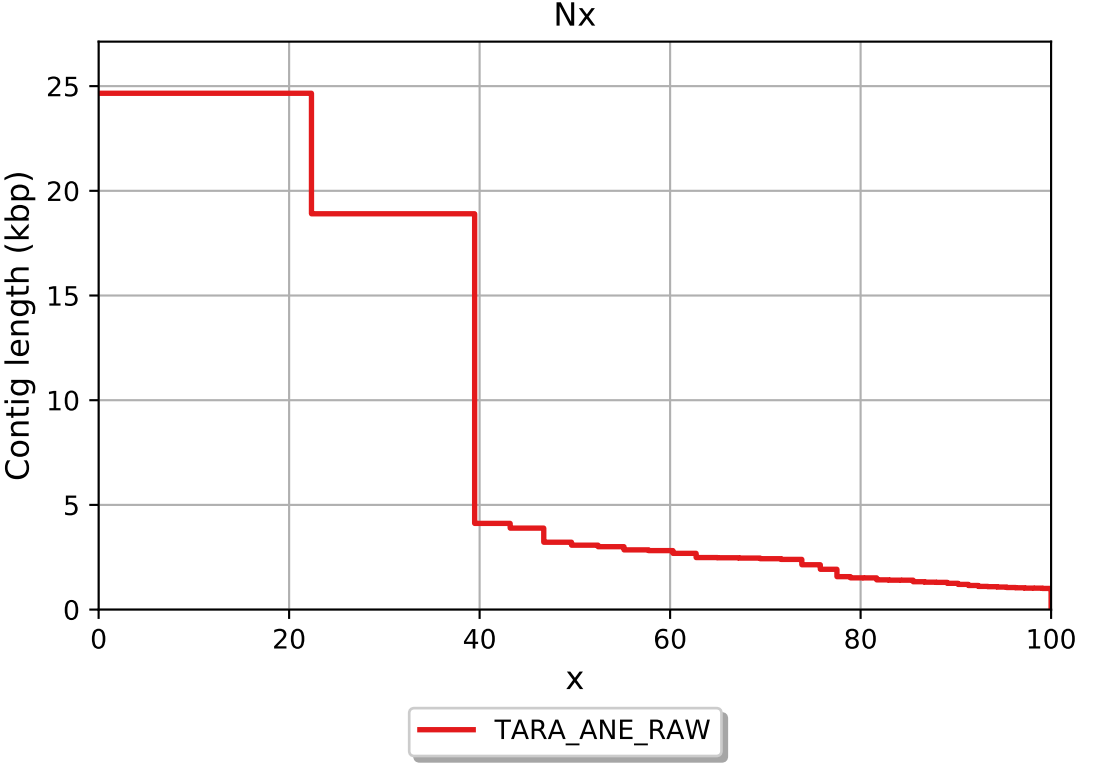
	TARA_ANE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	34
# possible misassemblies	35
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	90
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

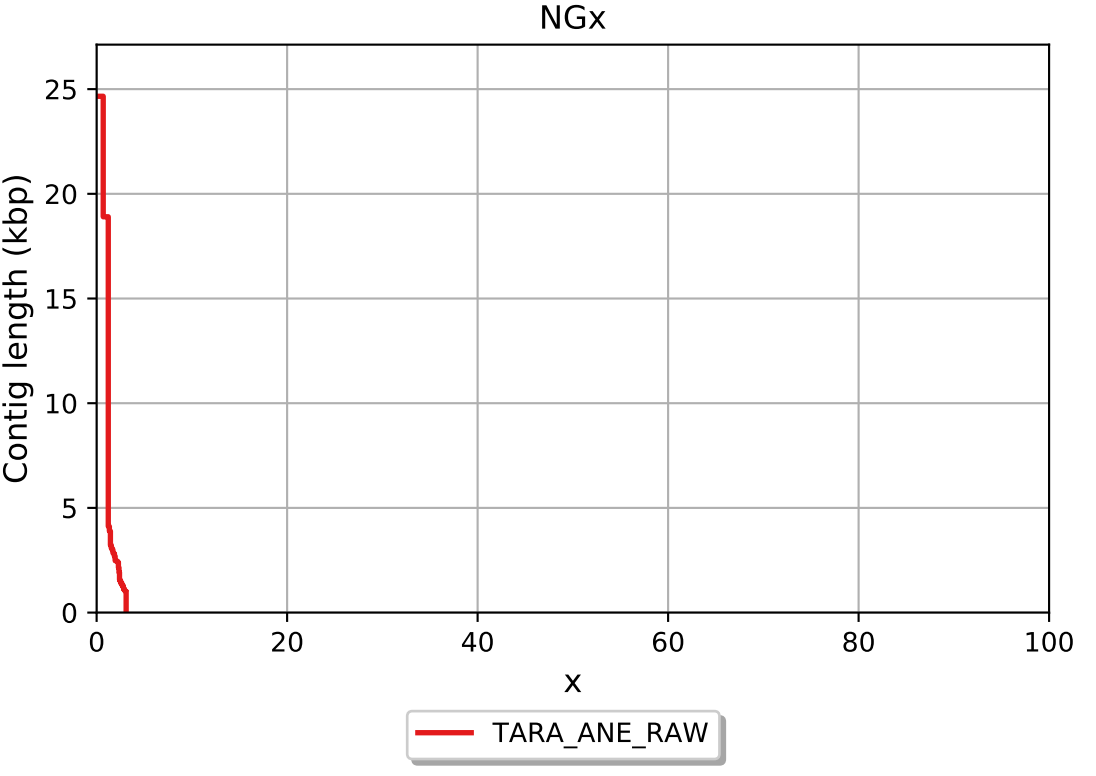
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

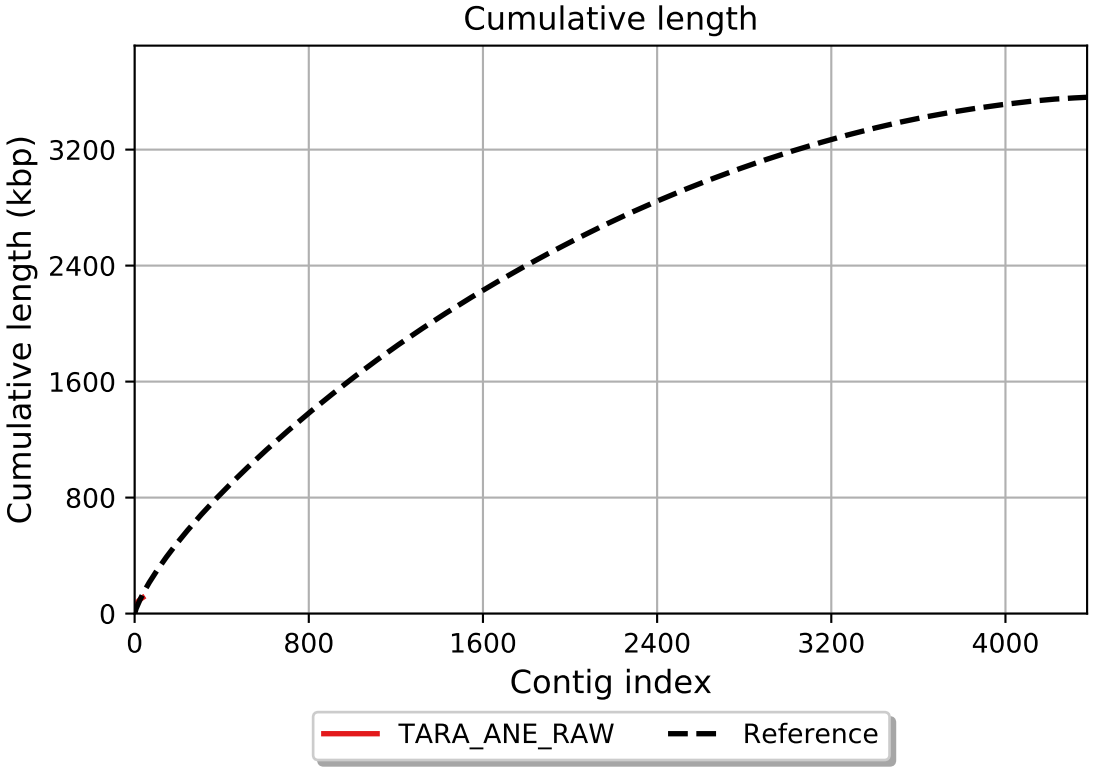
Unaligned report

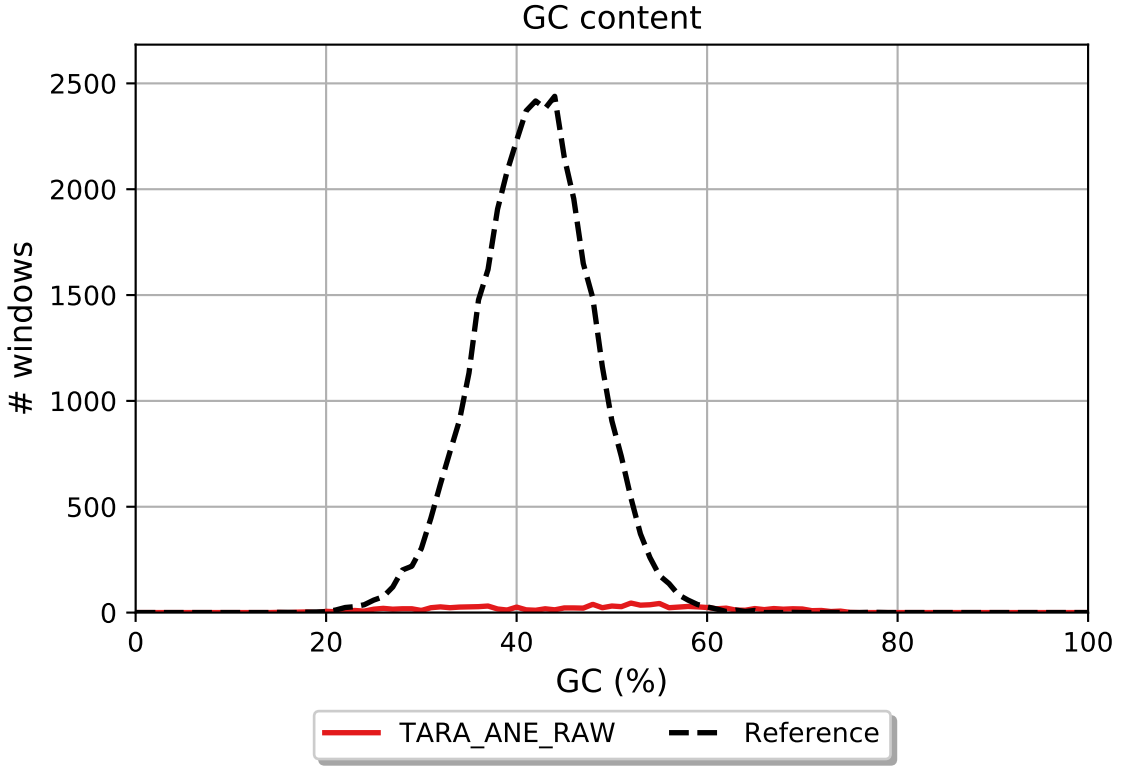
	TARA_ANE_RAW
# fully unaligned contigs	7
Fully unaligned length	14460
# partially unaligned contigs	30
Partially unaligned length	92906
# N's	0

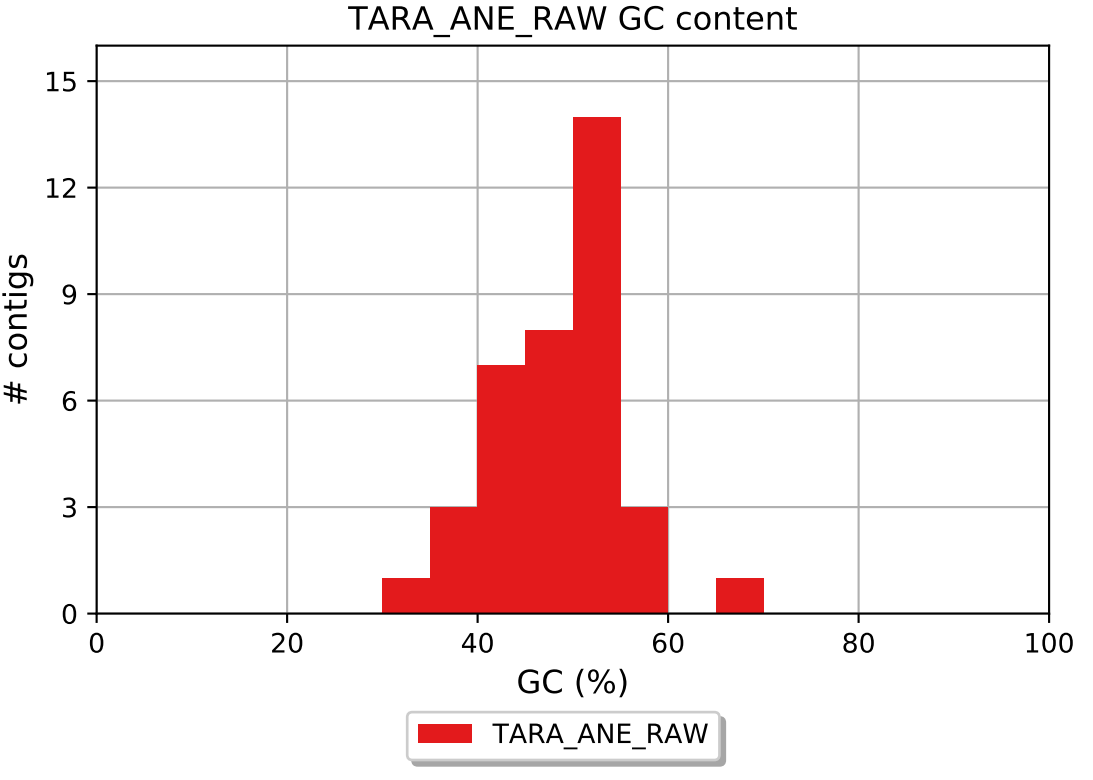
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

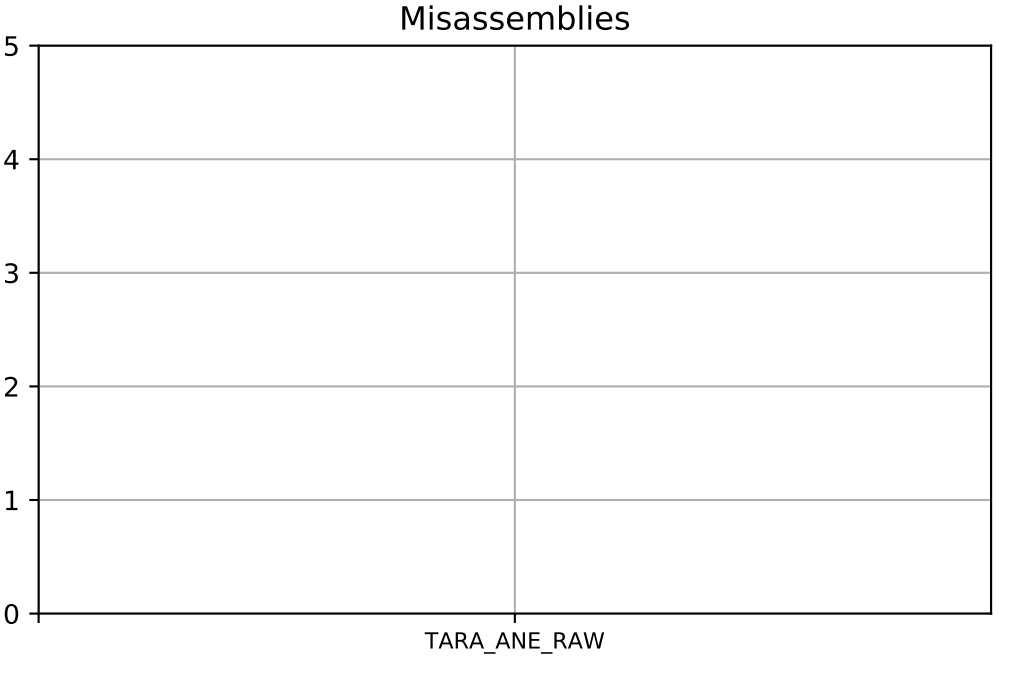

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
TARA_ANE_RAW

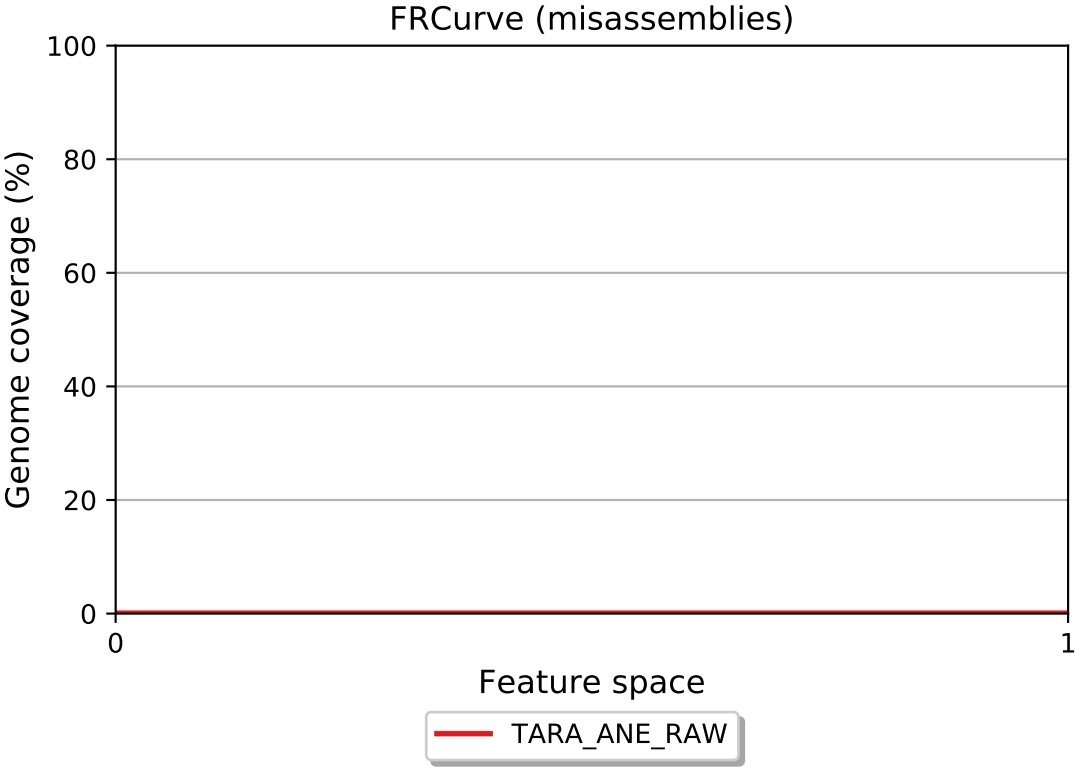

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
TARA_ANE_RAW

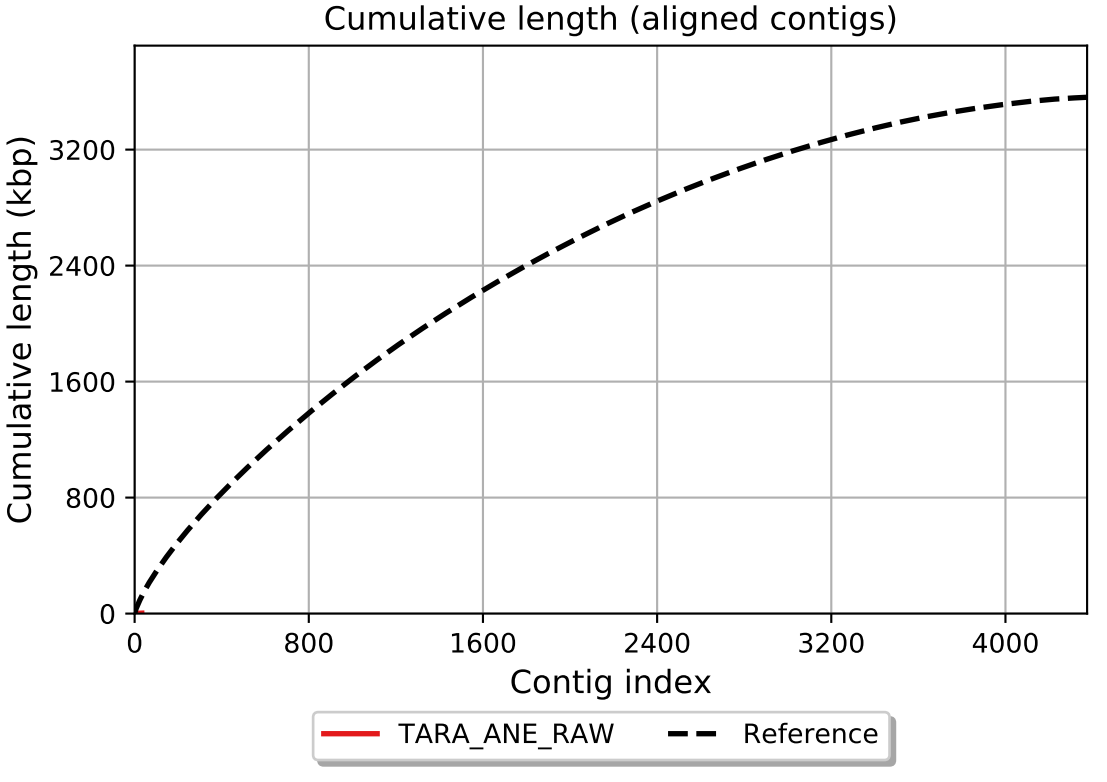

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
800
1600
2400
3200
4000
Contig index
TARA_ANE_RAW
Reference

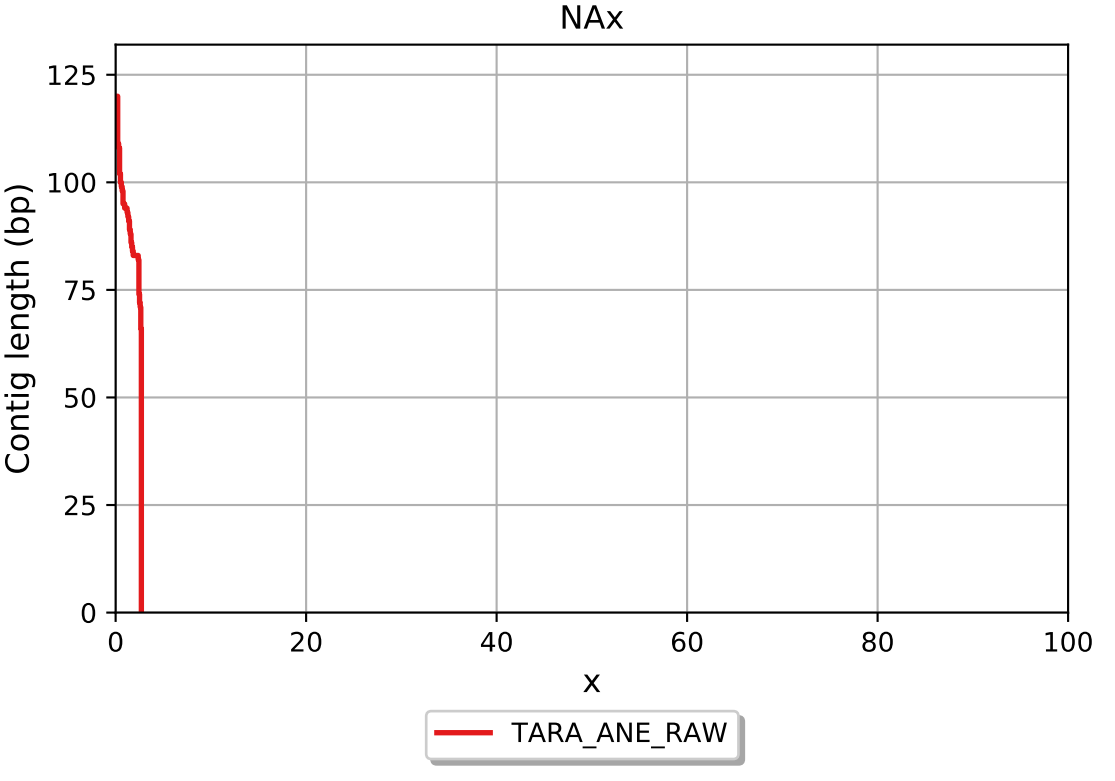

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
TARA_ANE_RAW
Reference

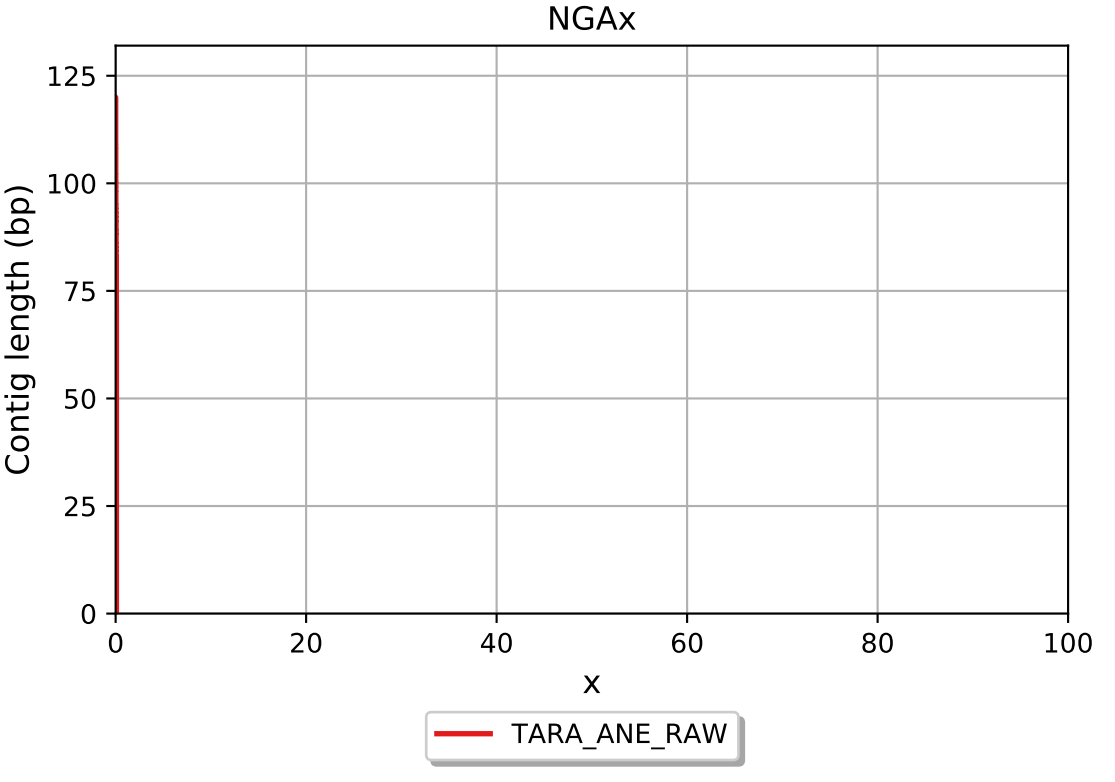

TARA_ANE_RAW GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
TARA_ANE_RAW


Misassemblies
5
4
3
2
1
0
TARA_ANE_RAW


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
800
1600
2400
3200
0
800
1600
2400
3200
4000
Contig index
TARA_ANE_RAW
Reference


NAx
Contig length (bp)
125
100
75
50
25
0
0
20
40
60
80
100
x
TARA_ANE_RAW


NGAx
Contig length (bp)
125
100
75
50
25
0
0
20
40
60
80
100
x
TARA_ANE_RAW