Report

	TARA_ANE_RAW
# contigs (>= 1000 bp)	392
# contigs (>= 5000 bp)	95
# contigs (>= 10000 bp)	45
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	2118981
Total length (>= 5000 bp)	1508060
Total length (>= 10000 bp)	1156199
Total length (>= 25000 bp)	703267
Total length (>= 50000 bp)	116677
# contigs	392
Largest contig	58665
Total length	2118981
Reference length	5854900
GC (%)	31.75
Reference GC (%)	63.53
N50	13453
N75	4269
L50	37
L75	113
# 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 + 387 part
Unaligned length	2087101
Genome fraction (%)	0.056
Duplication ratio	9.675
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16691.96
# indels per 100 kbp	0.00
Largest alignment	287
Total aligned length	31045
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

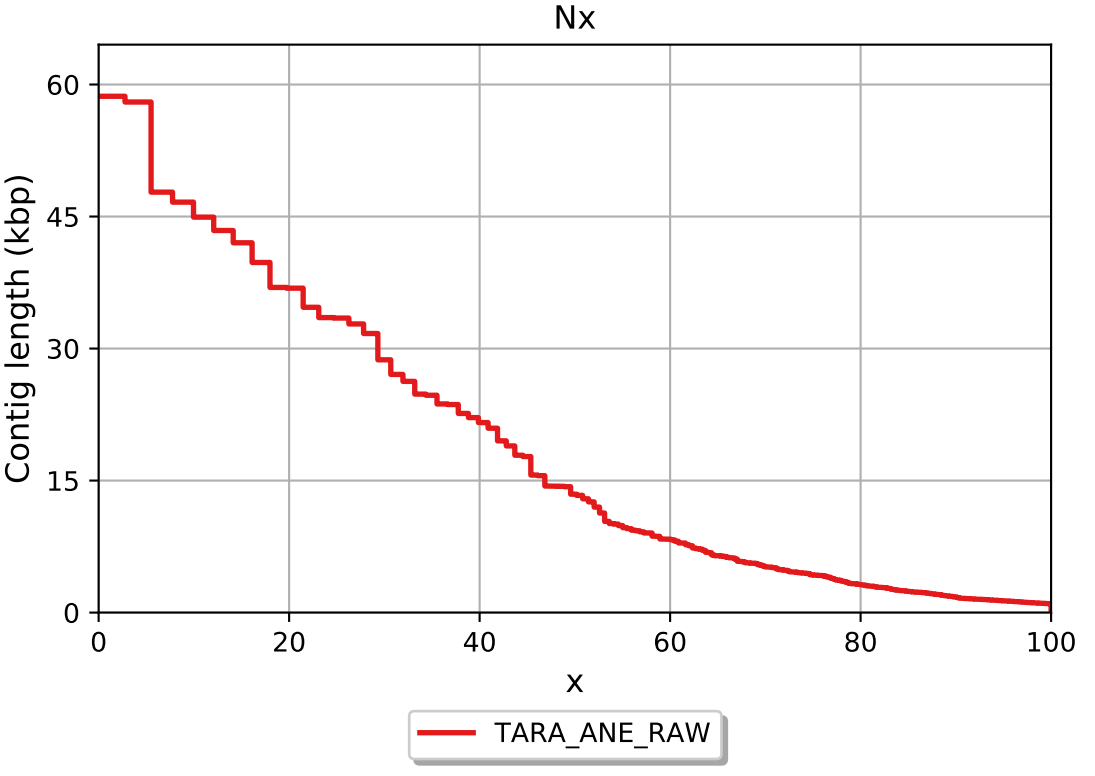
	TARA_ANE_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	390
# possible misassemblies	488
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	550
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

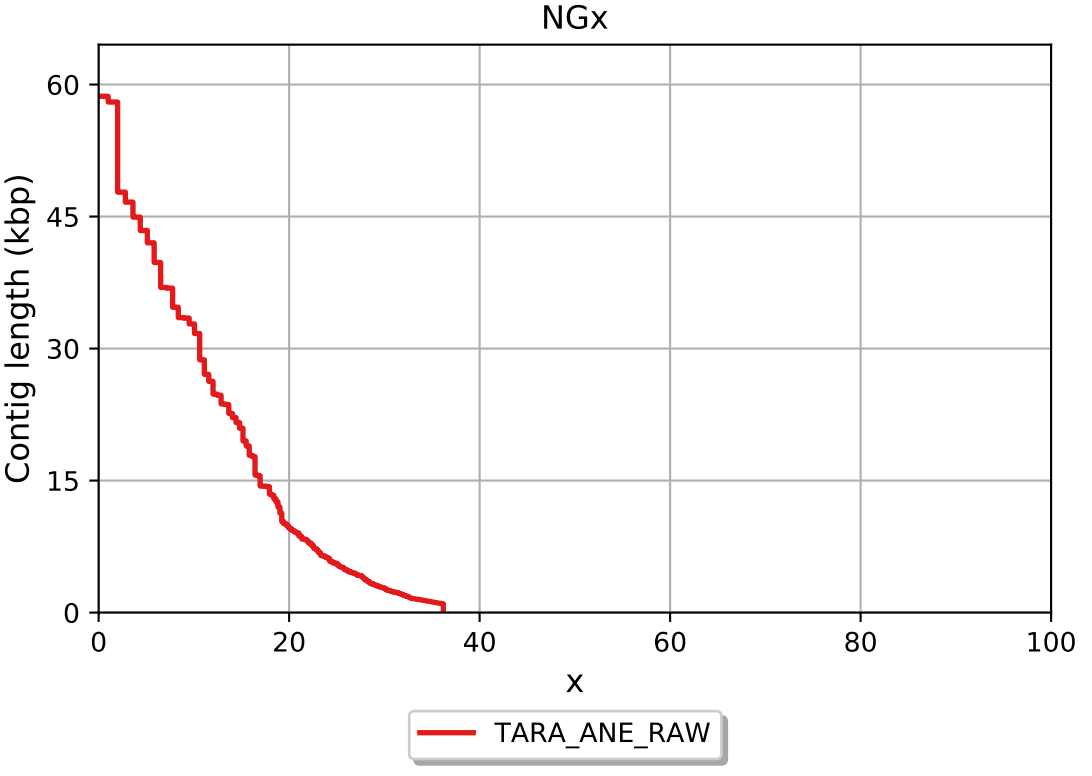
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

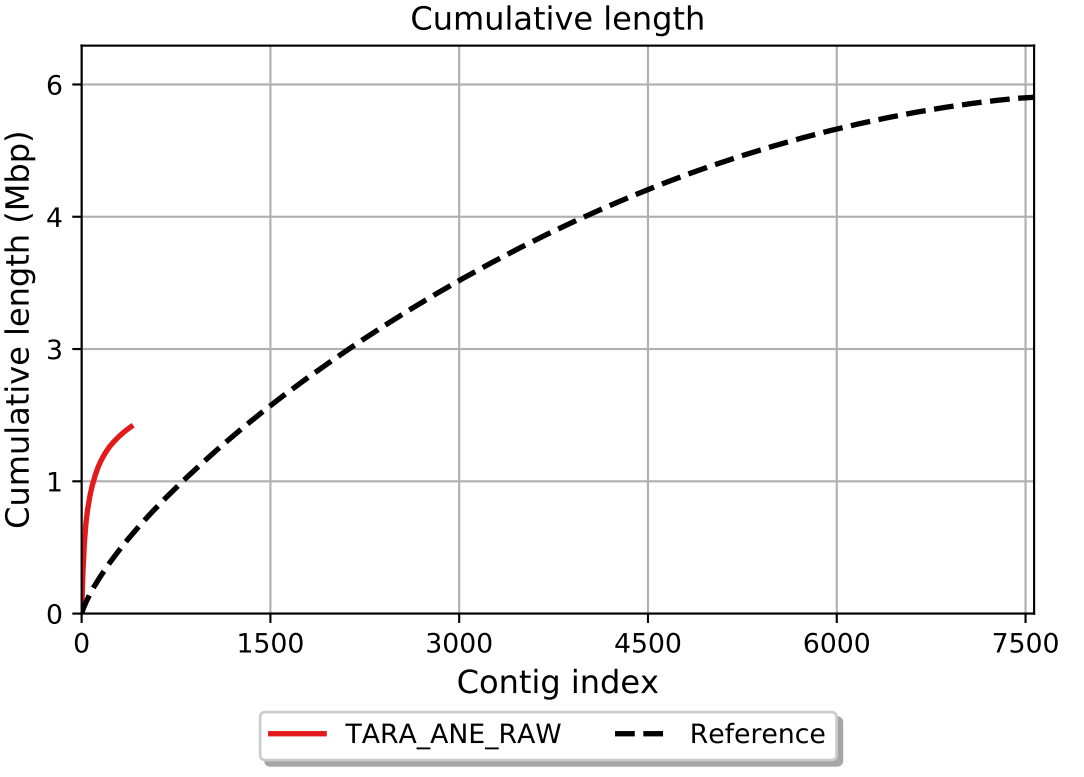
Unaligned report

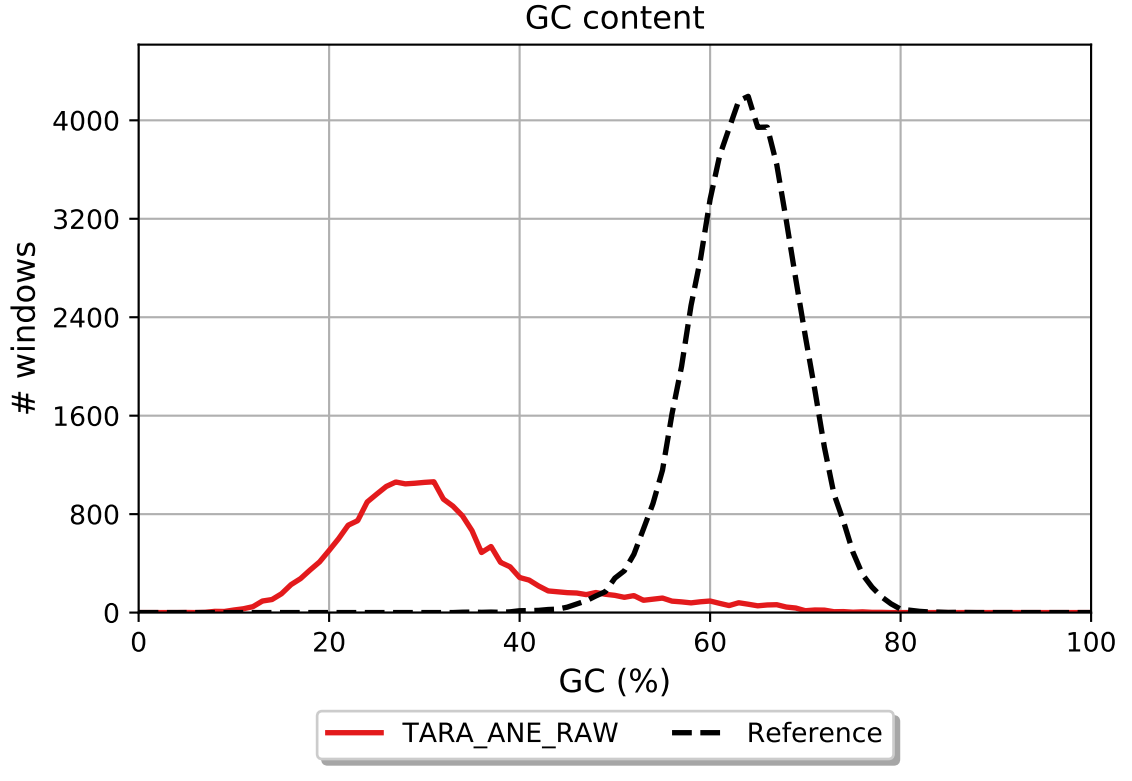
	TARA_ANE_RAW
# fully unaligned contigs	4
Fully unaligned length	9958
# partially unaligned contigs	387
Partially unaligned length	2077143
# N's	0

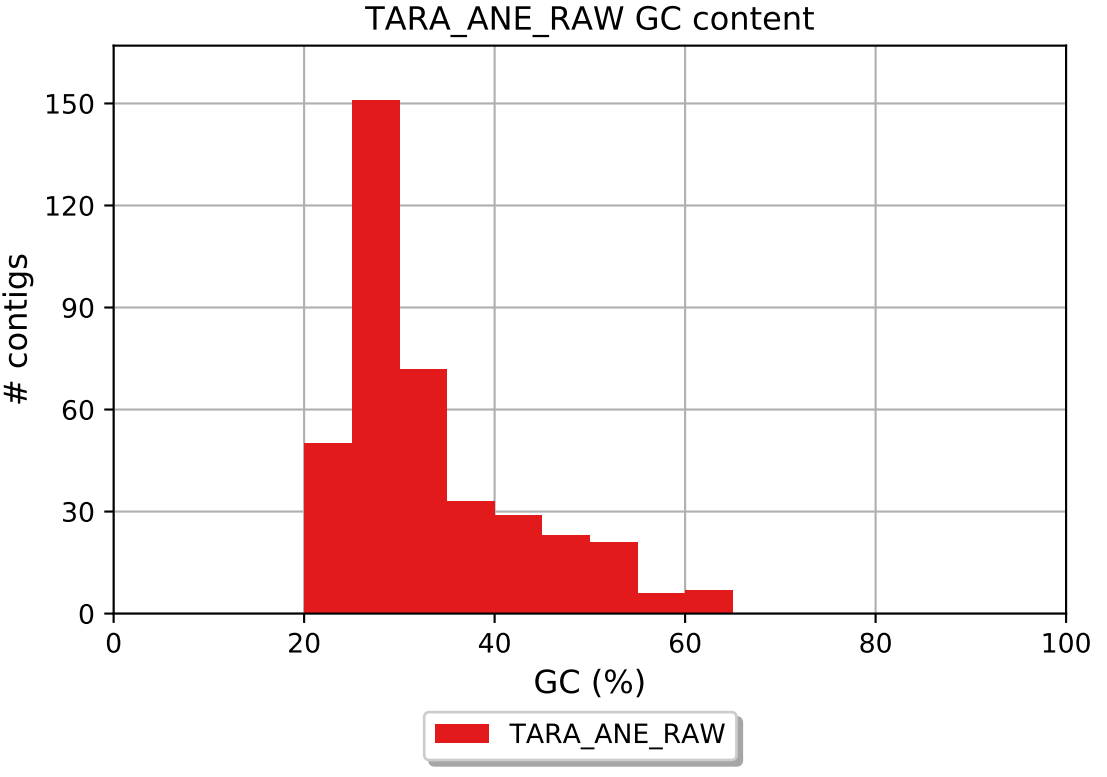
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

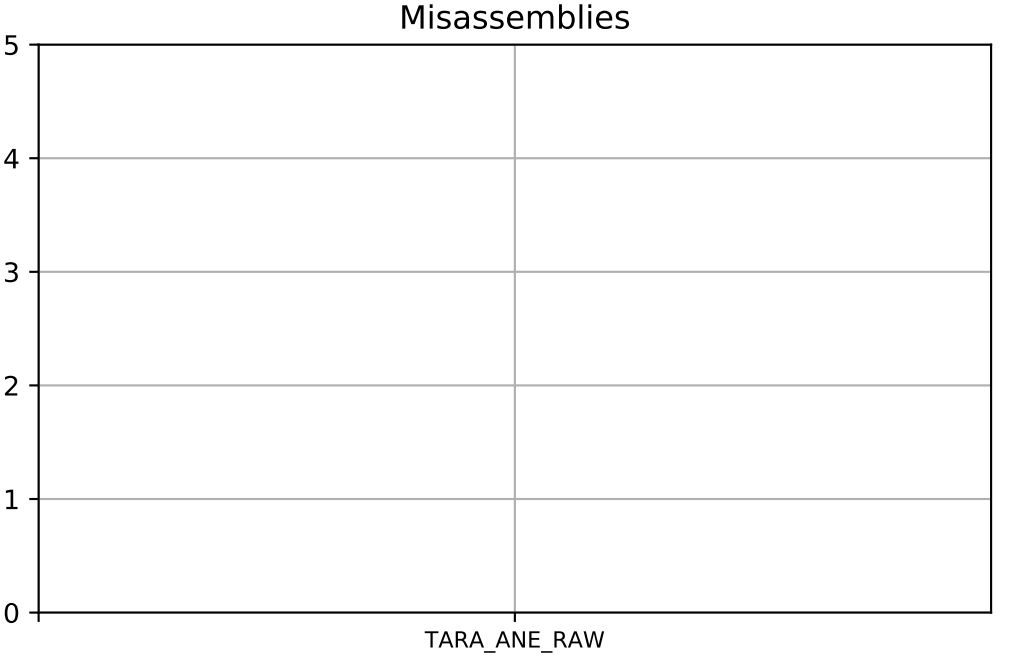

Nx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
TARA_ANE_RAW

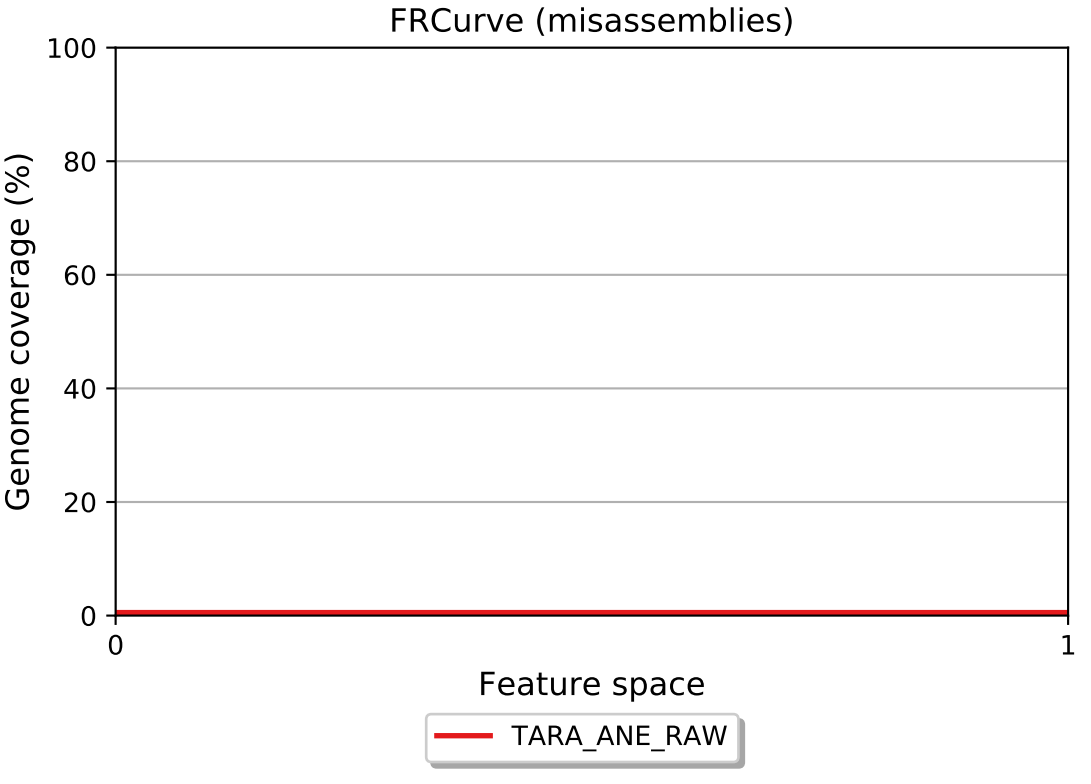

NGx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
TARA_ANE_RAW

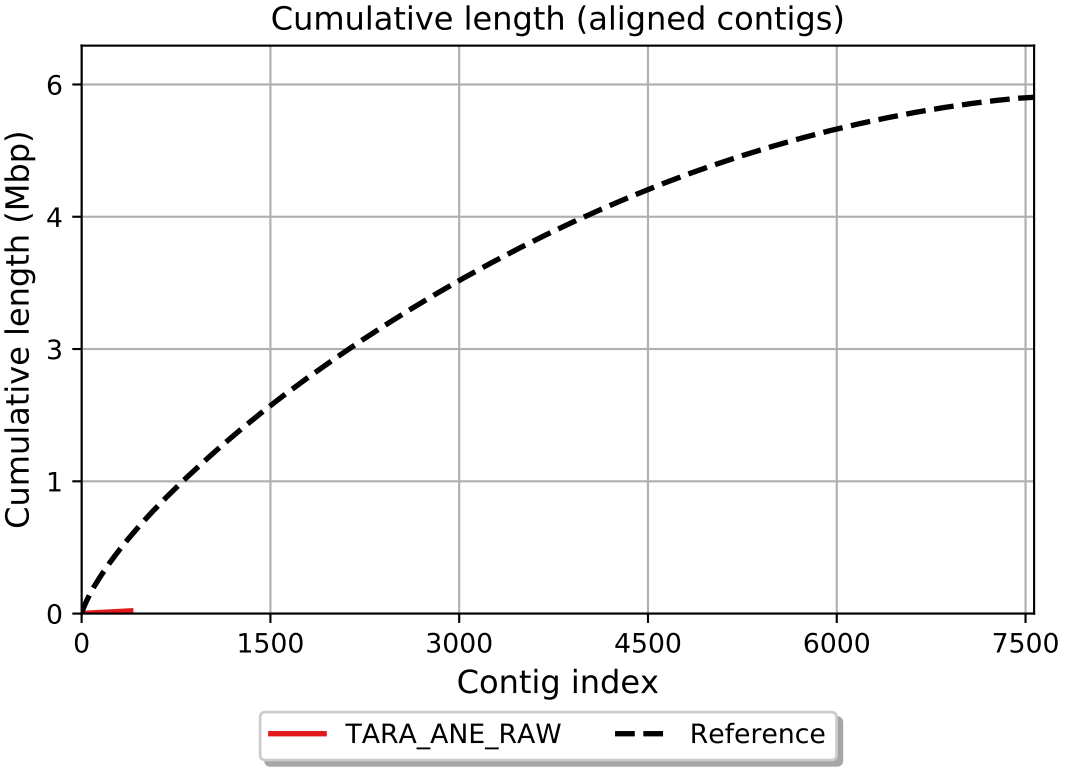

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
1500
3000
4500
6000
7500
Contig index
TARA_ANE_RAW
Reference

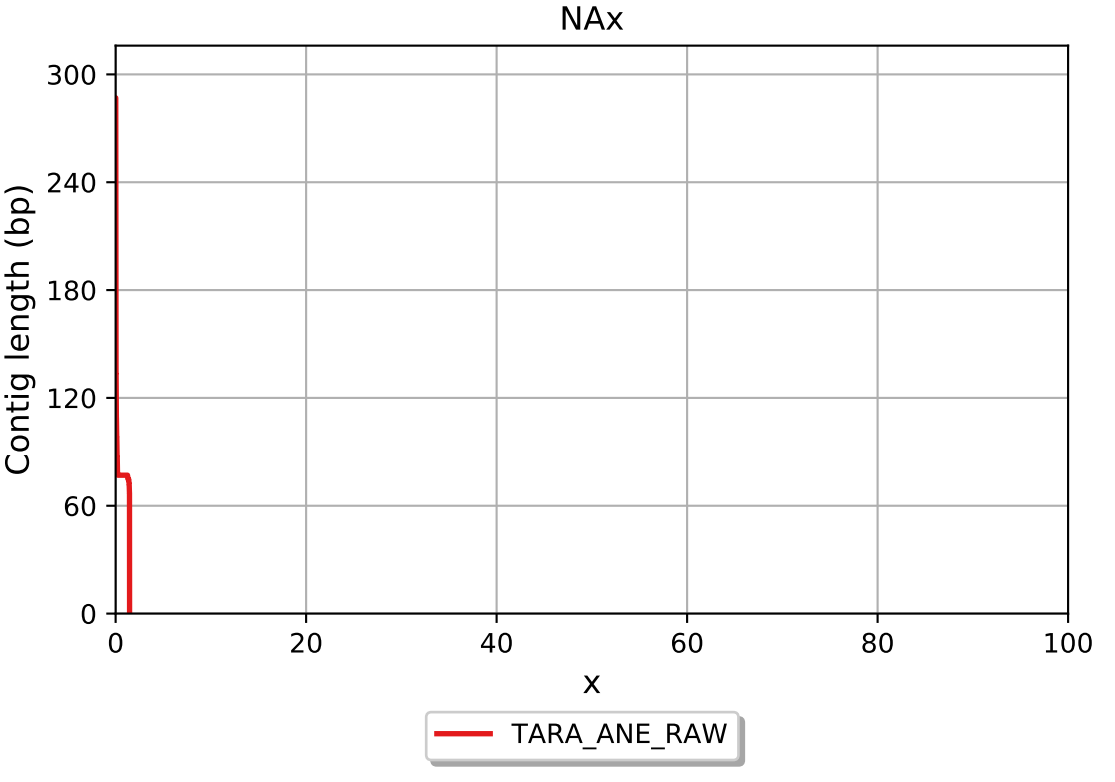

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
TARA_ANE_RAW
Reference

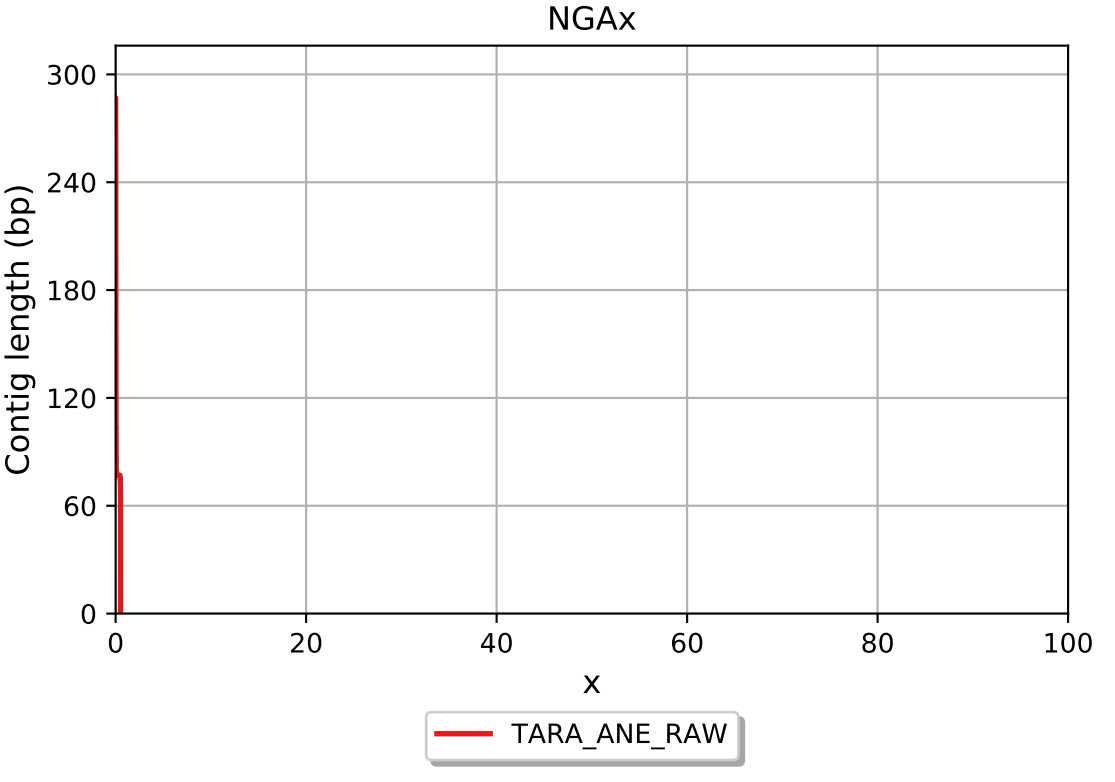

TARA_ANE_RAW GC content
contigs
150
120
90
60
30
0
0
20
40
60
80
100
GC (%)
TARA_ANE_RAW


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


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


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