Report

	TARA_MED_RAW
# contigs (>= 1000 bp)	442
# contigs (>= 5000 bp)	133
# contigs (>= 10000 bp)	80
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	15
Total length (>= 1000 bp)	3419112
Total length (>= 5000 bp)	2744796
Total length (>= 10000 bp)	2381034
Total length (>= 25000 bp)	1712683
Total length (>= 50000 bp)	987642
# contigs	442
Largest contig	107525
Total length	3419112
Reference length	5854900
GC (%)	34.04
Reference GC (%)	63.53
N50	25329
NG50	3545
N75	6912
L50	35
LG50	177
L75	103
# 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	3 + 439 part
Unaligned length	3384124
Genome fraction (%)	0.060
Duplication ratio	9.903
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19699.97
# indels per 100 kbp	28.30
Largest alignment	339
Total aligned length	34988
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

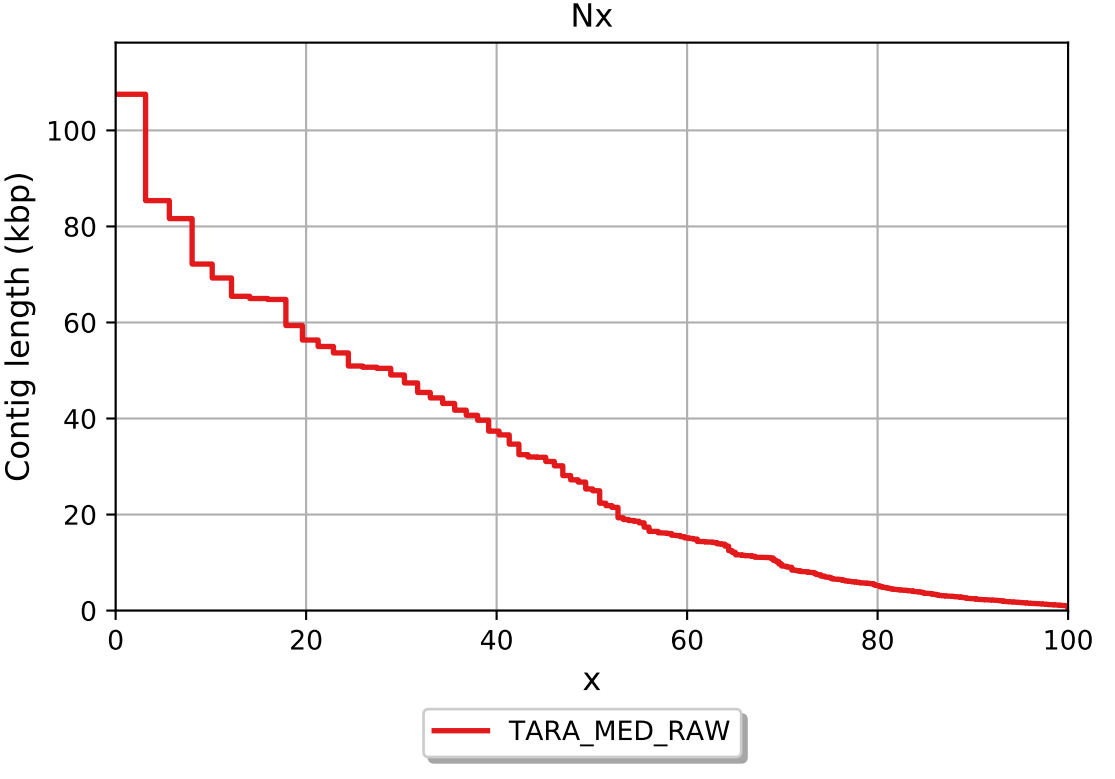
	TARA_MED_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	440
# possible misassemblies	554
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	696
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

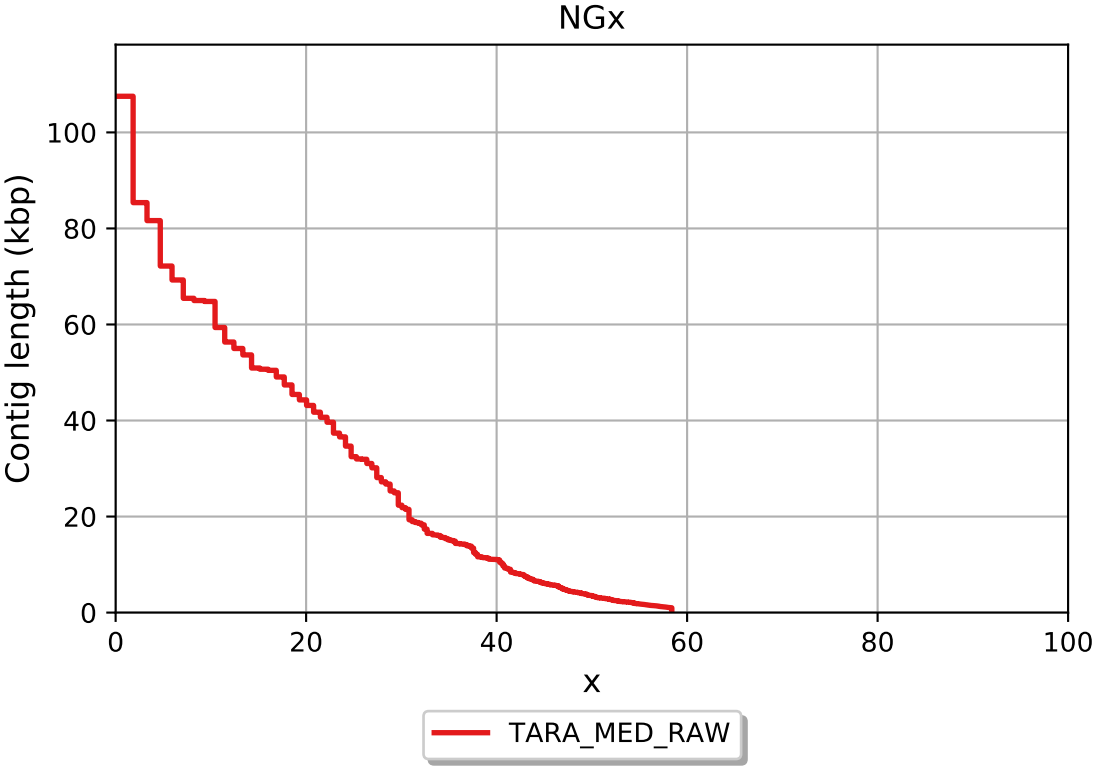
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

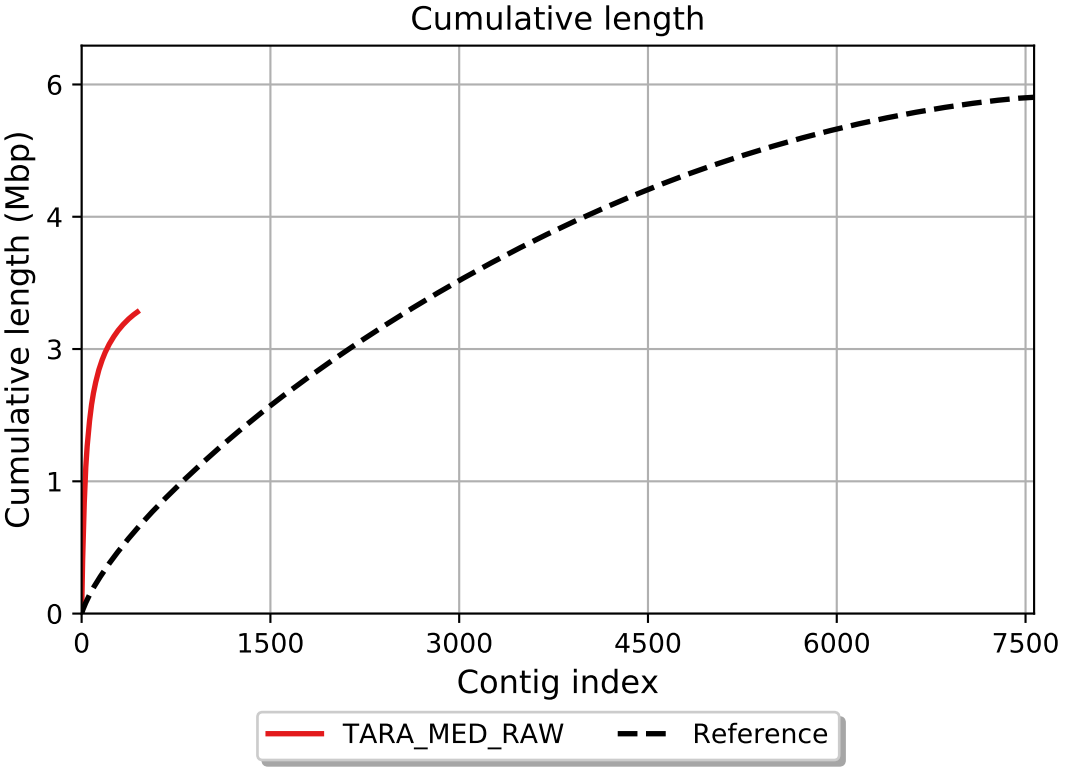
Unaligned report

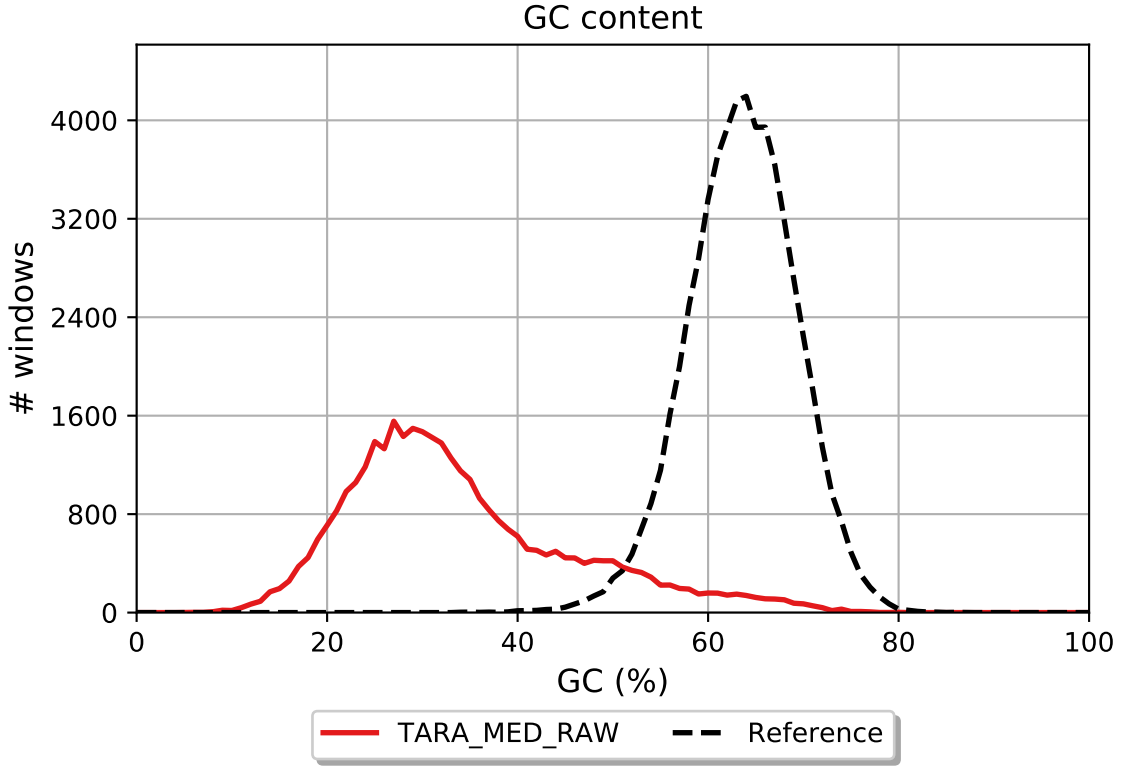
	TARA_MED_RAW
# fully unaligned contigs	3
Fully unaligned length	5580
# partially unaligned contigs	439
Partially unaligned length	3378544
# N's	0

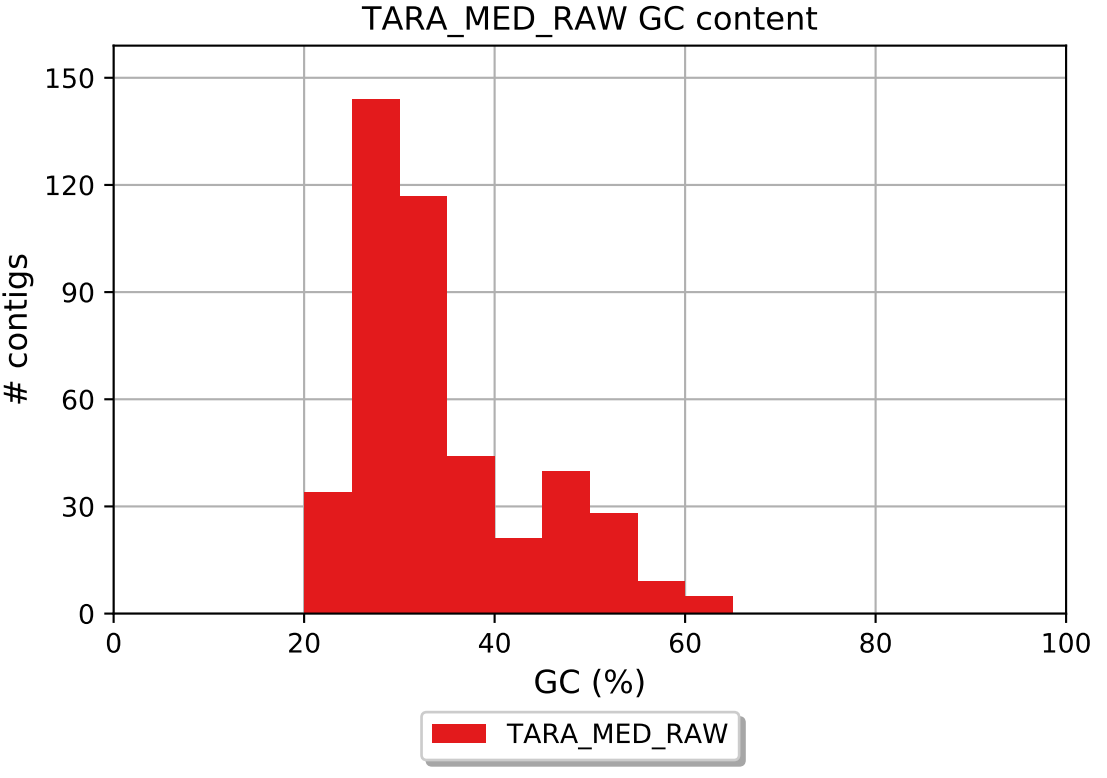
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

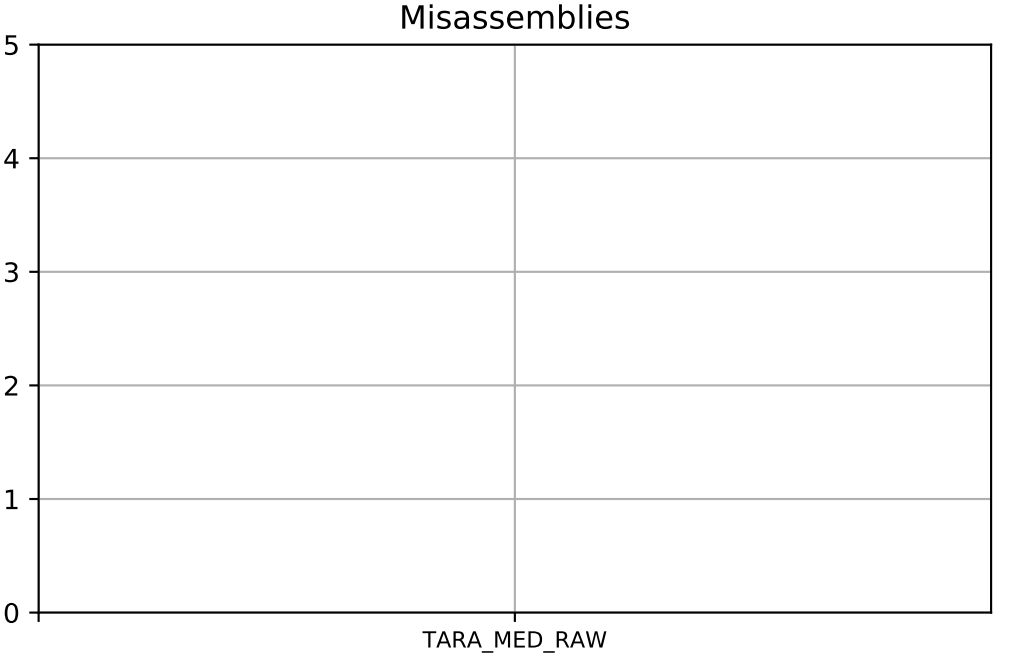

Nx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
TARA_MED_RAW

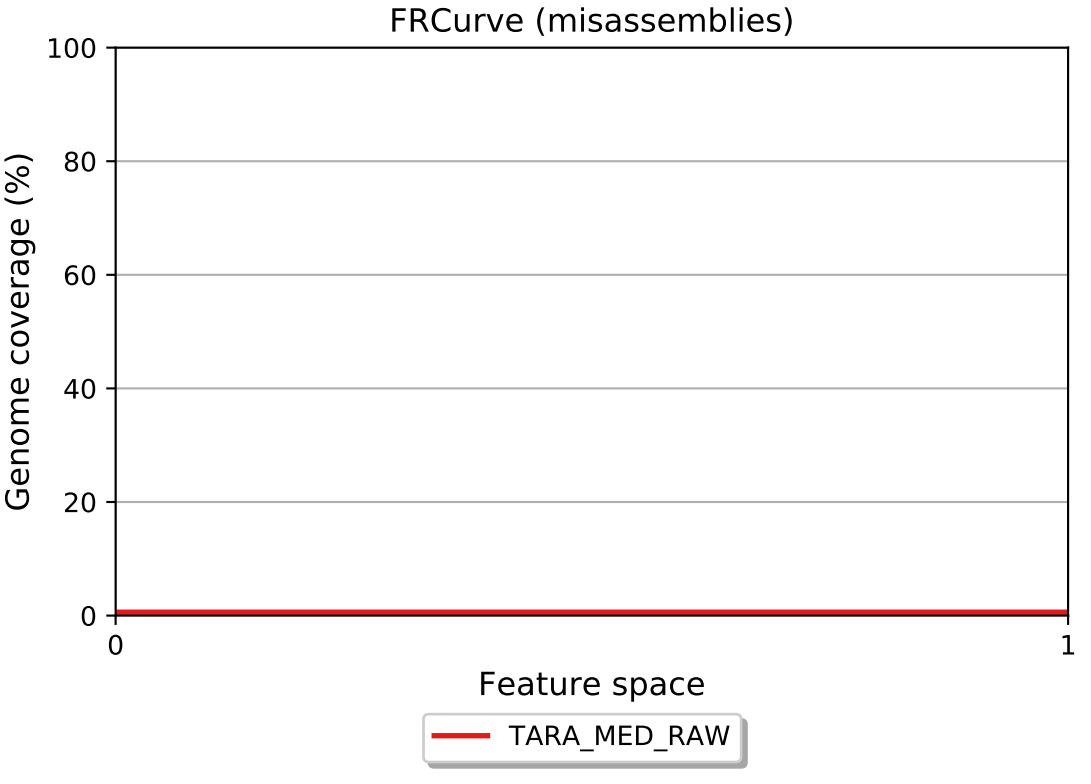

NGx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
TARA_MED_RAW

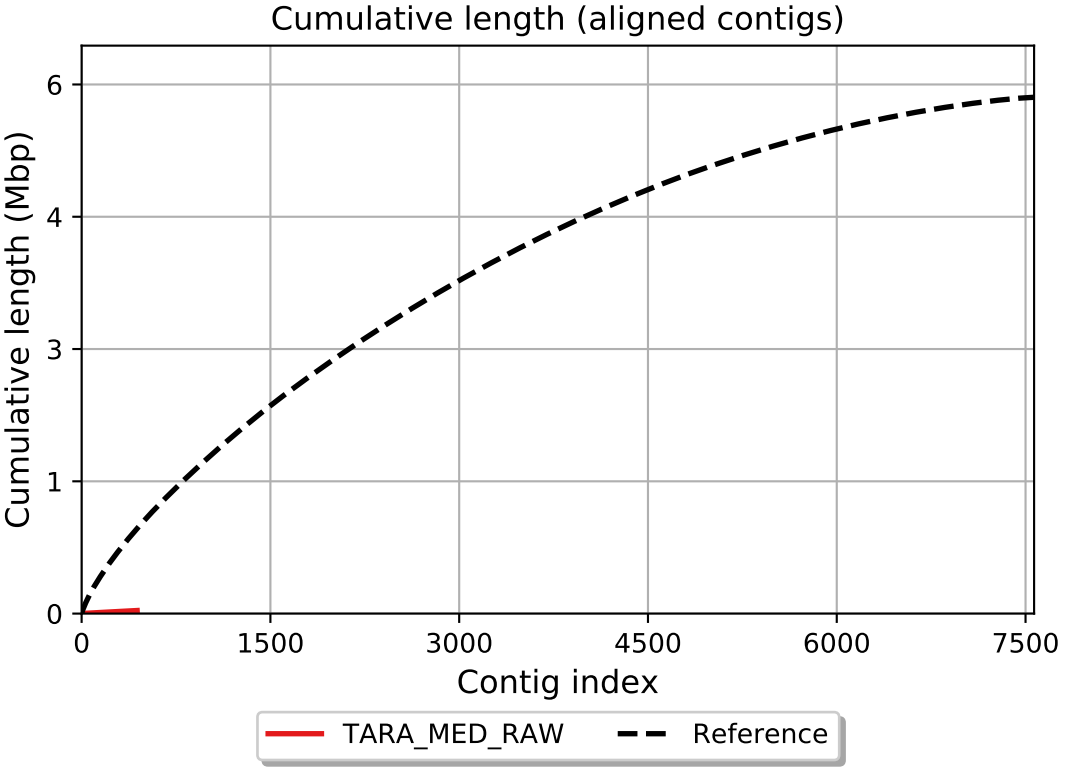

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
1500
3000
4500
6000
7500
Contig index
TARA_MED_RAW
Reference

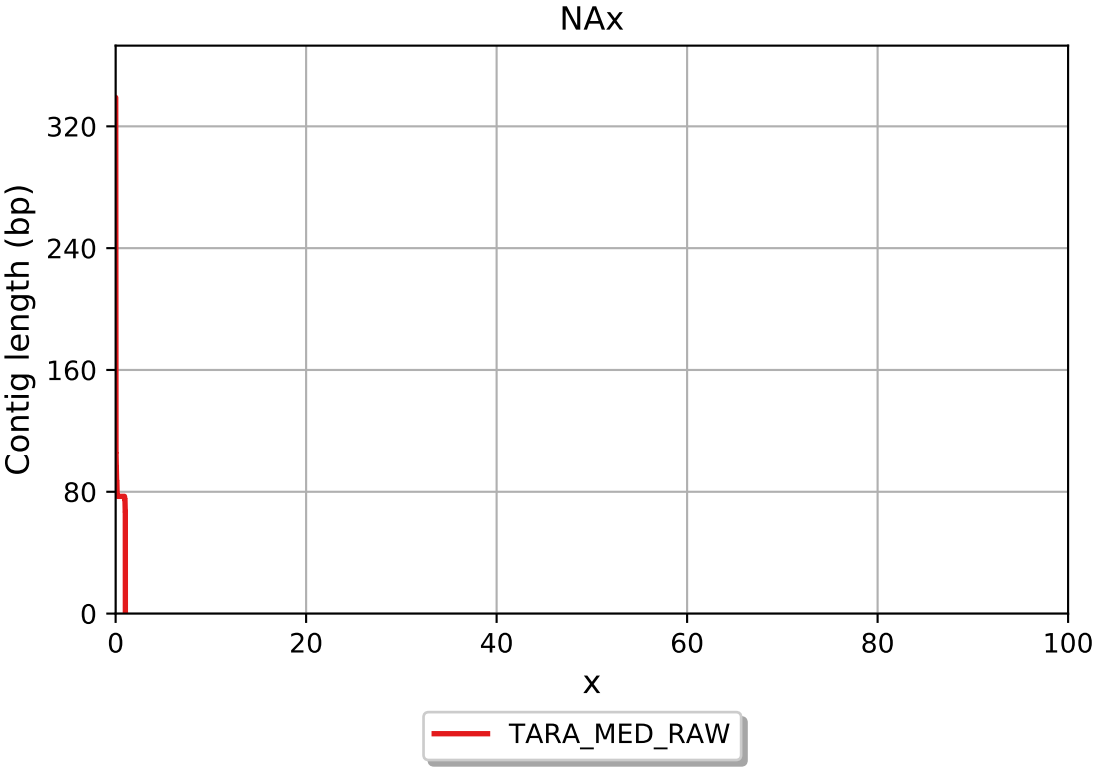

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
TARA_MED_RAW
Reference

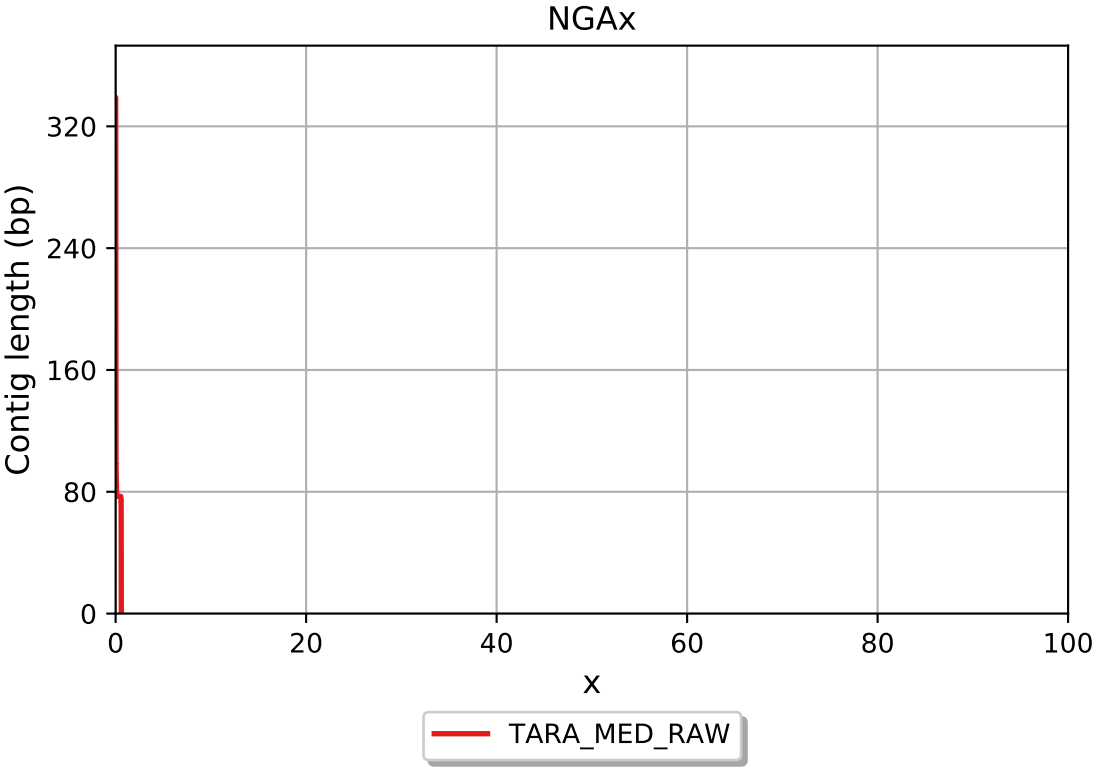

TARA_MED_RAW GC content
150
120
90
60
30
0
contigs
0
20
40
60
80
100
GC (%)
TARA_MED_RAW


Misassemblies
5
4
3
2
1
0
TARA_MED_RAW


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


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


NAx
Contig length (bp)
320
240
160
80
0
0
20
40
60
80
100
x
TARA_MED_RAW


NGAx
Contig length (bp)
320
240
160
80
0
0
20
40
60
80
100
x
TARA_MED_RAW