Report

	TARA_PSW_RAW
# contigs (>= 1000 bp)	315
# contigs (>= 5000 bp)	79
# contigs (>= 10000 bp)	38
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	10
Total length (>= 1000 bp)	2491709
Total length (>= 5000 bp)	2000758
Total length (>= 10000 bp)	1732218
Total length (>= 25000 bp)	1484672
Total length (>= 50000 bp)	1032498
# contigs	315
Largest contig	222419
Total length	2491709
Reference length	5854900
GC (%)	47.15
Reference GC (%)	63.53
N50	31460
N75	6629
L50	16
L75	56
# 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	11 + 304 part
Unaligned length	2466023
Genome fraction (%)	0.096
Duplication ratio	4.580
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8808.84
# indels per 100 kbp	53.50
Largest alignment	339
Total aligned length	25686
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

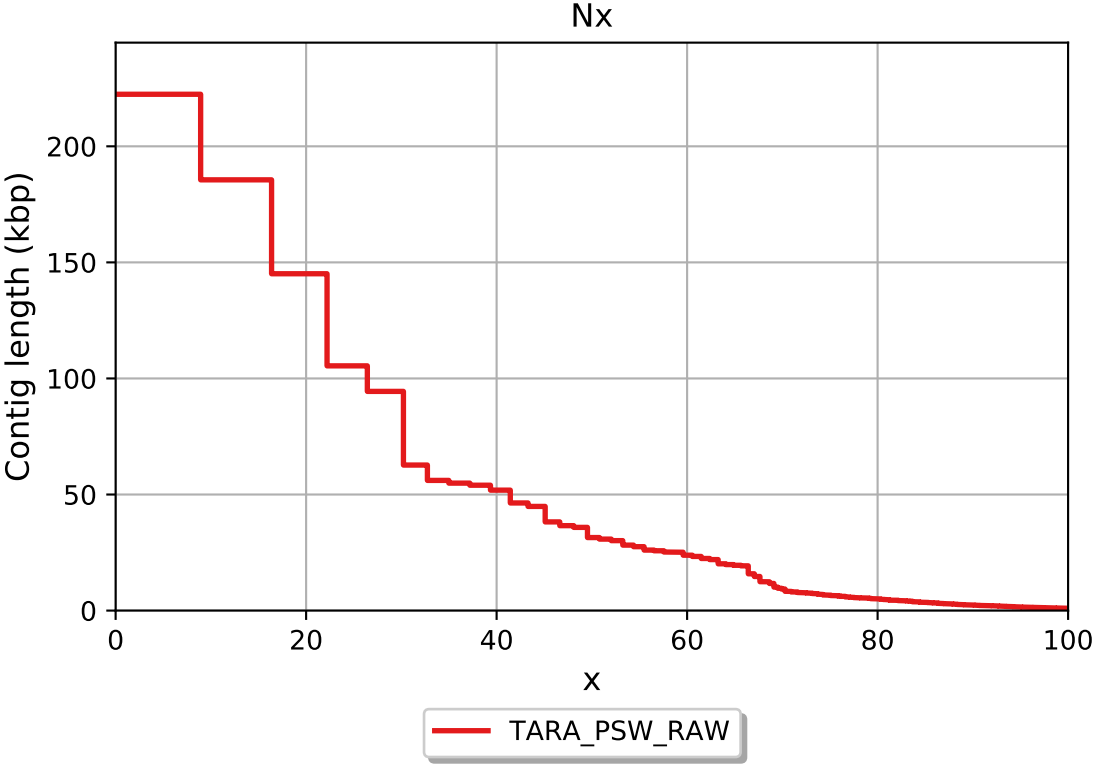
	TARA_PSW_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	311
# possible misassemblies	385
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	494
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	4

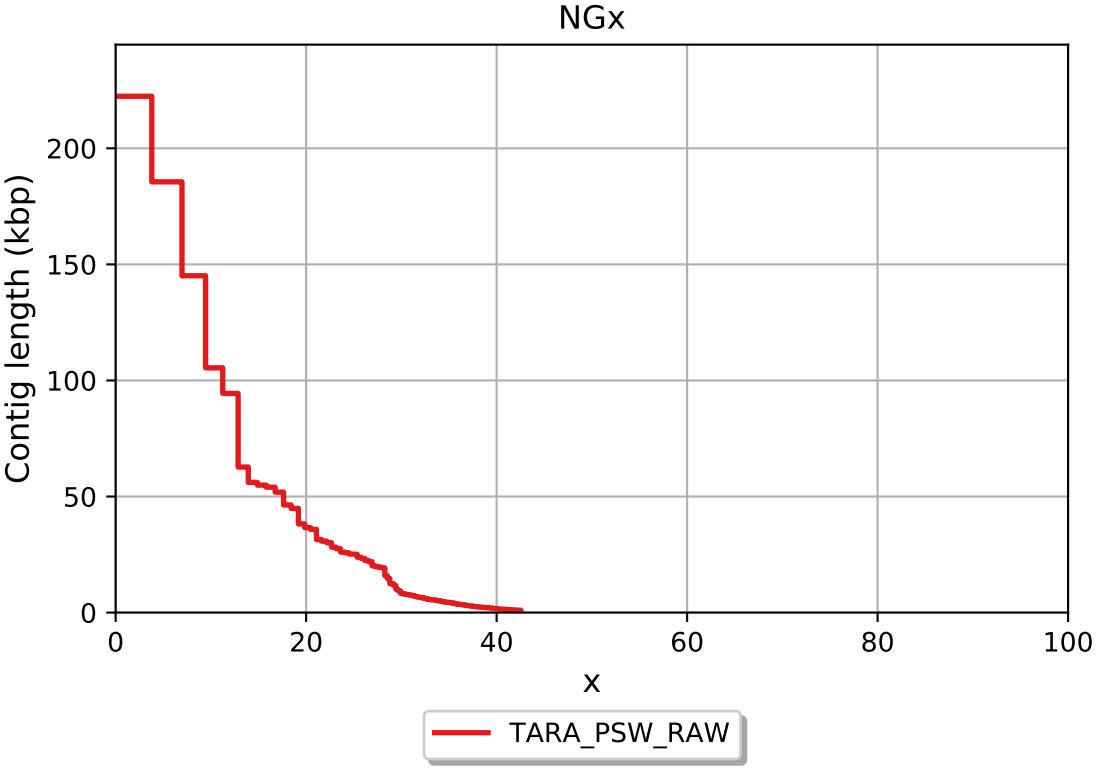
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

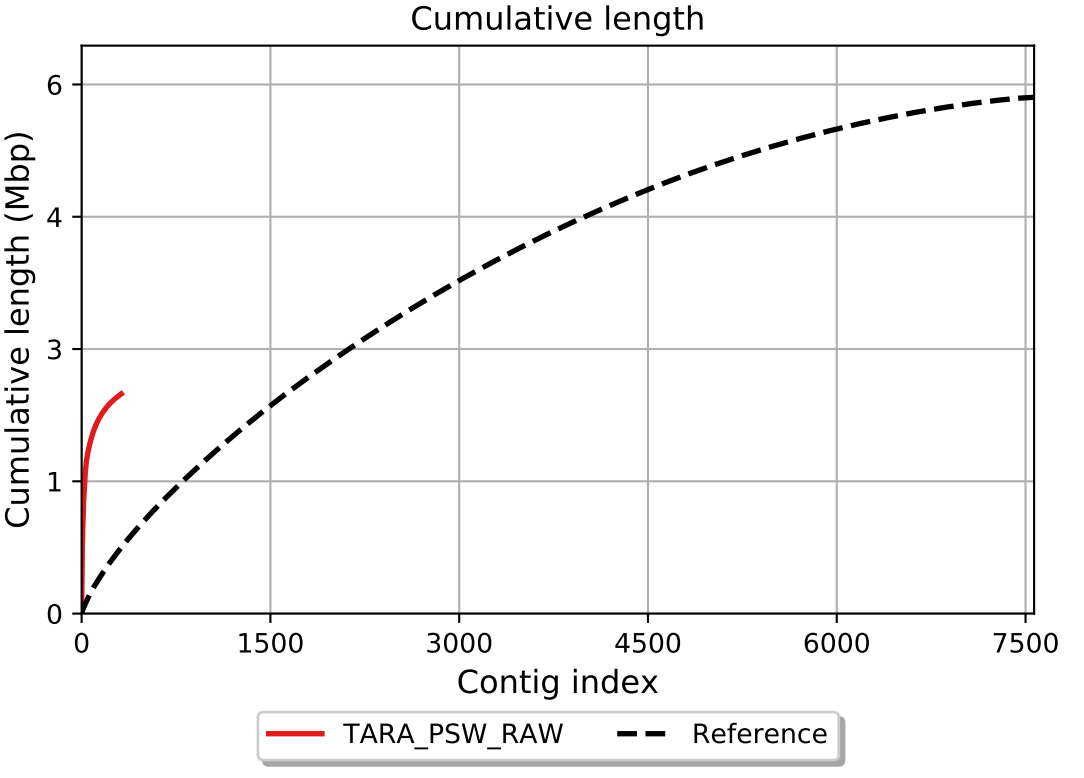
Unaligned report

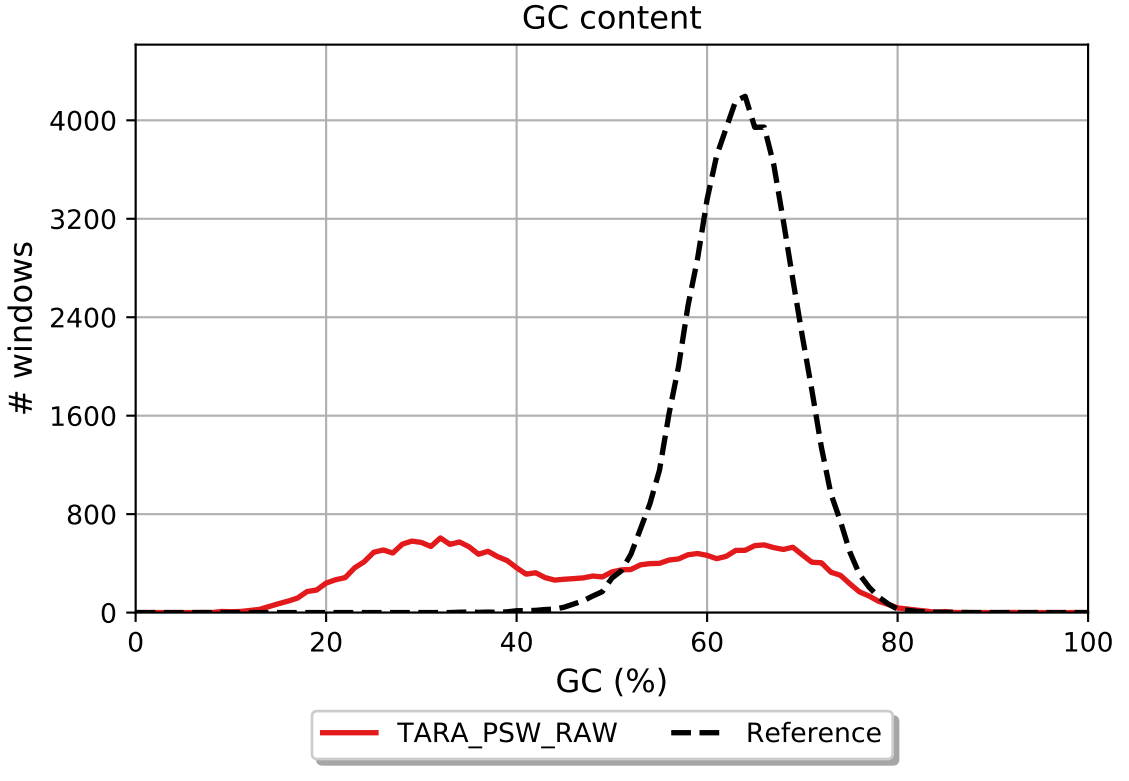
	TARA_PSW_RAW
# fully unaligned contigs	11
Fully unaligned length	177722
# partially unaligned contigs	304
Partially unaligned length	2288301
# N's	0

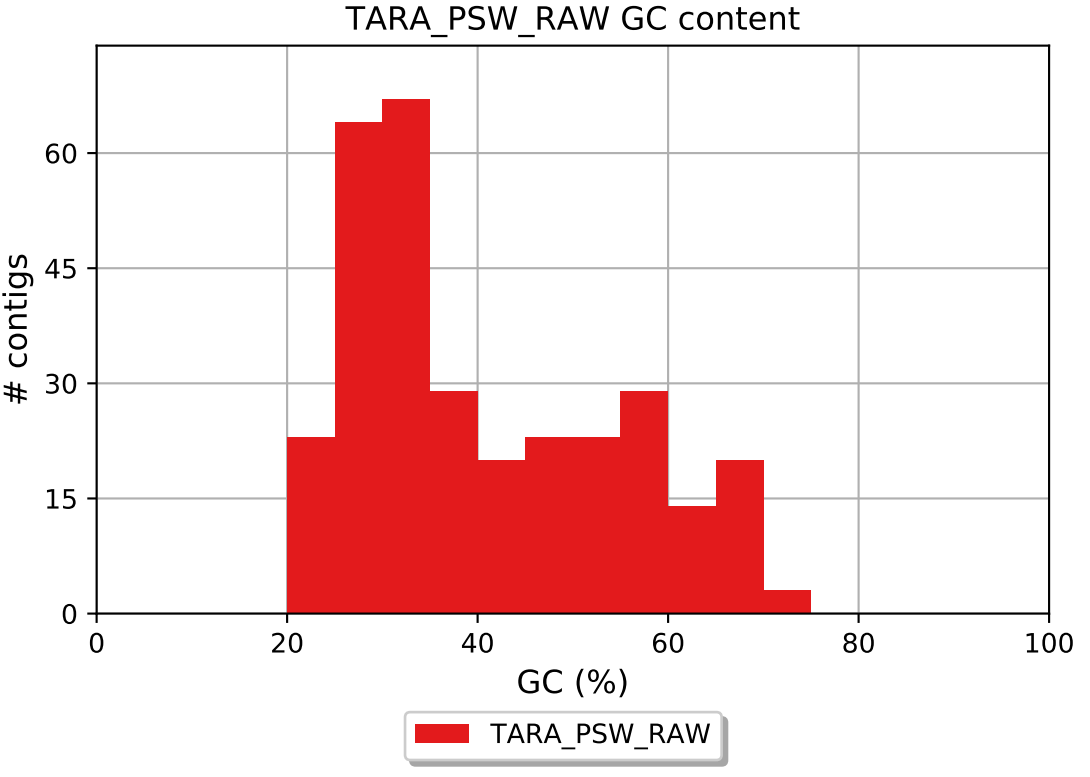
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

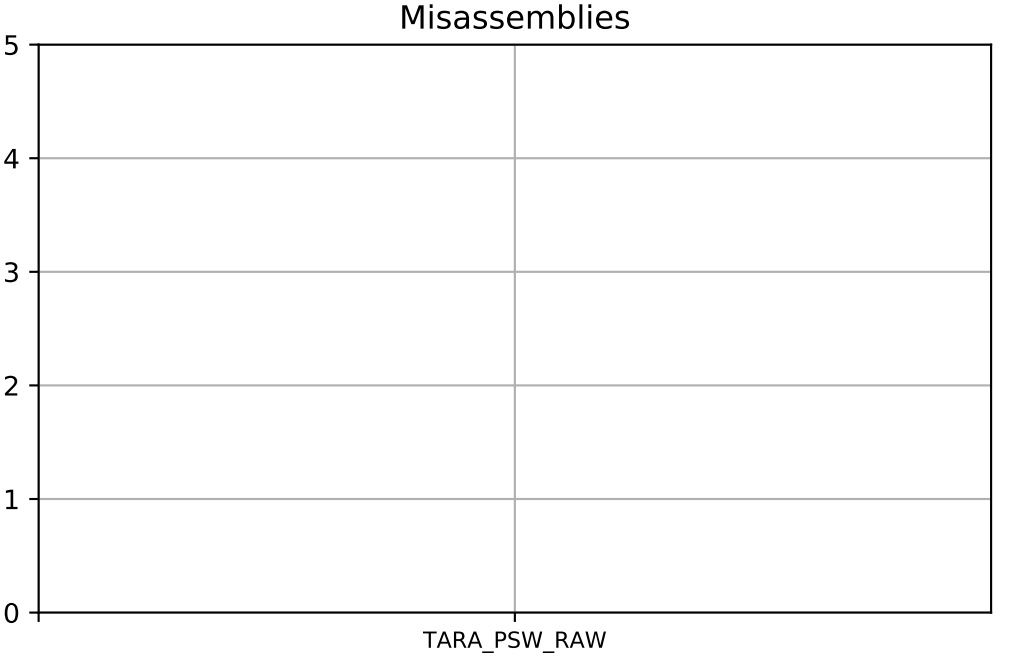

Nx
Contig length (kbp)
200
150
100
50
0
0
20
40
60
80
100
x
TARA_PSW_RAW

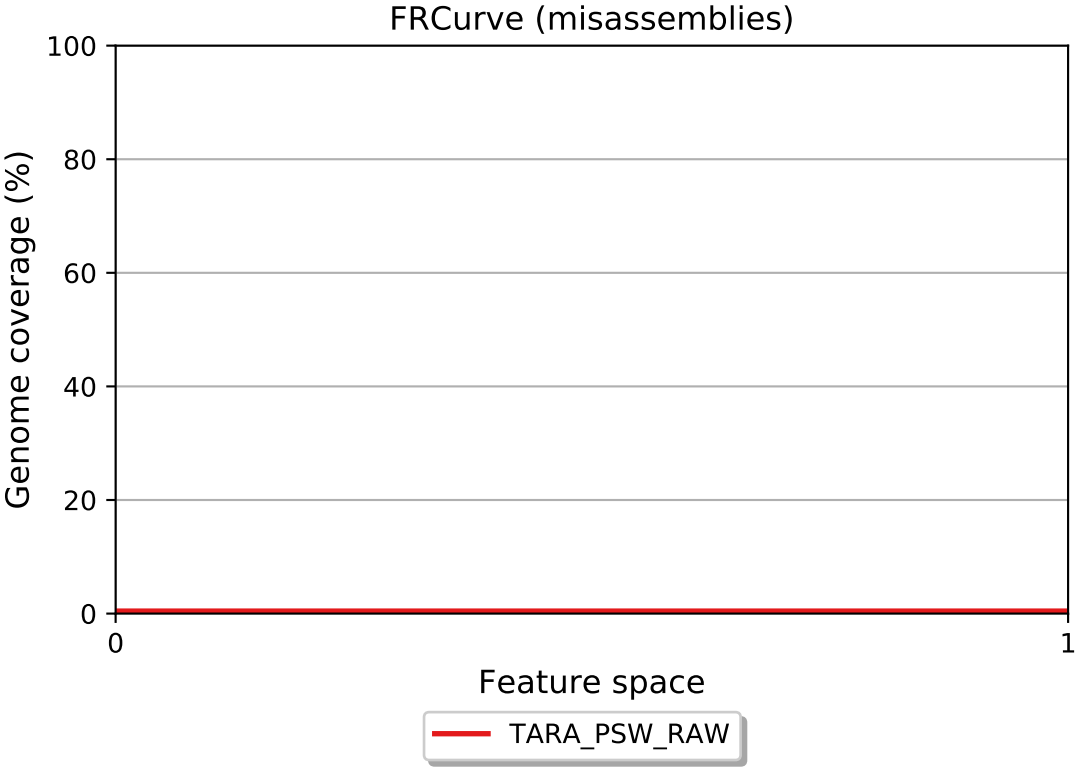

NGx
Contig length (kbp)
200
150
100
50
0
0
20
40
60
80
100
x
TARA_PSW_RAW

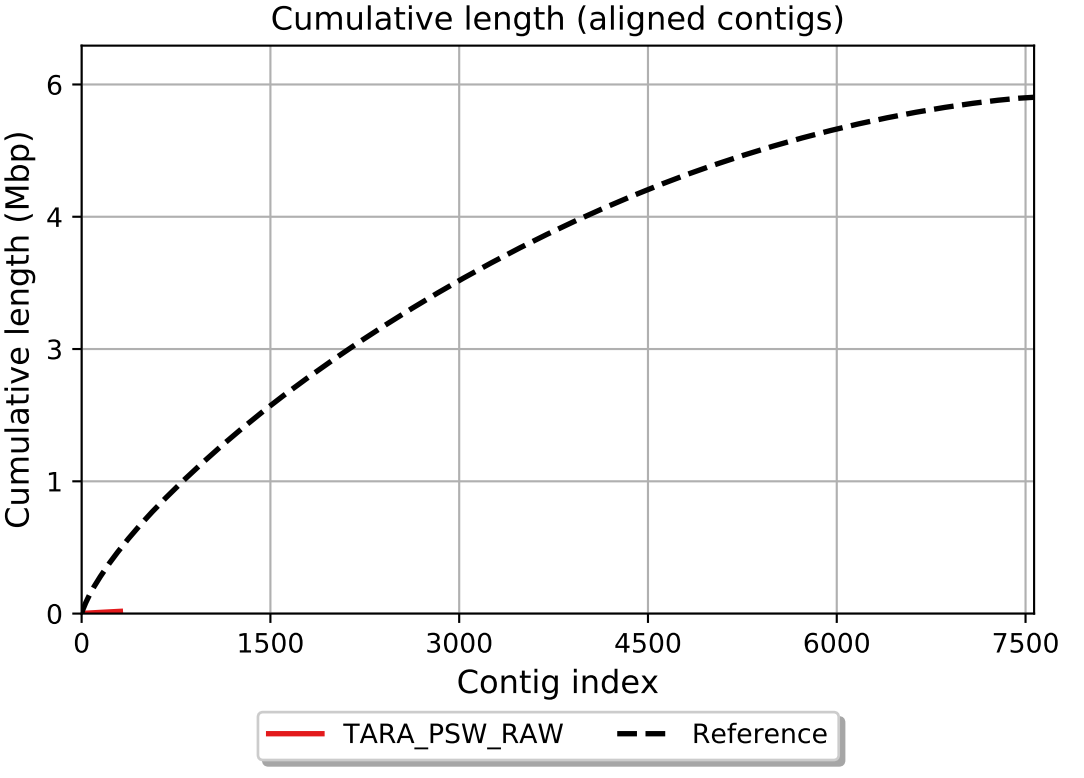

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
1500
3000
4500
6000
7500
Contig index
TARA_PSW_RAW
Reference

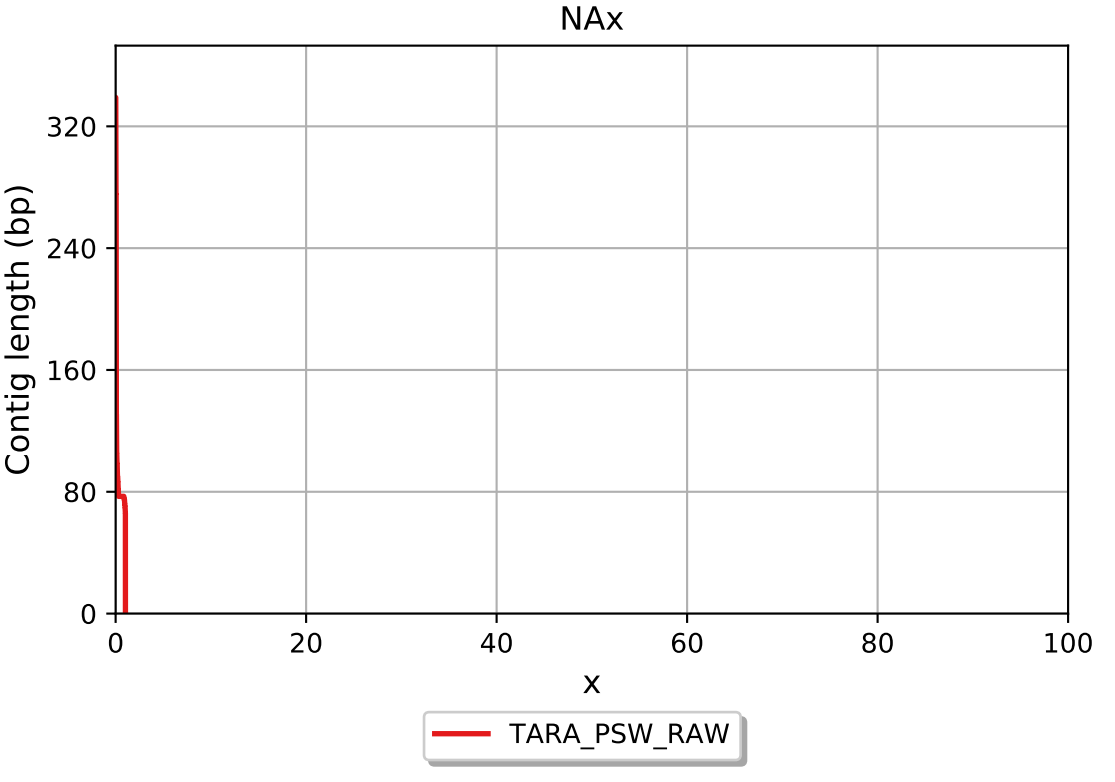

GC content
windows
4000
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
TARA_PSW_RAW
Reference

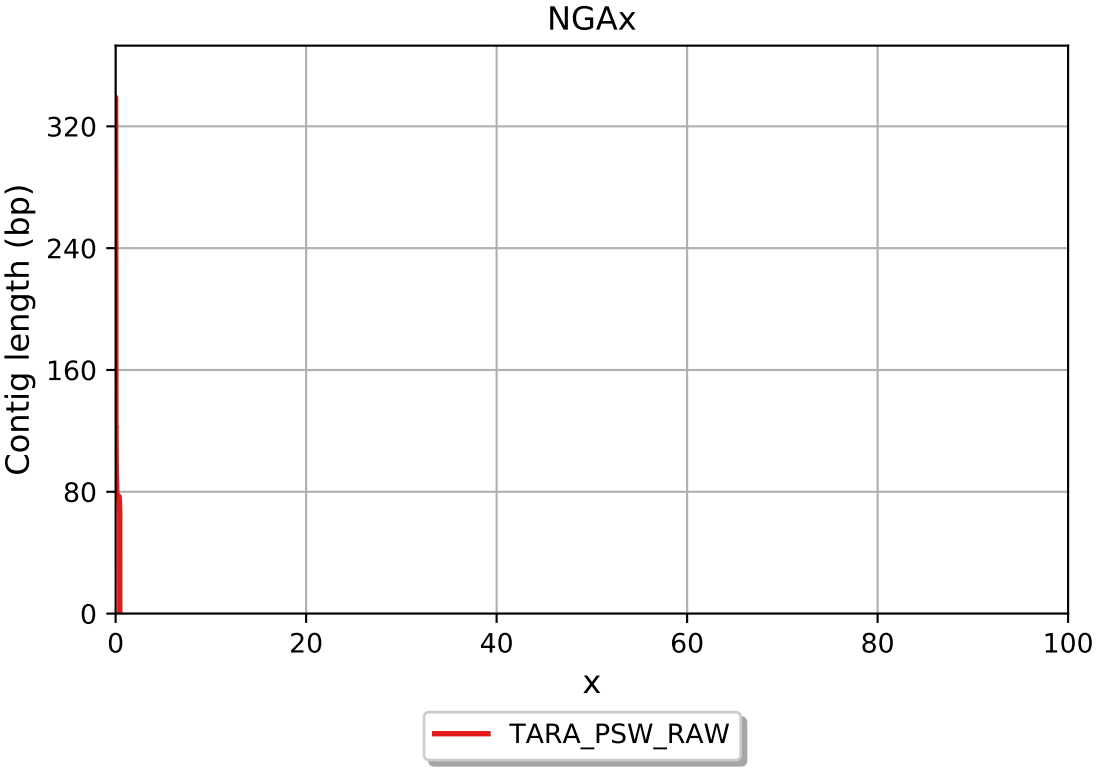

TARA_PSW_RAW GC content
contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
TARA_PSW_RAW


Misassemblies
5
4
3
2
1
0
TARA_PSW_RAW


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


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


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


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