Report

	TARA_PON_RAW
# contigs (>= 0 bp)	1663221
# contigs (>= 1000 bp)	1663221
# contigs (>= 5000 bp)	73322
# contigs (>= 10000 bp)	19113
# contigs (>= 25000 bp)	3249
# contigs (>= 50000 bp)	778
Total length (>= 0 bp)	3411305116
Total length (>= 1000 bp)	3411305116
Total length (>= 5000 bp)	739386287
Total length (>= 10000 bp)	376859143
Total length (>= 25000 bp)	150171410
Total length (>= 50000 bp)	67234015
# contigs	1663221
Largest contig	594166
Total length	3411305116
Reference length	7658814
N50	2072
N75	1355
L50	402266
L75	922394
# 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	8
# unaligned contigs	1662890 + 329 part
Unaligned length	3411274779
Genome fraction (%)	0.080
Duplication ratio	5.162
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10308.44
# indels per 100 kbp	162.34
Largest alignment	573
Total aligned length	28673

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

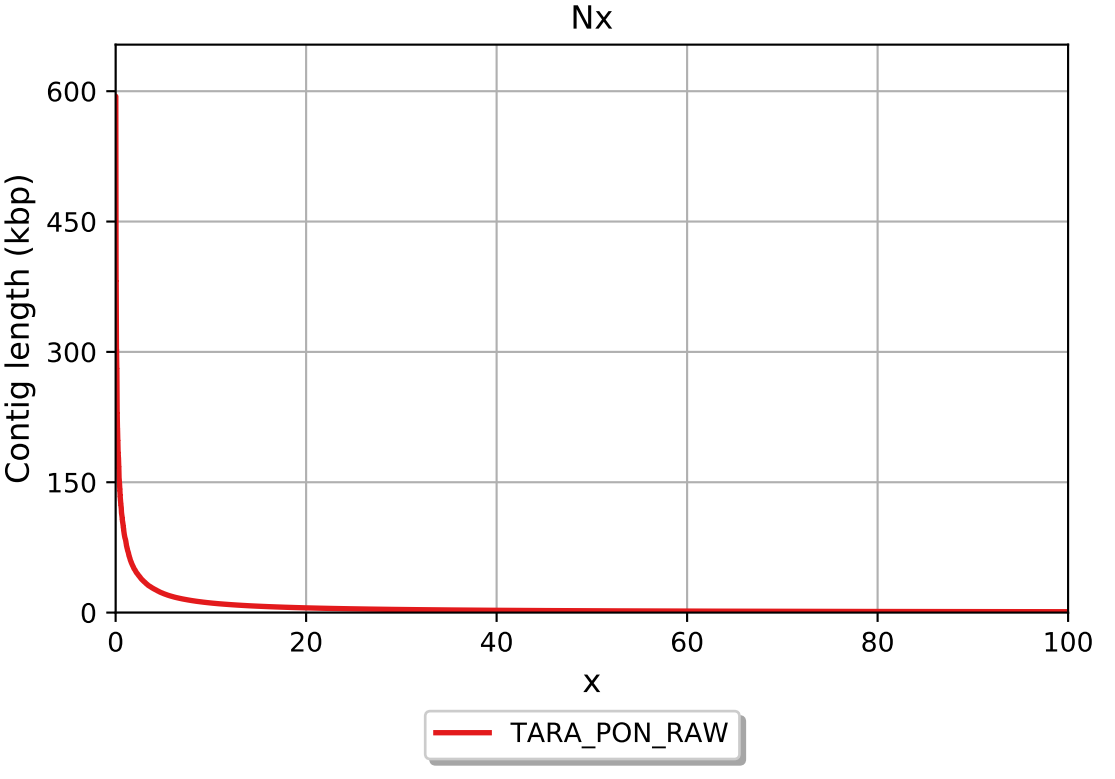
	TARA_PON_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	322
# possible misassemblies	384
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	635
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	11

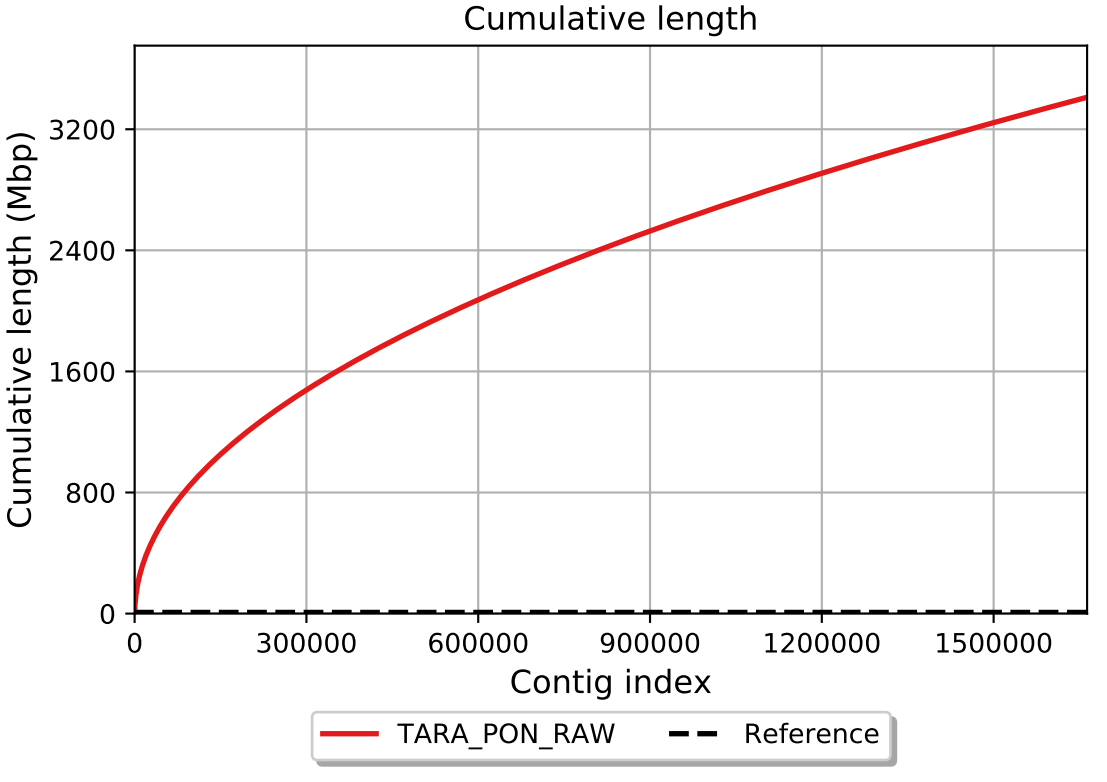
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

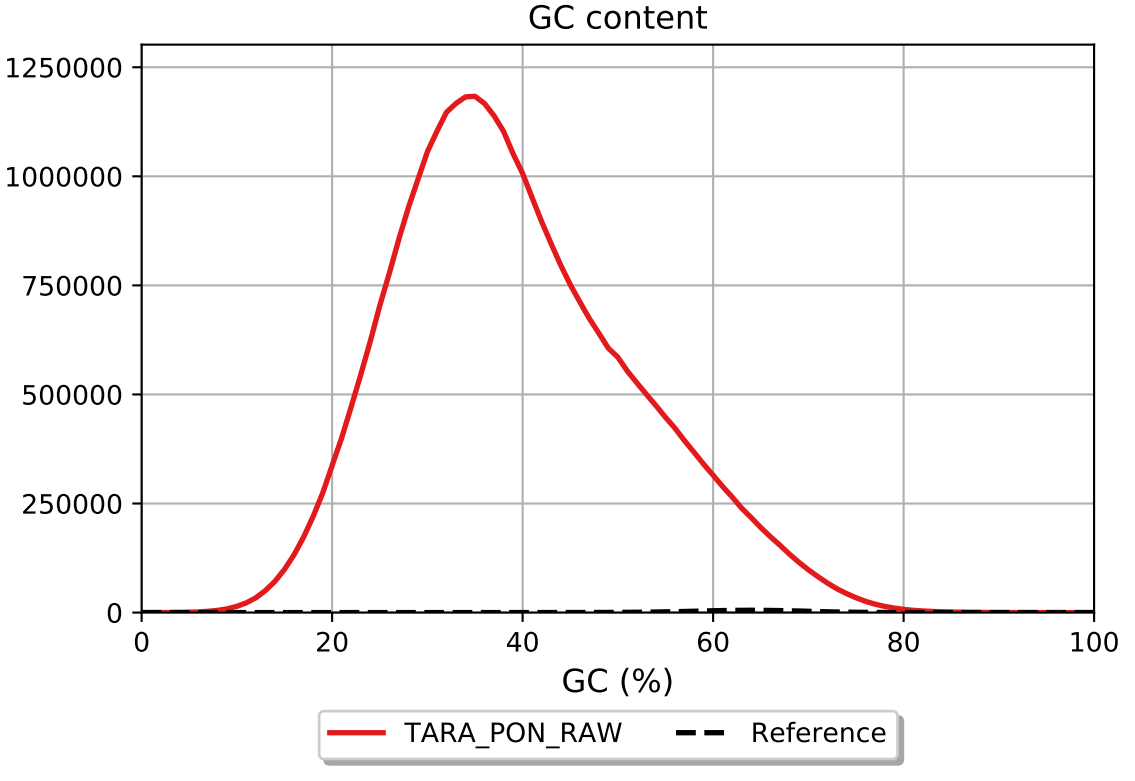
Unaligned report

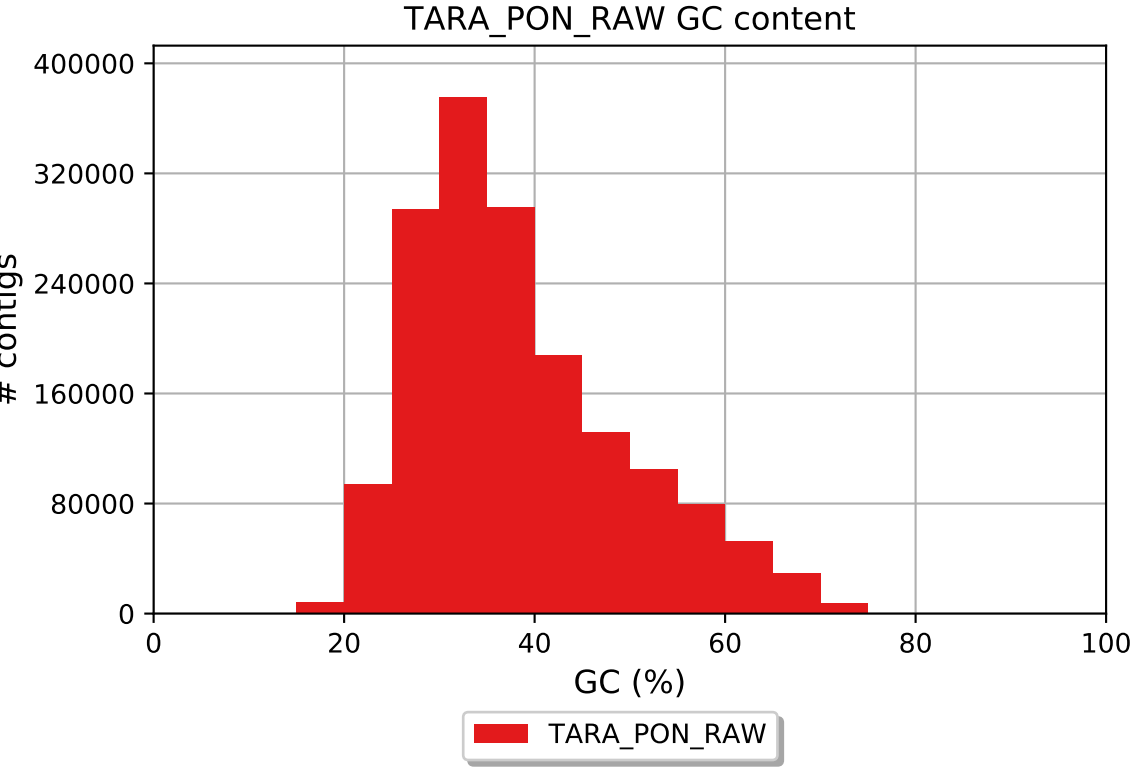
	TARA_PON_RAW
# fully unaligned contigs	1662890
Fully unaligned length	3409944341
# partially unaligned contigs	329
Partially unaligned length	1330438
# N's	0

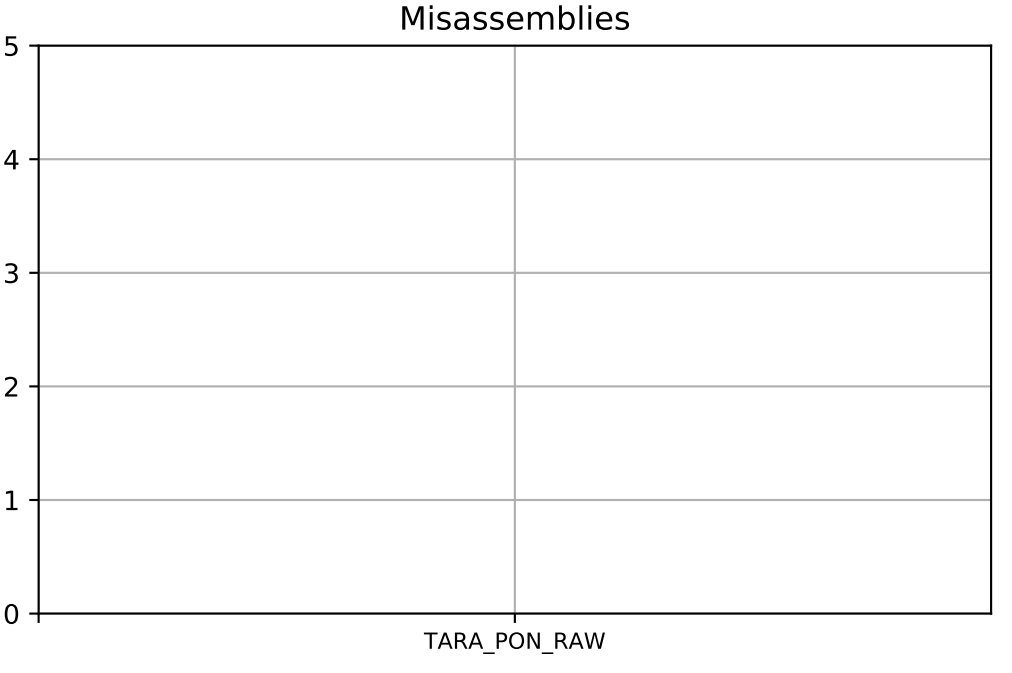
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

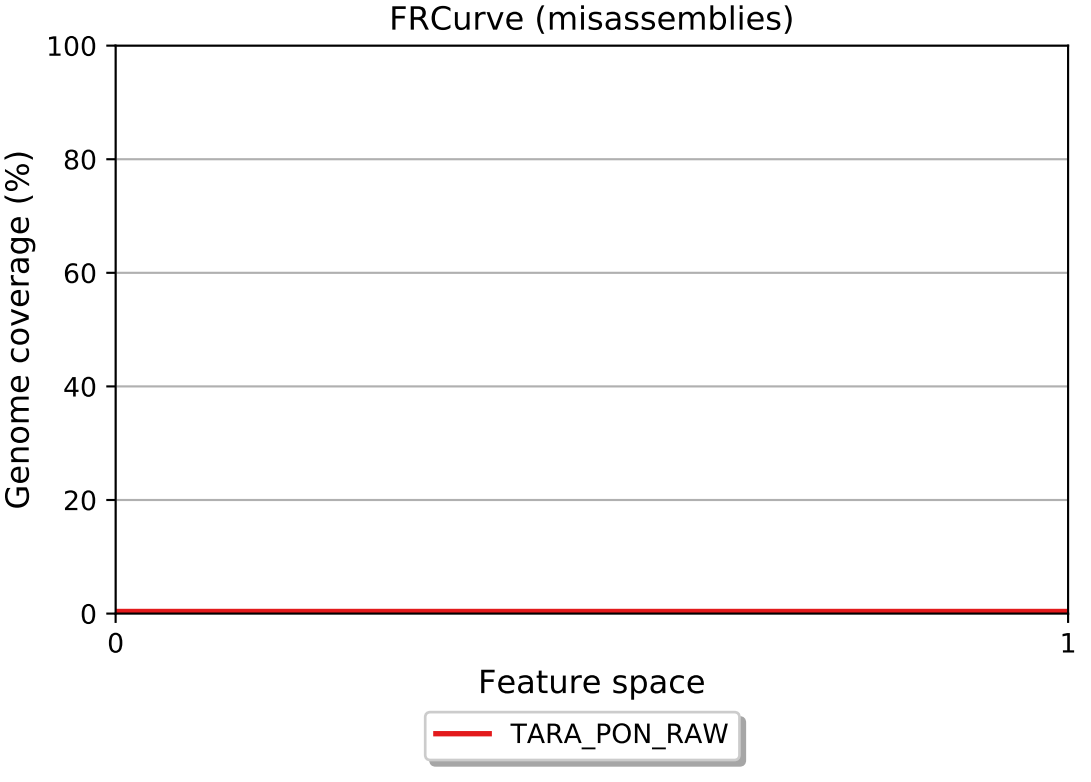

Nx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
TARA_PON_RAW

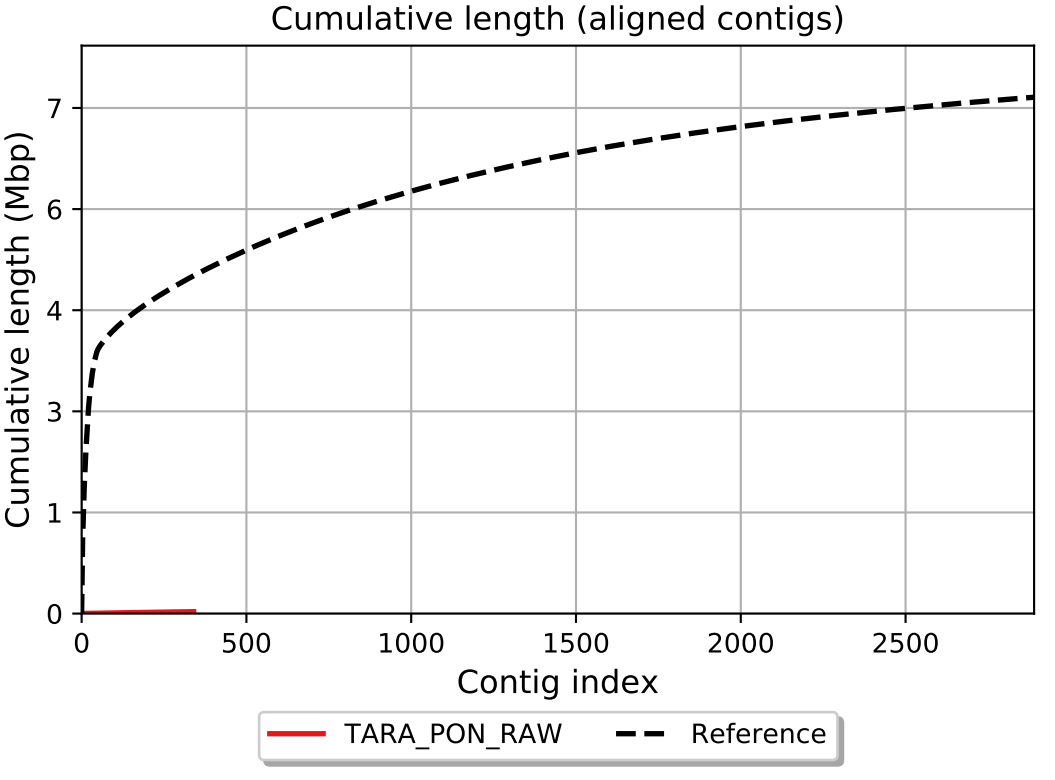

Cumulative length
Cumulative length (Mbp)
3200
2400
1600
800
0
0
300000
600000
900000
1200000
1500000
Contig index
TARA_PON_RAW
Reference

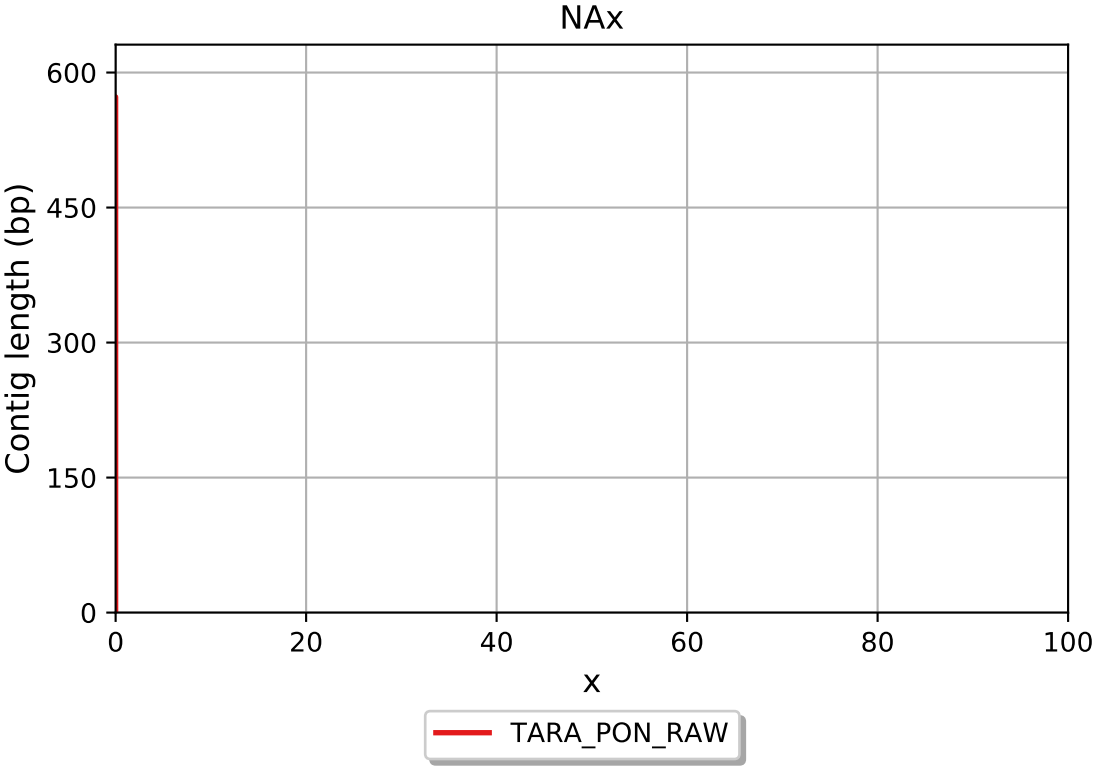

GC content
1250000
1000000
750000
500000
250000
0
0
20
40
60
80
100
GC (%)
TARA_PON_RAW
Reference


TARA_PON_RAW GC content
400000
320000
240000
160000
80000
0
contigs
0
20
40
60
80
100
GC (%)
TARA_PON_RAW


Misassemblies
5
4
3
2
1
0
TARA_PON_RAW


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
7
0
500
1000
1500
2000
2500
Contig index
TARA_PON_RAW
Reference


NAx
600
450
300
150
0
Contig length (bp)
0
20
40
60
80
100
x
TARA_PON_RAW