Report

	TARA_IOS_RAW
# contigs (>= 0 bp)	1475271
# contigs (>= 1000 bp)	1475271
# contigs (>= 5000 bp)	53523
# contigs (>= 10000 bp)	11784
# contigs (>= 25000 bp)	1601
# contigs (>= 50000 bp)	355
Total length (>= 0 bp)	2864496476
Total length (>= 1000 bp)	2864496476
Total length (>= 5000 bp)	494394129
Total length (>= 10000 bp)	217798872
Total length (>= 25000 bp)	74213818
Total length (>= 50000 bp)	32929696
# contigs	1475271
Largest contig	584819
Total length	2864496476
Reference length	4234461
N50	1934
N75	1323
L50	391314
L75	846793
# 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	0
# unaligned contigs	1475229 + 41 part
Unaligned length	2864491510
Genome fraction (%)	0.037
Duplication ratio	3.400
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8403.36
# indels per 100 kbp	129.28
Largest alignment	208
Total aligned length	4095

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

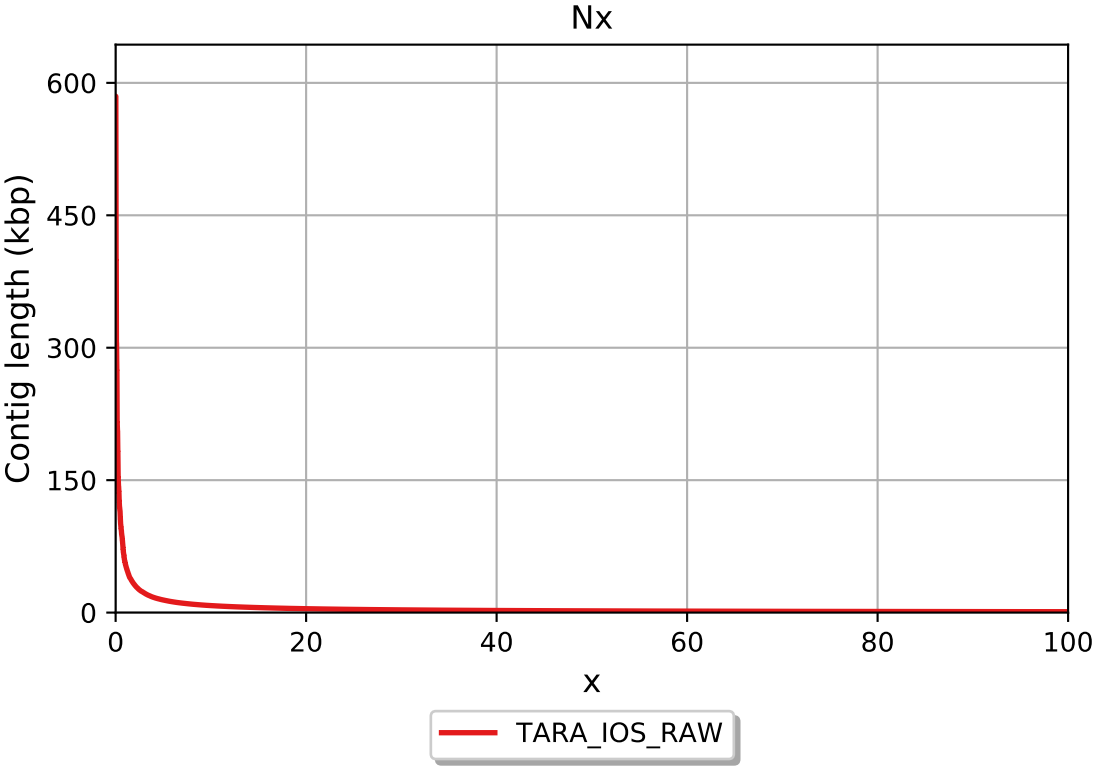
	TARA_IOS_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	41
# possible misassemblies	45
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	130
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	3

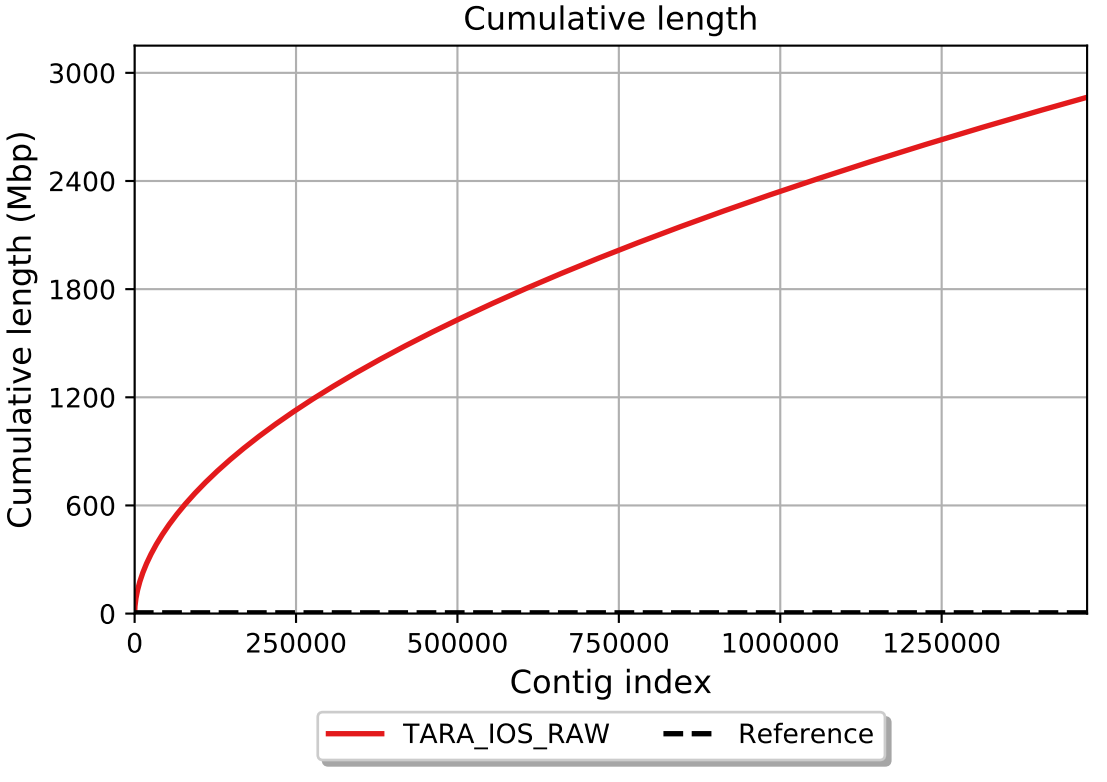
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

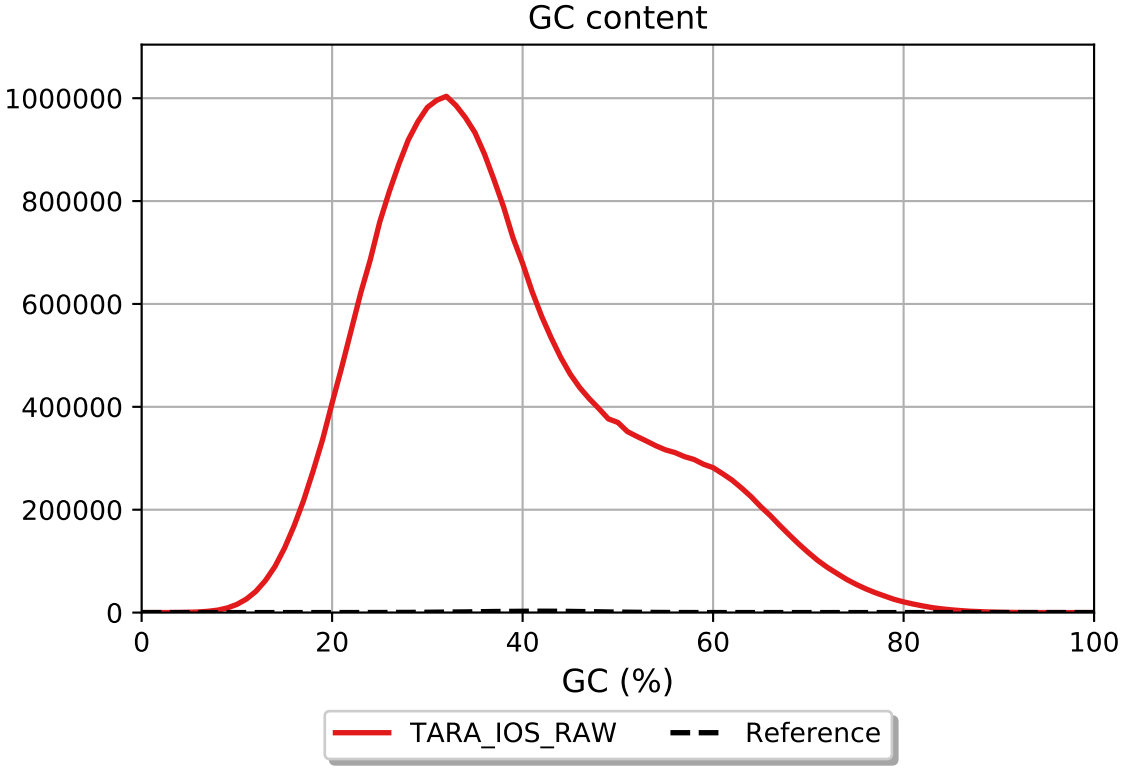
Unaligned report

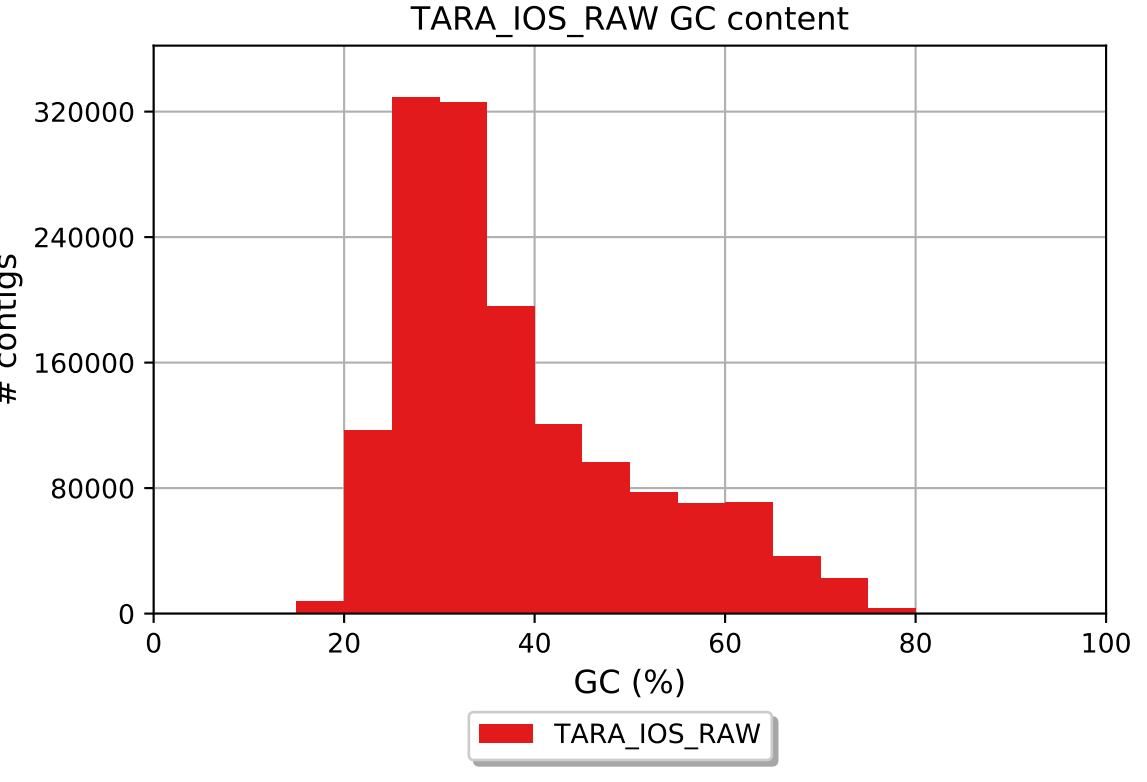
	TARA_IOS_RAW
# fully unaligned contigs	1475229
Fully unaligned length	2864345168
# partially unaligned contigs	41
Partially unaligned length	146342
# N's	0

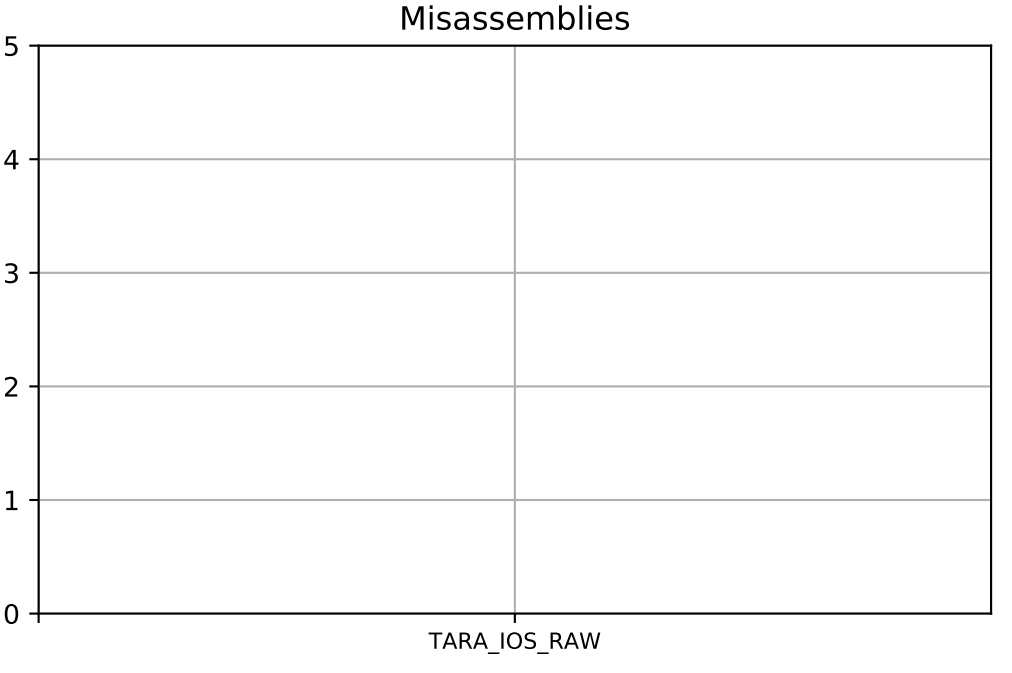
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

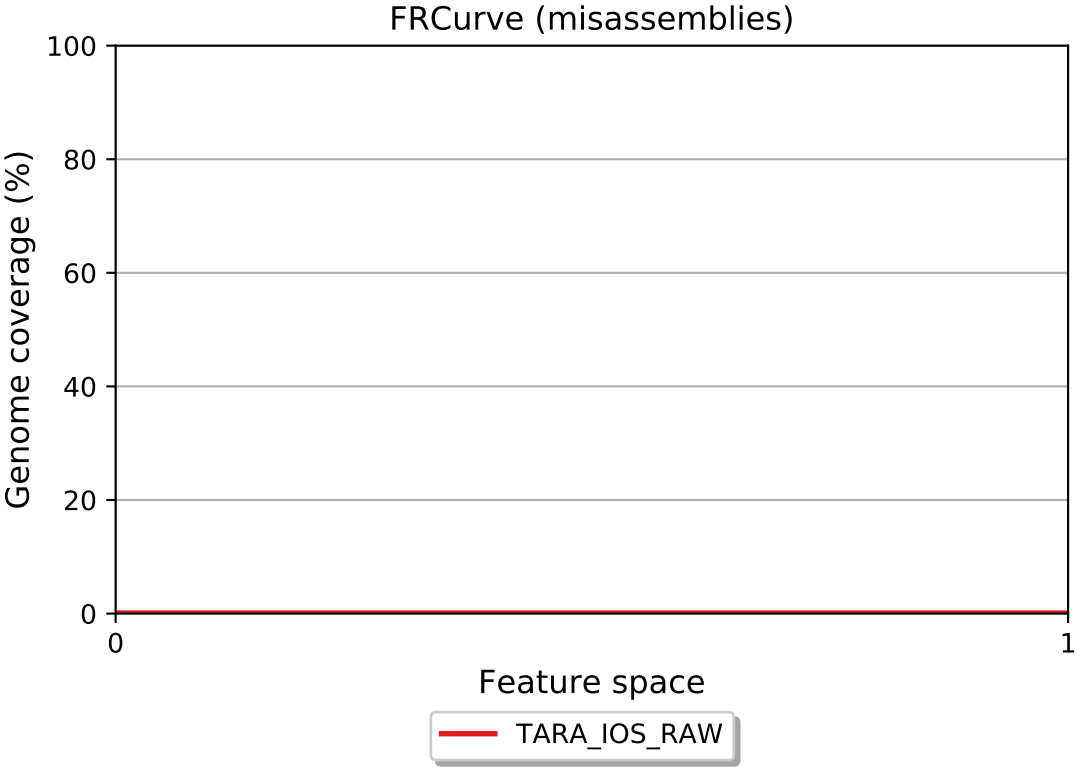

Nx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
TARA_IOS_RAW

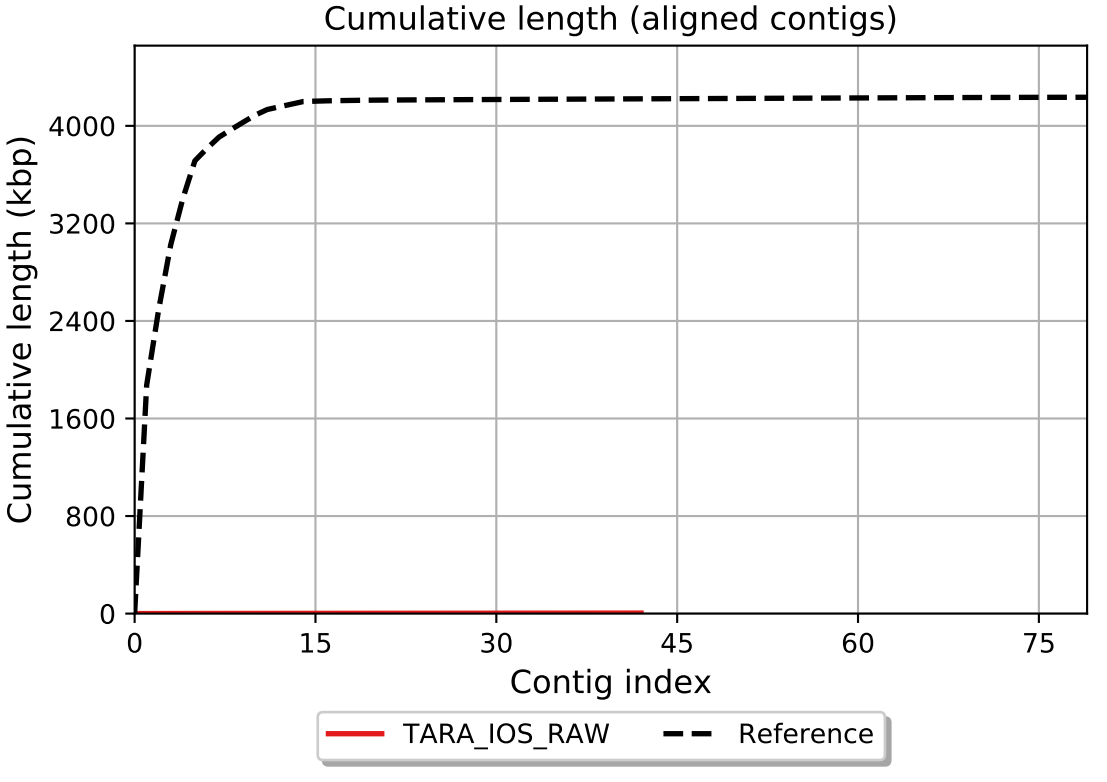

Cumulative length
Cumulative length (Mbp)
3000
2400
1800
1200
600
0
0
250000
500000
750000
1000000
1250000
Contig index
TARA_IOS_RAW
Reference

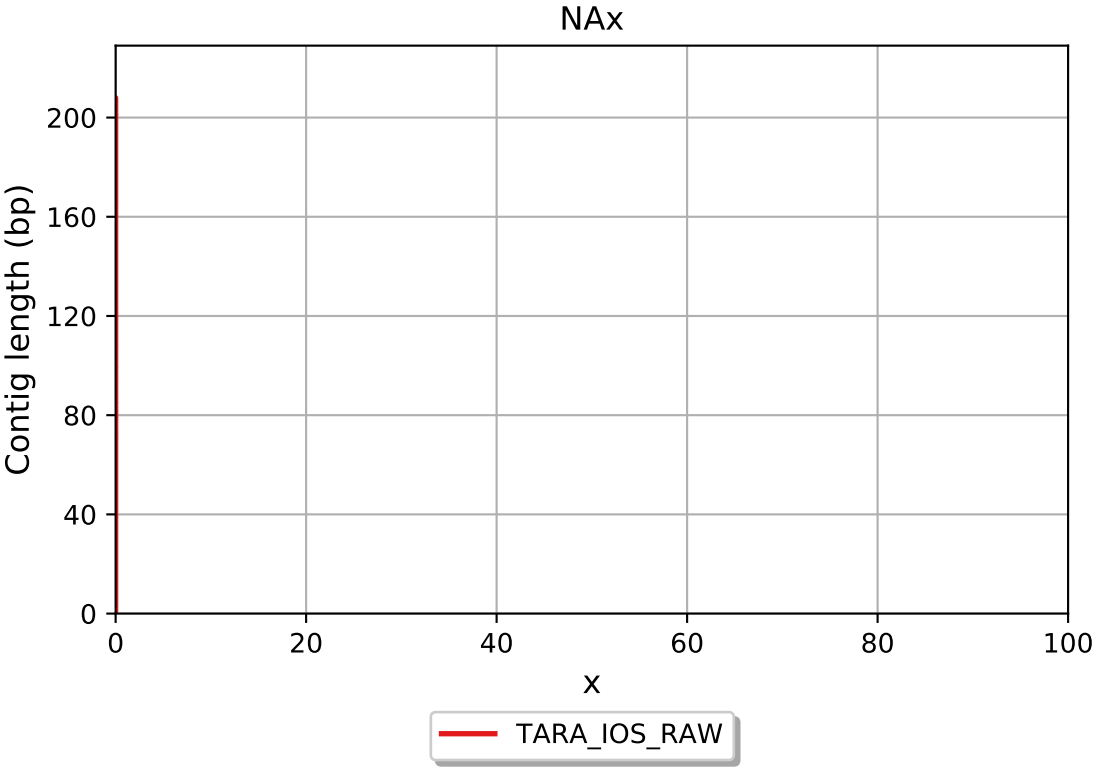

GC content
1000000
800000
600000
400000
200000
0
0
20
40
60
80
100
GC (%)
TARA_IOS_RAW
Reference


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


Misassemblies
5
4
3
2
1
0
TARA_IOS_RAW


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
15
30
45
60
75
Contig index
TARA_IOS_RAW
Reference


NAx
Contig length (bp)
200
160
120
80
40
0
0
20
40
60
80
100
x
TARA_IOS_RAW