Report

	TARA_SOC_RAW
# contigs (>= 0 bp)	415693
# contigs (>= 1000 bp)	415693
# contigs (>= 5000 bp)	19160
# contigs (>= 10000 bp)	4878
# contigs (>= 25000 bp)	753
# contigs (>= 50000 bp)	146
Total length (>= 0 bp)	867144156
Total length (>= 1000 bp)	867144156
Total length (>= 5000 bp)	185494017
Total length (>= 10000 bp)	90542706
Total length (>= 25000 bp)	31376935
Total length (>= 50000 bp)	11333585
# contigs	415693
Largest contig	377717
Total length	867144156
Reference length	4234461
N50	2133
N75	1393
L50	101886
L75	230070
# 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	415666 + 27 part
Unaligned length	867141540
Genome fraction (%)	0.018
Duplication ratio	3.483
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10386.15
# indels per 100 kbp	133.16
Largest alignment	201
Total aligned length	2616

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

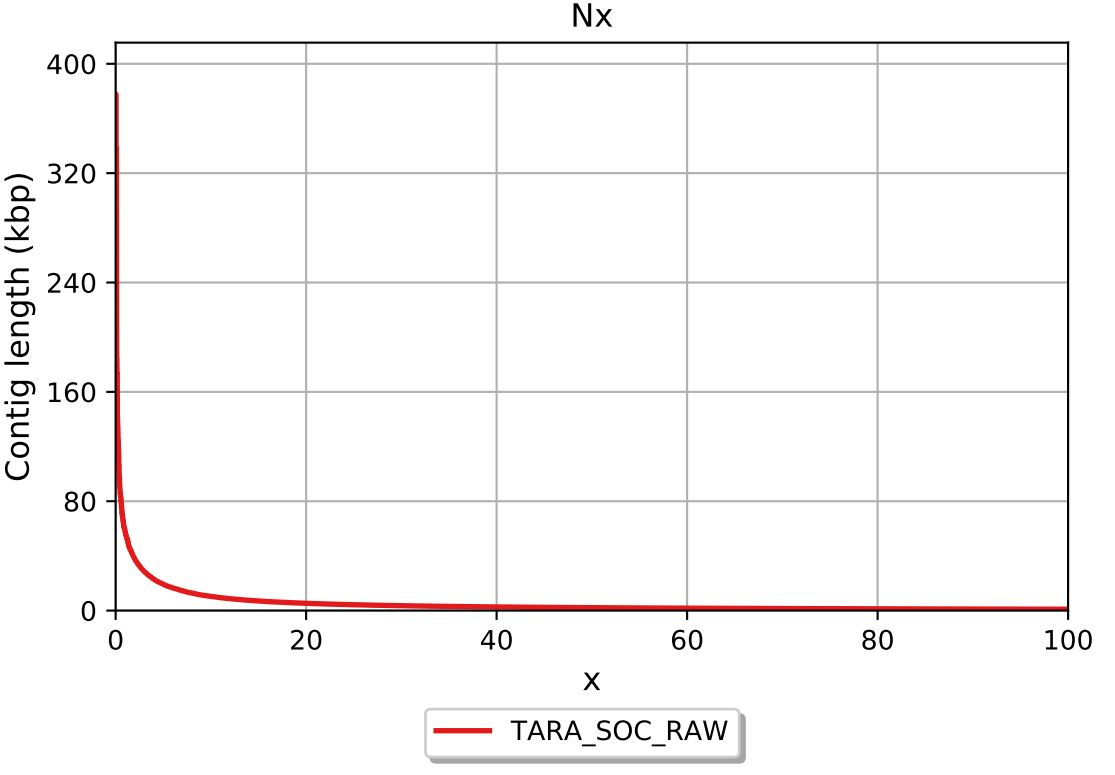
	TARA_SOC_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	25
# possible misassemblies	30
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	78
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

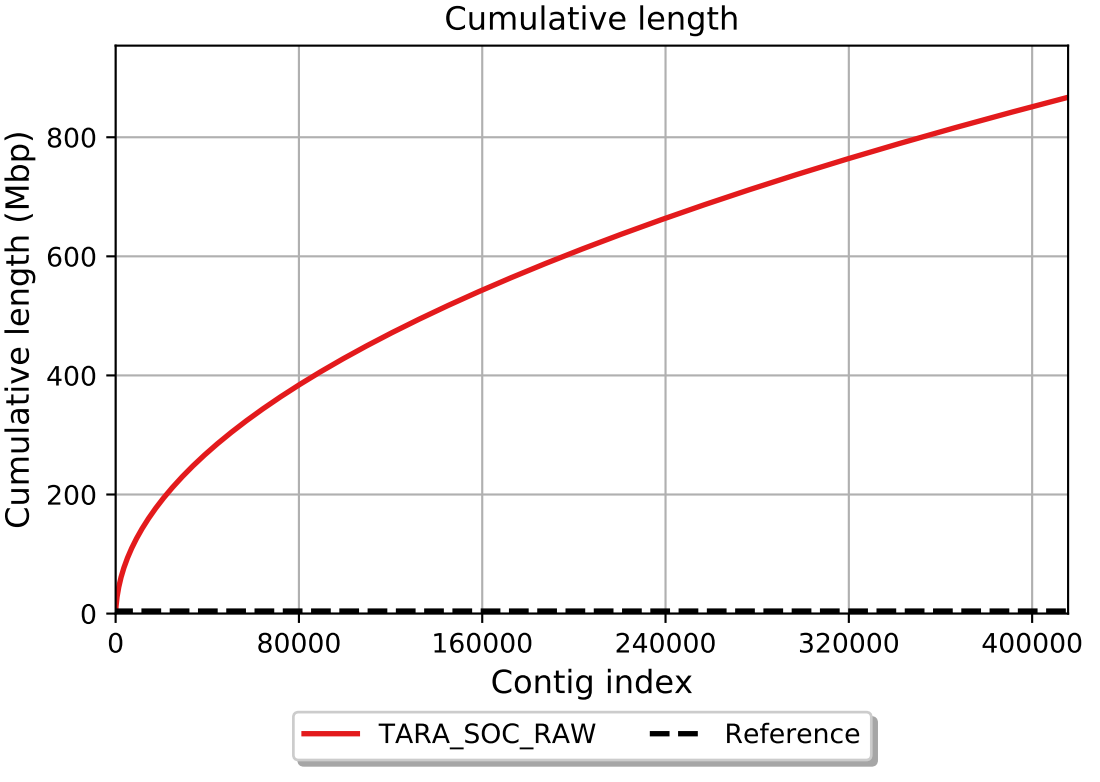
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

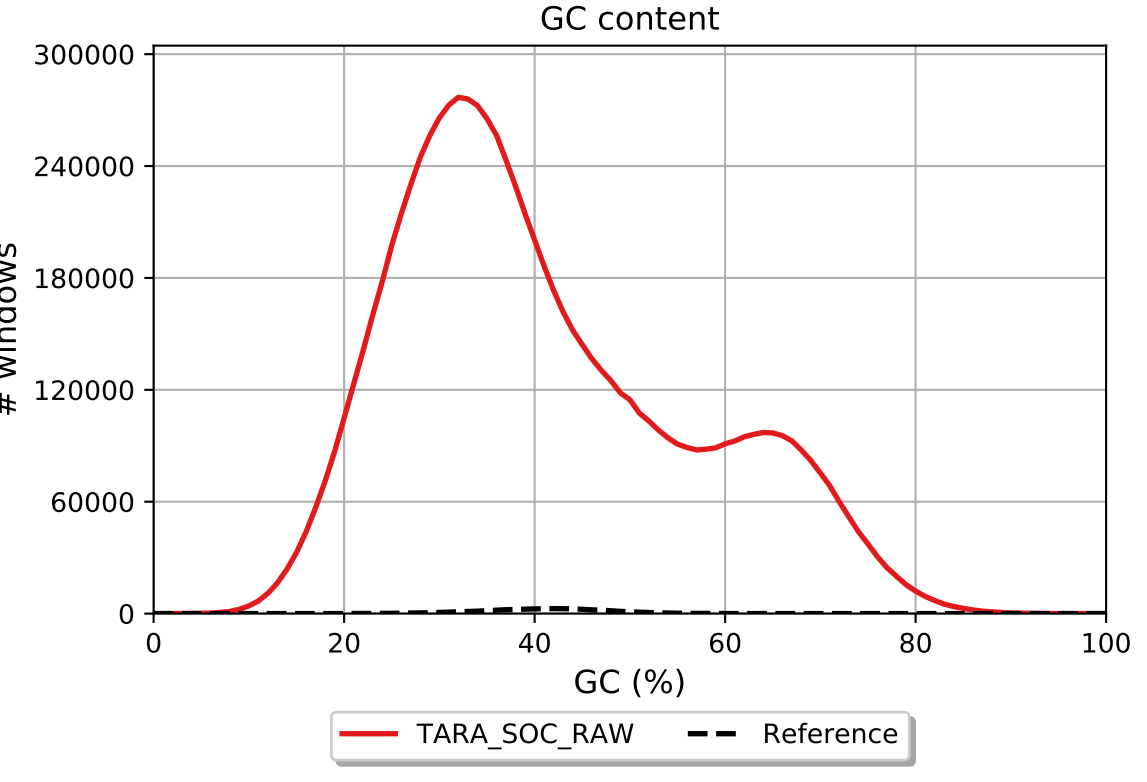
Unaligned report

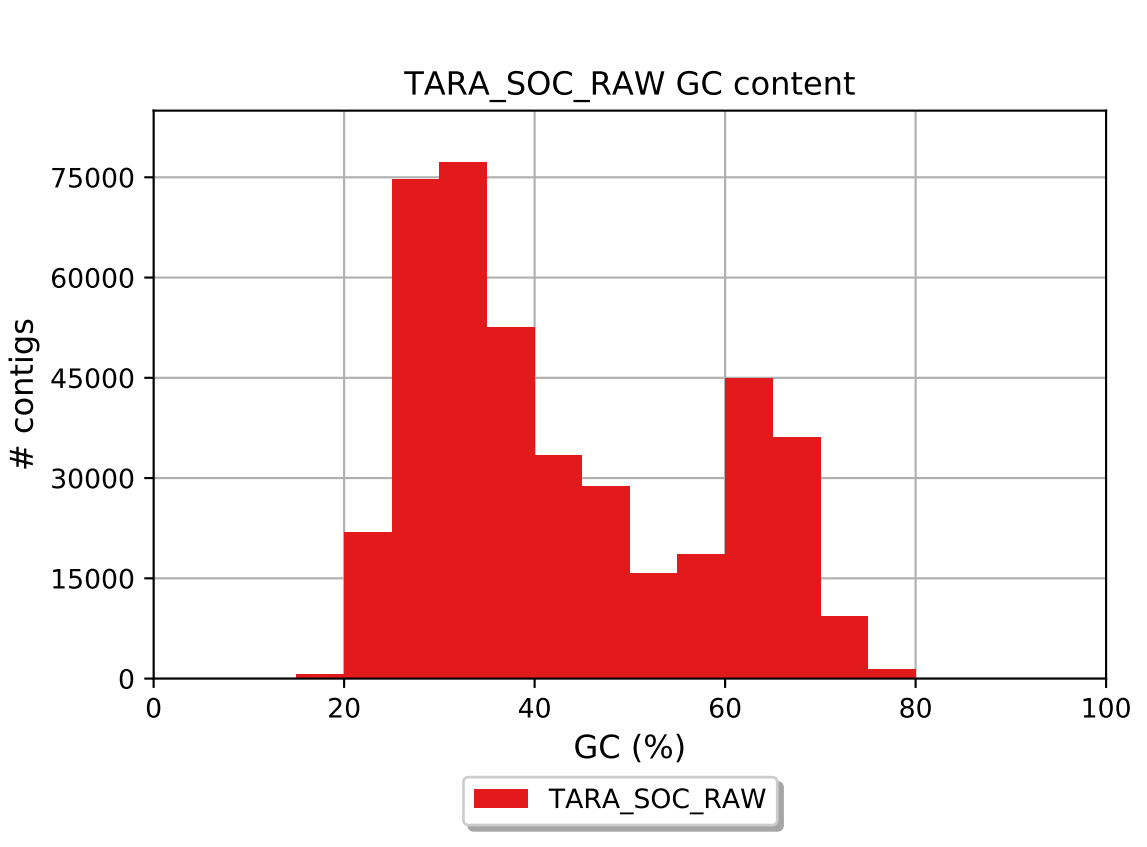
	TARA_SOC_RAW
# fully unaligned contigs	415666
Fully unaligned length	867081918
# partially unaligned contigs	27
Partially unaligned length	59622
# N's	0

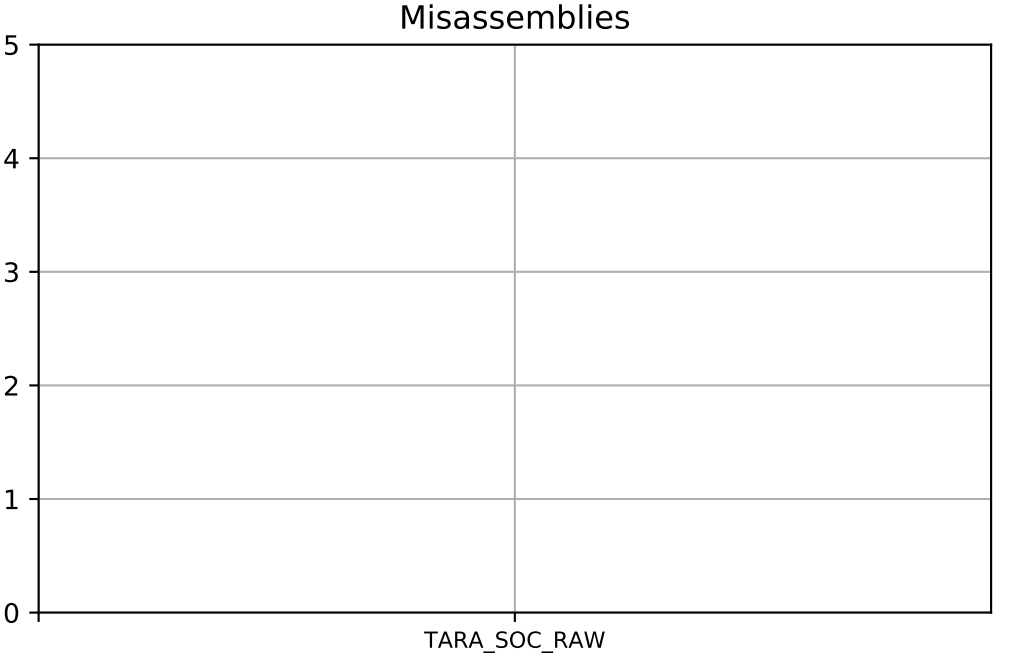
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

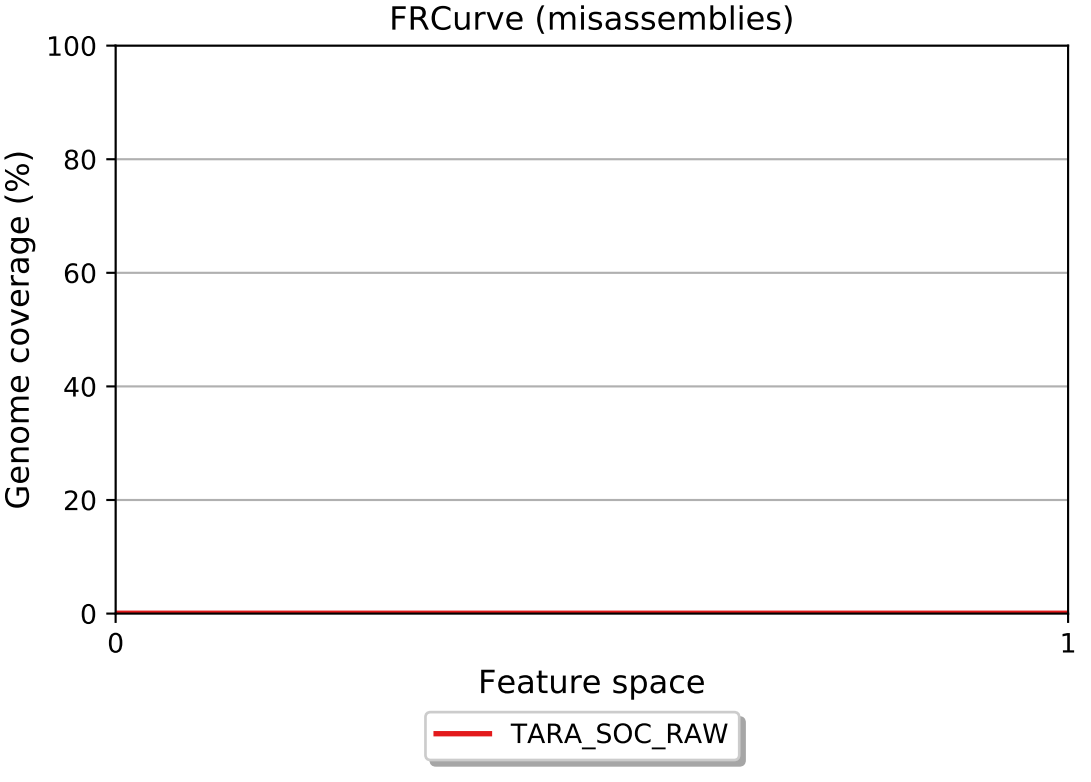

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
TARA_SOC_RAW

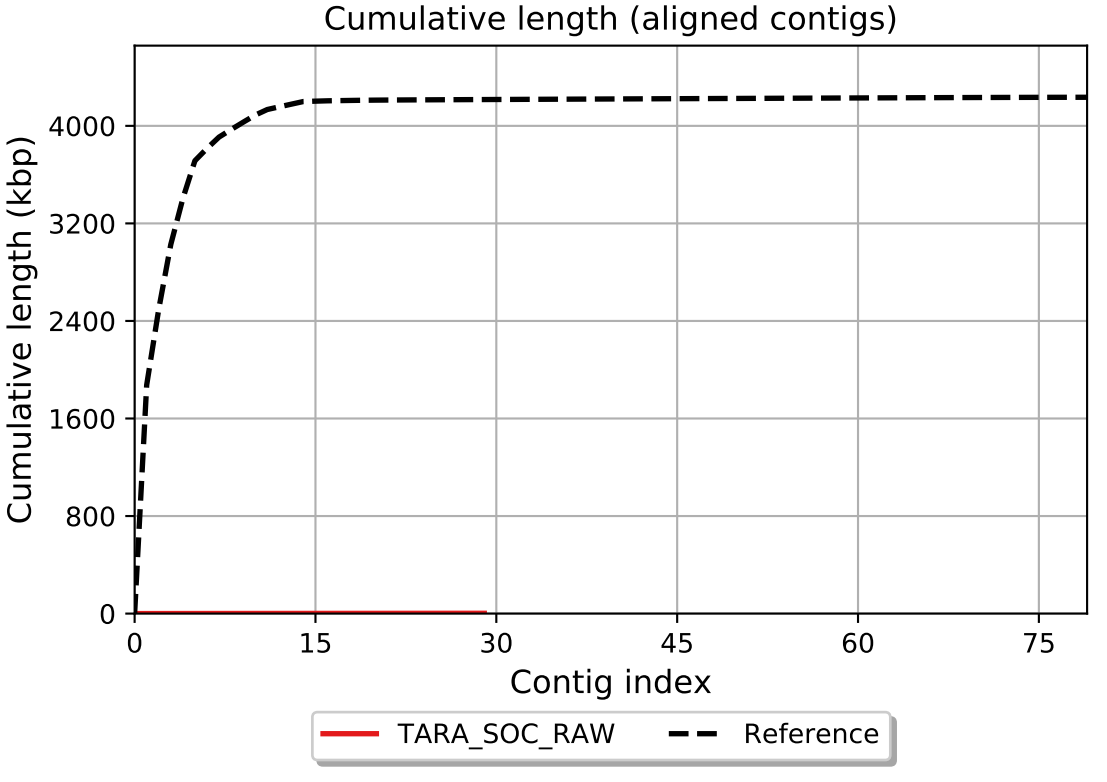

Cumulative length
Cumulative length (Mbp)
800
600
400
200
0
0
80000
160000
240000
320000
400000
Contig index
TARA_SOC_RAW
Reference

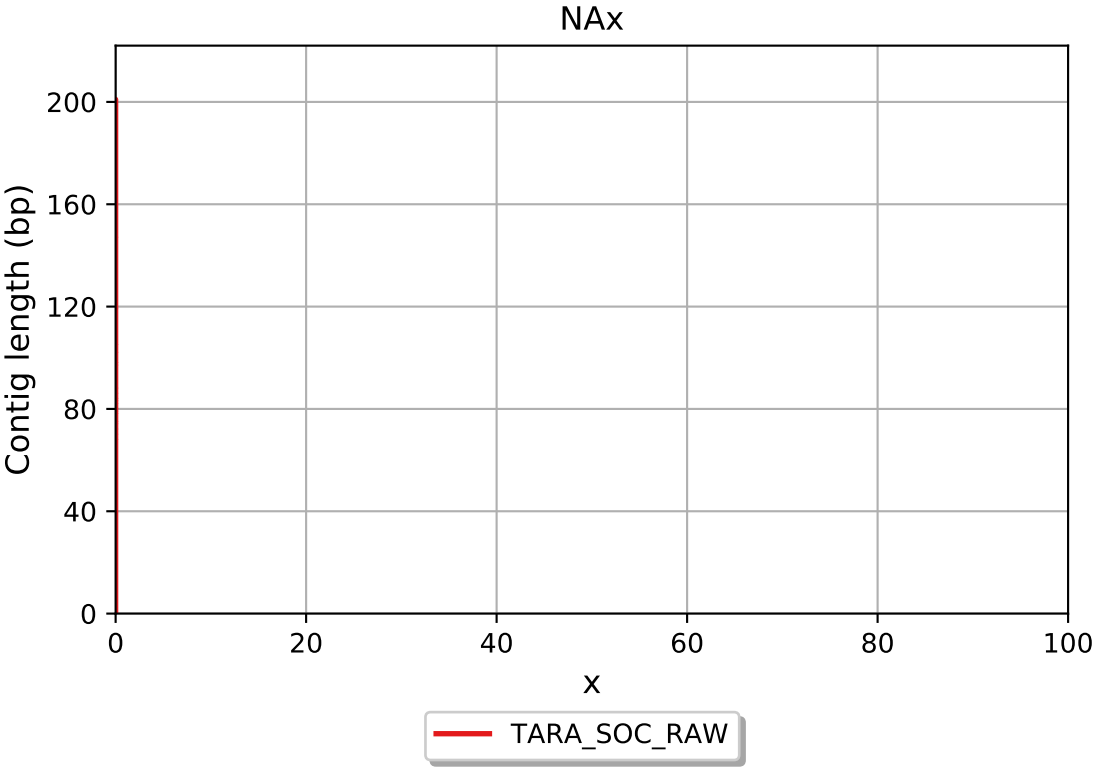

GC content
300000
240000
180000
120000
60000
0
windows
0
20
40
60
80
100
GC (%)
TARA_SOC_RAW
Reference


TARA_SOC_RAW GC content
contigs
75000
60000
45000
30000
15000
0
0
20
40
60
80
100
GC (%)
TARA_SOC_RAW


Misassemblies
5
4
3
2
1
0
TARA_SOC_RAW


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


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


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