## Report

| | tig00004064 |
|---|---|
| # contigs (>= 0 bp) | 1 |
| # contigs (>= 1000 bp) | 1 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 1 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 0 bp) | 2563357 |
| Total length (>= 1000 bp) | 2563357 |
| Total length (>= 5000 bp) | 2563357 |
| Total length (>= 10000 bp) | 2563357 |
| Total length (>= 25000 bp) | 2563357 |
| Total length (>= 50000 bp) | 2563357 |
| # contigs | 1 |
| Largest contig | 2563357 |
| Total length | 2563357 |
| Reference length | 2610531 |
| GC (%) | 54.21 |
| Reference GC (%) | 54.14 |
| N50 | 2563357 |
| NG50 | 2563357 |
| N75 | 2563357 |
| NG75 | 2563357 |
| L50 | 1 |
| LG50 | 1 |
| L75 | 1 |
| LG75 | 1 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 2563357 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 97.567 |
| Duplication ratio | 1.006 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.08 |
| # indels per 100 kbp | 6.44 |
| Largest alignment | 1463673 |
| Total aligned length | 2563357 |
| NA50 | 1463673 |
| NGA50 | 1463673 |
| NA75 | 1099684 |
| NGA75 | 1099684 |
| LA50 | 1 |
| LGA50 | 1 |
| LA75 | 2 |
| LGA75 | 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).

# Misassemblies report

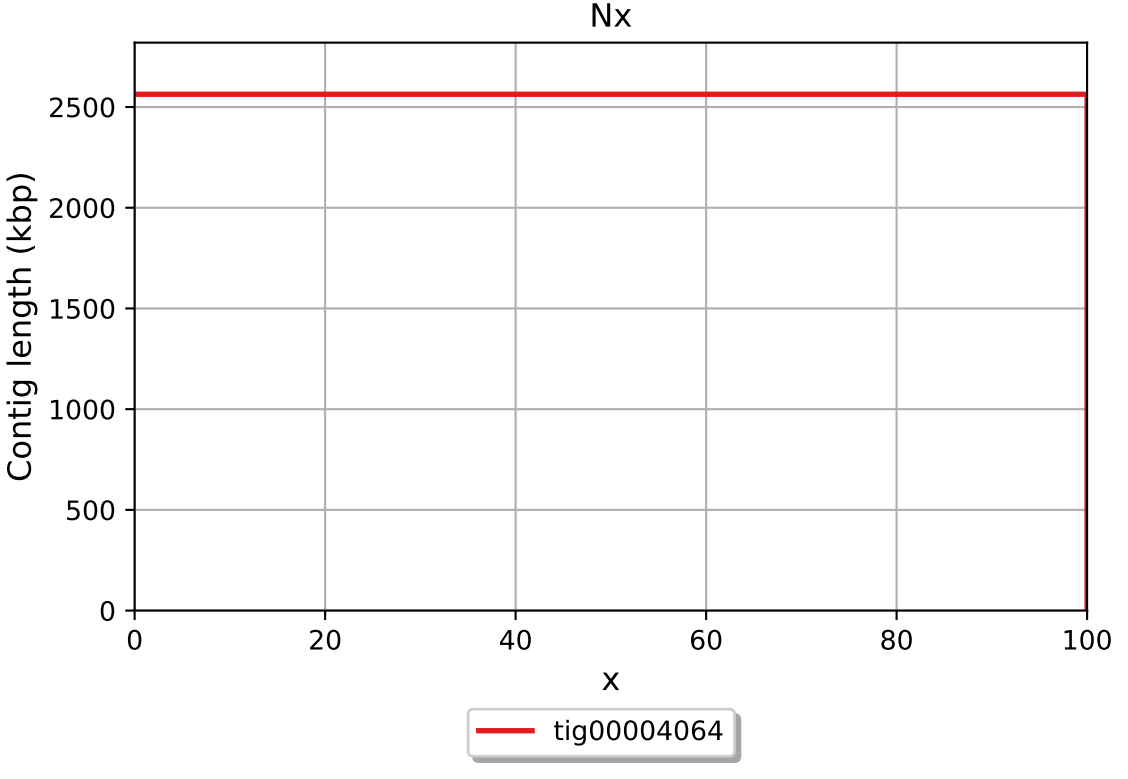
| | tig00004064 |
|---|---|
| # misassemblies | 1 |
| # contig misassemblies | 1 |
| # c. relocations | 1 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 2563357 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 2 |
| # indels | 164 |
| # indels (<= 5 bp) | 164 |
| # indels (> 5 bp) | 0 |
| Indels length | 168 |

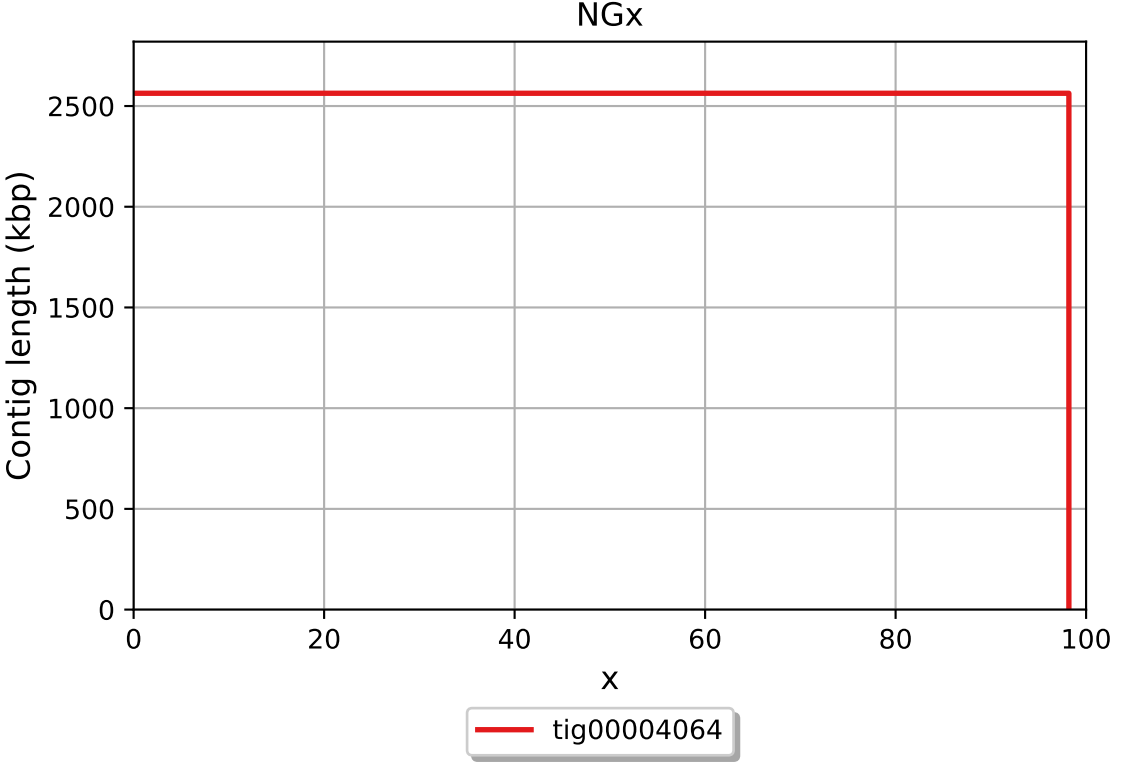
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

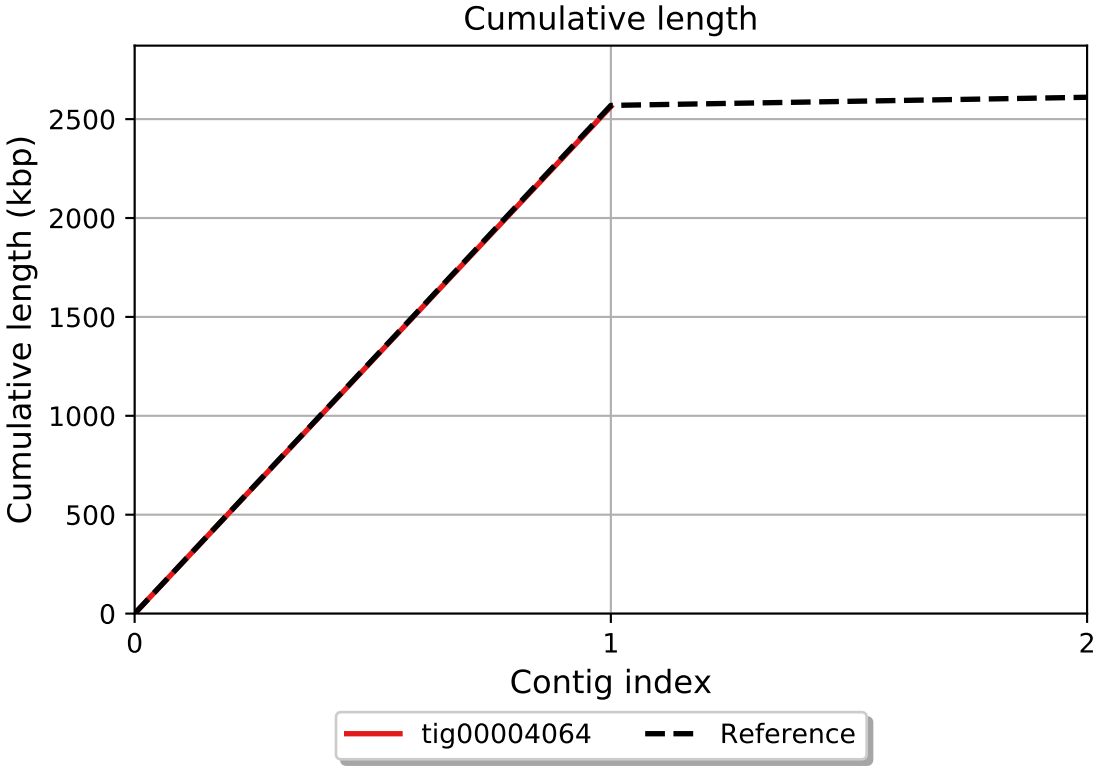
# Unaligned report

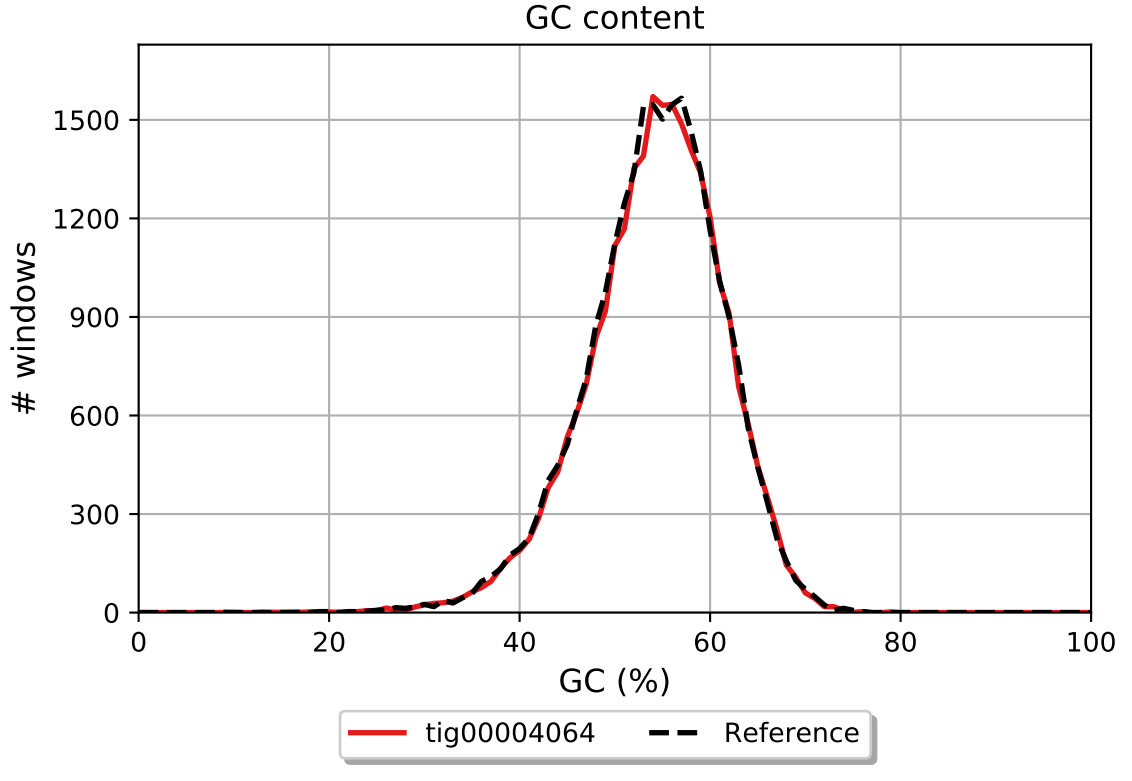
| | tig00004064 |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

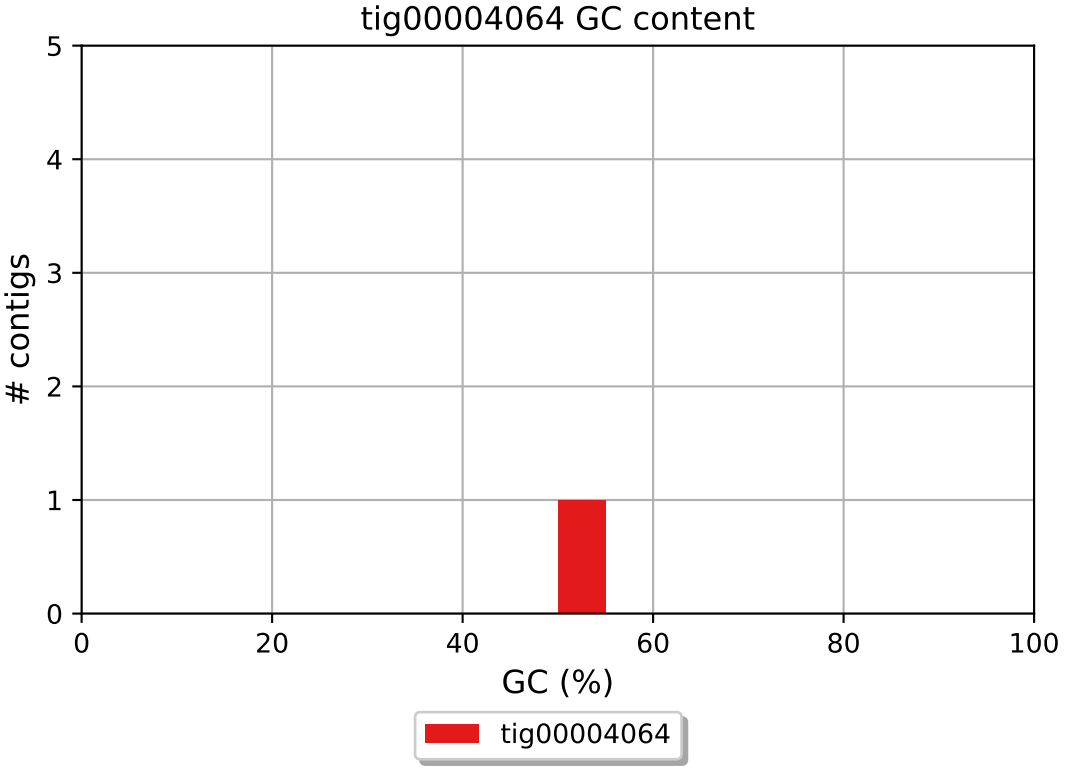
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
tig00004064

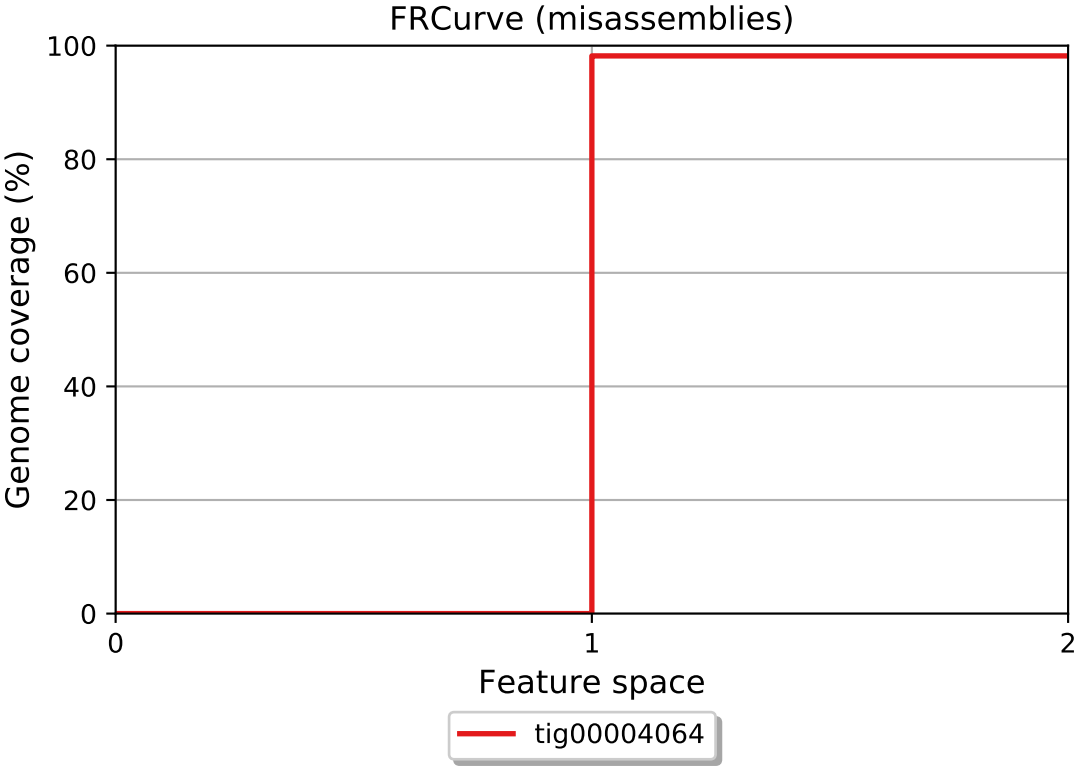

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
tig00004064

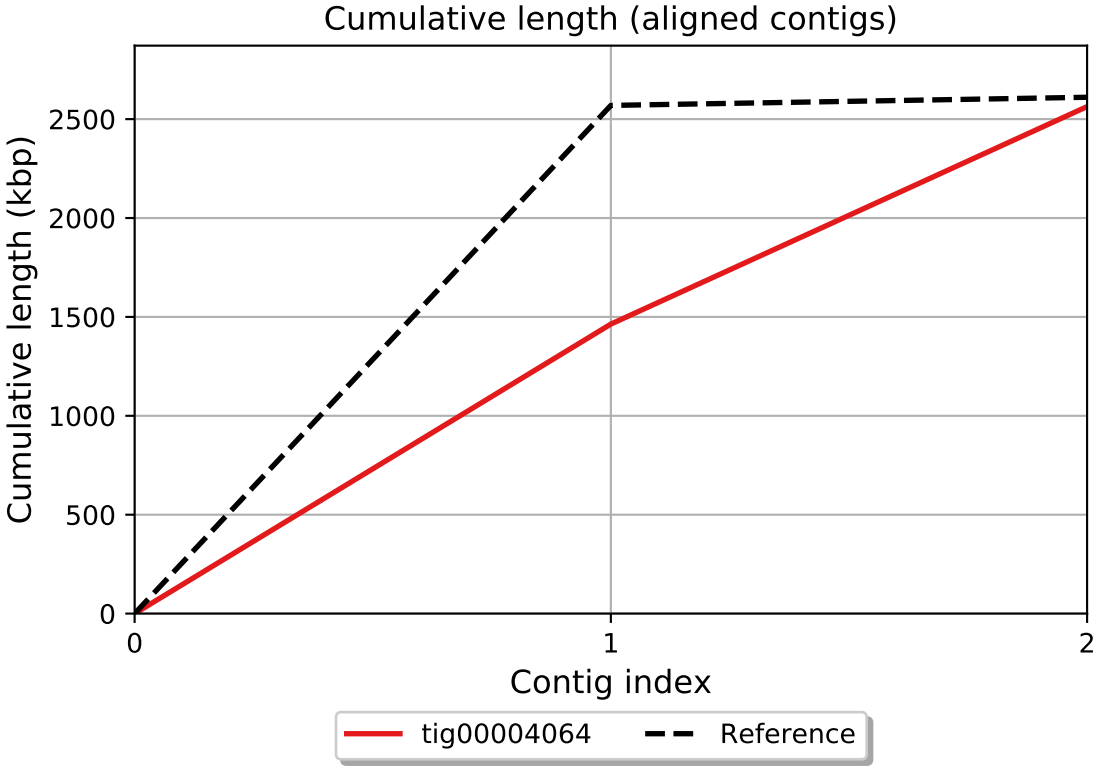

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
tig00004064
Reference

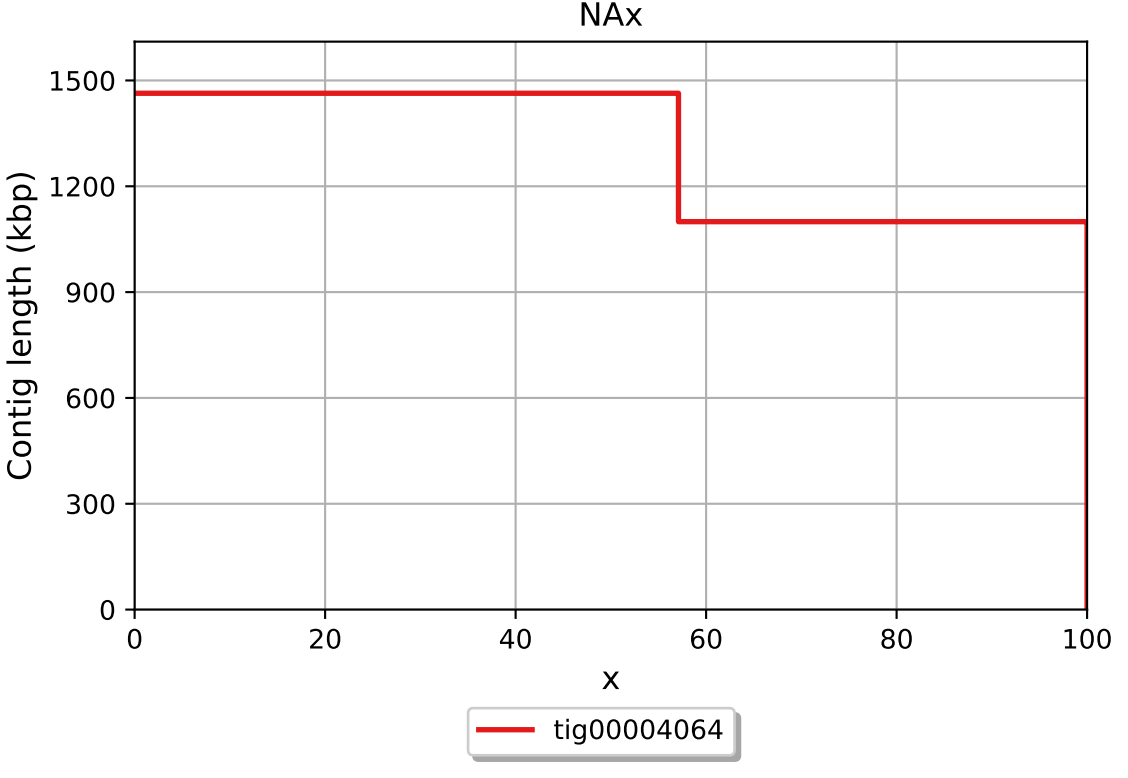

GC content
# windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
tig00004064
Reference

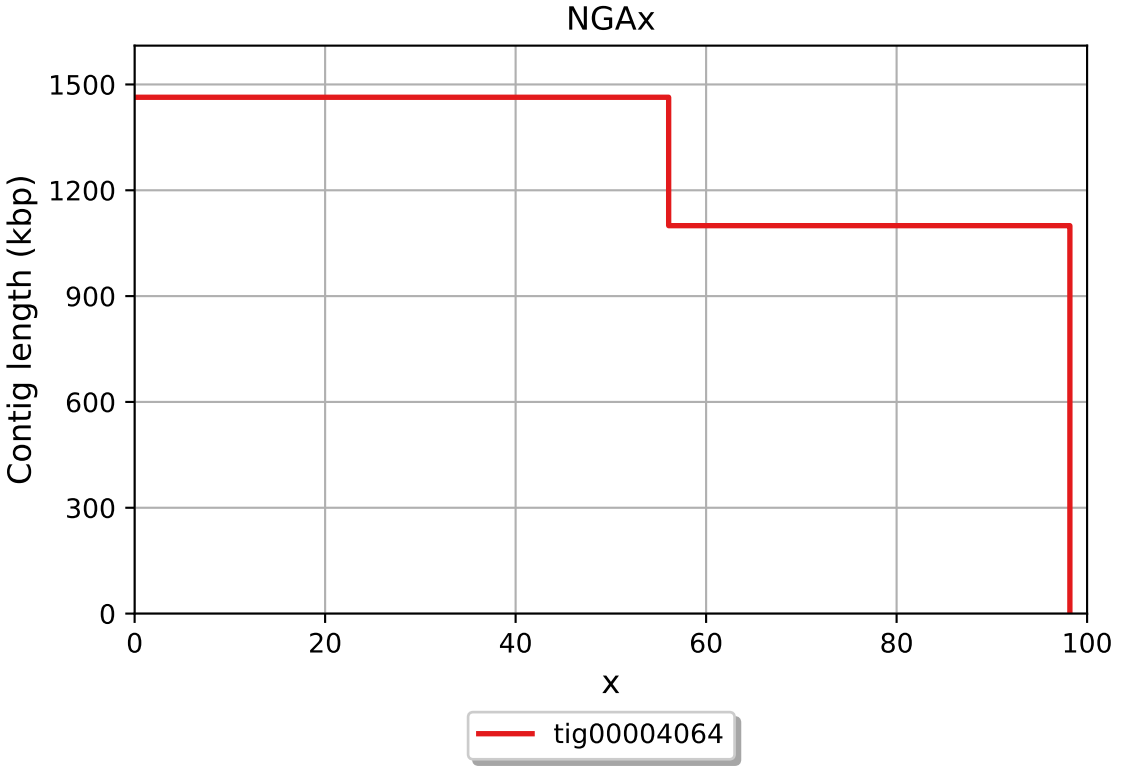

tig00004064 GC content
# contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
tig00004064

Misassemblies
5
4
3
2
1
0
tig00004064
# relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
tig00004064


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
tig00004064
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
tig00004064


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
tig00004064