Report

| | 33_380.30 |
|---|---|
| # contigs (>= 0 bp) | 39 |
| # contigs (>= 1000 bp) | 34 |
| # contigs (>= 5000 bp) | 20 |
| # contigs (>= 10000 bp) | 13 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 306475 |
| Total length (>= 1000 bp) | 302316 |
| Total length (>= 5000 bp) | 264045 |
| Total length (>= 10000 bp) | 208225 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 39 |
| Largest contig | 19255 |
| Total length | 306475 |
| Reference length | 29857 |
| N50 | 13909 |
| N75 | 8272 |
| L50 | 9 |
| L75 | 16 |
| # 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 | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 98.458 |
| Duplication ratio | 10.435 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 20.43 |
| # indels per 100 kbp | 71.50 |
| Largest alignment | 19255 |
| Total aligned length | 306445 |
| NA50 | 13908 |
| NA75 | 8271 |
| LA50 | 9 |
| LA75 | 16 |

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

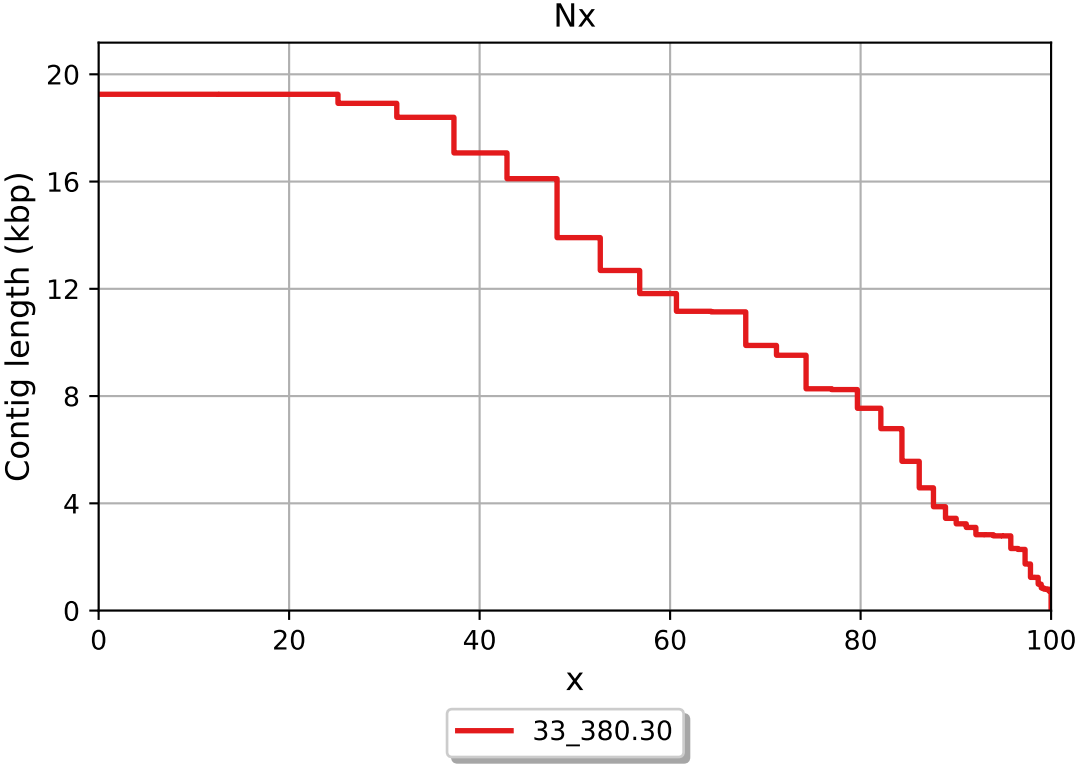
| | 33_380.30 |
|---|---|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # c. interspecies translocations | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # s. interspecies translocations | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 6 |
| # indels | 21 |
| # indels (<= 5 bp) | 21 |
| # indels (> 5 bp) | 0 |
| Indels length | 21 |

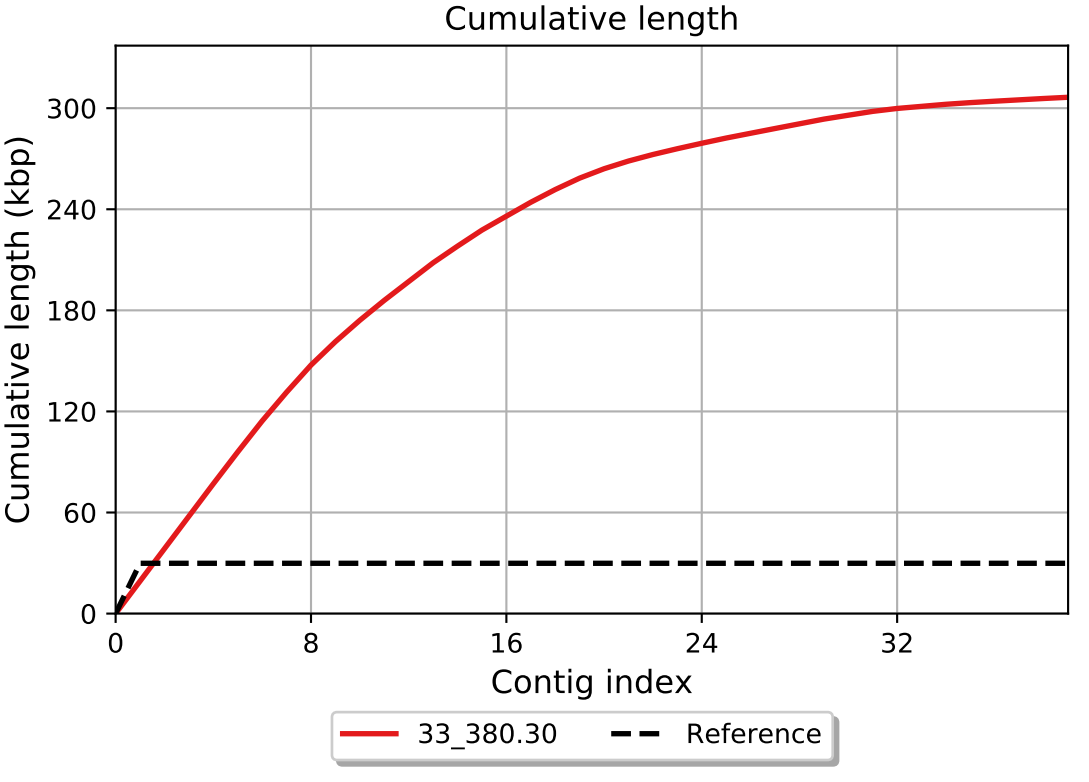
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

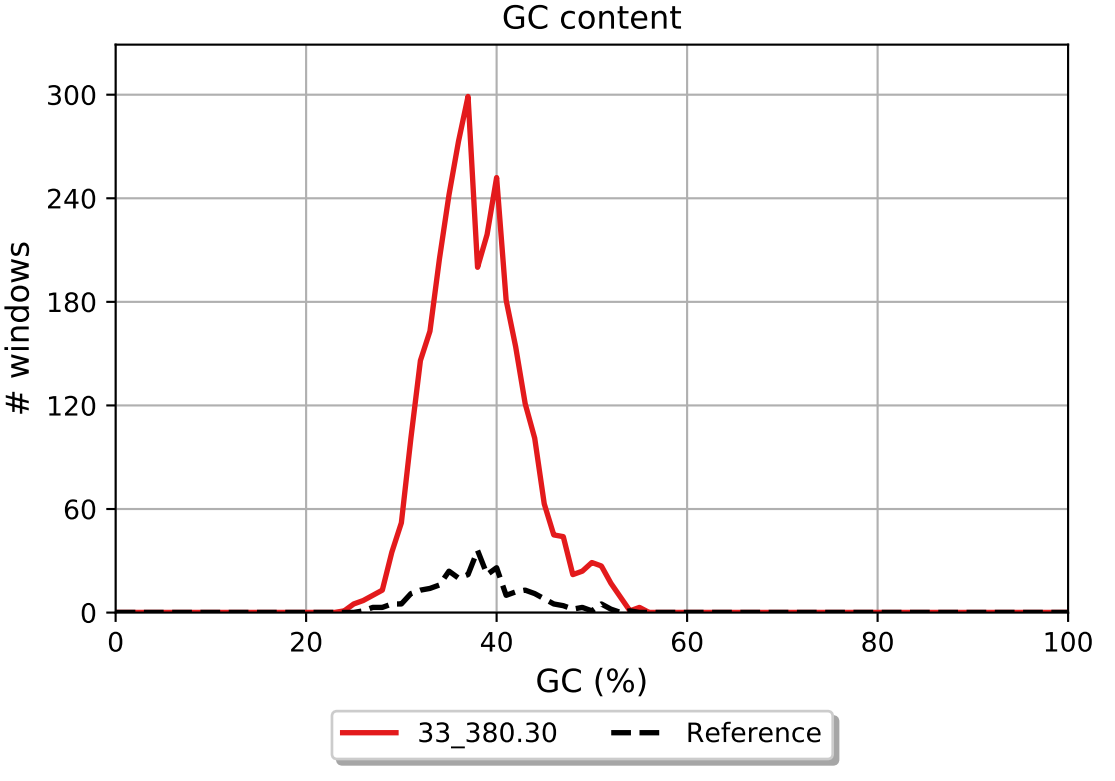
# Unaligned report

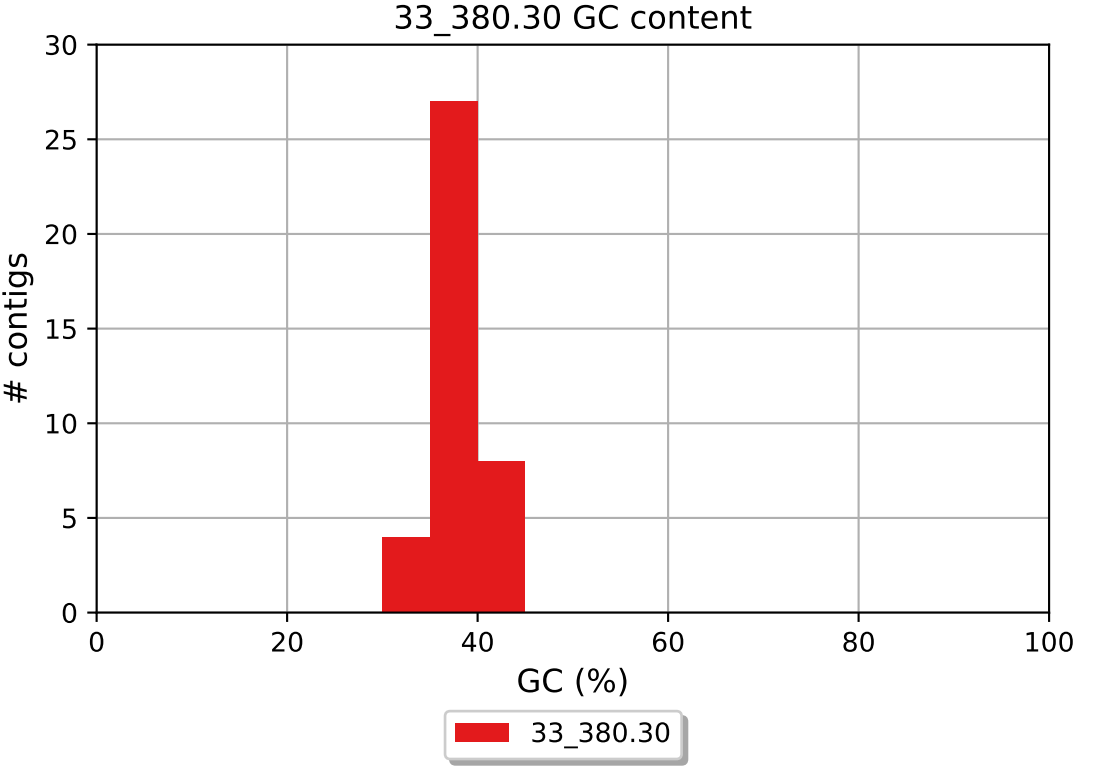
| | 33_380.30 |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

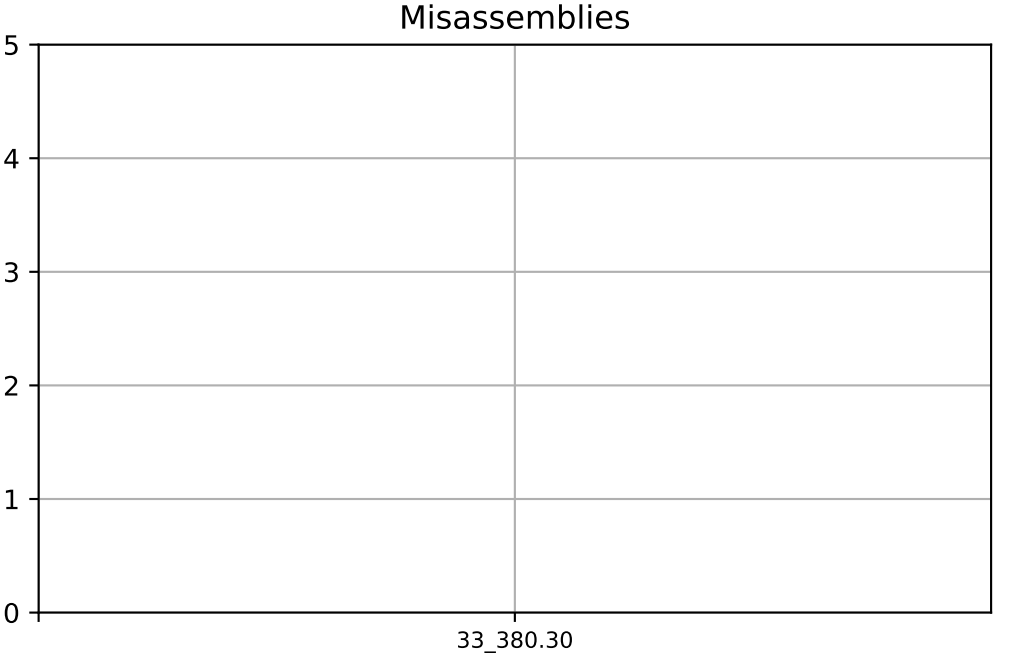
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

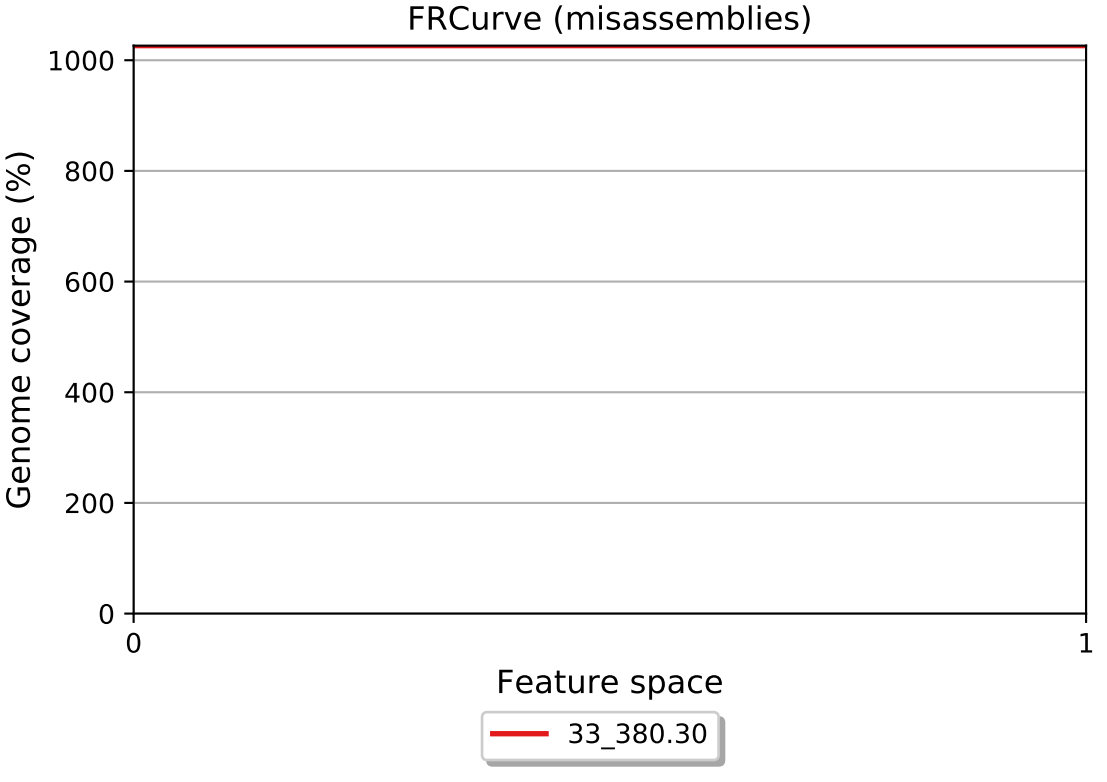

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
33_380.30

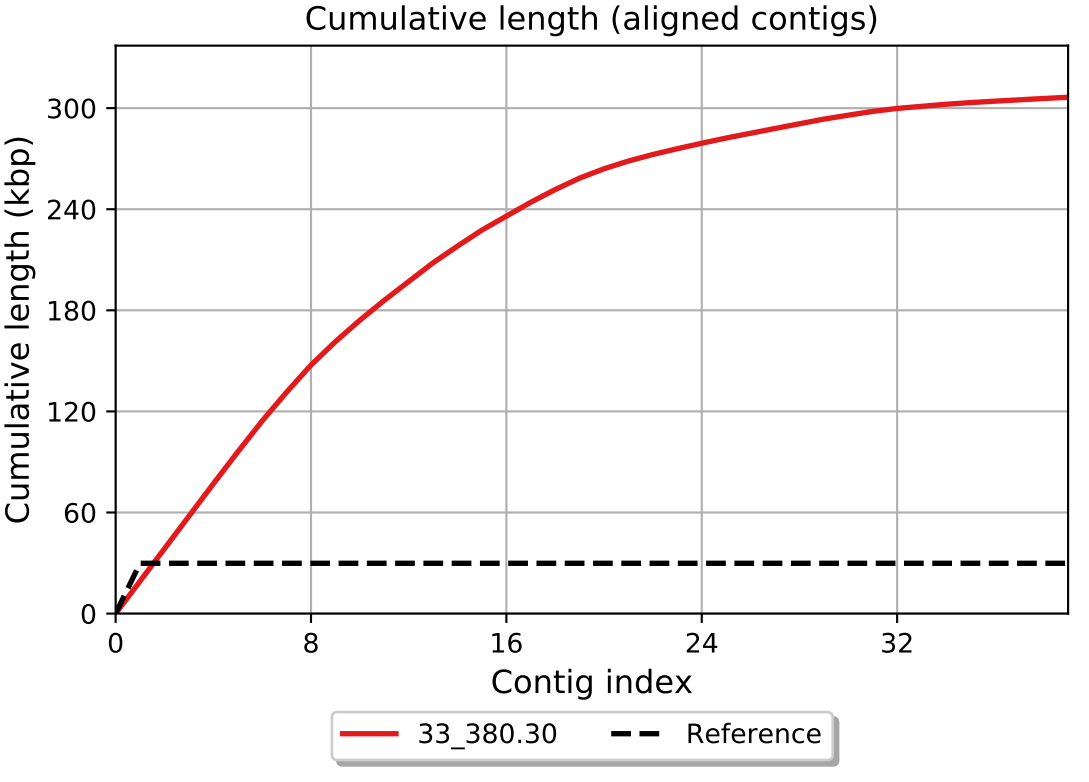

Cumulative length
Cumulative length (kbp)
300
240
180
120
60
0
0
8
16
24
32
Contig index
33_380.30
Reference

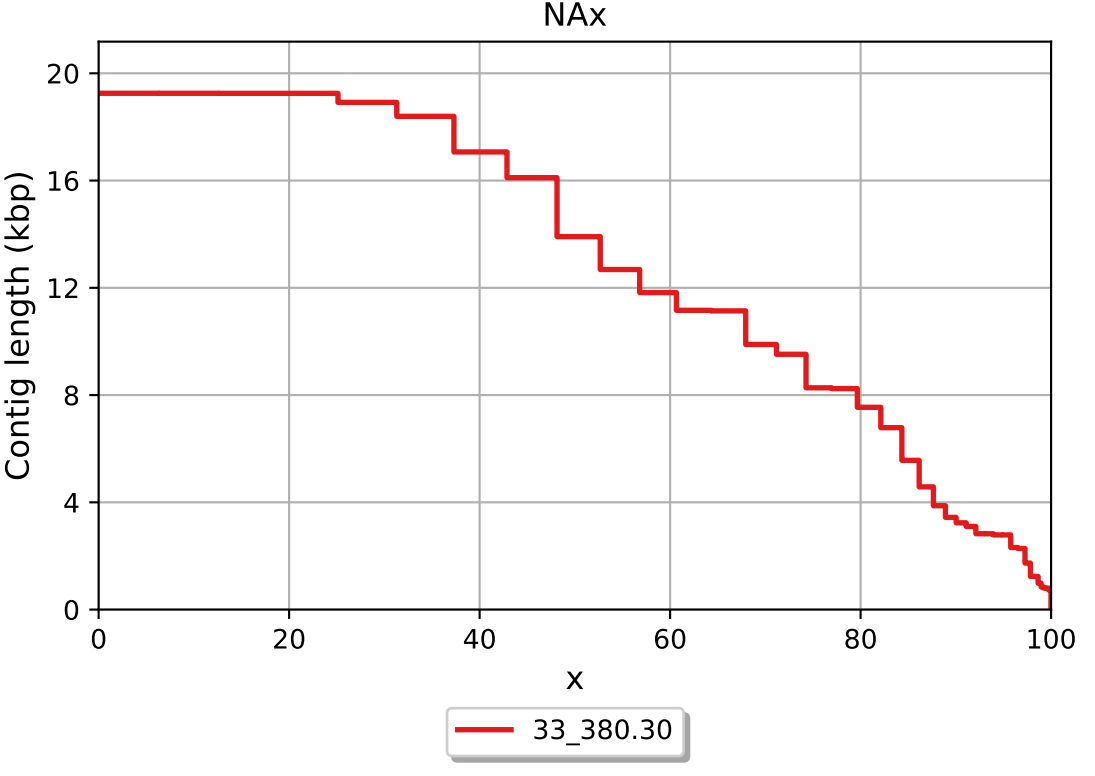

GC content
# windows
300
240
180
120
60
0
0
20
40
60
80
100
GC (%)
33_380.30
Reference


33_380.30 GC content
# contigs
GC (%)
0
5
10
15
20
25
30
0
20
40
60
80
100
33_380.30


Misassemblies
5
4
3
2
1
0
33_380.30


FRCurve (misassemblies)
Genome coverage (%)
1000
800
600
400
200
0
0
1
Feature space
33_380.30


Cumulative length (aligned contigs)
Cumulative length (kbp)
300
240
180
120
60
0
0
8
16
24
32
Contig index
33_380.30
Reference


NAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
33_380.30