# Report

| | klebsiellapneumoniae-8_fa | klebsiellapneumoniae-8_fa_broken |
|---|---|---|
| # contigs (>= 0 bp) | 367 | - |
| # contigs (>= 1000 bp) | 84 | 95 |
| Total length (>= 0 bp) | 5611755 | - |
| Total length (>= 1000 bp) | 5563416 | 5560075 |
| # contigs | 90 | 107 |
| Largest contig | 526031 | 526031 |
| Total length | 5567208 | 5566344 |
| Reference length | 5682322 | 5682322 |
| GC (%) | 57.19 | 57.19 |
| Reference GC (%) | 57.12 | 57.12 |
| N50 | 142249 | 129474 |
| NG50 | 142249 | 129474 |
| N90 | 35266 | 30124 |
| NG90 | 27500 | 25906 |
| auN | 165398.4 | 155470.9 |
| auNG | 162047.8 | 152297.7 |
| L50 | 14 | 15 |
| LG50 | 14 | 15 |
| L90 | 41 | 46 |
| LG90 | 44 | 50 |
| # misassemblies | 76 | 75 |
| # misassembled contigs | 37 | 38 |
| Misassembled contigs length | 4397977 | 4164417 |
| # local misassemblies | 26 | 26 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 2 | - |
| # unaligned mis. contigs | 4 | 4 |
| # unaligned contigs | 14 + 47 part | 15 + 52 part |
| Unaligned length | 728218 | 728389 |
| Genome fraction (%) | 84.851 | 85.229 |
| Duplication ratio | 1.011 | 1.011 |
| # N's per 100 kbp | 16.04 | 0.52 |
| # mismatches per 100 kbp | 686.13 | 687.57 |
| # indels per 100 kbp | 20.20 | 19.42 |
| # genomic features | 9715 + 228 part | 9695 + 266 part |
| Complete BUSCO (%) | 97.97 | 97.97 |
| Partial BUSCO (%) | 0.00 | 0.00 |
| # predicted rRNA genes | 4 + 3 part | 4 + 2 part |
| Largest alignment | 313363 | 313363 |
| Total aligned length | 4836224 | 4835113 |
| NA50 | 60731 | 59395 |
| NGA50 | 59395 | 58133 |
| NA90 | - | - |
| NGA90 | - | - |
| auNA | 76812.2 | 73778.9 |
| auNGA | 75256.1 | 72273.1 |
| LA50 | 27 | 28 |
| LGA50 | 28 | 29 |
| LA90 | - | - |
| LGA90 | - | - |

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

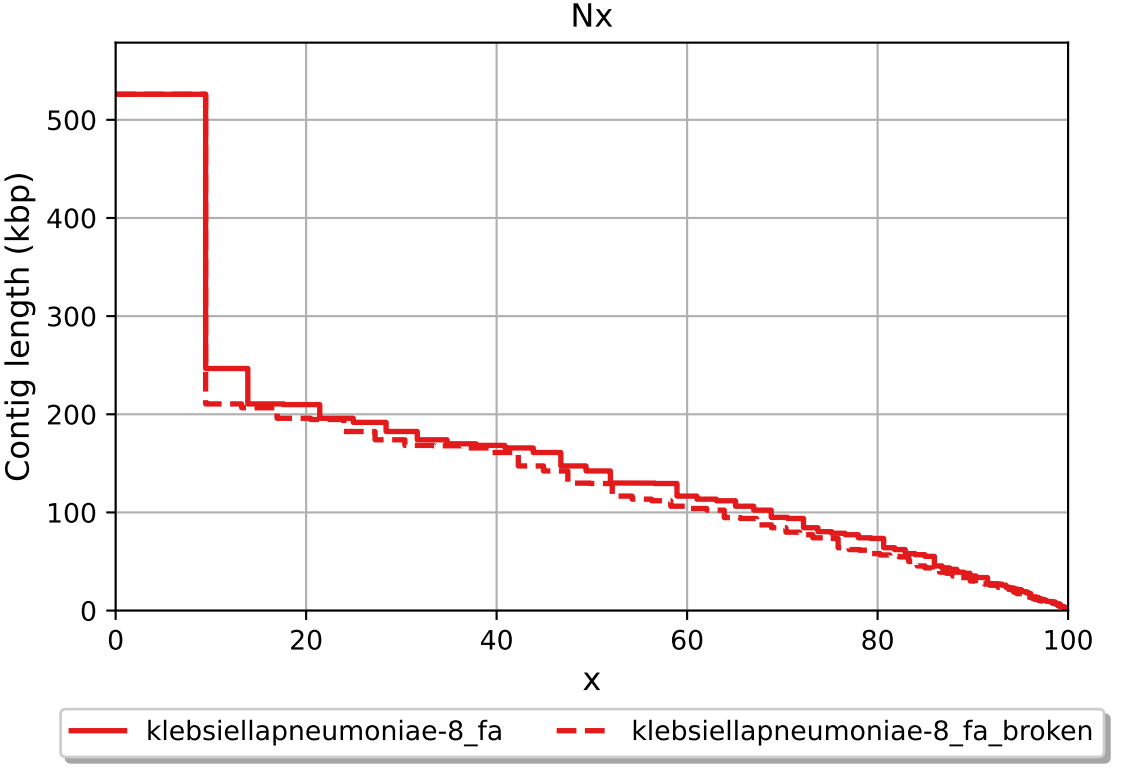
| | klebsiellapneumoniae-8_fa | klebsiellapneumoniae-8_fa_broken |
|---|---|---|
| # misassemblies | 76 | 75 |
| # contig misassemblies | 75 | 75 |
| # c. relocations | 71 | 71 |
| # c. translocations | 4 | 4 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 1 | 0 |
| # s. relocations | 1 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 37 | 38 |
| Misassembled contigs length | 4397977 | 4164417 |
| # local misassemblies | 26 | 26 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 2 | - |
| # unaligned mis. contigs | 4 | 4 |
| # mismatches | 33183 | 33245 |
| # indels | 977 | 939 |
| # indels (<= 5 bp) | 860 | 839 |
| # indels (> 5 bp) | 117 | 100 |
| Indels length | 8717 | 7758 |

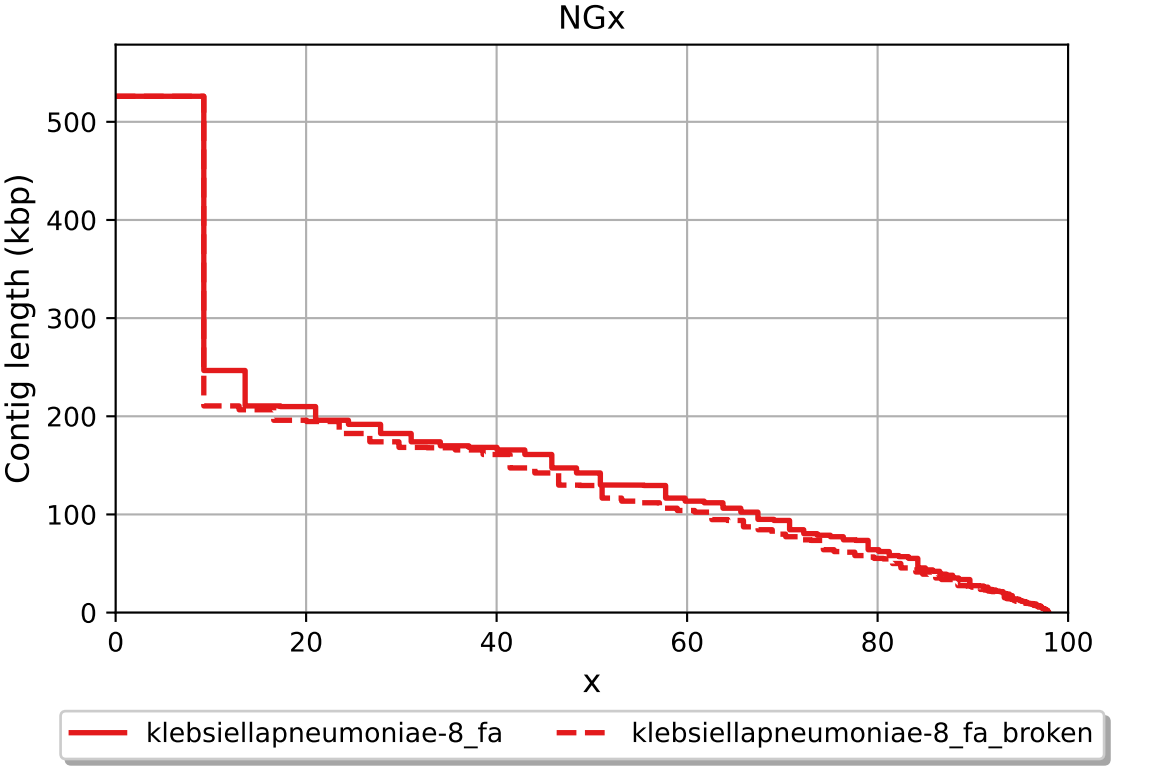
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

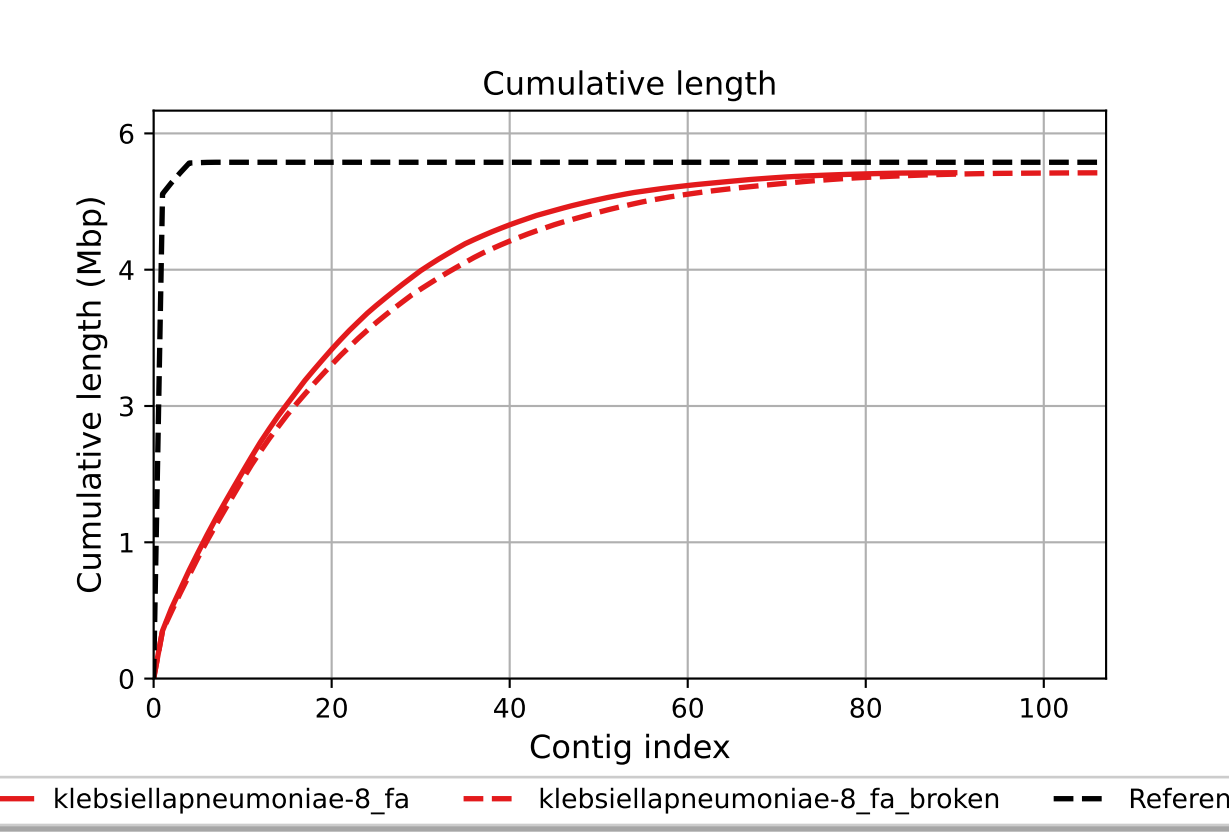
# Unaligned report

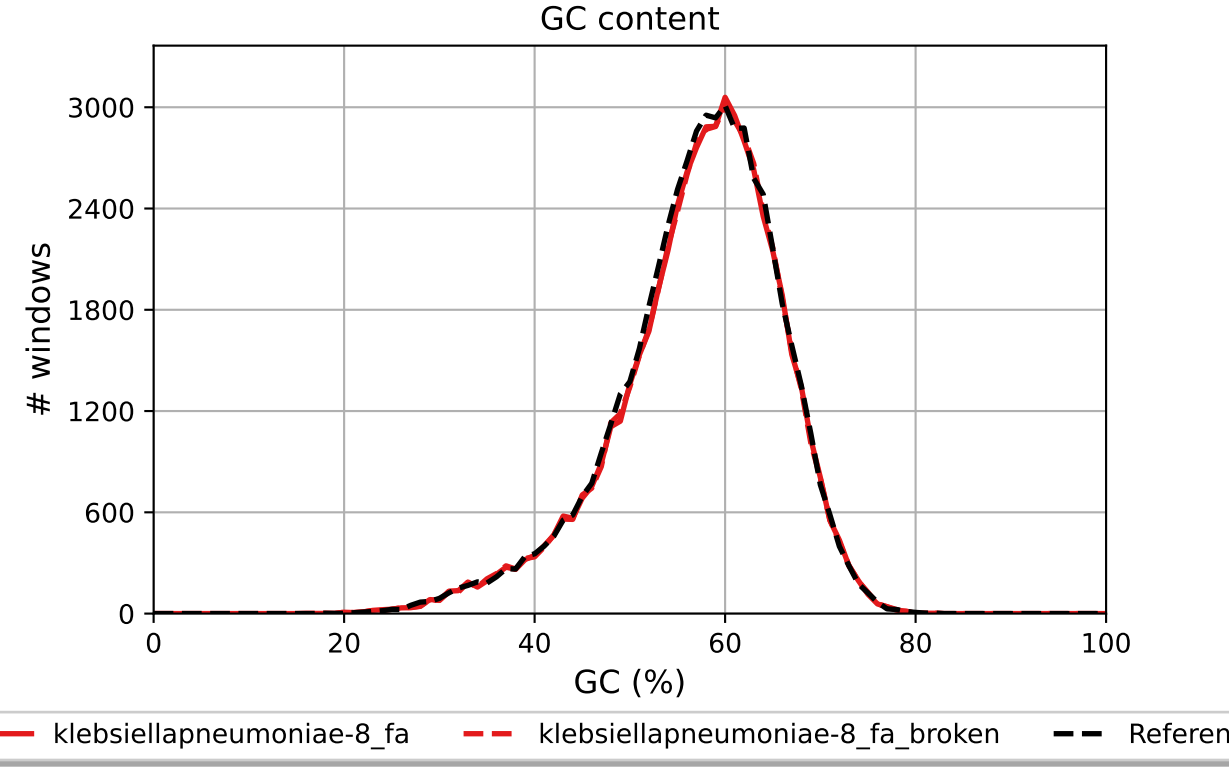
| | klebsiellapneumoniae-8_fa | klebsiellapneumoniae-8_fa_broken |
|---|---|---|
| # fully unaligned contigs | 14 | 15 |
| Fully unaligned length | 84781 | 85048 |
| # partially unaligned contigs | 47 | 52 |
| Partially unaligned length | 643437 | 643341 |
| # N's | 893 | 29 |

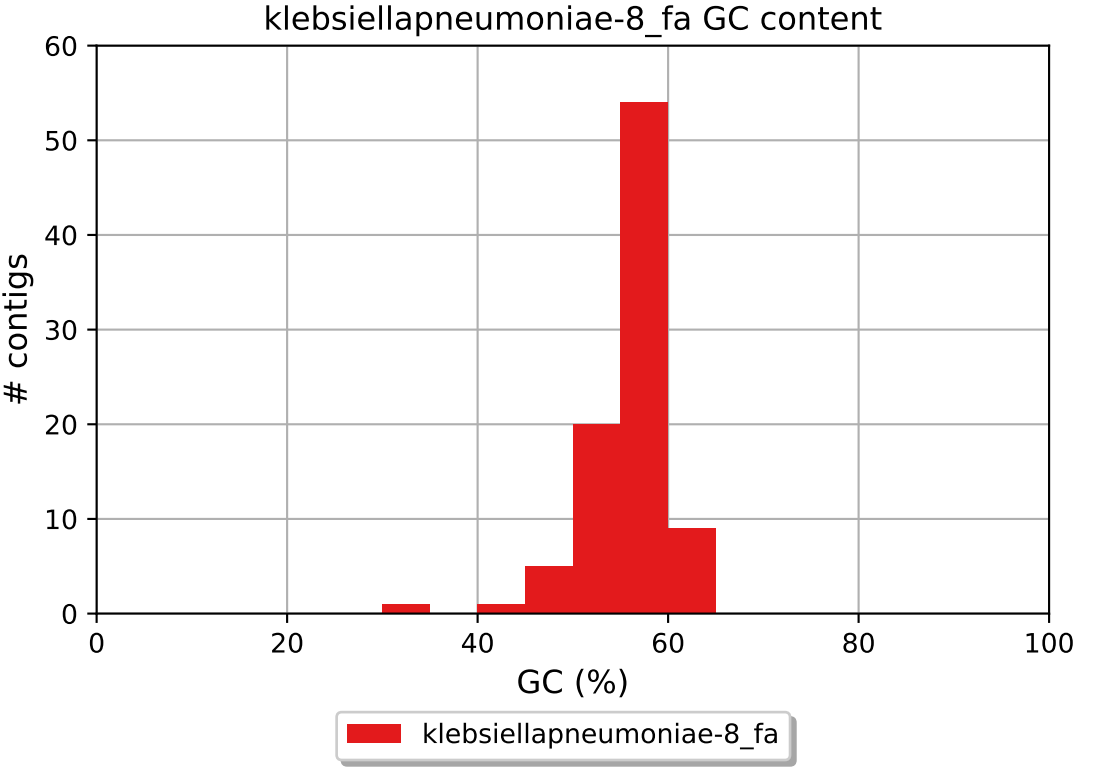
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

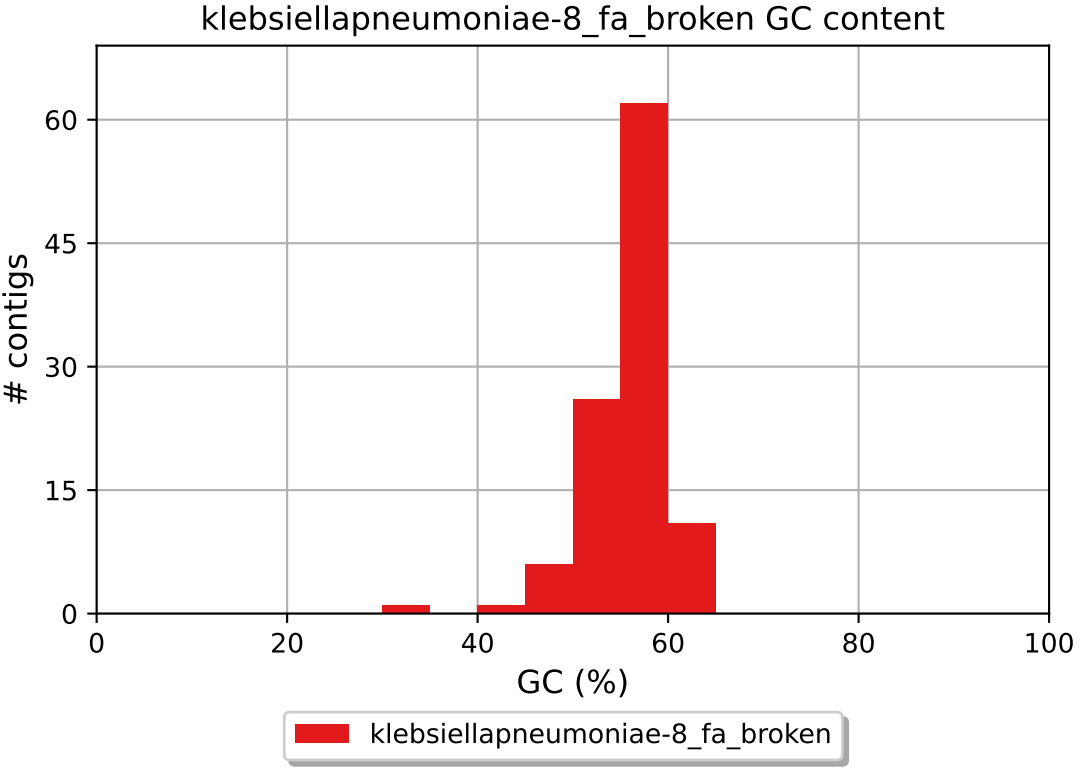

Nx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken

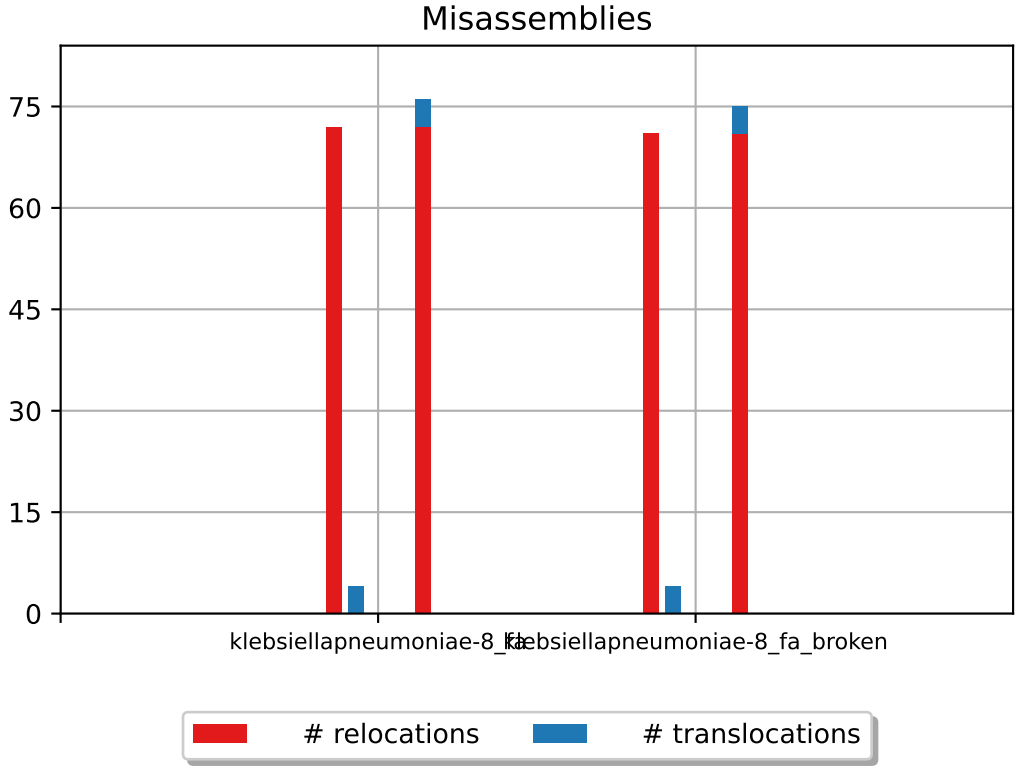

NGx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken

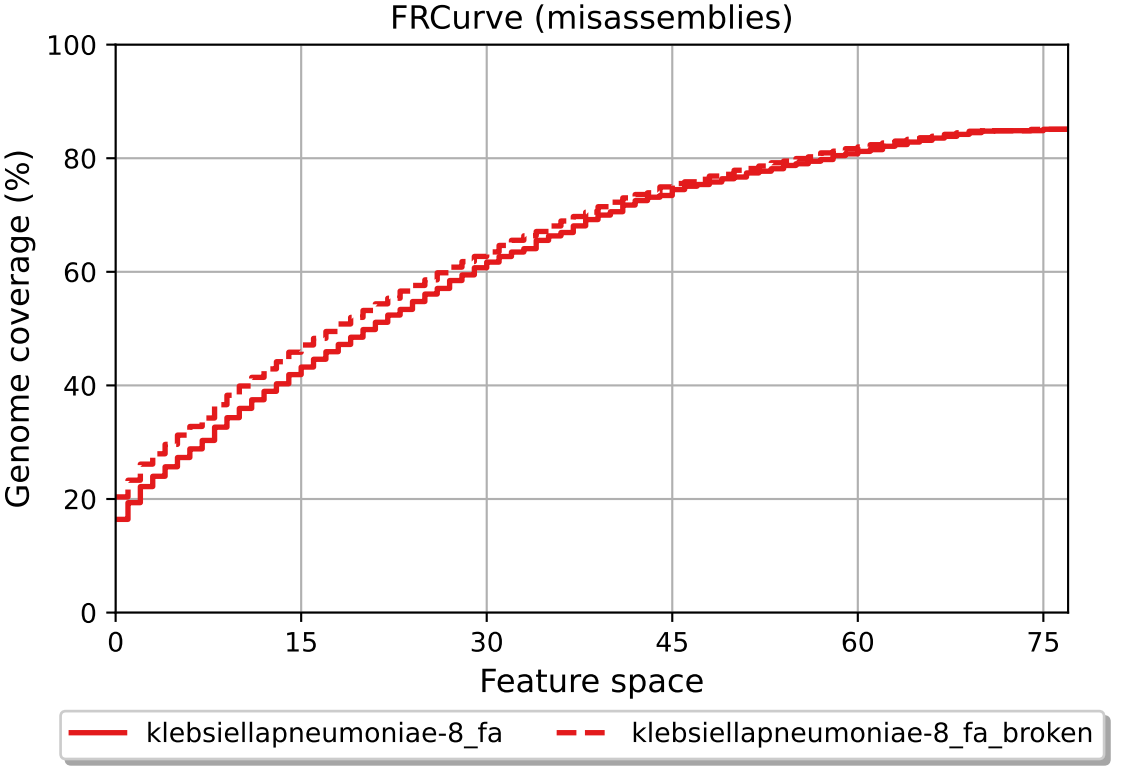

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
Contig index
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken
Referen

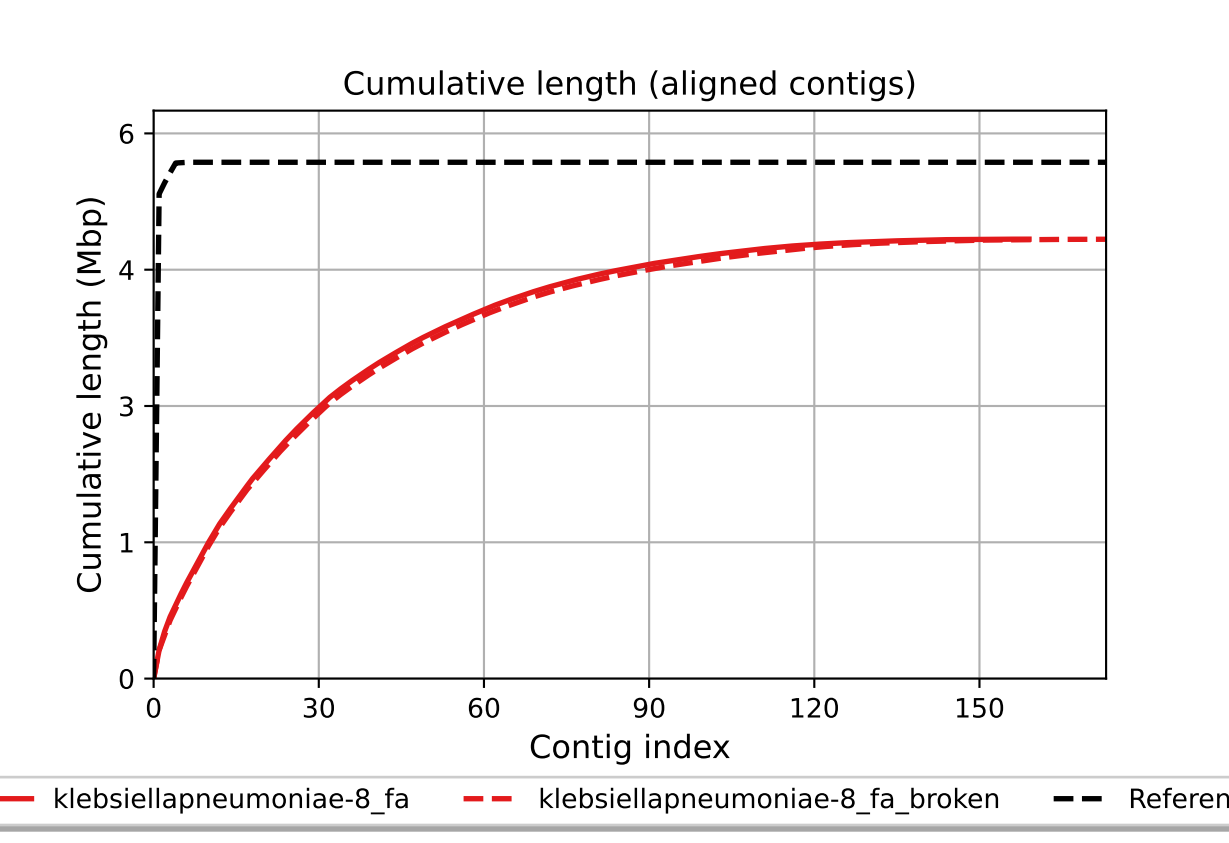

GC content
3000
2400
1800
1200
600
0
# windows
0
20
40
60
80
100
GC (%)
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken
Referen

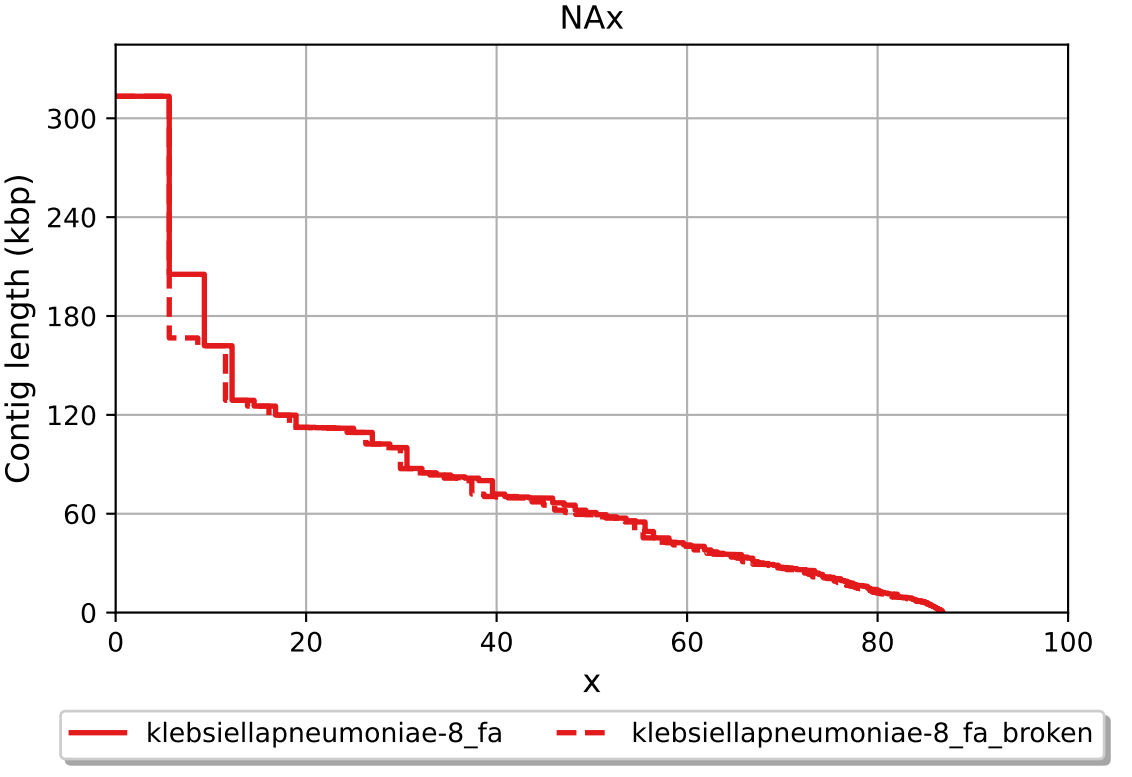

klebsiellapneumoniae-8_fa GC content
# contigs
GC (%)
0
10
20
30
40
50
60
0
20
40
60
80
100
klebsiellapneumoniae-8_fa

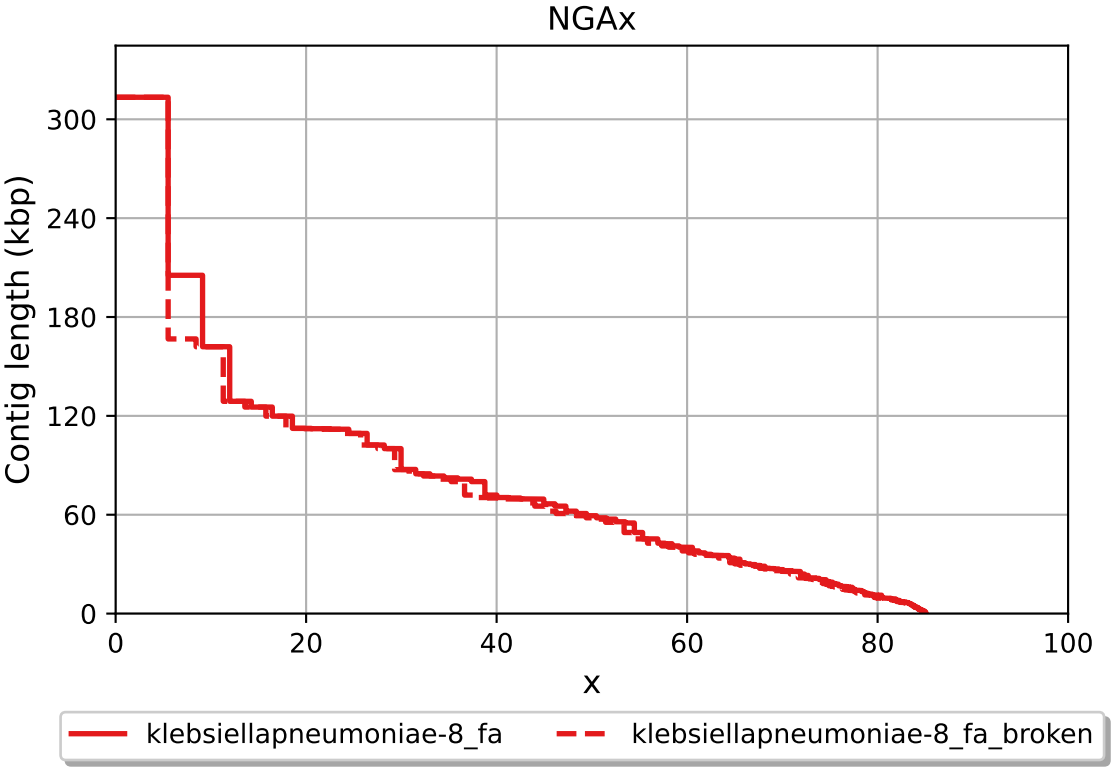

klebsiellapneumoniae-8_fa_broken GC content
# contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
klebsiellapneumoniae-8_fa_broken

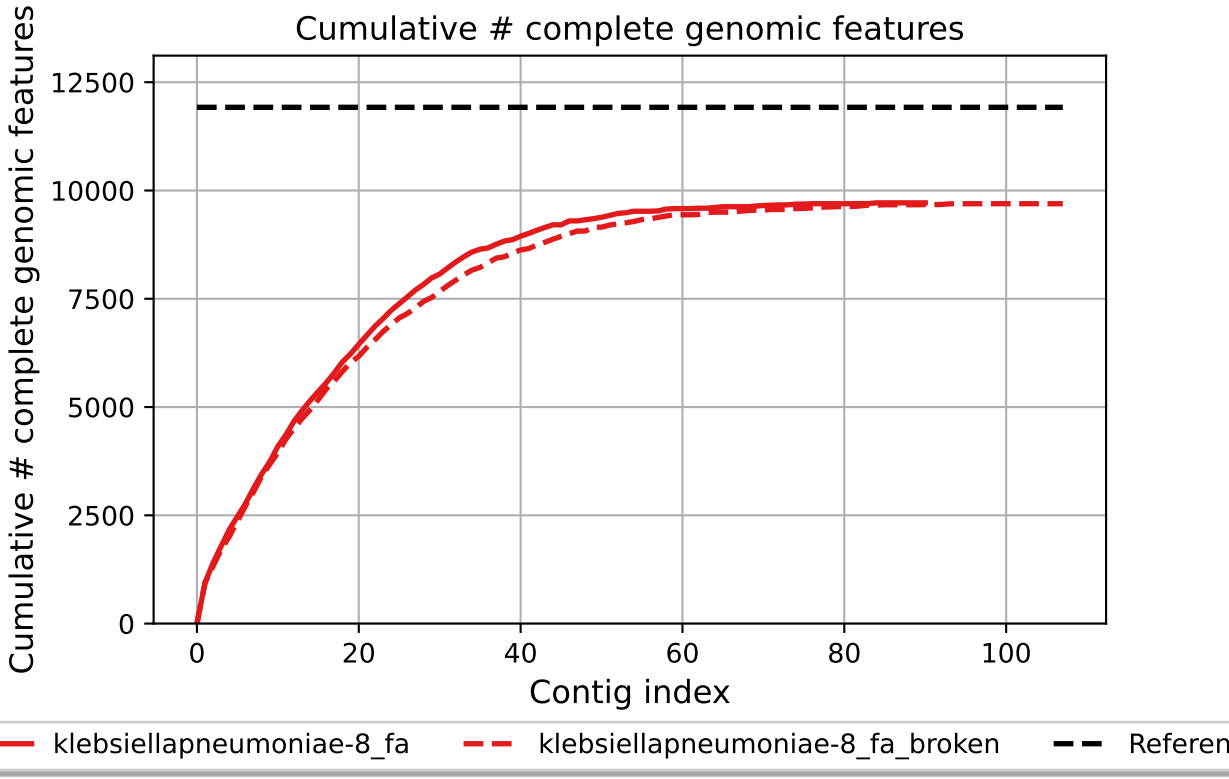

Misassemblies
75
60
45
30
15
0
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken
# relocations
# translocations

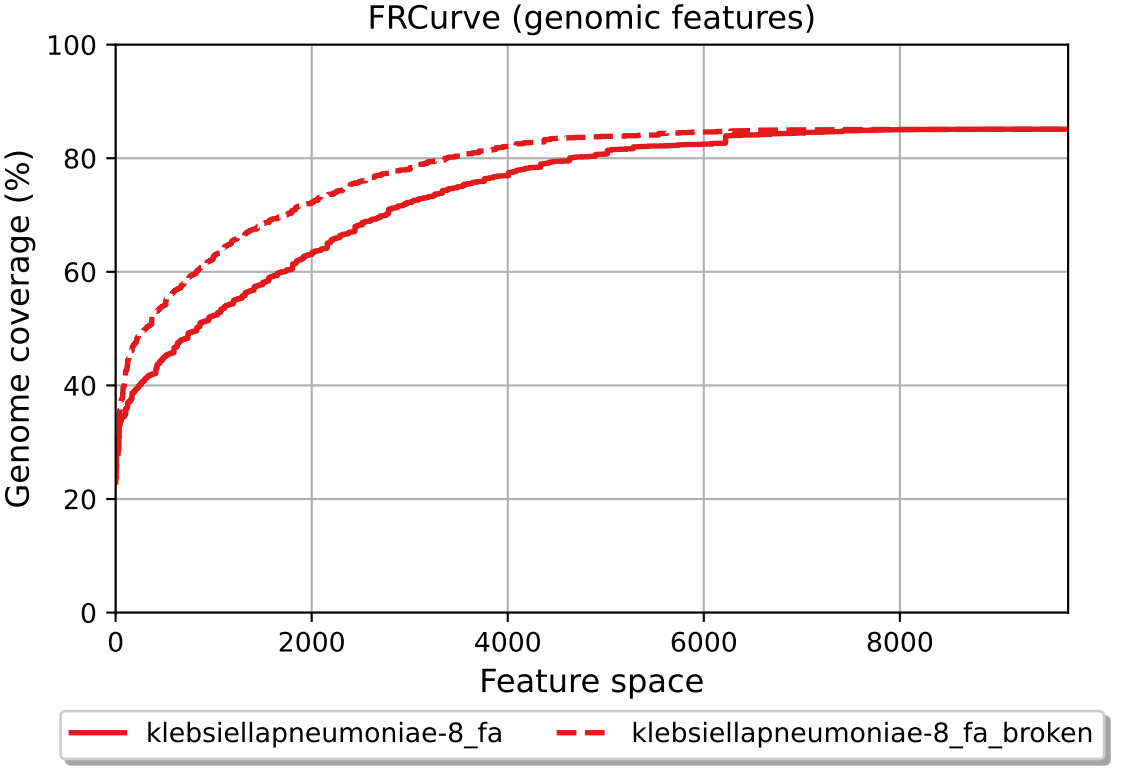

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
75
Feature space
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken

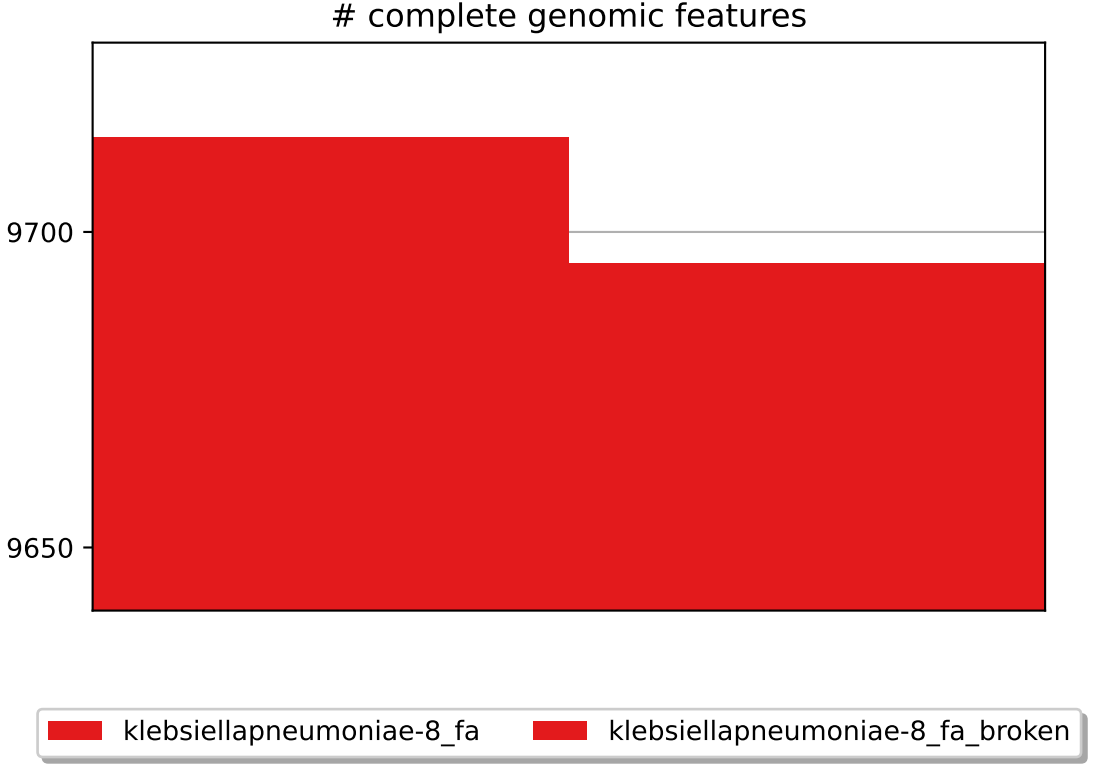

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
30
60
90
120
150
Contig index
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken
Referen

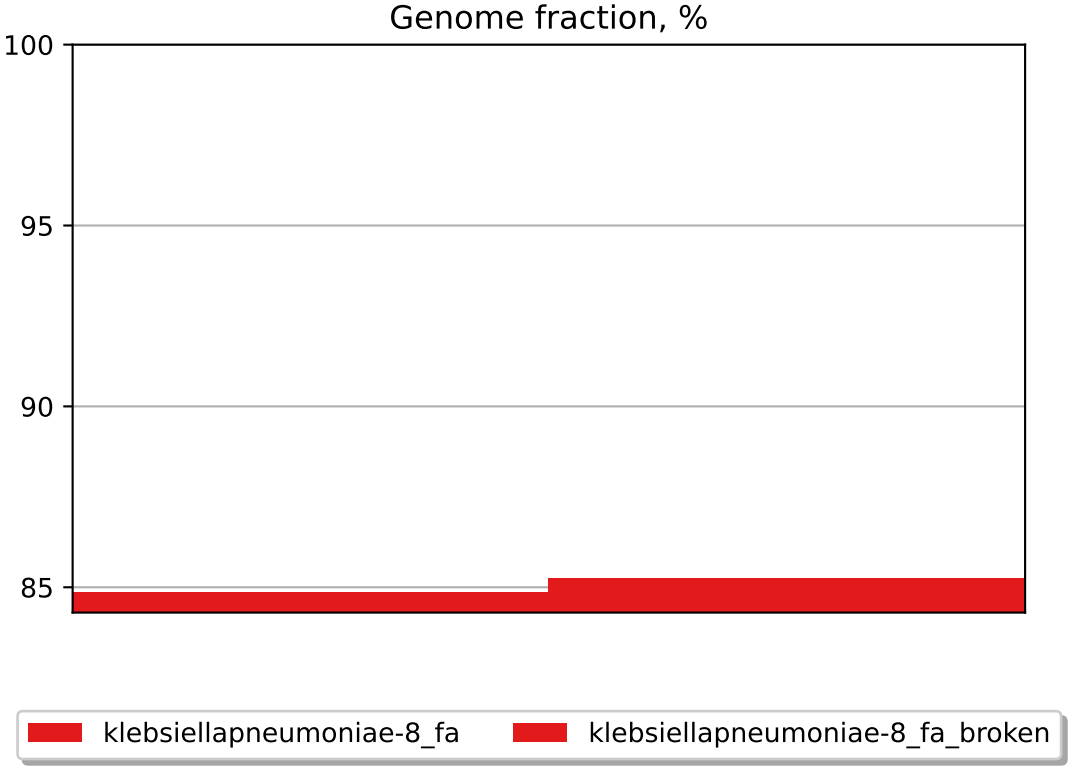

NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken


Cumulative # complete genomic features
Cumulative # complete genomic features
12500
10000
7500
5000
2500
0
0
20
40
60
80
100
Contig index
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken
Referen


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
2000
4000
6000
8000
Feature space
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken


# complete genomic features
9700
9650
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken


Genome fraction, %
100
95
90
85
klebsiellapneumoniae-8_fa
klebsiellapneumoniae-8_fa_broken