Psq_fq_fp1_clmp_fp2_fqscrn_rprd_jfsh
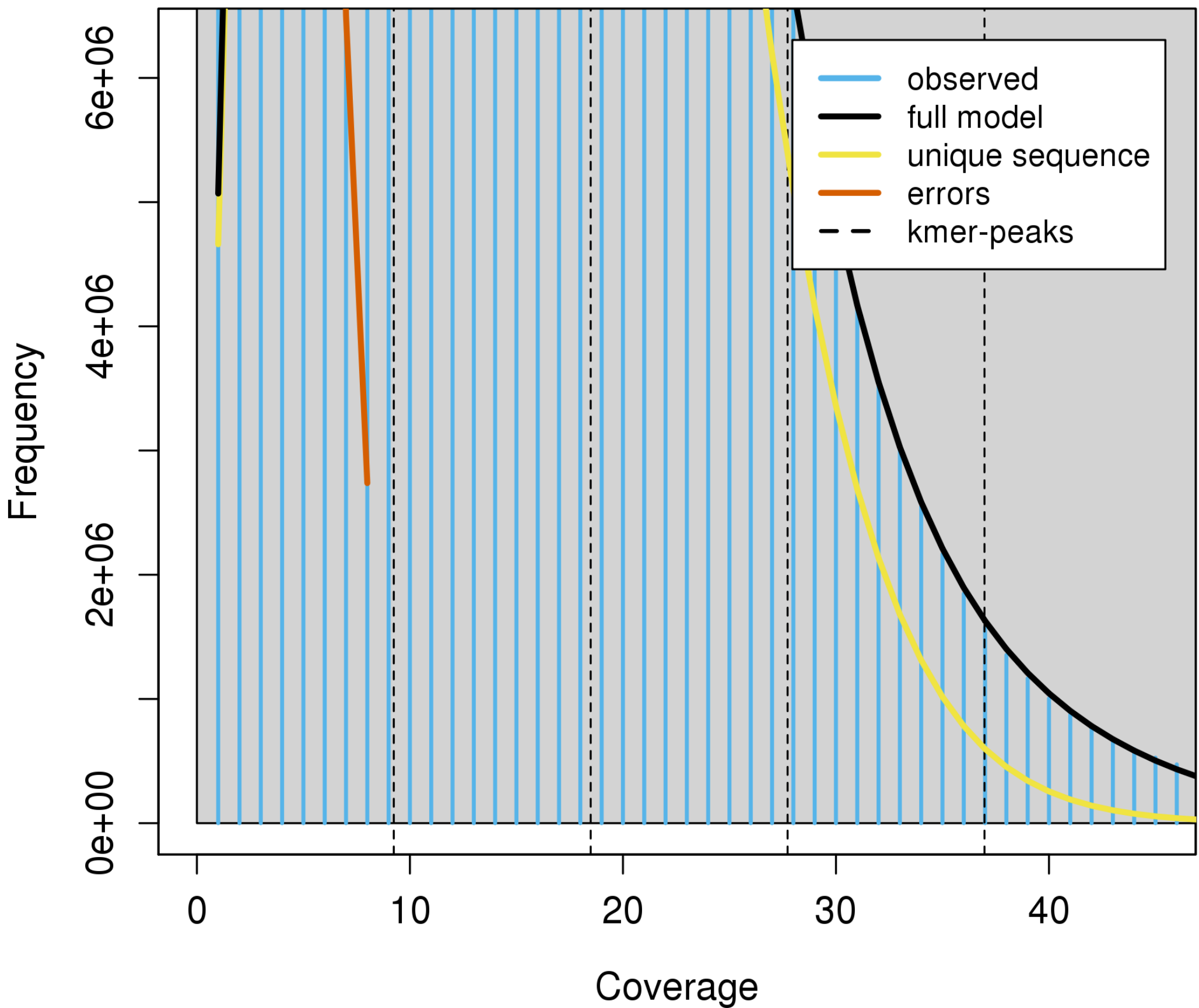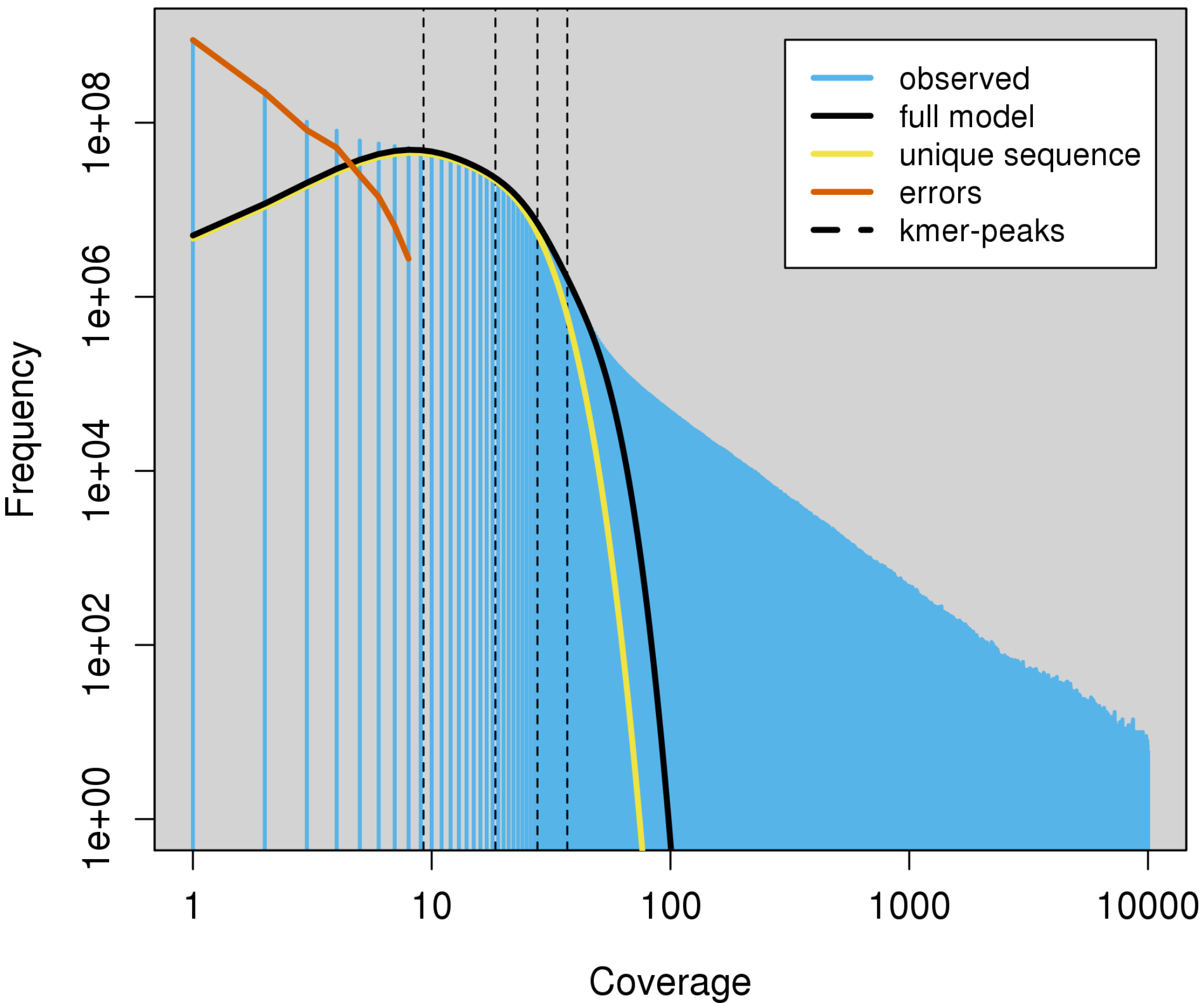
GenomeScope Profile

len:724,828,529bp uniq:69.9%
aa:97.1% ab:2.87%
kcov:9.24 err:0.708% dup:1.27 k:21 p:2

GenomeScope Profile

len:724,828,529bp uniq:69.9%
aa:97.1% ab:2.87%
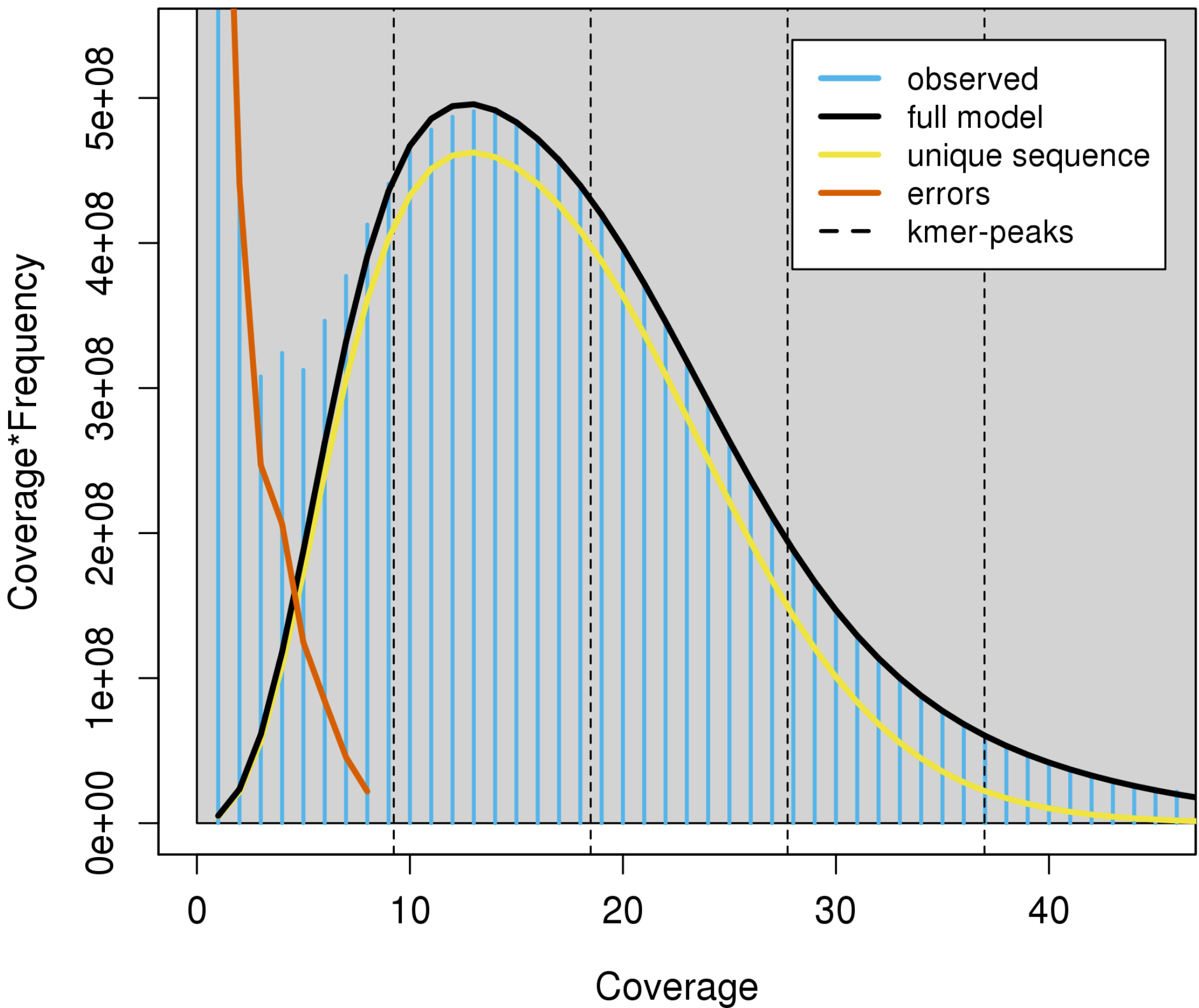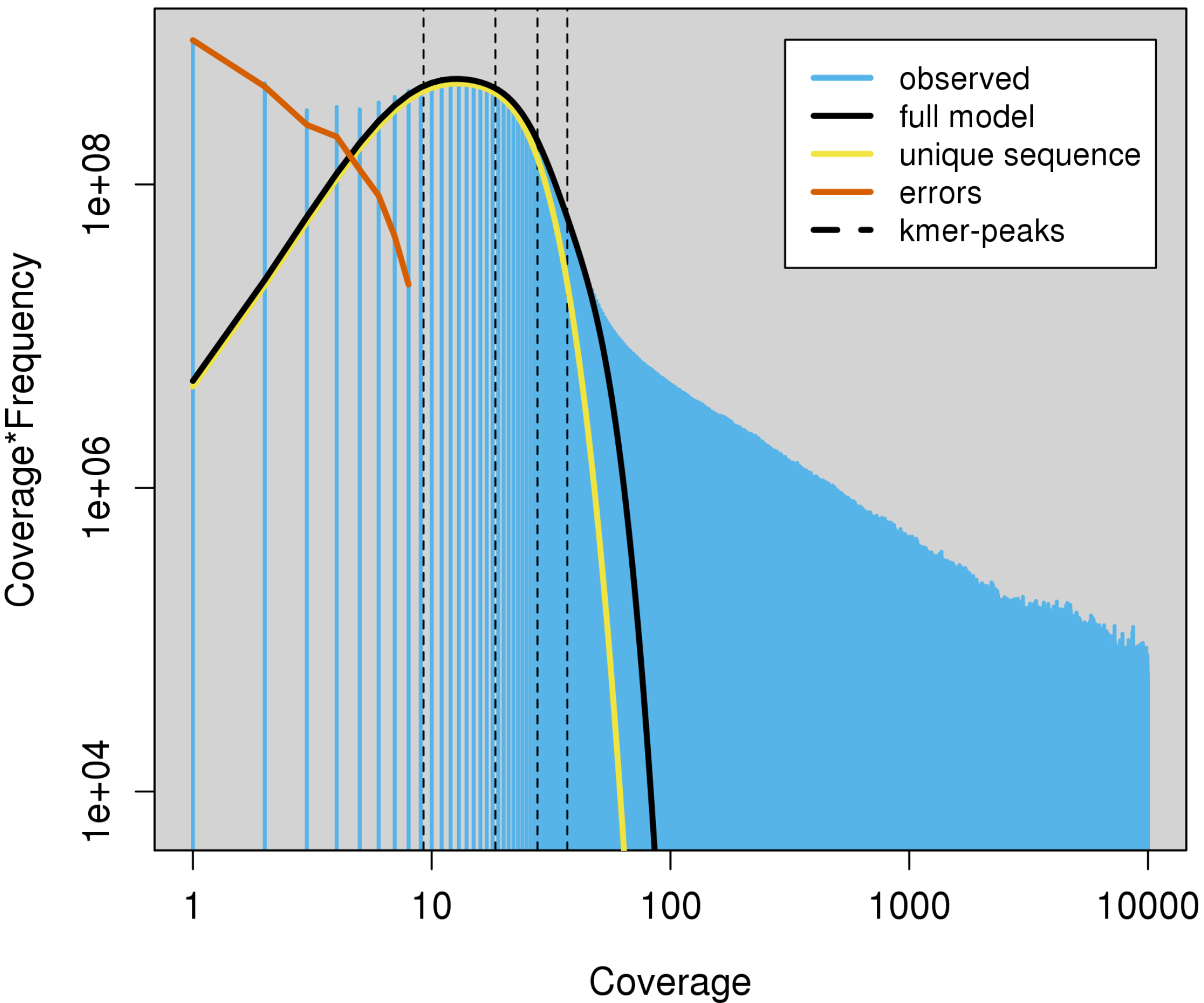kcov:9.24 err:0.708% dup:1.27 k:21 p:2

GenomeScope Profile

len:724,828,529bp uniq:69.9%
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GenomeScope Profile

len:724,828,529bp uniq:69.9%
aa:97.1% ab:2.87%
kcov:9.24 err:0.708% dup:1.27 k:21 p:2

Results

```
GenomeScope version 2.0
input file = user_uploads/007aRKrRMe59JUDgGHKk
output directory = user_data/007aRKrRMe59JUDgGHKk
p = 2
k = 21

property                     min              max
Homozygous (aa)              96.4631%         97.7971%
Heterozygous (ab)            2.20286%         3.53694%
Genome Haploid Length        664,252,616 bp   724,828,529 bp
Genome Repeat Length         200,186,444 bp   218,442,265 bp
Genome Unique Length         464,066,171 bp   506,386,264 bp
Model Fit                    79.7202%         99.1775%
Read Error Rate              0.707981%        0.707981%
```

Model

```
Formula: y_transform ~ x^transform_exp * length * predict2_0(r1, k, d,
    kmercov, bias, x)

Parameters:
          Estimate Std. Error t value Pr(>|t|)
d        8.076e-02  5.193e-03  15.552  <2e-16 ***
r1       2.870e-02  3.335e-03   8.605  <2e-16 ***
kmercov  9.243e+00  2.015e-01  45.862  <2e-16 ***
bias     1.274e+00  1.461e-01   8.720  <2e-16 ***
length   5.269e+08  4.729e+06 111.416  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1464000 on 1995 degrees of freedom

Number of iterations to convergence: 19
Achieved convergence tolerance: 1.49e-08
```

View analysis later

Return to view your results at any time:

http://genomescope.org/genomescope2.0/analysis.php?code=0O7aRKrRMe59JUDgGHKk

Progress

starting

round 0 trimming to 3 trying 2p peak model... converged. score: 16801575251641252

round 1 trimming to 8 trying 2p peak model... converged. score: 4563412582448055

round 2 trimming to 13 trying 2p peak model... converged. score: 4525162010974586

round 3 trimming to 18 trying 2p peak model... converged. score: 5008041298377410

done