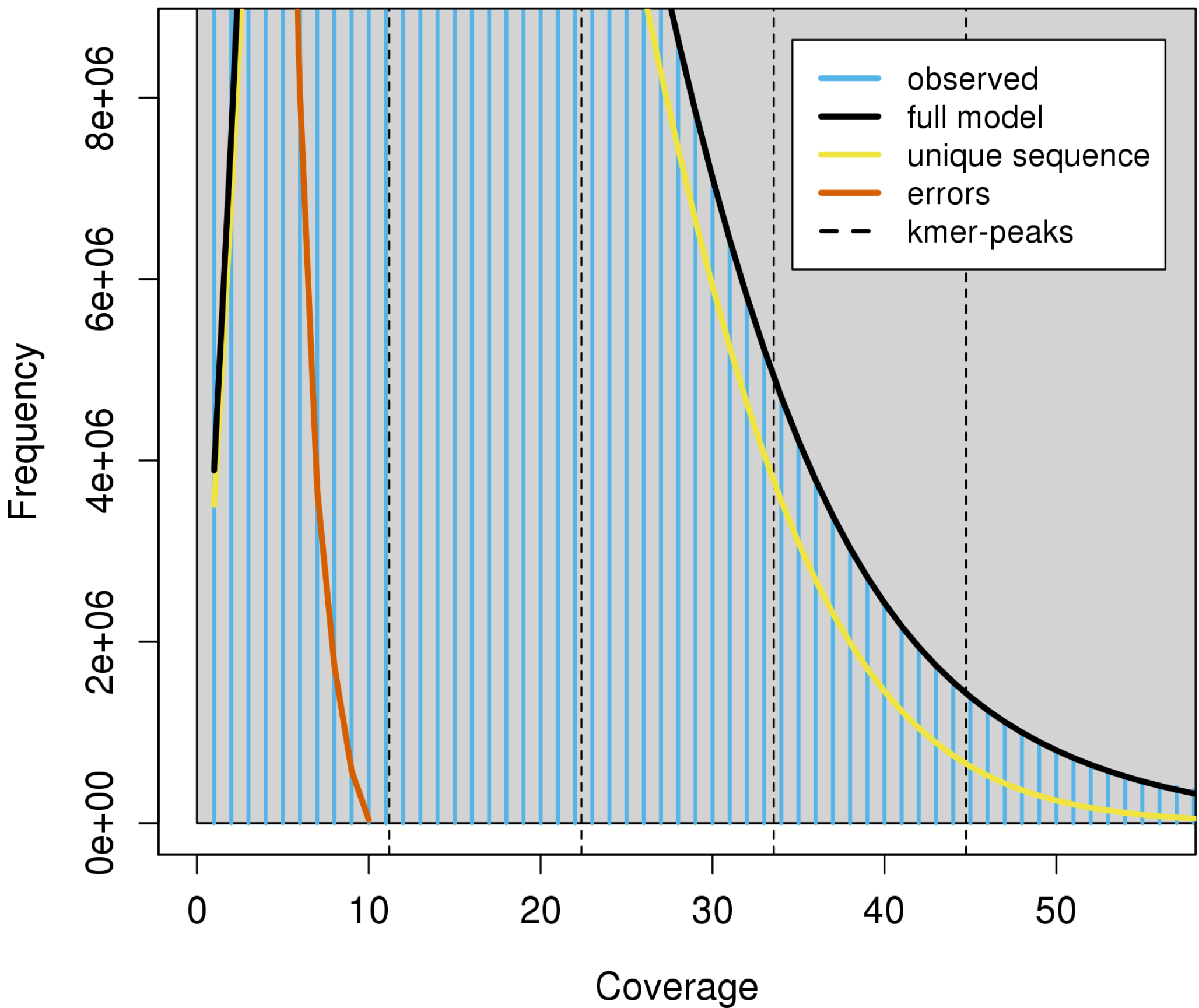# Pbb_fq_fp1_clmp_fp2_fqscrn_rprd_jfsh
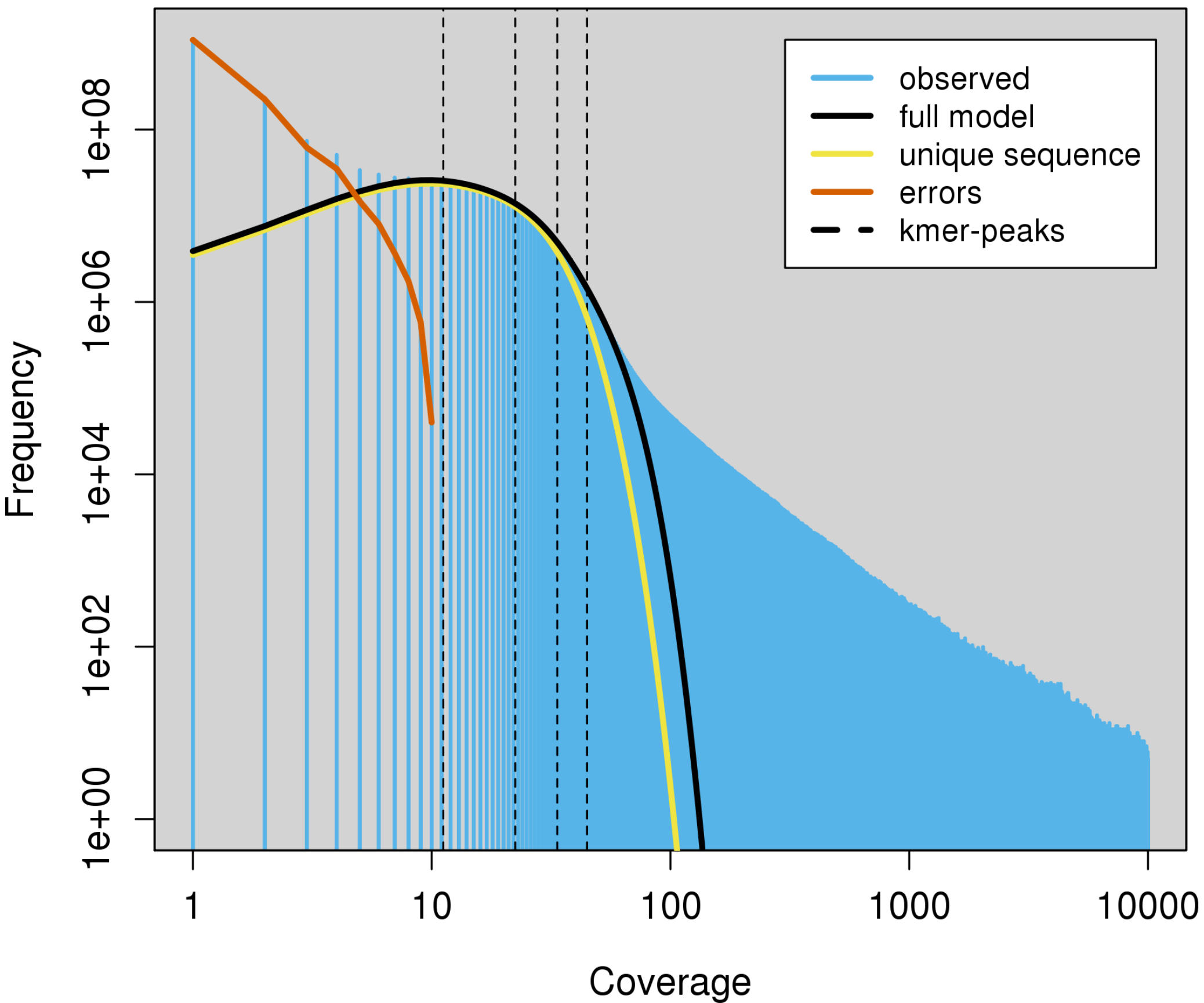
GenomeScope Profile

len:514,541,162bp uniq:70%
aa:97.5% ab:2.51%
kcov:11.2 err:0.789% dup:2.53 k:21 p:2
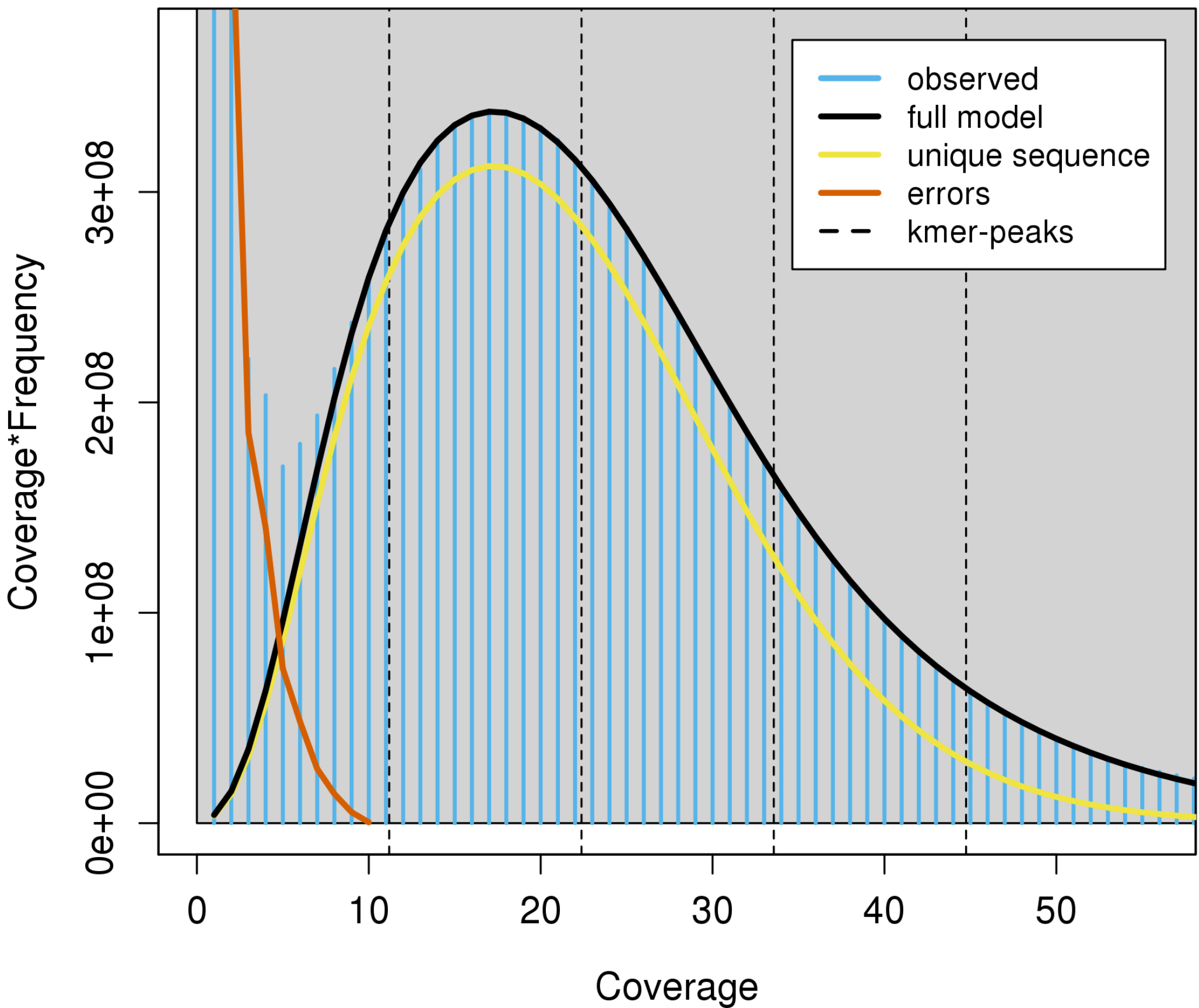

GenomeScope Profile

len:514,541,162bp uniq:70%
aa:97.5% ab:2.51%
kcov:11.2 err:0.789% dup:2.53 k:21 p:2

GenomeScope Profile

len:514,541,162bp uniq:70%
aa:97.5% ab:2.51%
kcov:11.2 err:0.789% dup:2.53 k:21 p:2

GenomeScope Profile

len:514,541,162bp uniq:70%
aa:97.5% ab:2.51%
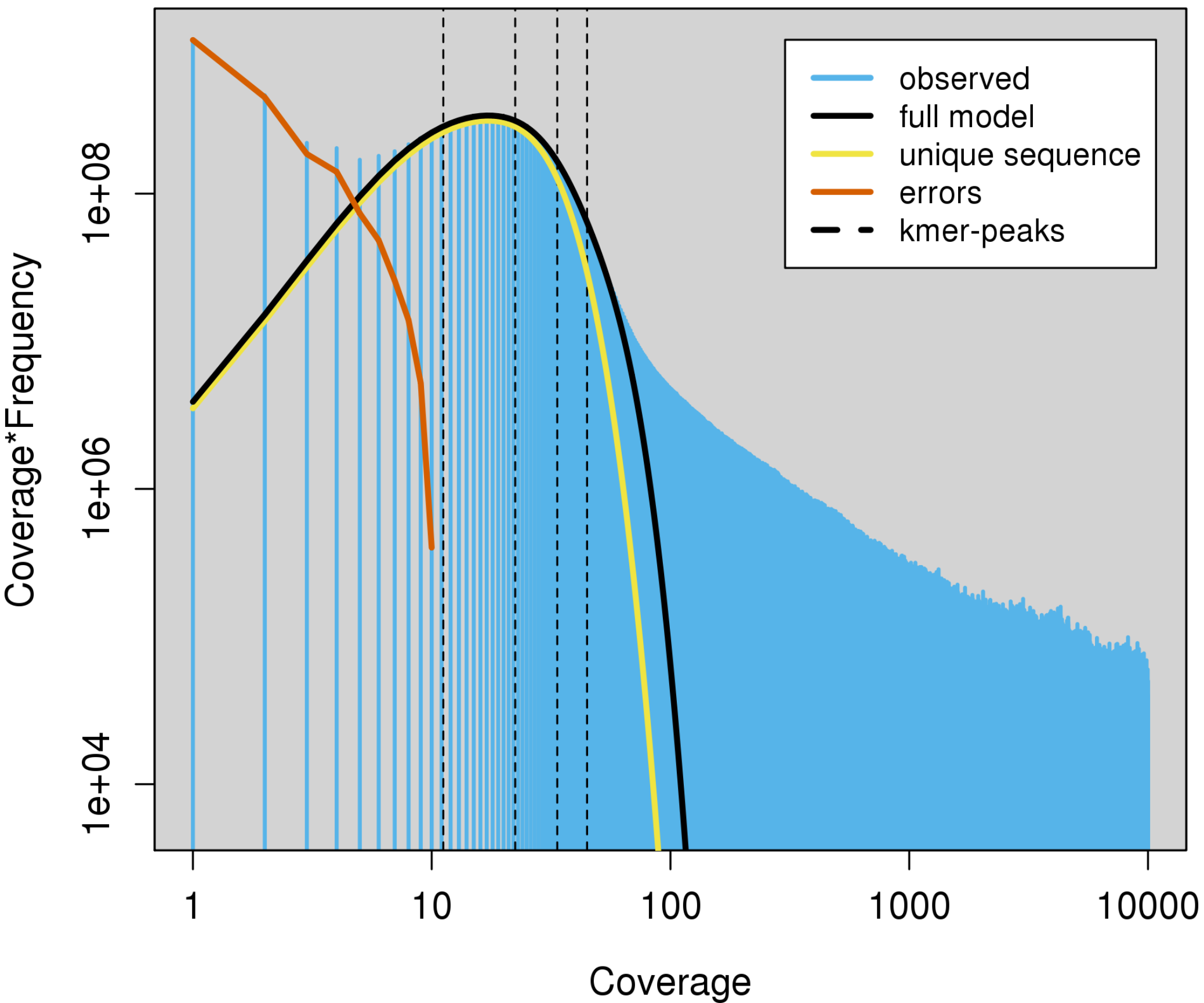**kcov:11.2 err:0.789% dup:2.53 k:21 p:2**

Results

```
GenomeScope version 2.0
input file = user_uploads/ODJXe1HpeNXrGSQULxn3
output directory = user_data/ODJXe1HpeNXrGSQULxn3
p = 2
k = 21

property                 min              max
Homozygous (aa)          97.3556%         97.6324%
Heterozygous (ab)        2.3676%          2.64441%
Genome Haploid Length    493,648,332 bp   514,541,162 bp
Genome Repeat Length     148,212,888 bp   154,485,748 bp
Genome Unique Length     345,435,444 bp   360,055,414 bp
Model Fit                83.1216%         99.4707%
Read Error Rate          0.78907%         0.78907%
```

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         9.819e-02  4.175e-03   23.52   <2e-16 ***
r1        2.506e-02  6.920e-04   36.21   <2e-16 ***
kmercov   1.119e+01  1.159e-01   96.51   <2e-16 ***
bias      2.530e+00  1.321e-01   19.15   <2e-16 ***
length    3.910e+08  5.147e+06   75.96   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1134000 on 1995 degrees of freedom

Number of iterations to convergence: 36
Achieved convergence tolerance: 1.49e-08
```

View analysis later

Return to view your results at any time:

Progress

starting

round 0 trimming to 5 trying 2p peak model... converged. score: 3567796552891662

round 1 trimming to 10 trying 2p peak model... converged. score: 2618662311288935

round 2 trimming to 15 trying 2p peak model... converged. score: 2639868038478599

round 3 trimming to 20 trying 2p peak model... converged. score: 2477156870641636

done