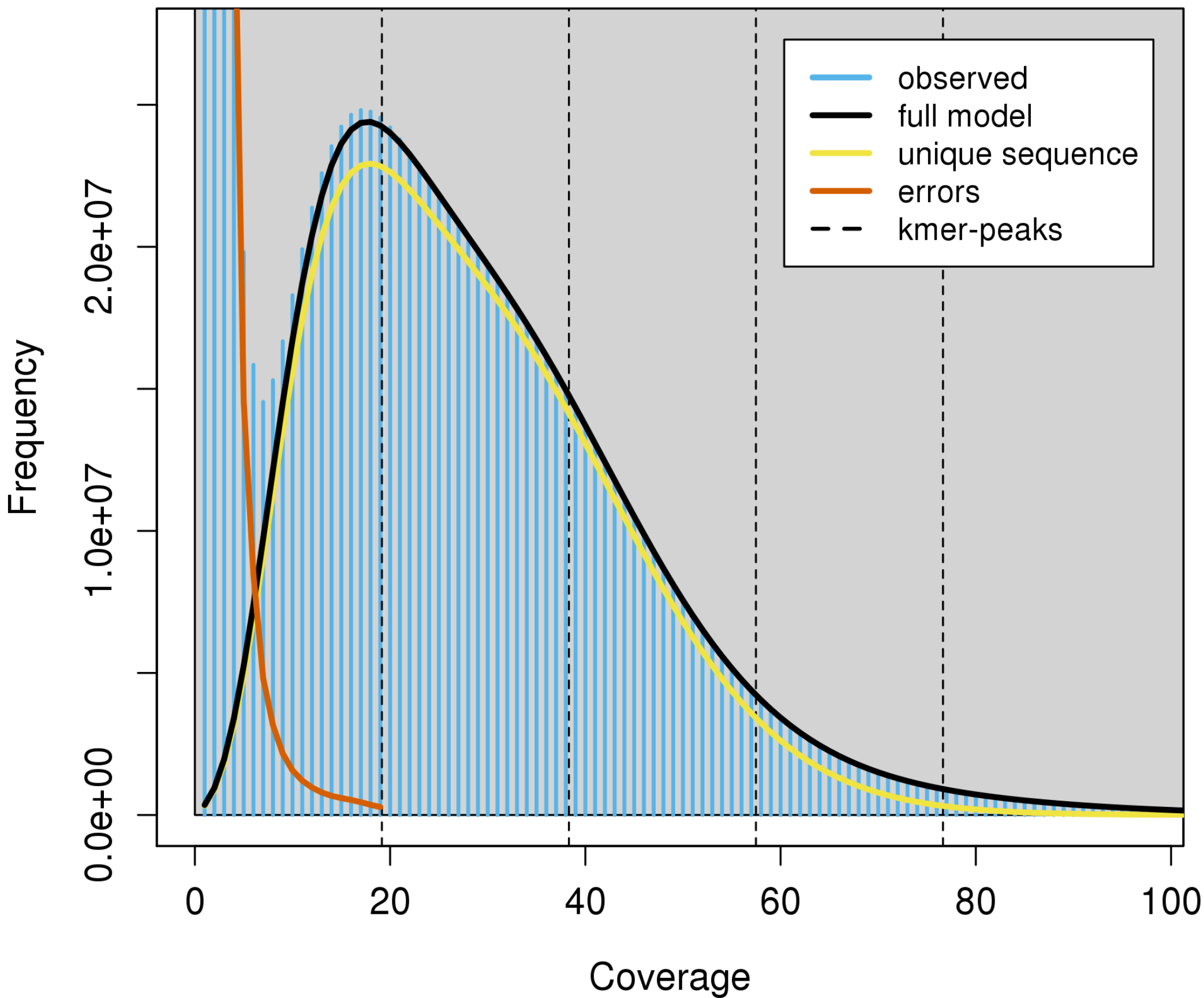Dar_fq_fp1_clmp_fp2_fqscrn_rprd_jfsh
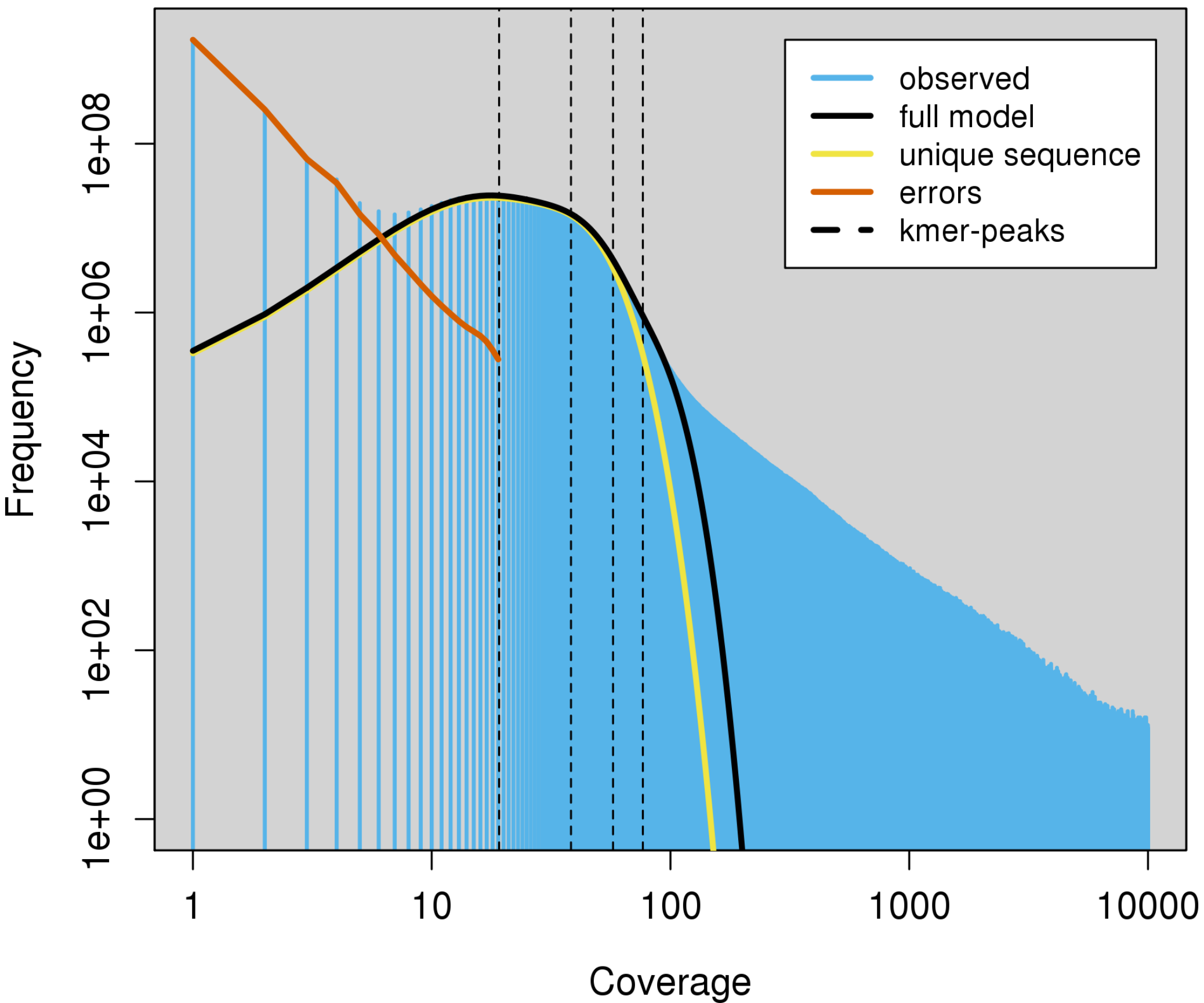
GenomeScope Profile

len:781,687,328bp uniq:75.7%
aa:97.9% ab:2.11%
kcov:19.2 err:0.433% dup:3.11 k:21 p:2

GenomeScope Profile

len:781,687,328bp uniq:75.7%
aa:97.9% ab:2.11%
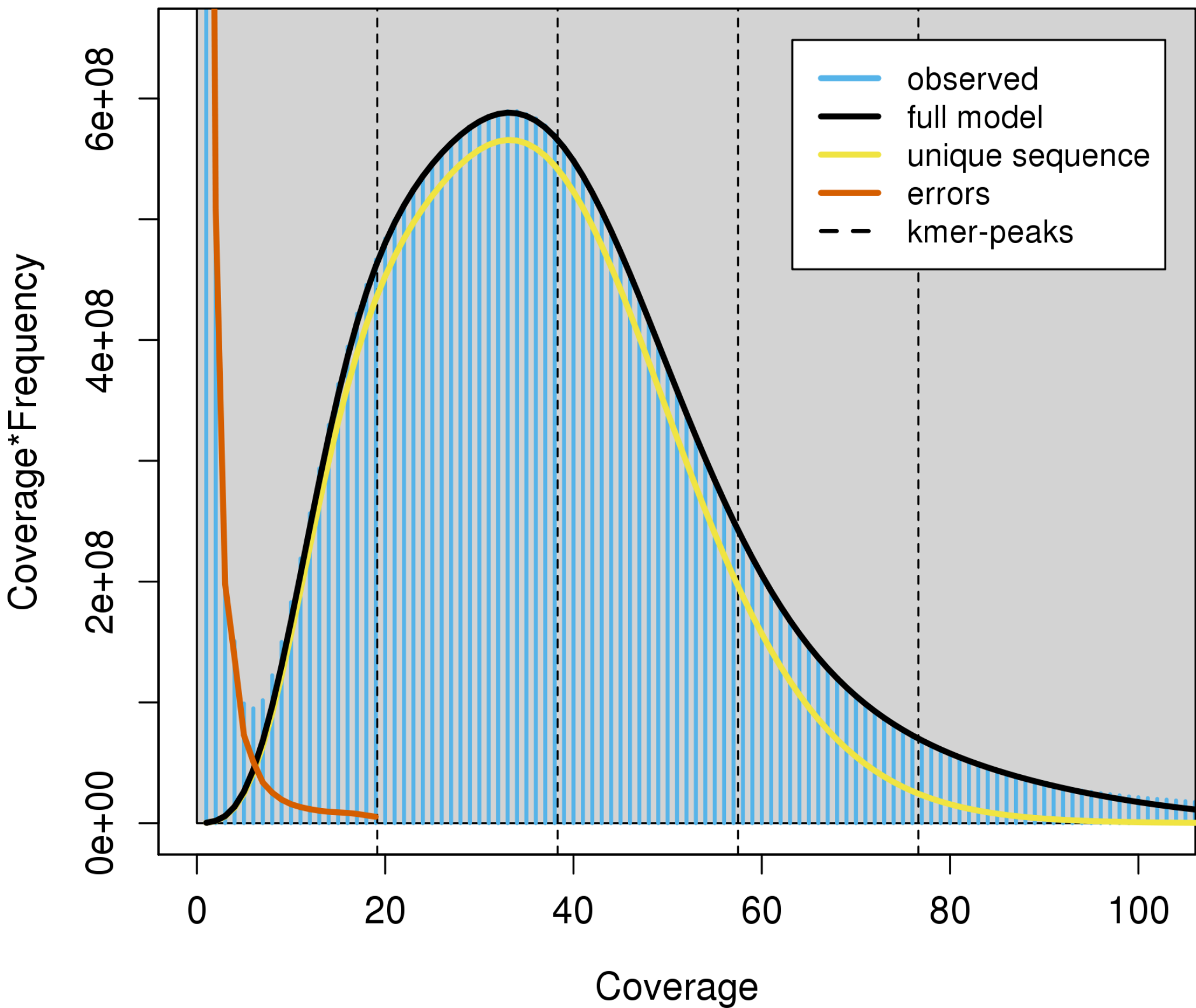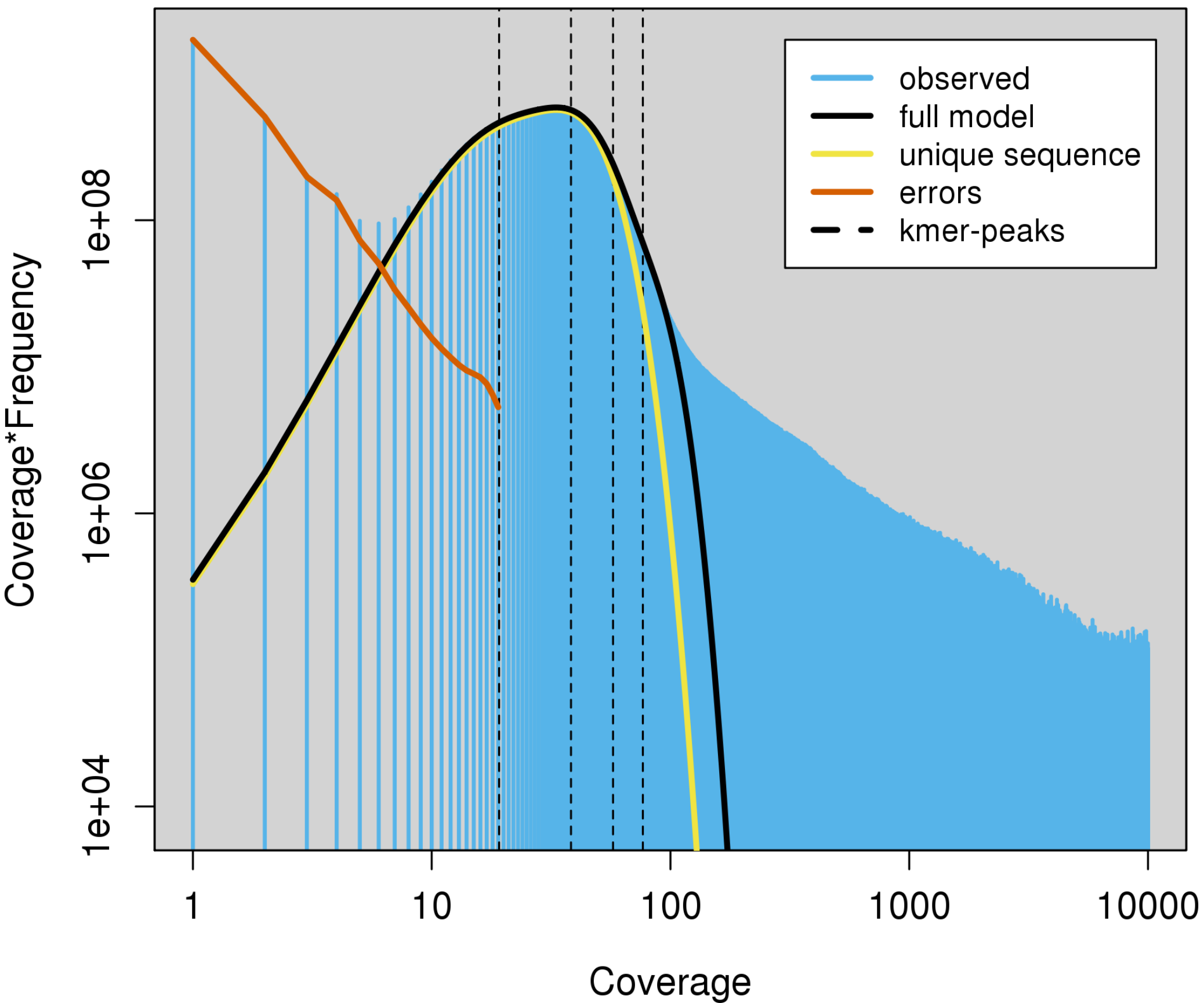kcov:19.2 err:0.433% dup:3.11 k:21 p:2

GenomeScope Profile

len:781,687,328bp uniq:75.7%
aa:97.9% ab:2.11%
kcov:19.2 err:0.433% dup:3.11 k:21 p:2

GenomeScope Profile

len:781,687,328bp uniq:75.7%
aa:97.9% ab:2.11%
kcov:19.2 err:0.433% dup:3.11 k:21 p:2

Results

```
GenomeScope version 2.0
input file = user_uploads/XpLyoyXZWdV8cSlB6VfW
output directory = user_data/XpLyoyXZWdV8cSlB6VfW
p = 2
k = 21

property                  min              max
Homozygous (aa)           97.8616%         97.9159%
Heterozygous (ab)         2.0841%          2.13843%
Genome Haploid Length     776,256,569 bp   781,687,328 bp
Genome Repeat Length      188,761,296 bp   190,081,887 bp
Genome Unique Length      587,495,273 bp   591,605,441 bp
Model Fit                 84.4545%         99.5482%
Read Error Rate           0.432528%        0.432528%
```

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        6.710e-02  1.281e-03   52.39   <2e-16 ***
r1       2.111e-02  1.358e-04  155.43   <2e-16 ***
kmercov  1.916e+01  3.339e-02  573.75   <2e-16 ***
bias     3.111e+00  3.904e-02   79.69   <2e-16 ***
length   6.319e+08  1.302e+06  485.26   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2325000 on 1995 degrees of freedom

Number of iterations to convergence: 9
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=XpLyoyXZWdV8cSlB6VfW

Progress

starting

round 0 trimming to 6 trying 2p peak model... converged. score: 12252747151510026

round 1 trimming to 11 trying 2p peak model... converged. score: 11168693554045106

round 2 trimming to 16 trying 2p peak model... converged. score: 11053401202395214

round 3 trimming to 21 trying 2p peak model... converged. score: 11047279746645982

done