KG_A.japonica_k21_default
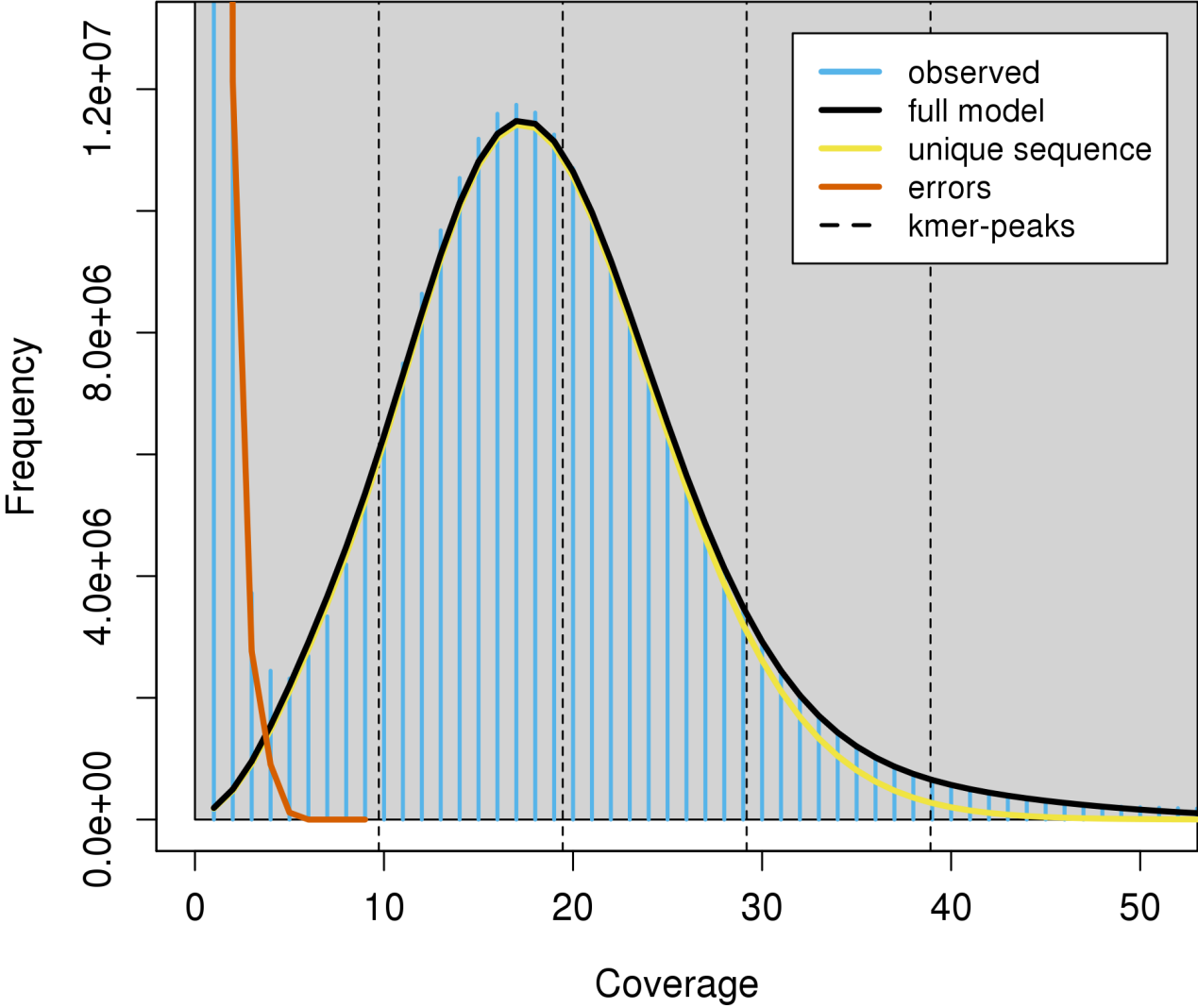
GenomeScope Profile
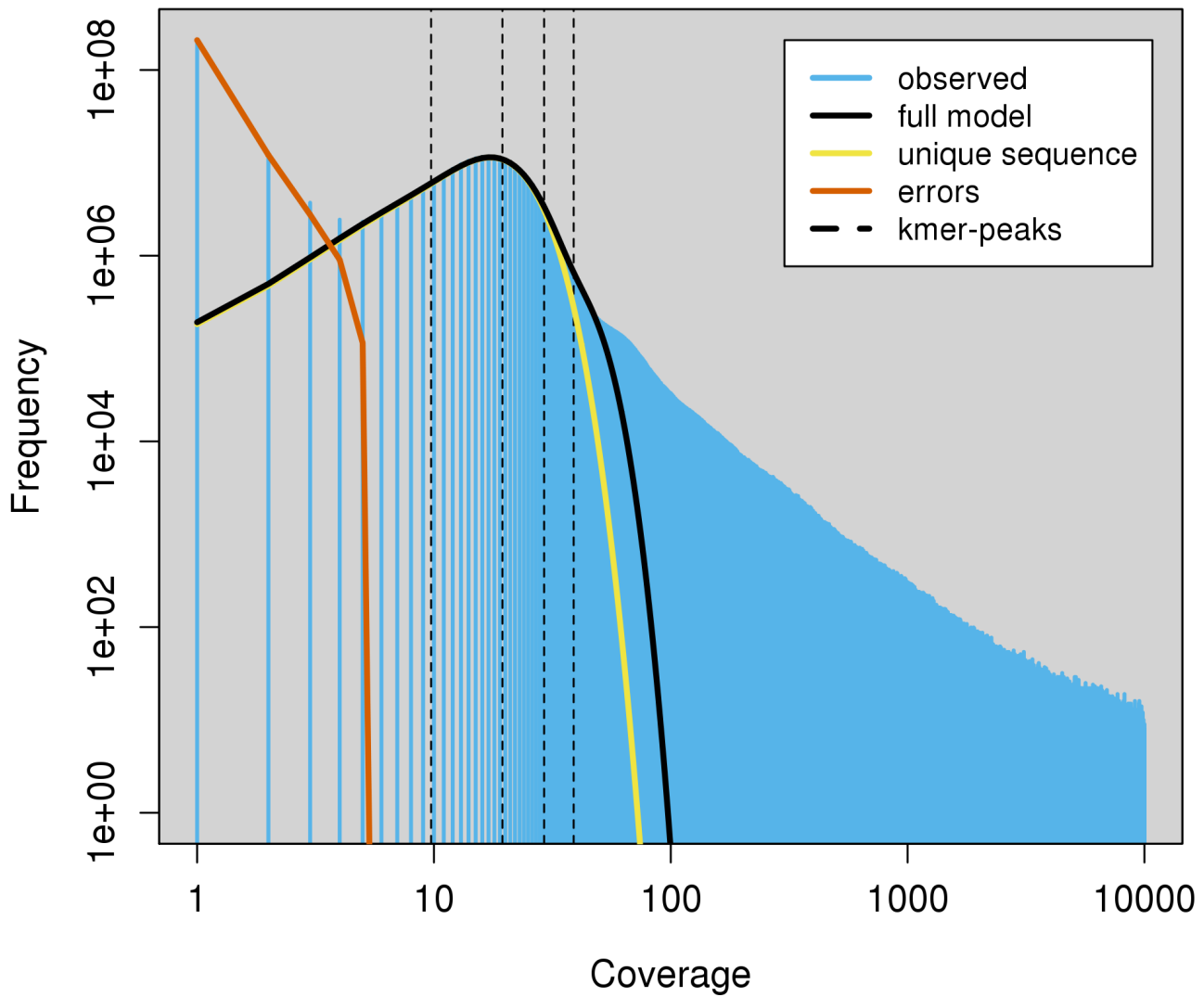
len:304,068,716bp uniq:63.3%
aa:99.6% ab:0.351%
kcov:9.73 err:0.202% dup:1.13 k:21 p:2

Legend:
- observed
- full model
- unique sequence
- errors
- kmer-peaks

Y-axis: Frequency
X-axis: Coverage

(user_data/pl28nXUll0povpWlov7F/linear_plot.png)

(user_data/pl28nXUll0povpWlov7F/log_plot.png)

GenomeScope Profile

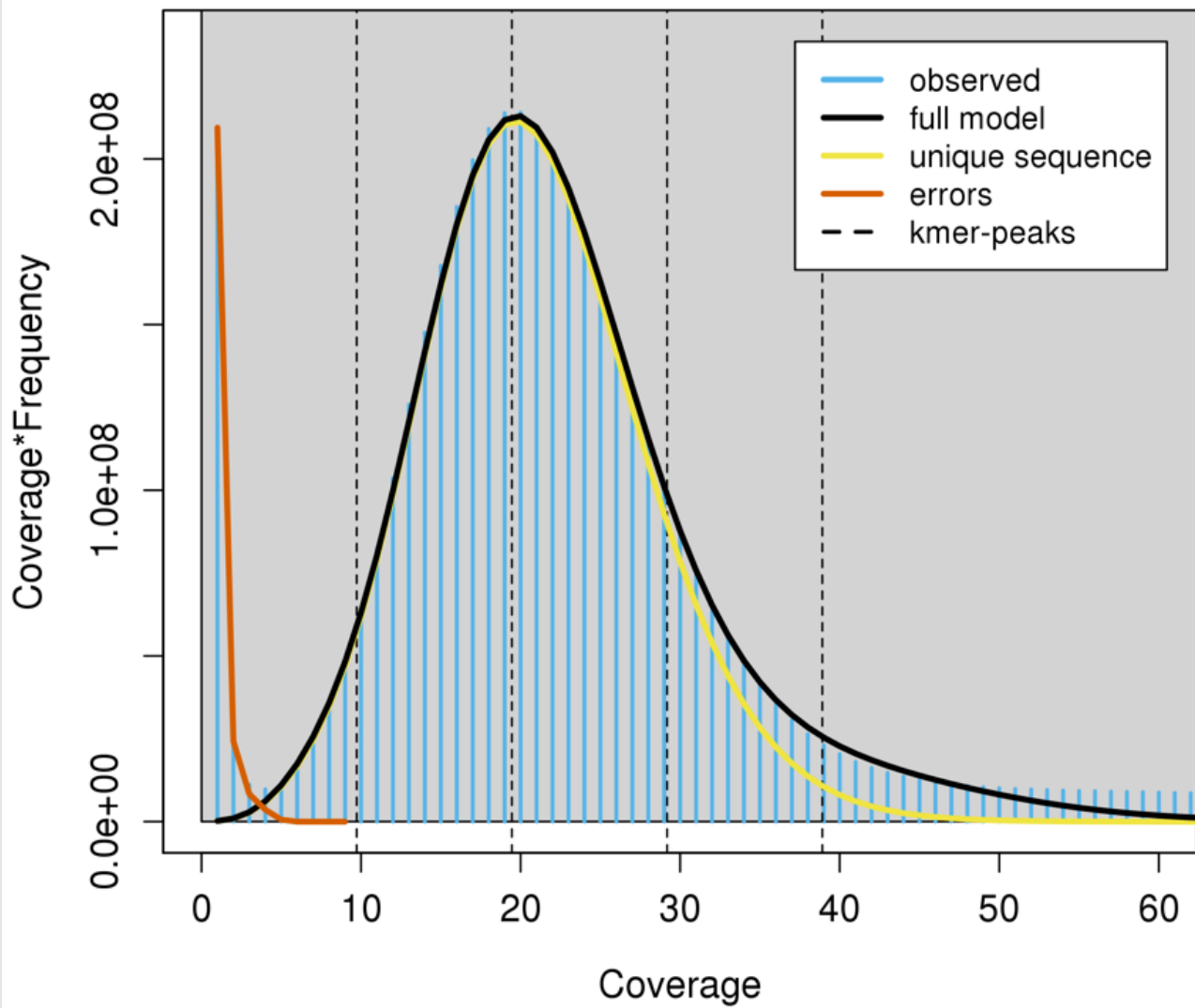**len:304,068,716bp uniq:63.3%**
aa:99.6% ab:0.351%
kcov:9.73 err:0.202% dup:1.13 k:21 p:2

(user_data/pI28nXUlI0povpWlov7F/transformed_linear_plot.png)
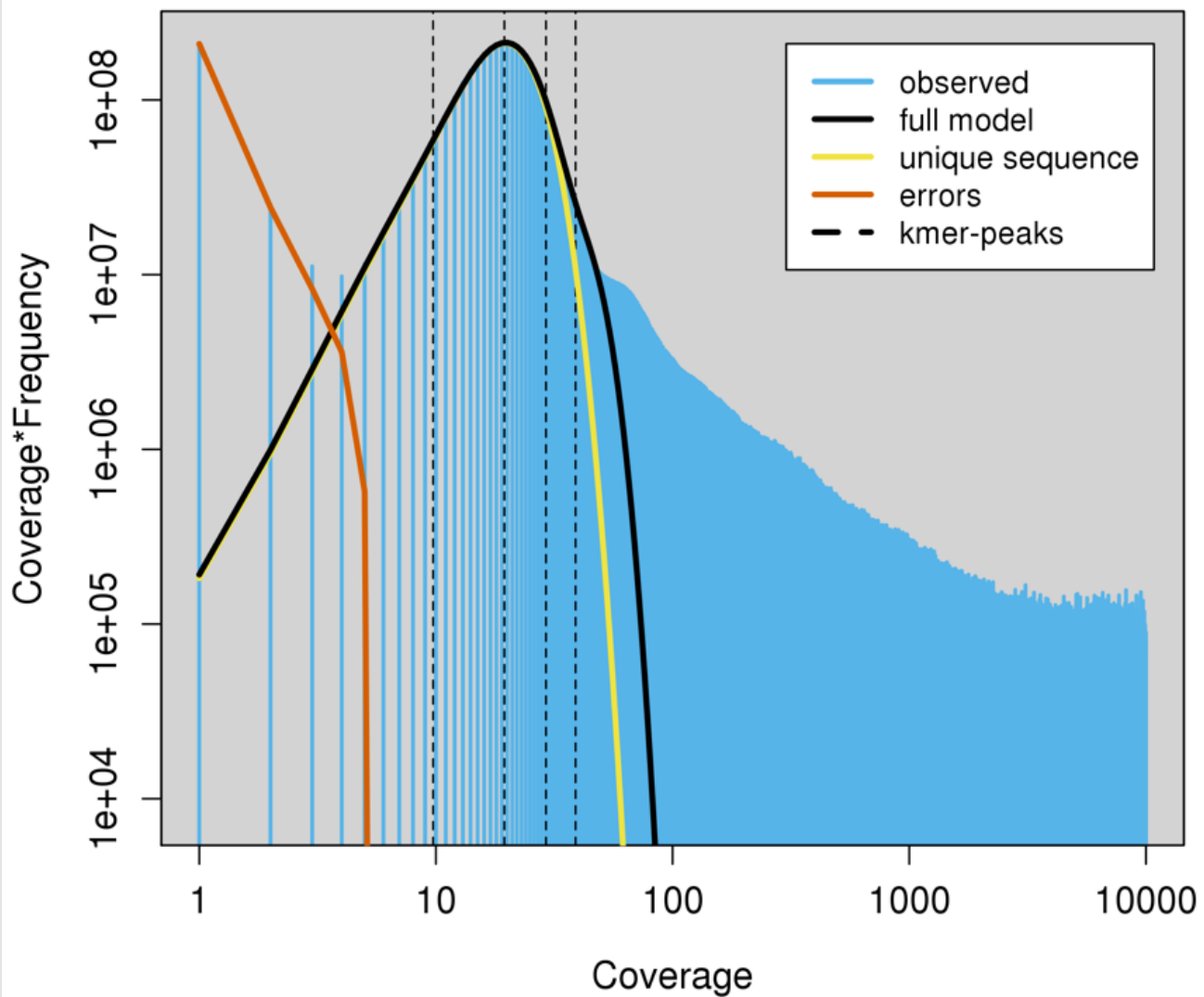
GenomeScope Profile

len:304,068,716bp uniq:63.3%
aa:99.6% ab:0.351%
kcov:9.73 err:0.202% dup:1.13 k:21 p:2

(user_data/pI28nXUll0povpWlov7F/transformed_log_plot.png)

Results

Model

```
GenomeScope version 2.0
input file = user_uploads/pI28nXUlI0povpWlov7F
output directory = user_data/pI28nXUlI0povpWlov7F
p = 2
k = 21

property                    min              max
Homozygous (aa)             98.367%          100%
Heterozygous (ab)           0%               1.63296%
Genome Haploid Length       281,591,179 bp   304,068,716 bp
Genome Repeat Length        103,295,487 bp   111,540,873 bp
Genome Unique Length        178,295,693 bp   192,527,843 bp
Model Fit                   68.4998%         98.0812%
Read Error Rate             0.201522%        0.201522%
```

```
Formula: y_transform ~ x^transform_exp * length * predict
    kmercov, bias, x)

Parameters:
          Estimate Std. Error t value Pr(>|t|)
d         4.847e-02  5.734e-03   8.454  <2e-16 ***
r1        3.512e-03  6.409e-03   0.548   0.584
kmercov   9.727e+00  1.867e-01  52.111  <2e-16 ***
bias      1.129e+00  1.219e-01   9.260  <2e-16 ***
length    1.946e+08  1.032e+07  18.857  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1

Residual standard error: 1083000 on 1995 degrees of freed

Number of iterations to convergence: 13
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=pI28nXUlI0povpWlov7F

Progress

starting

round 0 trimming to 4 trying 2p peak model... converged. score: 2411110707914454

round 1 trimming to 9 trying 2p peak model... converged. score: 2410503542144946

round 2 trimming to 14 trying 2p peak model... converged. score: 2202613830057960

round 3 trimming to 19 trying 2p peak model... converged. score: 2574506723647969

done