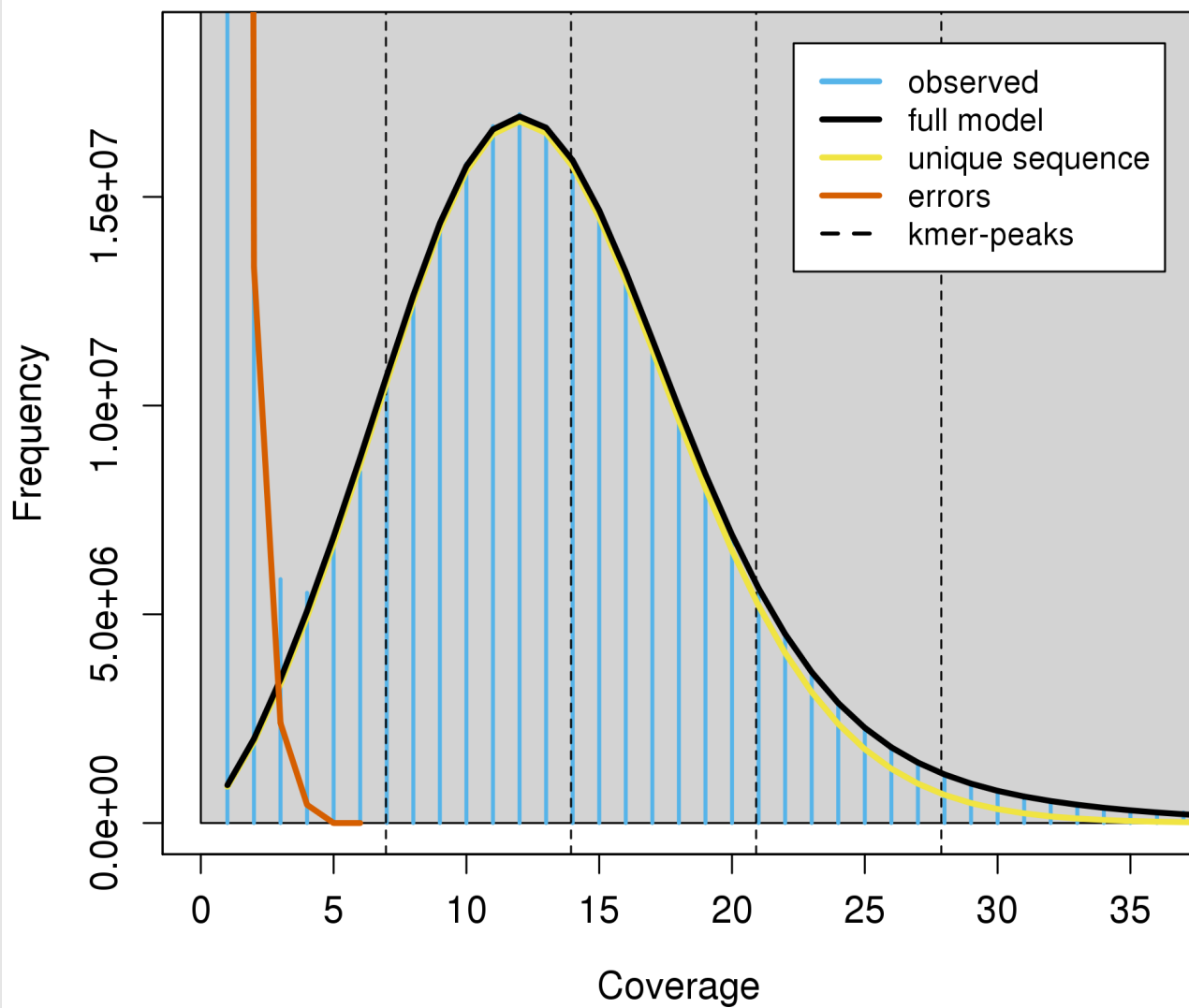# kg_A.japonica_k41_default

GenomeScope Profile
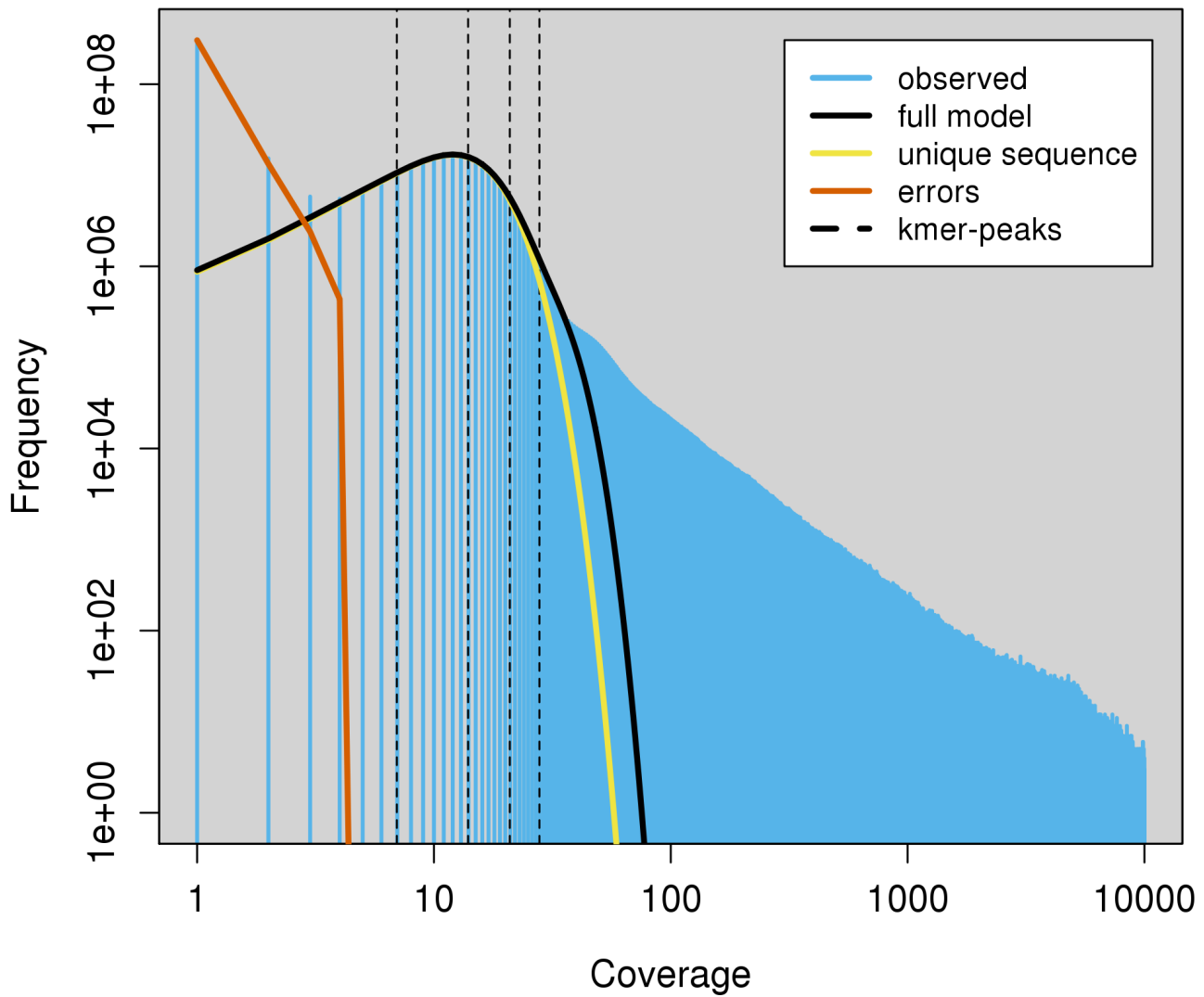
len:324,234,867bp uniq:66.1%
aa:99.8% ab:0.192%
kcov:6.97 err:0.177% dup:0.879 k:41 p:2

(user_data/T52ri5URhNsSLSYn7csY/linear_plot.png)
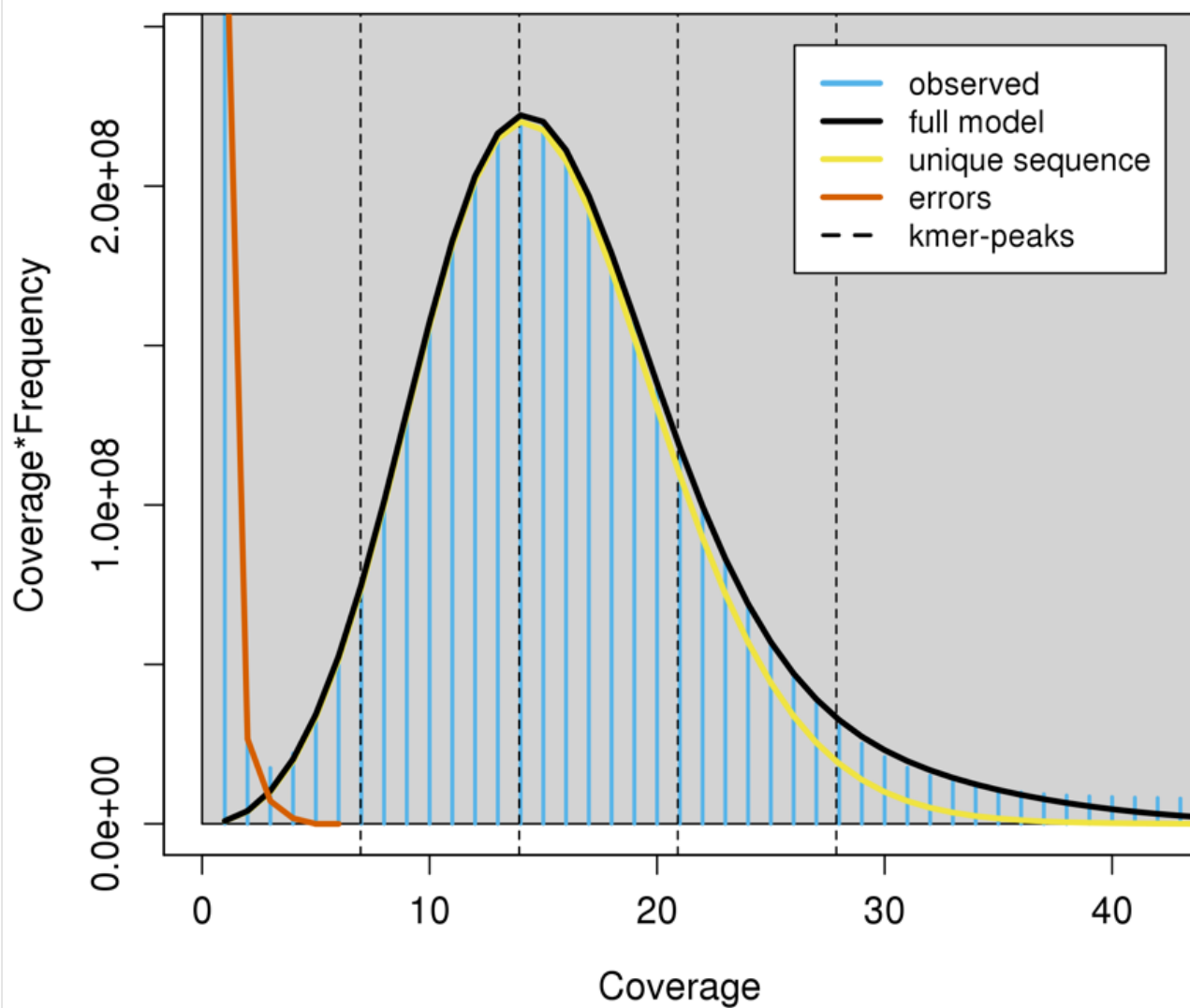
GenomeScope Profile

len:324,234,867bp uniq:66.1%
aa:99.8% ab:0.192%
kcov:6.97 err:0.177% dup:0.879 k:41 p:2

(user_data/T52ri5URhNsSLSYn7csY/log_plot.png)

(user_data/T52ri5URhNsSLSYn7csY/transformed_linear_plot.png)
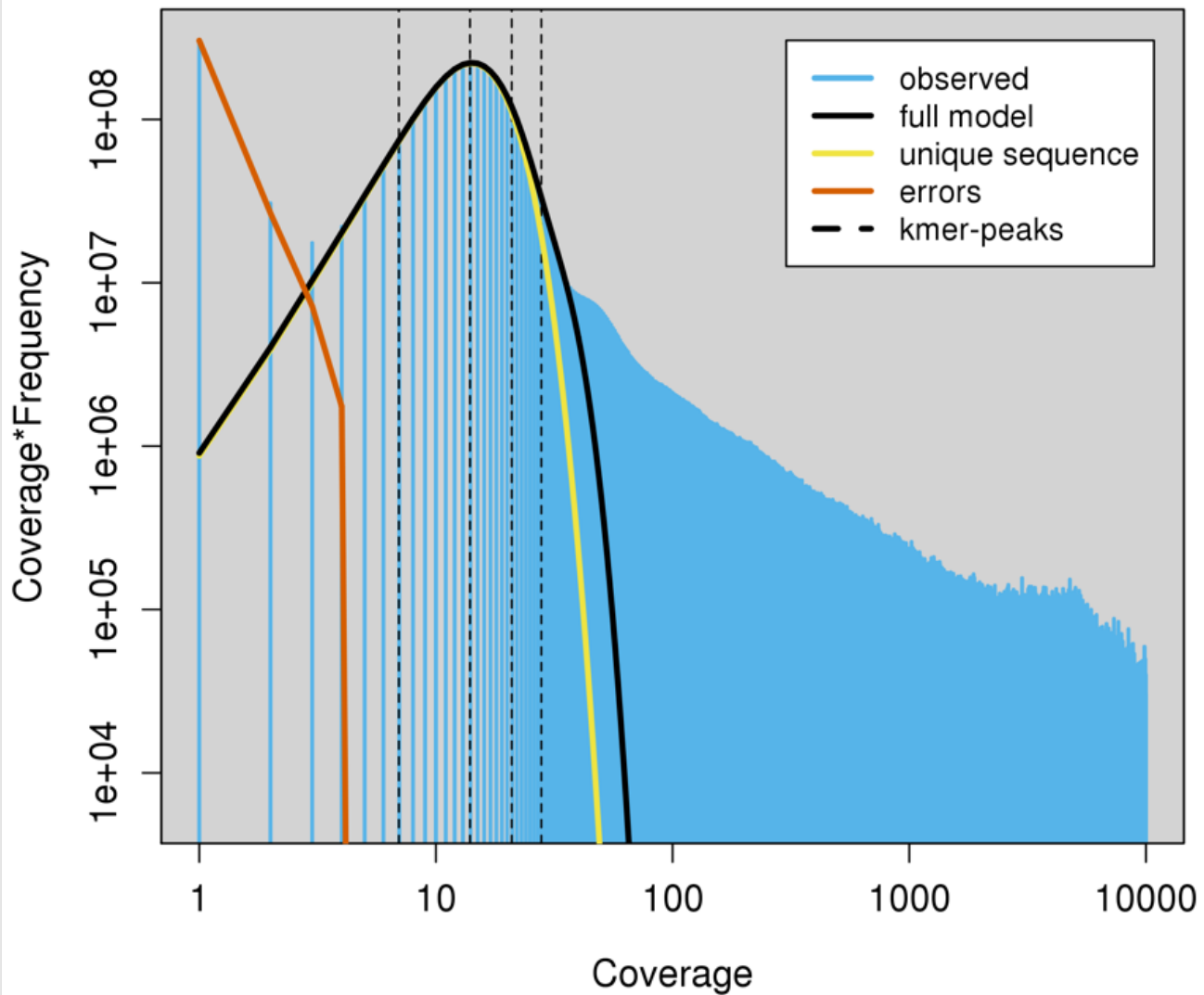
GenomeScope Profile

len:324,234,867bp uniq:66.1%
aa:99.8% ab:0.192%
kcov:6.97 err:0.177% dup:0.879 k:41 p:2

(user_data/T52ri5URhNsSLSYn7csY/transformed_log_plot.png)

Results

Model

```
GenomeScope version 2.0
input file = user_uploads/T52ri5URhNsSLSYn7csY
output directory = user_data/T52ri5URhNsSLSYn7csY
p = 2
k = 41

property                      min               max
Homozygous (aa)               99.7741%          99.8422%
Heterozygous (ab)             0.157833%         0.225918%
Genome Haploid Length         320,428,149 bp    324,234,867 bp
Genome Repeat Length          108,738,737 bp    110,030,564 bp
Genome Unique Length          211,689,413 bp    214,204,303 bp
Model Fit                     70.7731%          99.2527%
Read Error Rate               0.177313%         0.177313%
```

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

Parameters:
         Estimate Std. Error t value Pr(>|t|)
d        4.324e-02  1.519e-03   28.47   <2e-16 ***
r1       1.919e-03  1.702e-04   11.27   <2e-16 ***
kmercov  6.970e+00  2.058e-02  338.70   <2e-16 ***
bias     8.788e-01  2.281e-02   38.53   <2e-16 ***
length   2.226e+08  6.162e+05  361.17   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1

Residual standard error: 848400 on 1995 degrees of freedom

Number of iterations to convergence: 8
Achieved convergence tolerance: 1.49e-08
```

View analysis later

Return to view your results at any time:

Progress

starting

round 0 trimming to 3 trying 2p peak model... converged. score: 1474520470176671

round 1 trimming to 8 trying 2p peak model... converged. score: 1475147102000463

round 2 trimming to 13 trying 2p peak model... converged. score: 1352592459611652

round 3 trimming to 18 trying 2p peak model... converged. score: 2952583489070402

done