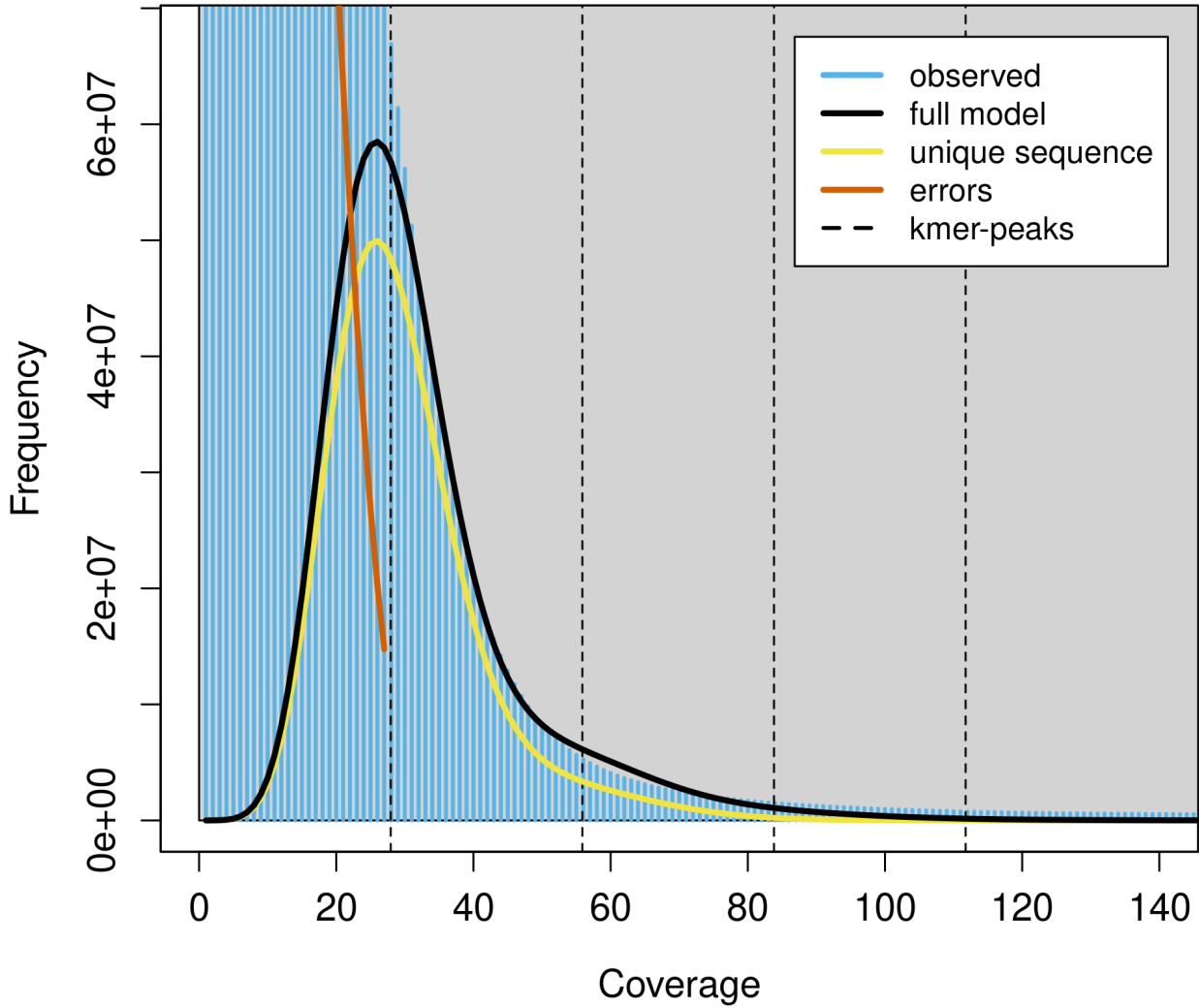


my sample

### GenomeScope Profile

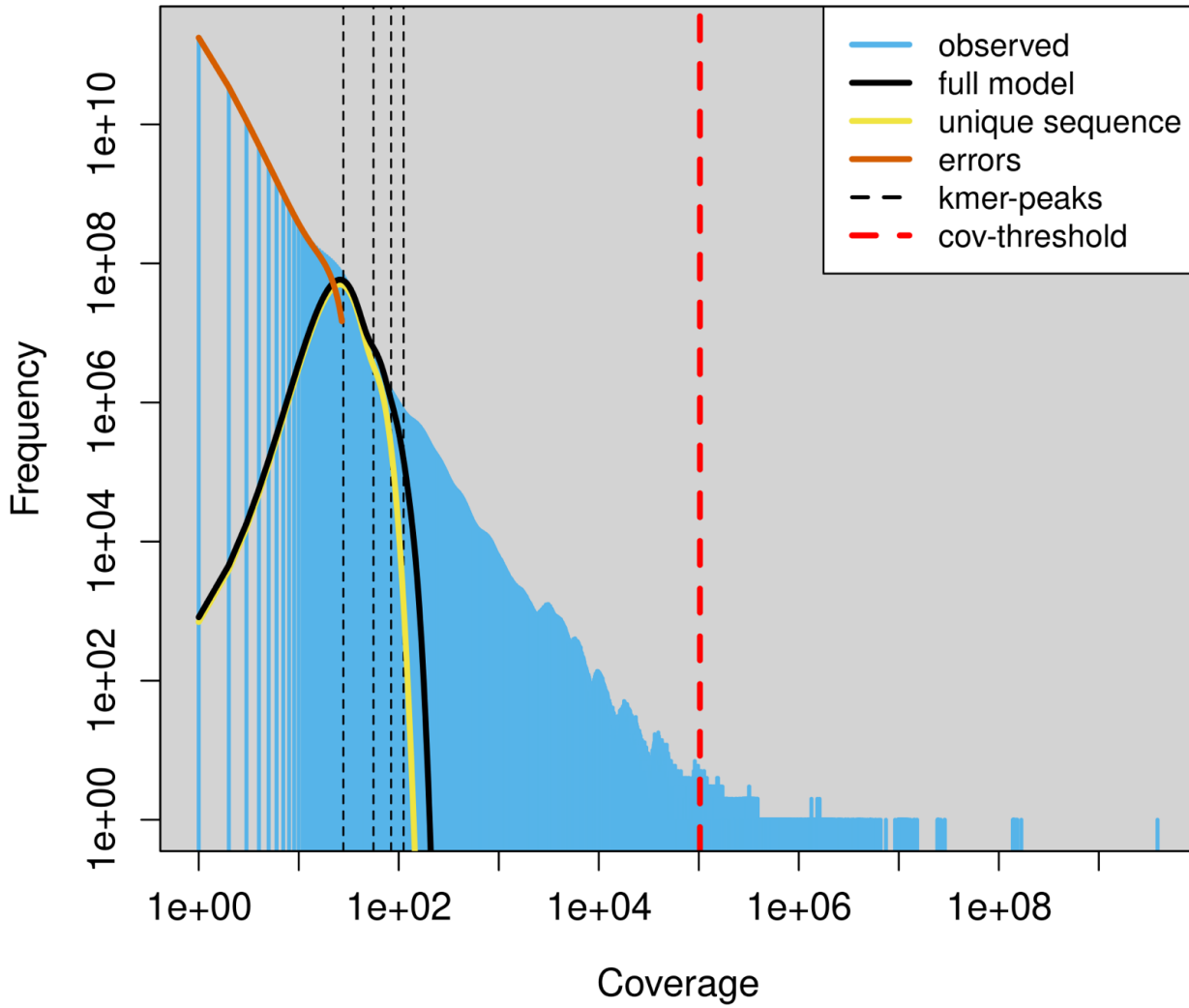
len:2,035,832,037bp uniq:30%  
aa:90.7% ab:9.27%  
kcov:27.9 err:6.72% dup:1.63 k:21 p:2



(user\_data/yBjMcjqLewzuFzsam89n/linear\_plot.png)

# GenomeScope Profile

len:2,035,832,037bp uniq:30%  
aa:90.7% ab:9.27%  
kcov:27.9 err:6.72% dup:1.63 k:21 p:2



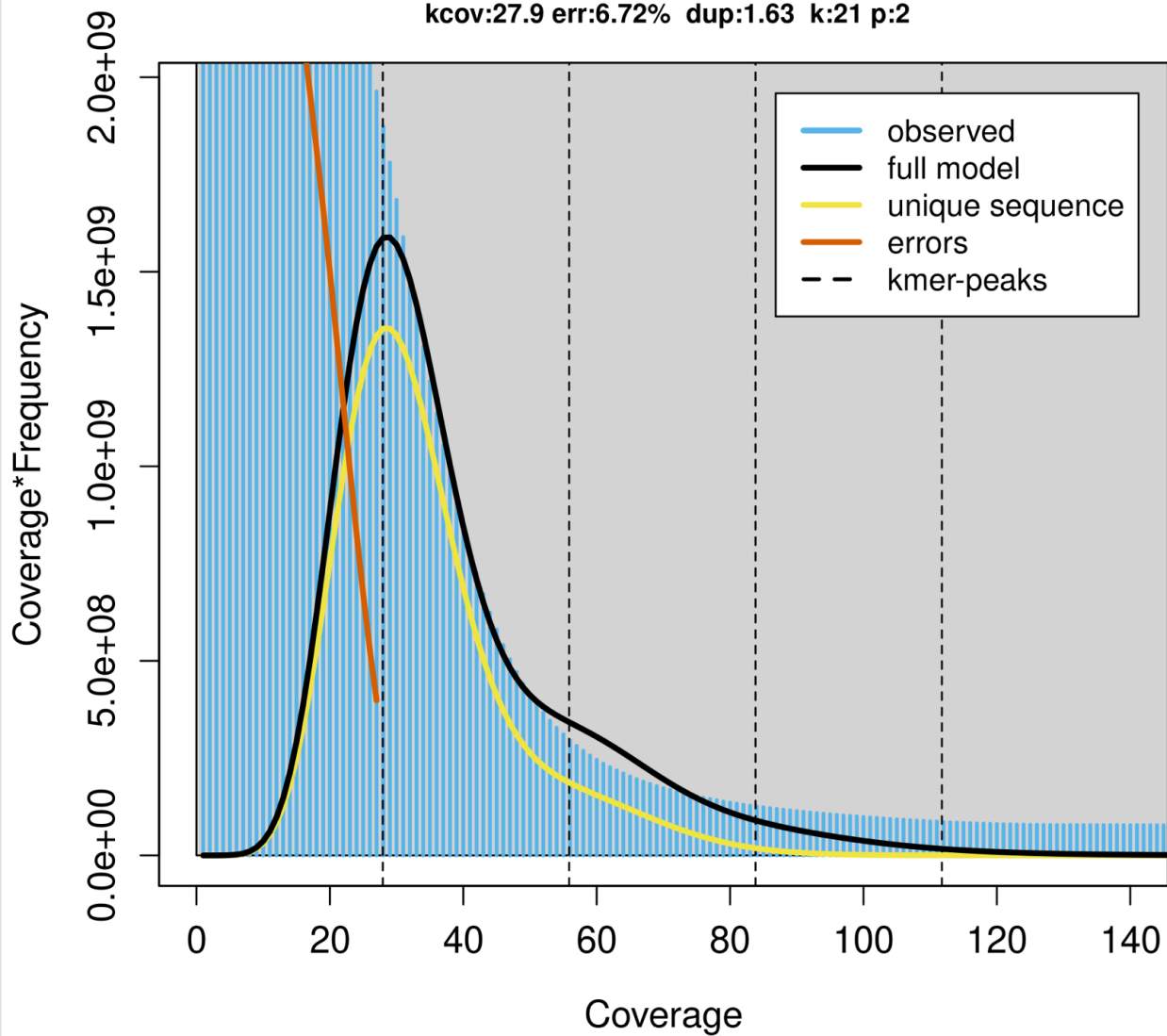
(user\_data/yBjMcjqLewzuFzsam89n/log\_plot.png)

# GenomeScope Profile

len:2,035,832,037bp uniq:30%

aa:90.7% ab:9.27%

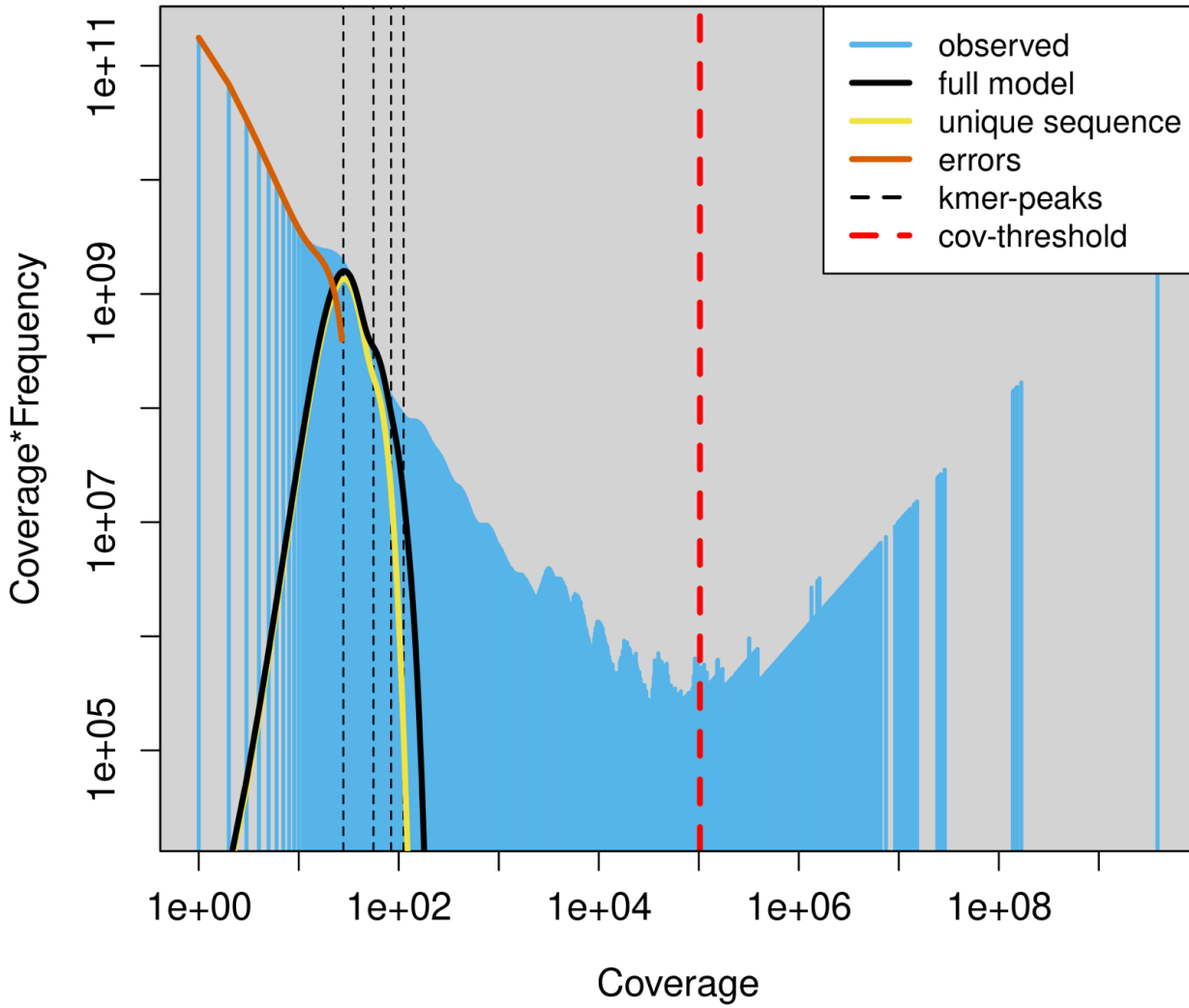
kcov:27.9 err:6.72% dup:1.63 k:21 p:2



(user\_data/yBjMcjqLewzuFzsam89n/transformed\_linear\_plot.png)

# GenomeScope Profile

len:2,035,832,037bp uniq:30%  
aa:90.7% ab:9.27%  
kcov:27.9 err:6.72% dup:1.63 k:21 p:2



(user\_data/yBjMcjqLewzuFzsam89n/transformed\_log\_plot.png)

Results

Model

```
GenomeScope version 2.0
input file = user_uploads/yBjMcjqLewzuFzsam89n
output directory = user_data/yBjMcjqLewzuFzsam89n
p = 2
k = 21
```

property	min	max
Homozygous (aa)	84.9896%	96.4684%
Heterozygous (ab)	3.53158%	15.0104%
Genome Haploid Length	1,967,515,747 bp	2,035,832,037 bp
Genome Repeat Length	1,377,538,845 bp	1,425,369,894 bp
Genome Unique Length	589,976,902 bp	610,462,142 bp
Model Fit	30.9033%	84.2117%
Read Error Rate	6.71809%	6.71809%

```
Formula: y_transform ~ x^transform_exp * length * predict2
kmercov, bias, x)
```

Parameters:

	Estimate	Std. Error	t value	Pr(> t )
d	1.457e-01	1.112e-01	1.310	0.19039
r1	9.271e-02	2.870e-02	3.231	0.00126 **
kmercov	2.794e+01	2.384e-01	117.200	< 2e-16 ***
bias	1.628e+00	5.369e-02	30.324	< 2e-16 ***
length	7.024e+08	6.360e+07	11.044	< 2e-16 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 21460000 on 1995 degrees of freedom

Number of iterations to convergence: 14  
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=yBjMcjqLewzuFzsam89n>

## Progress

starting

round 0 trimming to 15 trying 2p peak model... converged. score: 1847728803671195392

round 1 trimming to 20 trying 2p peak model... converged. score: 1644963802680406528

round 2 trimming to 25 trying 2p peak model... converged. score: 1663372621907594496

round 3 trimming to 30 trying 2p peak model... converged. score: 1734451232854149632

done