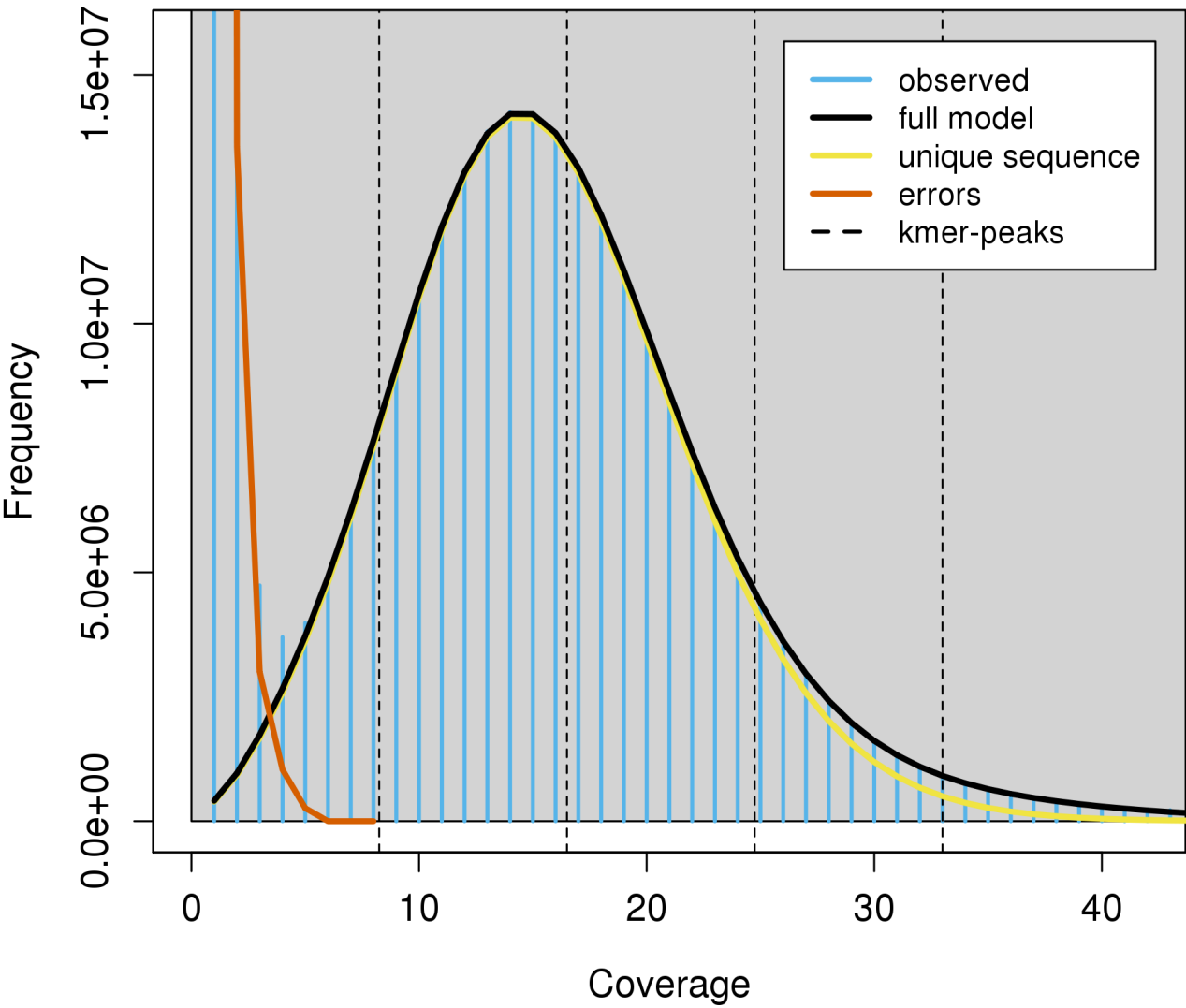


KG\_A.japonica\_k31\_default

GenomeScope Profile

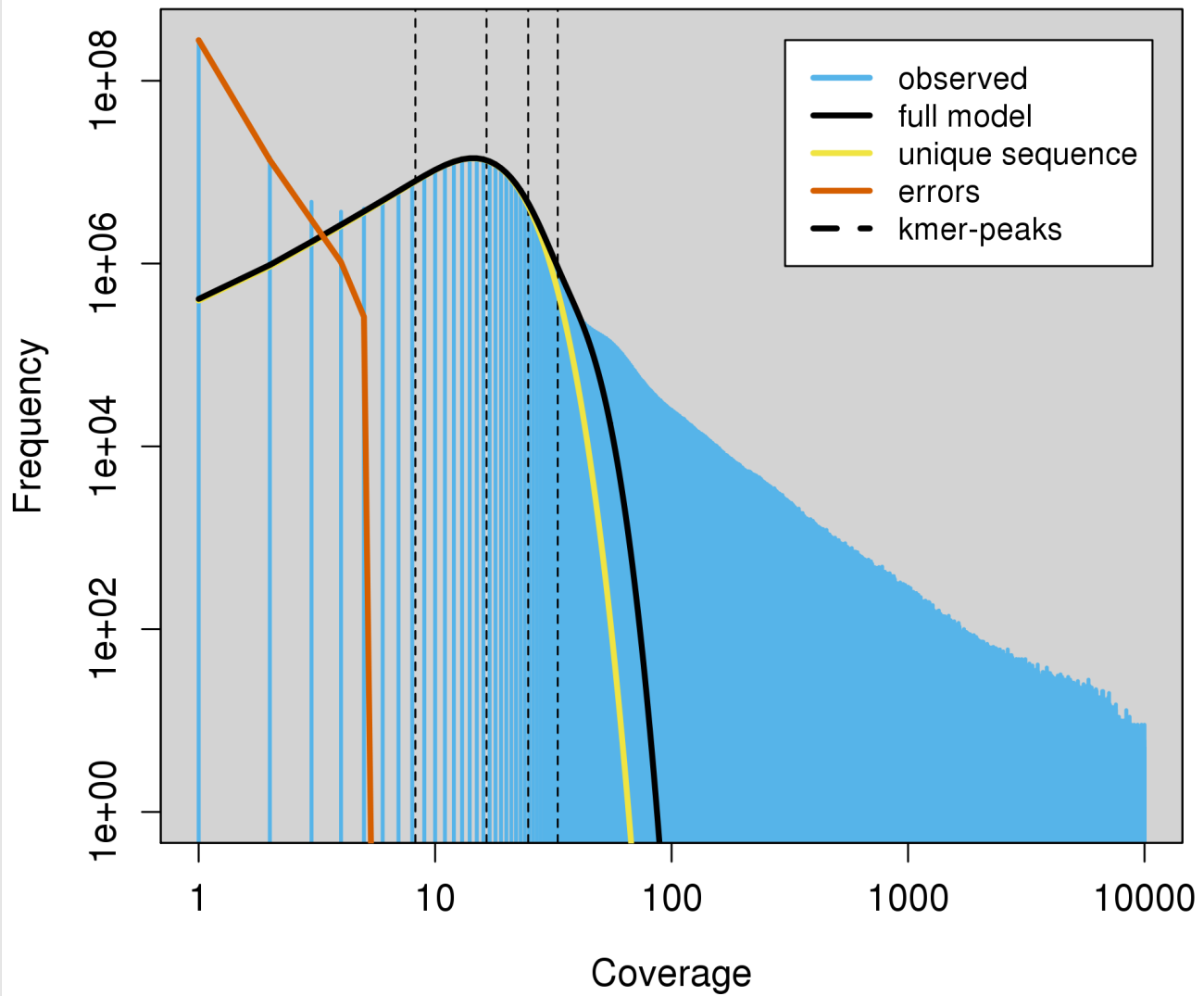
len:313,873,679bp uniq:65.7%  
aa:99.8% ab:0.209%  
kcov:8.25 err:0.194% dup:1.06 k:31 p:2



(user\_data/wzOxPMMnIDutflT3D7ys/linear\_plot.png)

# GenomeScope Profile

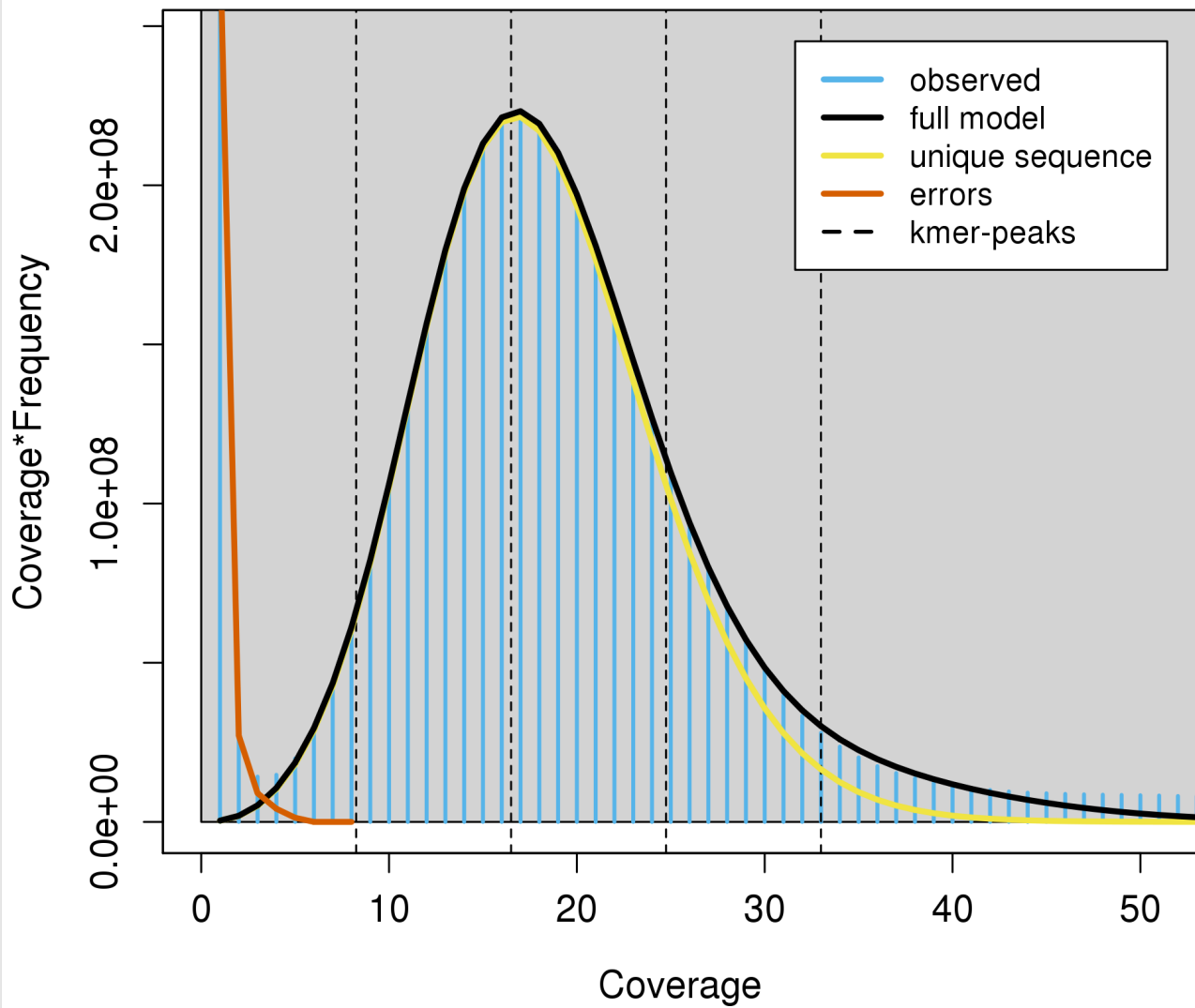
len:313,873,679bp uniq:65.7%  
aa:99.8% ab:0.209%  
kcov:8.25 err:0.194% dup:1.06 k:31 p:2



(user\_data/wzOxPMMnIDutfLt3D7ys/log\_plot.png)

# GenomeScope Profile

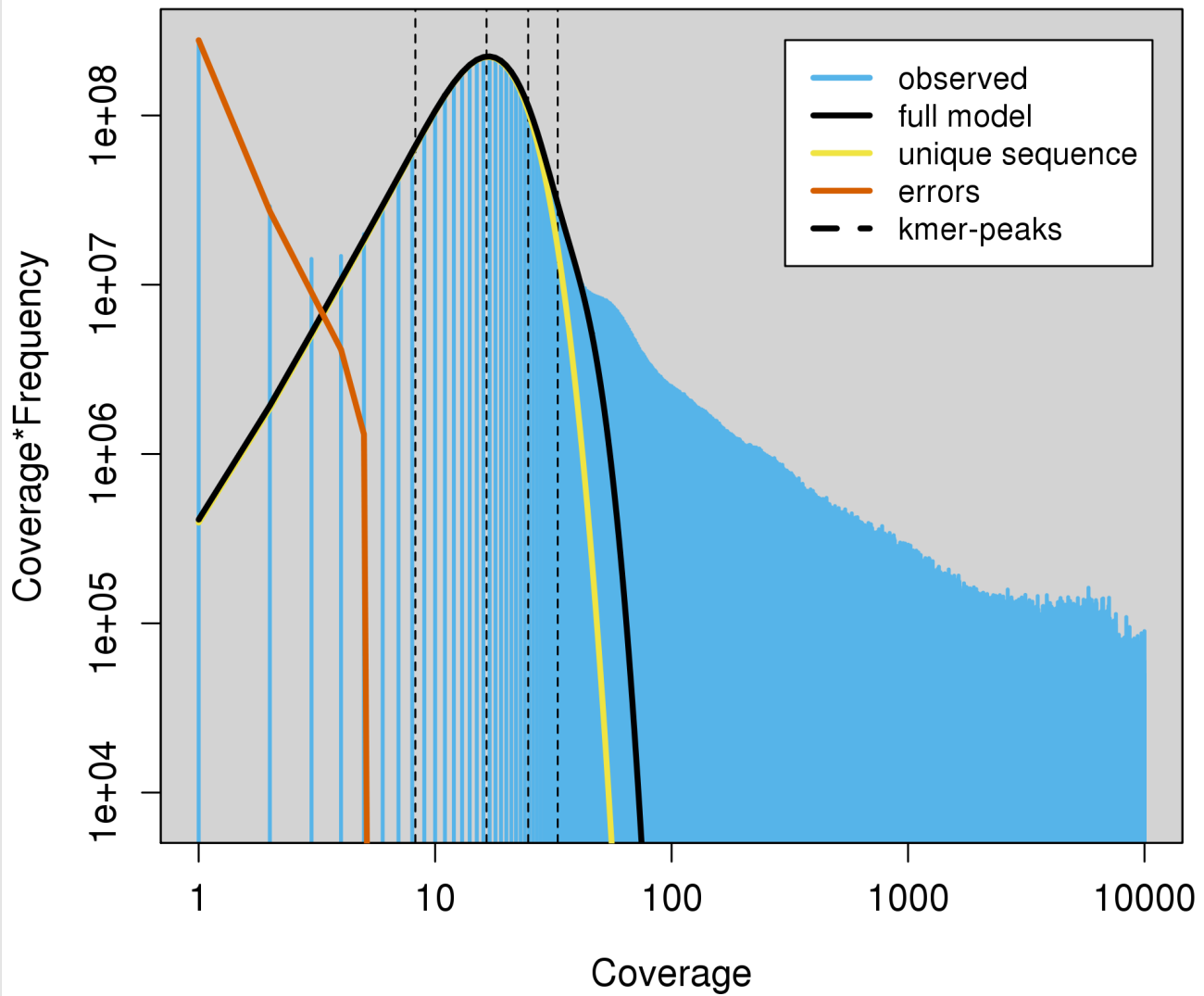
len:313,873,679bp uniq:65.7%  
aa:99.8% ab:0.209%  
kcov:8.25 err:0.194% dup:1.06 k:31 p:2



(user\_data/wzOxPMMnIDutflT3D7ys/transformed\_linear\_plot.png)

# GenomeScope Profile

len:313,873,679bp uniq:65.7%  
aa:99.8% ab:0.209%  
kcov:8.25 err:0.194% dup:1.06 k:31 p:2



(user\_data/wzOxPMMnIDutflT3D7ys/transformed\_log\_plot.png)

Results

Model

GenomeScope version 2.0  
input file = user\_uploads/wzOxPMMnlDutflT3D7ys  
output directory = user\_data/wzOxPMMnlDutflT3D7ys  
p = 2  
k = 31

property	min	max
Homozygous (aa)	99.7617%	99.8202%
Heterozygous (ab)	0.179786%	0.238327%
Genome Haploid Length	311,336,385 bp	313,873,679 bp
Genome Repeat Length	106,862,307 bp	107,733,202 bp
Genome Unique Length	204,474,077 bp	206,140,477 bp
Model Fit	70.4095%	99.2159%
Read Error Rate	0.193904%	0.193904%

Formula: y\_transform ~ x^transform\_exp \* length \* predict.kmercov, bias, x)

Parameters:

	Estimate	Std. Error	t value	Pr(> t )
d	4.237e-02	1.352e-03	31.34	<2e-16 ***
r1	2.091e-03	1.464e-04	14.28	<2e-16 ***
kmercov	8.249e+00	1.674e-02	492.82	<2e-16 ***
bias	1.061e+00	2.019e-02	52.57	<2e-16 ***
length	2.144e+08	4.935e+05	434.42	<2e-16 ***

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

Residual standard error: 941900 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:

<http://genomescope.org/genomescope2.0/analysis.php?code=wzOxPMMnlDutflT3D7ys>

Progress

starting

round 0 trimming to 3 trying 2p peak model... converged. score: 1818875735645419

round 1 trimming to 8 trying 2p peak model... converged. score: 1813195688248264

round 2 trimming to 13 trying 2p peak model... converged. score: 1680254220577933

round 3 trimming to 18 trying 2p peak model... converged. score: 1806013134379097

done