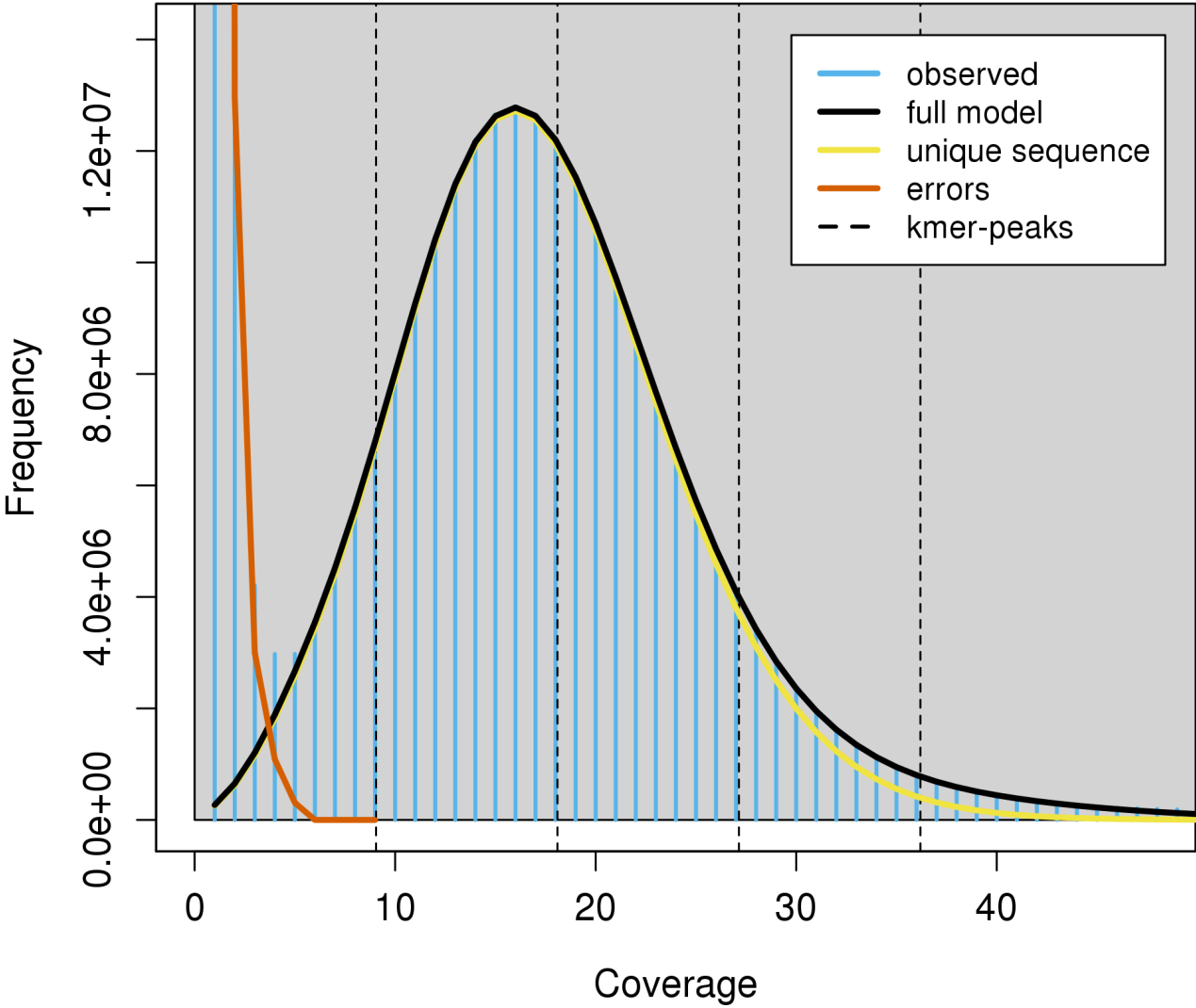


KG\_A.japonica\_k25\_default

GenomeScope Profile

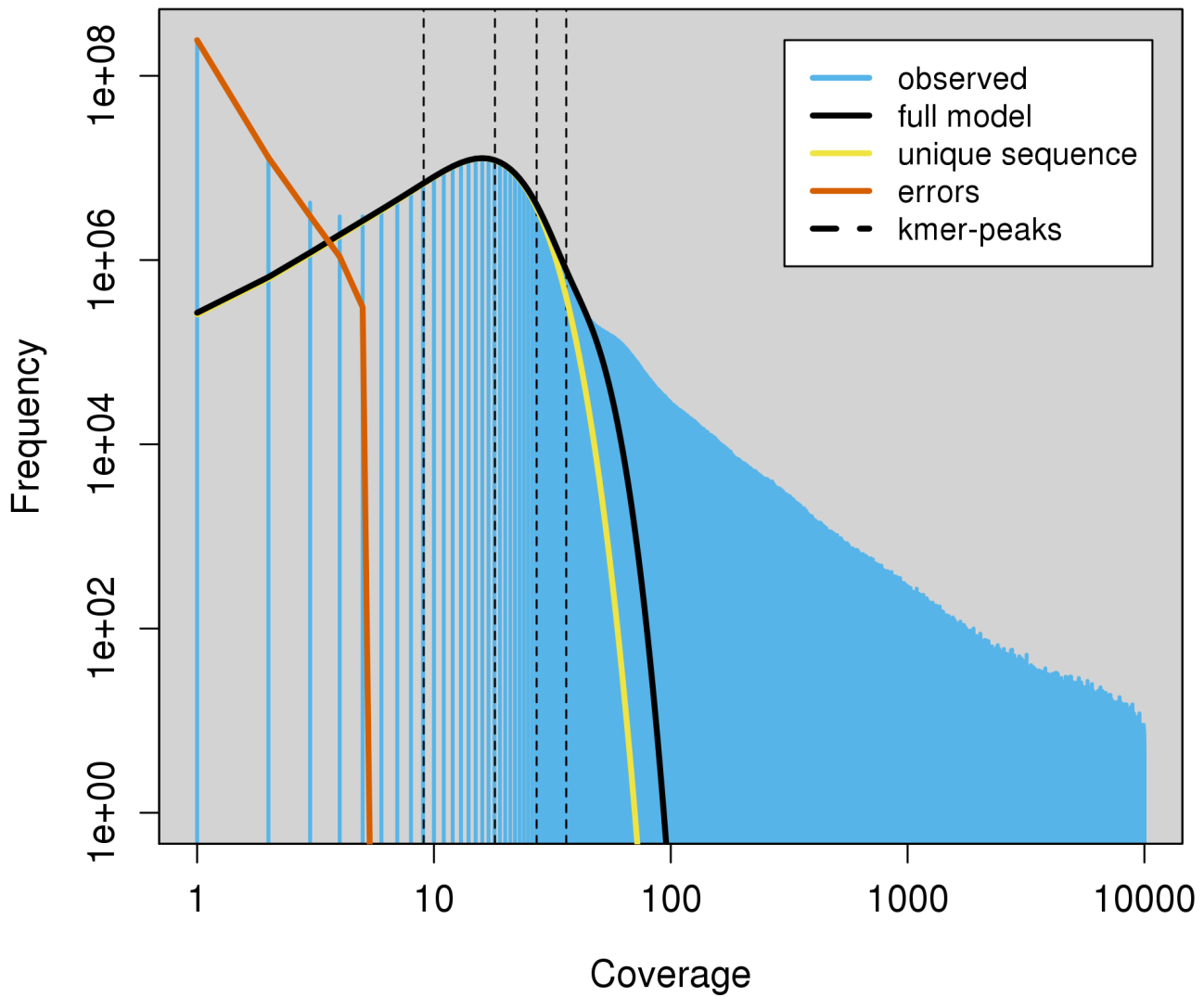
len:305,170,863bp uniq:65%  
aa:99.7% ab:0.299%  
kcov:9.05 err:0.24% dup:1.16 k:21 p:2



(user\_data/93S8LzwWZNY9CJ99L05e/linear\_plot.png )

# GenomeScope Profile

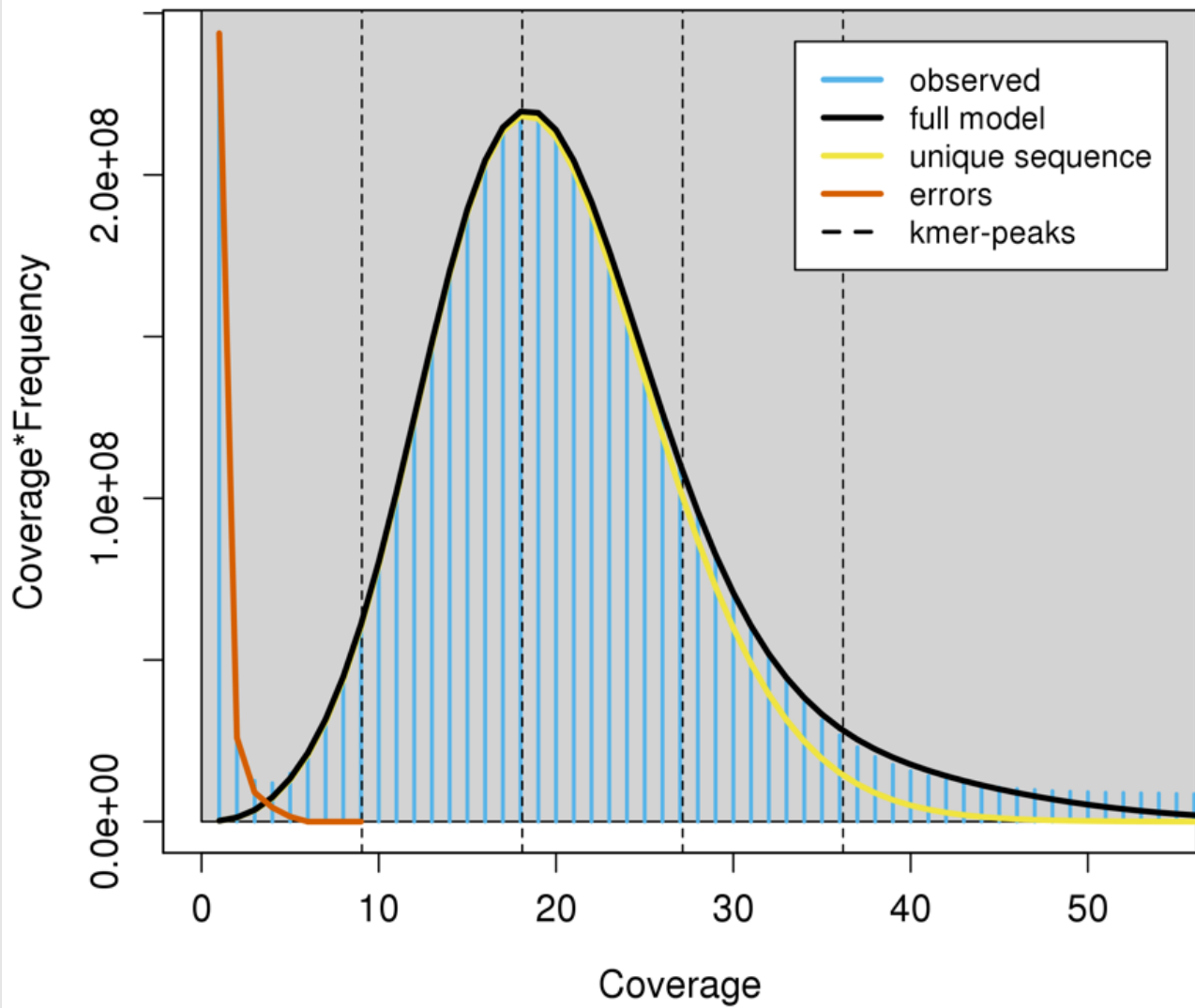
len:305,170,863bp uniq:65%  
aa:99.7% ab:0.299%  
kcov:9.05 err:0.24% dup:1.16 k:21 p:2



(user\_data/93S8LzwWZNY9CJ99L05e/log\_plot.png )

# GenomeScope Profile

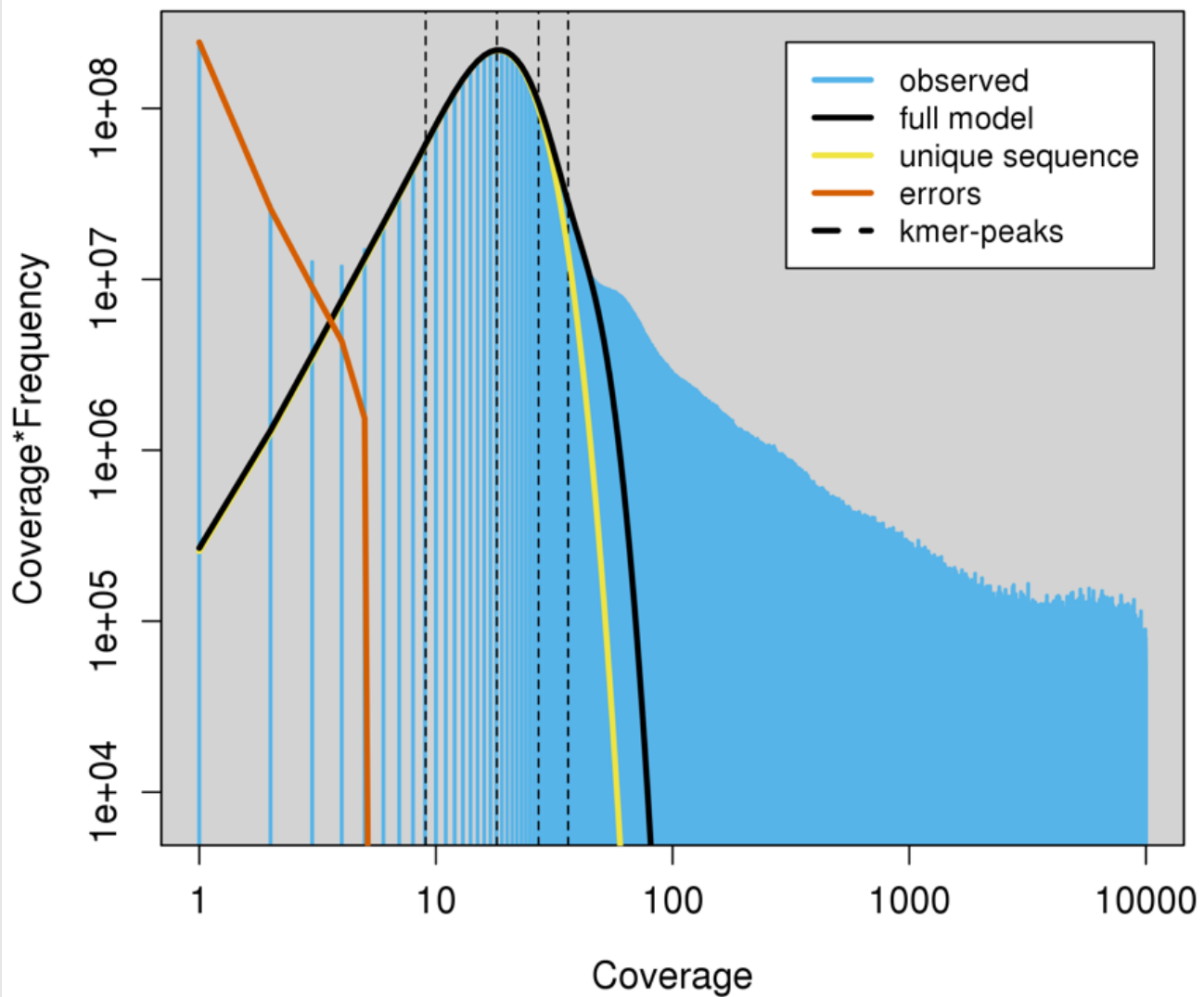
len:305,170,863bp uniq:65%  
aa:99.7% ab:0.299%  
kcov:9.05 err:0.24% dup:1.16 k:21 p:2



(user\_data/93S8LzwWZNY9CJ99L05e/transformed\_linear\_plot.png)

## GenomeScope Profile

len:305,170,863bp uniq:65%  
aa:99.7% ab:0.299%  
kcov:9.05 err:0.24% dup:1.16 k:21 p:2



(user\_data/93S8LzwWZNY9CJ99L05e/transformed\_log\_plot.png )

Results

Model

GenomeScope version 2.0  
input file = user\_uploads/93S8LzwWZNY9CJ99L05e  
output directory = user\_data/93S8LzwWZNY9CJ99L05e  
p = 2  
k = 21

property	min	max
Homozygous (aa)	99.6561%	99.7456%
Heterozygous (ab)	0.254356%	0.343917%
Genome Haploid Length	302,714,438 bp	305,170,863 bp
Genome Repeat Length	105,878,950 bp	106,738,122 bp
Genome Unique Length	196,835,488 bp	198,432,742 bp
Model Fit	69.8825%	99.1481%
Read Error Rate	0.239951%	0.239951%

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

Parameters:

	Estimate	Std. Error	t value	Pr(> t )
d	4.373e-02	1.358e-03	32.21	<2e-16 ***
r1	2.991e-03	2.239e-04	13.36	<2e-16 ***
kmercov	9.048e+00	1.828e-02	494.94	<2e-16 ***
bias	1.155e+00	2.149e-02	53.76	<2e-16 ***
length	2.067e+08	4.698e+05	439.92	<2e-16 ***

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

Residual standard error: 1015000 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=93S8LzwWZNY9CJ99L05e>

Progress

starting

round 0 trimming to 4 trying 2p peak model... converged. score: 2107899263985634

round 1 trimming to 9 trying 2p peak model... converged. score: 2107348256810438

round 2 trimming to 14 trying 2p peak model... converged. score: 1939473130810613

round 3 trimming to 19 trying 2p peak model... converged. score: 1916665904872116

done