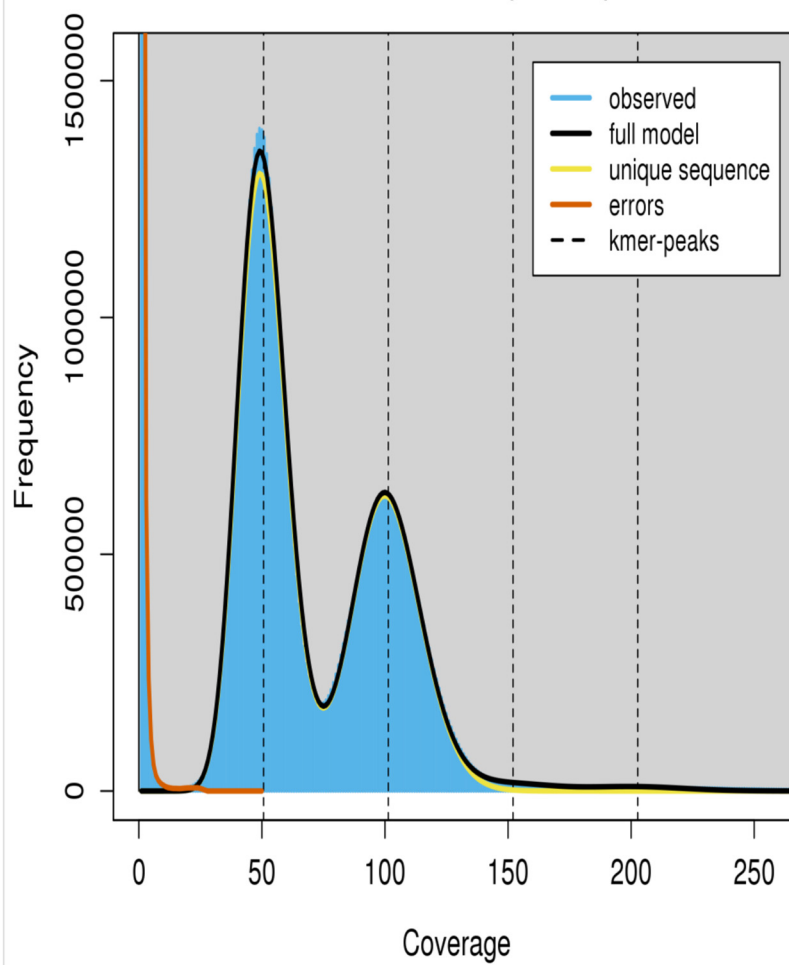


GenomeScope Profile

len:44,895,640bp uniq:83.6%
aa:97.4% ab:2.59%
kcov:50.7 err:0.0742% dup:0.9 k:21 p:2



```
GenomeScope version 2.0
input file = user_uploads/3ZGtdEQ9yidRAYrvKddc
output directory = user_data/3ZGtdEQ9yidRAYrvKddc
p = 2
k = 21
```

property	min	max
Homozygous (aa)	97.3963%	97.4139%
Heterozygous (ab)	2.58608%	2.60366%
Genome Haploid Length	44,851,312 bp	44,895,640 bp
Genome Repeat Length	7,349,356 bp	7,356,619 bp
Genome Unique Length	37,501,956 bp	37,539,020 bp
Model Fit	85.8514%	95.4174%
Read Error Rate	0.0741602%	0.0741602%

Model

```
Formula: y_transform ~ x^transform_exp * length * predict2_0(r1, k, d,
  kmercov, bias, x)
```

Parameters:

	Estimate	Std. Error	t value	Pr(> t)
d	3.485e-02	8.608e-04	40.48	<2e-16 ***
r1	2.595e-02	4.396e-05	590.34	<2e-16 ***
kmercov	5.067e+01	1.251e-02	4049.23	<2e-16 ***
bias	9.004e-01	5.090e-03	176.89	<2e-16 ***
length	3.888e+07	4.836e+04	803.84	<2e-16 ***

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

Residual standard error: 448900 on 1995 degrees of freedom

Number of iterations to convergence: 6

Achieved convergence tolerance: 1.49e-08