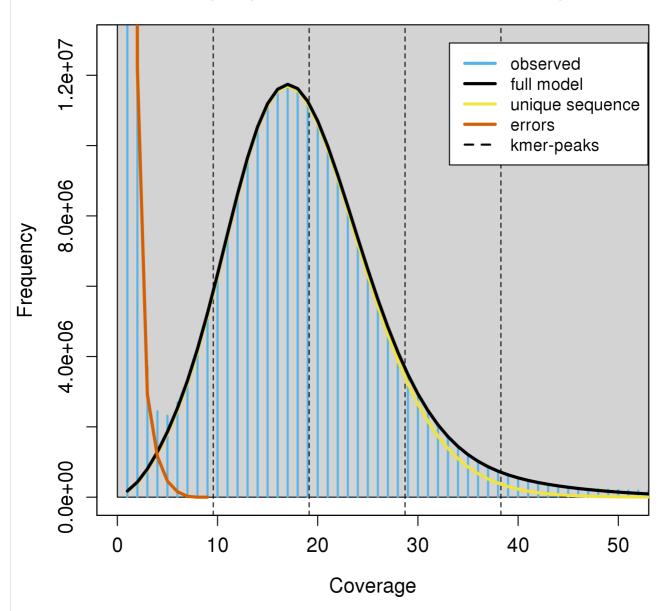
# KG\_A.japonica\_km21

# **GenomeScope Profile**

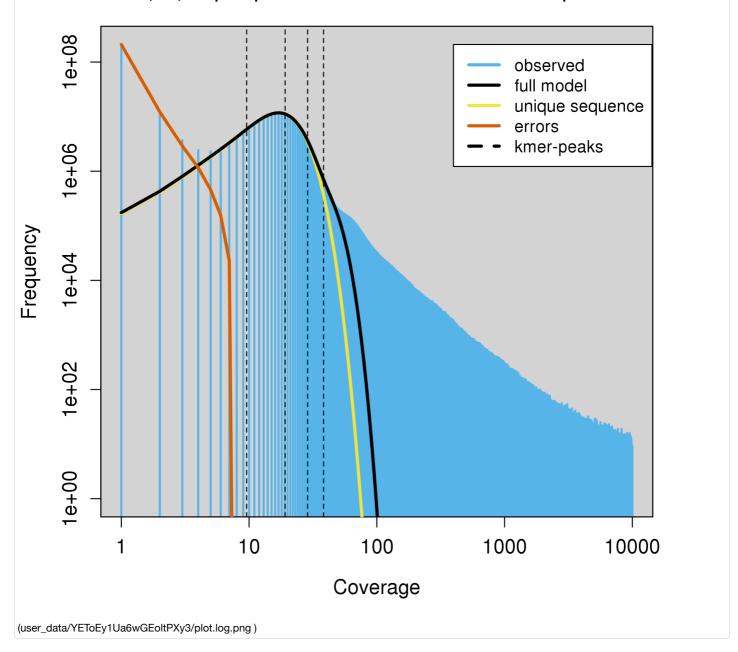
len:297,054,563bp uniq:64.3% het:0.234% kcov:9.57 err:0.207% dup:1.27% k:21

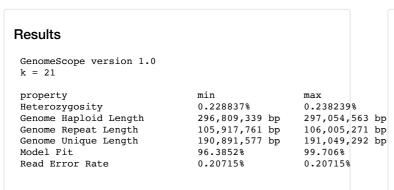


(user\_data/YEToEy1Ua6wGEoltPXy3/plot.png)

## **GenomeScope Profile**

len:297,054,563bp uniq:64.3% het:0.234% kcov:9.57 err:0.207% dup:1.27% k:21





Model

```
Formula: y \sim (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d) *
r)^k)^2) +
                 (2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * dnbinom(x,
kmercov/bias,
                 mu = kmercov) * length + (((1 - d) * ((1 - r)^k)) + ((1 - r)^k))
                  (1 - (1 - r)^k)^2) * dnbinom(x, size = kmercov * 2/b mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (
                  \begin{array}{lll} & \text{find} & -\text{kine Fcov} & 2) & \text{Fength} + \left(2 & \text{d.s.} \left((1-1) & \text{k}\right)\right) \\ & \left(1-r\right)^{k}\right) & \text{dnbinom}(x, \text{size} = \text{kmercov} & 3/\text{bias}, \text{mu} \\ & 3) & \text{length} + \left(d & \left(1-r\right)^{k}\right) & \text{dnbinom}(x, \text{size} \\ & 4/\text{bias}, \text{mu} = \text{kmercov} & 4\right) & \text{length}) \end{array}
Parameters:
                                        Estimate Std. Error t value Pr(>|t|)
d 4.209e-02 3.031e-04 138.86 r 2.335e-03 2.350e-05 99.37 kmercov 9.571e+00 1.976e-03 4843.43 bias 1.272e+00 3.243e-03 392.09
                                                                                                                                                                                       <2e-16 ***
                                                                                                                                                                                       <2e-16 ***
                                                                                                                                                                                     <2e-16 ***
<2e-16 ***
length 1.993e+08 5.452e+04 3656.08 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
Residual standard error: 6207 on 9977 degrees of freedom
Number of iterations to convergence: 7
Achieved convergence tolerance: 9.519e-06
```

## View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=YEToEy1Ua6wGEoltPXy3

## **Progress**

starting

round 0 trimming to 5 trying 4peak model... converged. score: 427906342532.956 round 1 trimming to 10 trying 4peak model... converged. score: 385175958999.953 round 2 trimming to 15 trying 4peak model... converged. score: 1583023569428.89 round 3 trimming to 20 trying 4peak model... converged. score: 140094633475759 done