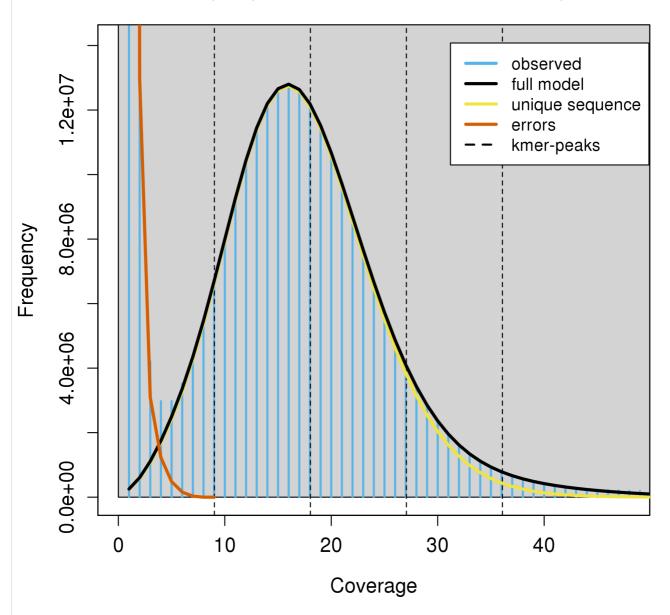
# KG\_A.japonica\_km25

## **GenomeScope Profile**

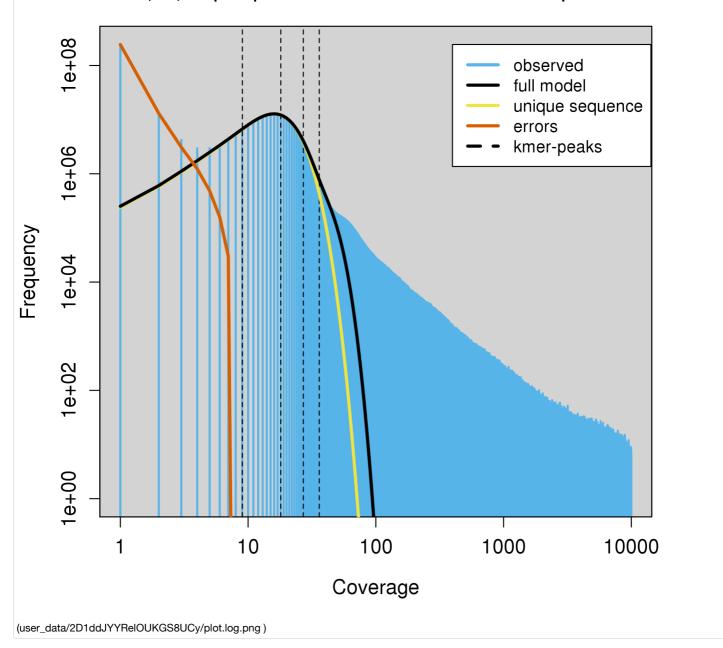
len:304,822,358bp uniq:65.3% het:0.216% kcov:9.02 err:0.201% dup:1.21% k:25

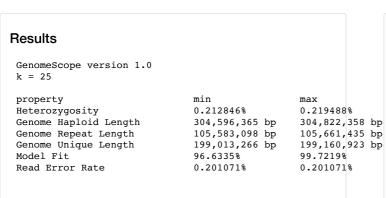


(user\_data/2D1ddJYYRelOUKGS8UCy/plot.png)

### **GenomeScope Profile**

len:304,822,358bp uniq:65.3% het:0.216% kcov:9.02 err:0.201% dup:1.21% k:25





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 3.934e-02 2.882e-04 136.5 r 2.162e-03 1.661e-05 130.2 kmercov 9.020e+00 1.672e-03 5393.3 bias 1.206e+00 2.878e-03 418.9
                                                                                                                                                                                  <2e-16 ***
                                                                                                                                                                                   <2e-16 ***
                                                                                                                                                                                  <2e-16 ***
                                                                                                                                                                                    <2e-16 ***
length 2.072e+08 5.330e+04 3888.1 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
Residual standard error: 6096 on 9961 degrees of freedom
Number of iterations to convergence: 7
Achieved convergence tolerance: 8.325e-06
```

### View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=2D1ddJYYRelOUKGS8UCy

#### **Progress**

#### starting

round 0 trimming to 4 trying 4peak model... converged. score: 610504951842.003 round 1 trimming to 9 trying 4peak model... converged. score: 370479211606.776 round 2 trimming to 14 trying 4peak model... converged. score: 1679037099087.22 round 3 trimming to 19 trying 4peak model... converged. score: 241622308774182 done