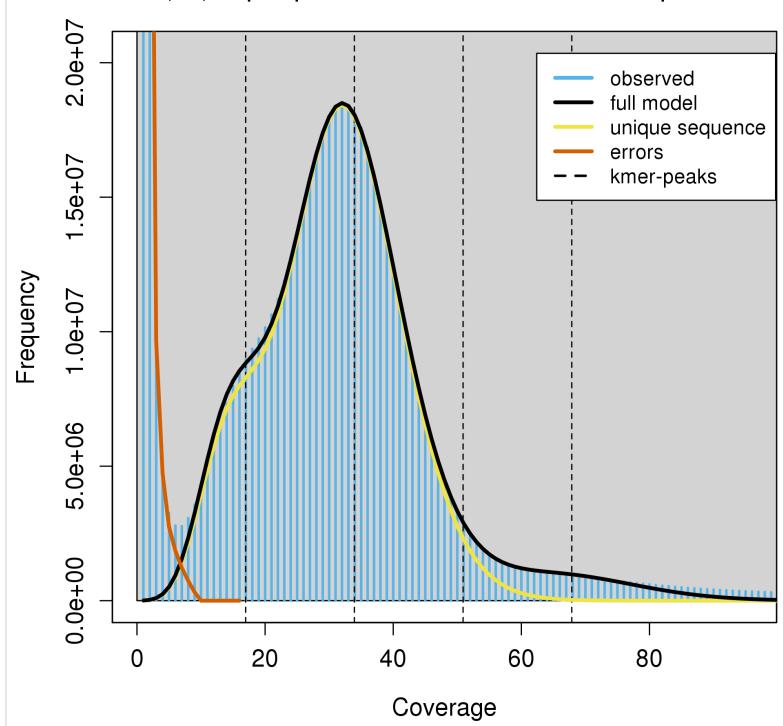
# Lamellibrachia

## **GenomeScope Profile**

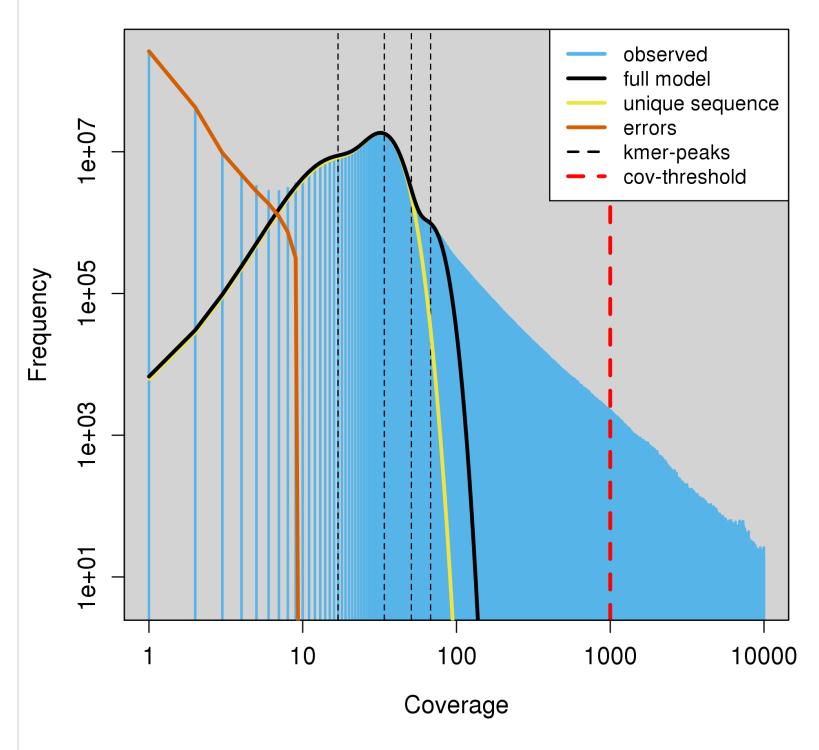
len:646,236,226bp uniq:64.5% het:0.597% kcov:17 err:0.0941% dup:0.984% k:21



(user\_data/S4jZX0MhN8zIsUN4mWYA/plot.png)

## **GenomeScope Profile**

len:646,236,226bp uniq:64.5% het:0.597% kcov:17 err:0.0941% dup:0.984% k:21



(user\_data/S4jZX0MhN8zlsUN4mWYA/plot.log.png)

## **Results**

```
<html class="gr__qb_cshl_edu"><head></head><body data-gr-c-s-
loaded="true">GenomeScope version 1.0
k = 21
```

property	min	max			
Heterozygosity	0.592237%	0.602461%			
Genome Haploid Length	645,021,920 bp	646,236,226 bp			
Genome Repeat Length	229,265,329 bp	229,696,940 bp			
Genome Unique Length	415,756,591 bp	416,539,286 bp			
Model Fit	93.4663%	98.4255%			
Read Error Rate	0.0941112%	0.0941112%			
<pre></pre> <div class="grammarlv-disable-indicator"></div>					

### Model

```
<html class="gr qb cshl edu"><head></head><body data-gr-c-s-</pre>
loaded="true">
Formula: y \sim (((2 * (1 - d) * (1 - (1 - r)^k)) + (2 * d * (1 - (1 - r)^k))))
r)^k)^2) +
           (2 * d * ((1 - r)^k) * (1 - (1 - r)^k))) * dnbinom(x, size =
kmercov/bias,
          mu = kmercov) * length + (((1 - d) * ((1 - r)^k)) + (d *
           (1 - (1 - r)^k)^2) * dnbinom(x, size = kmercov * 2/bias,
          mu = kmercov * 2) * length + (2 * d * ((1 - r)^k) * (1 - r)^k) * (1 - r)^k
           (1 - r)^k) * dnbinom(x, size = kmercov * 3/bias, mu = kmercov *
           3) * length + (d * (1 - r)^(2 * k)) * dnbinom(x, size = kmercov * kmercov 
           4/bias, mu = kmercov * 4) * length)
Parameters:
                       Estimate Std. Error t value Pr(> |t|)
                     7.375e-02 1.161e-03 63.52 <2e-16 ***
                      5.973e-03 2.556e-05 233.71 <2e-16 ***
kmercov 1.697e+01 7.978e-03 2126.74 <2e-16 ***
bias 9.845e-01 7.196e-03 136.81 <2e-16 ***
length 4.488e+08 5.740e+05 781.88 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 71550 on 984 degrees of freedom
Number of iterations to convergence: 7
```

### View analysis later

Return to view your results at any time:

http://genomescope.org/analysis.php?code=S4jZX0MhN8zIsUN4mWYA

### **Progress**

starting

round 0 trimming to 7 trying 4peak model... converged. score: 5190588663463.45 round 1 trimming to 12 trying 4peak model... converged. score: 5114744397475.79 round 2 trimming to 17 trying 4peak model... converged. score: 6844561709731.1 round 3 trimming to 22 trying 4peak model... converged. score: 18694391768740.6 done