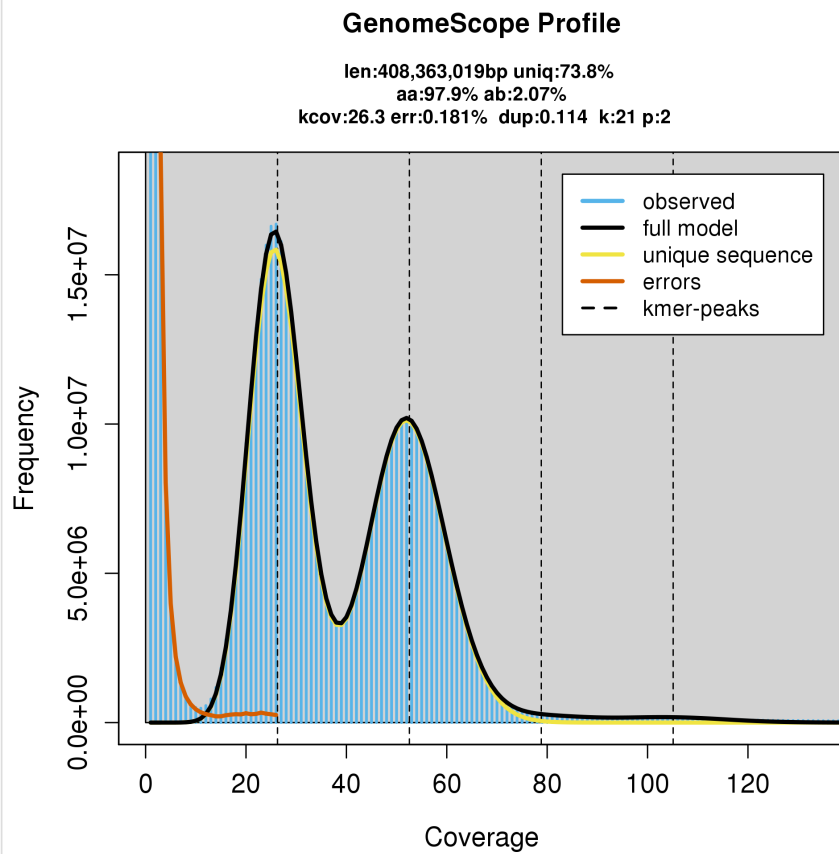
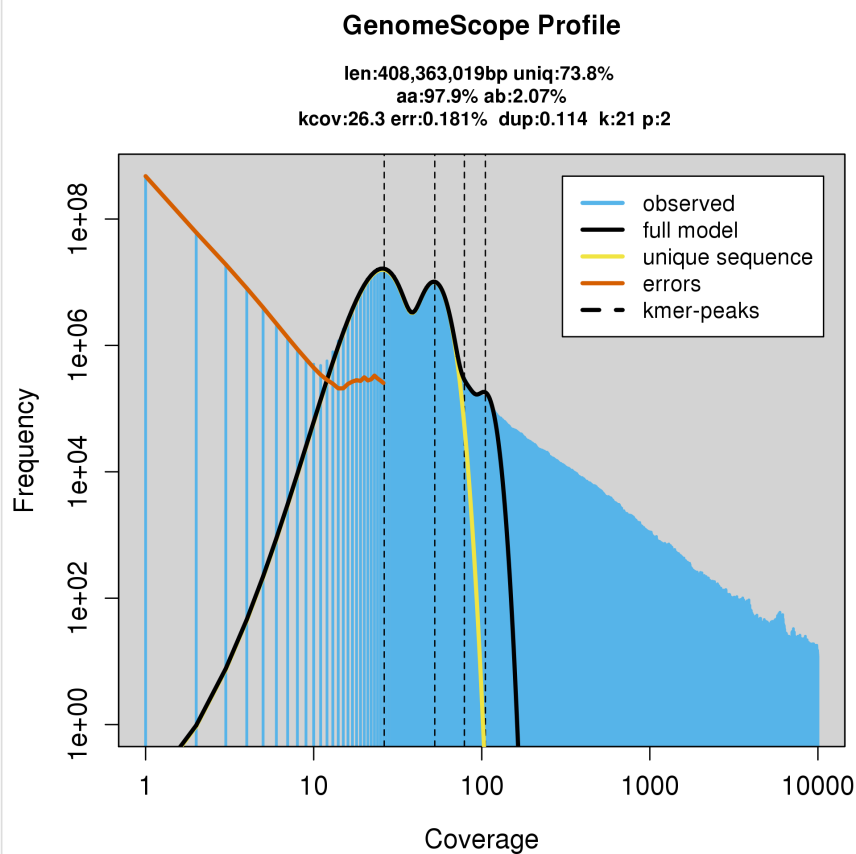


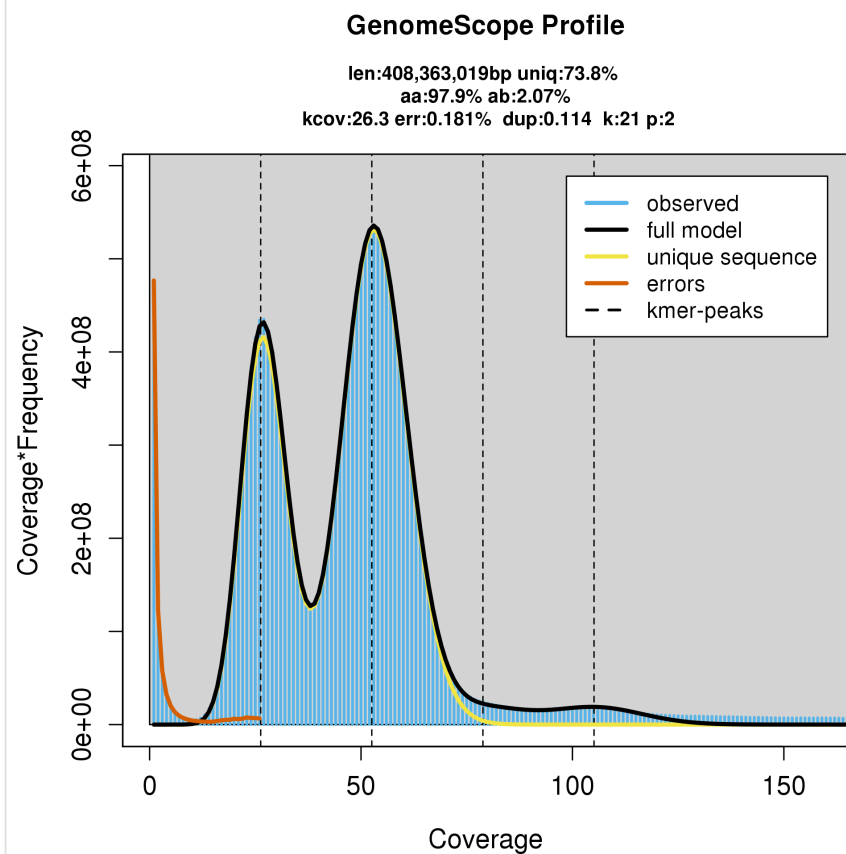
css_reads_O_imp



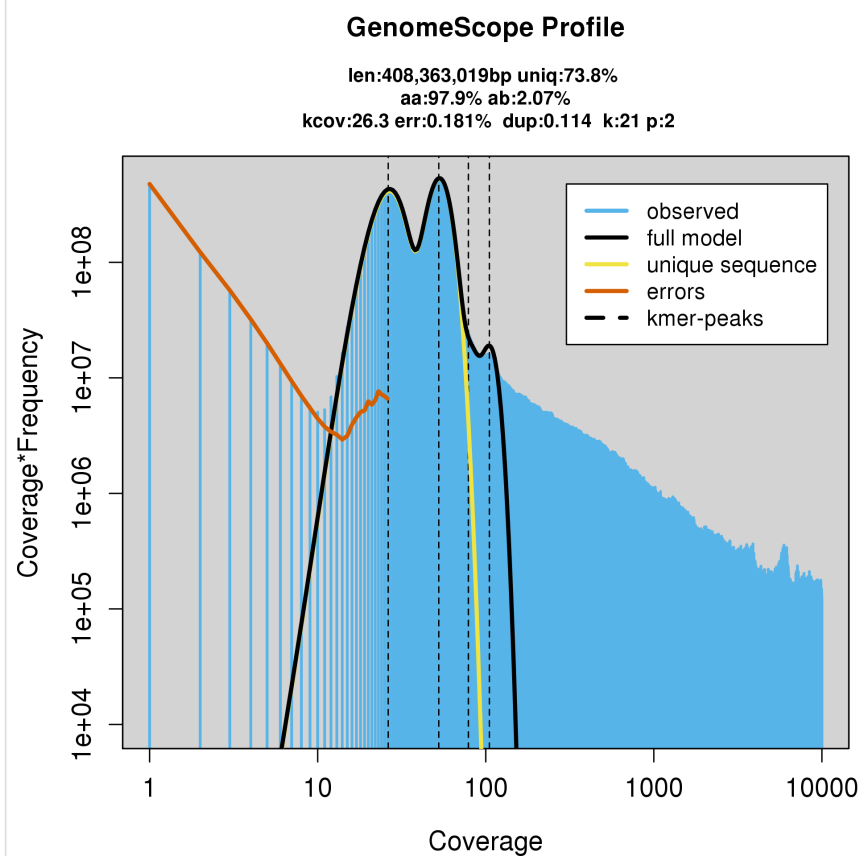
(user_data/VGLsrc4Tn2tFZCc9ewC/linear_plot.png)



(user_data/VGLsrc4Tn2tFZCc9ewC/log_plot.png)



(user_data/VGLsrc4Tn2tFZCc9ewC/transformed_linear_plot.png)



(user_data/VGLsrc4Tn2tFZCc9ewC/transformed_log_plot.png)

Results

GenomeScope version 2.0
input file = user_uploads/VGLsrIc4Tn2tFZCc9ewC
output directory = user_data/VGLsrIc4Tn2tFZCc9ewC
p = 2
k = 21

property	min	max
Homozygous (aa)	97.9174%	97.9331%
Heterozygous (ab)	2.0669%	2.08263%
Genome Haploid Length	407,964,586 bp	408,363,019 bp
Genome Repeat Length	107,017,720 bp	107,122,237 bp
Genome Unique Length	300,946,866 bp	301,240,782 bp
Model Fit	76.032%	98.5172%
Read Error Rate	0.180646%	0.180646%

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	3.670e-02	7.018e-04	52.30	<2e-16 ***
r1	2.075e-02	3.932e-05	527.64	<2e-16 ***
kmercov	2.628e+01	6.412e-03	4097.69	<2e-16 ***
bias	1.140e-01	2.736e-03	41.69	<2e-16 ***
length	3.126e+08	3.785e+05	825.88	<2e-16 ***

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

Residual standard error: 2255000 on 1995 degrees of freedom

Number of iterations to convergence: 5
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=VGLsrIc4Tn2tFZCc9ewC>

Progress

starting

round 0 trimming to 10 trying 2p peak model... converged. score: 10494026884791292

round 1 trimming to 15 trying 2p peak model... converged. score: 10491586166552396

round 2 trimming to 20 trying 2p peak model... converged. score: 10467507706368798

round 3 trimming to 25 trying 2p peak model... converged. score: 10392006398608126

done