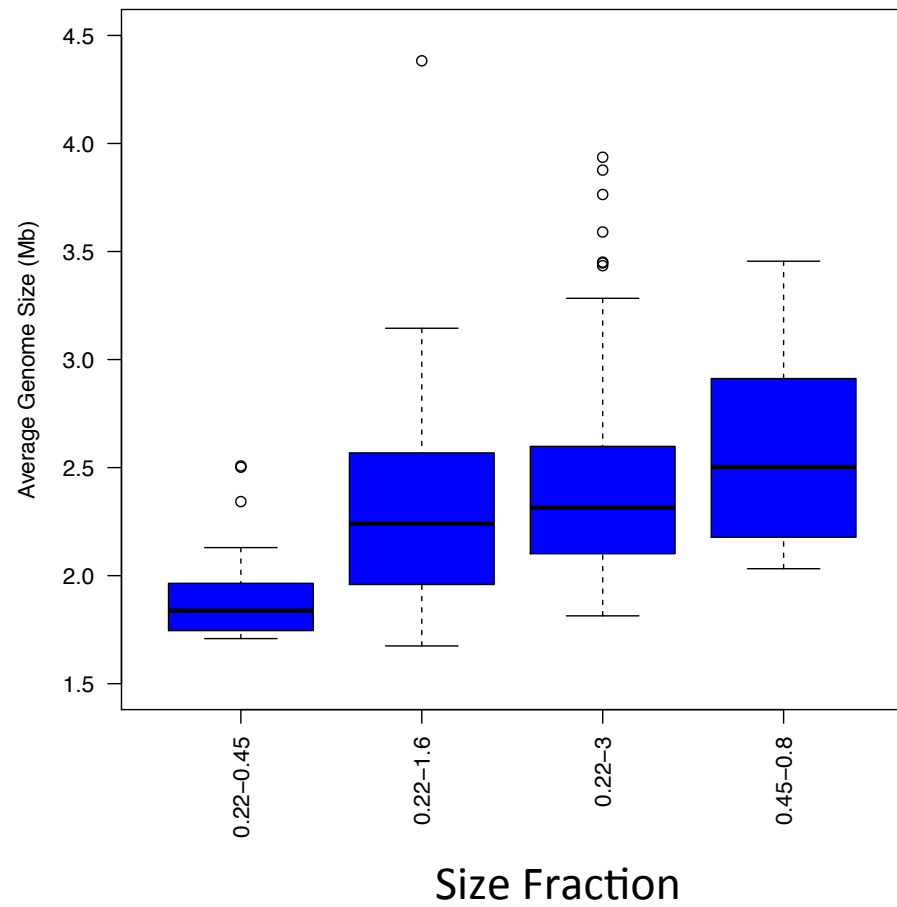
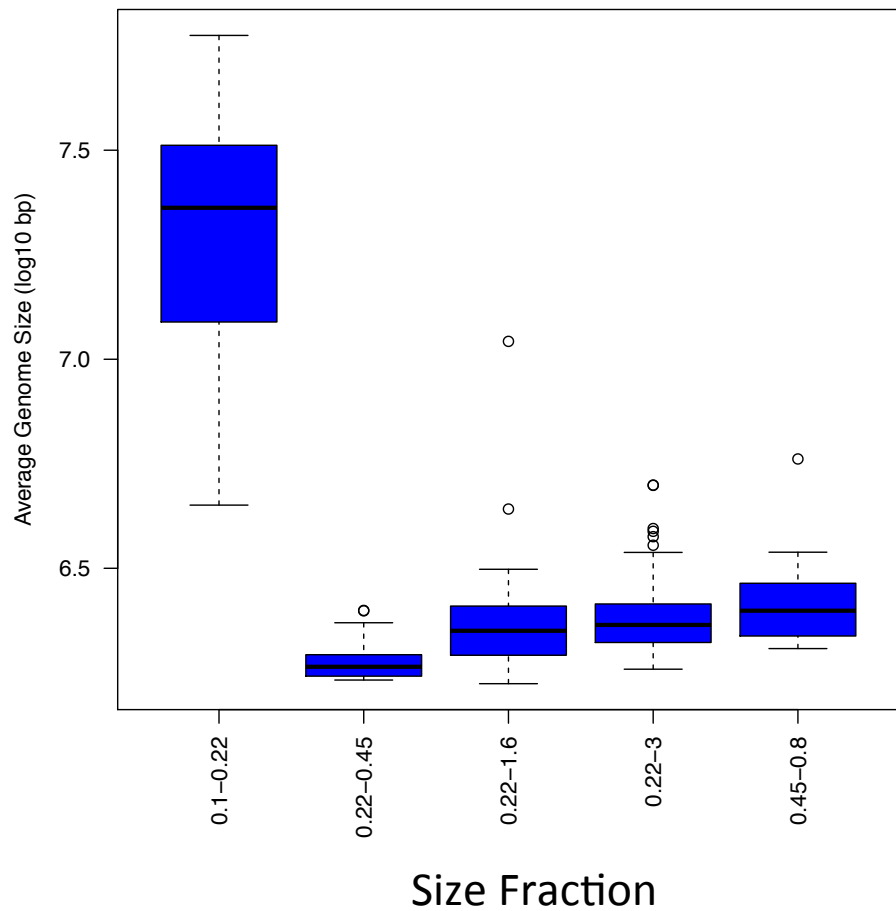
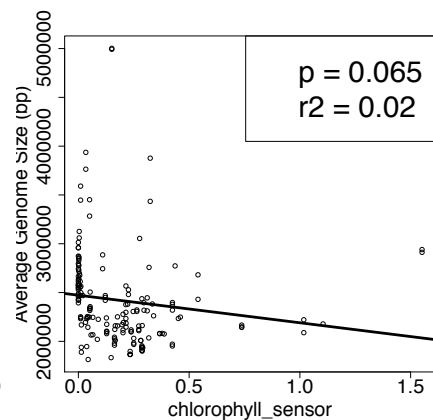
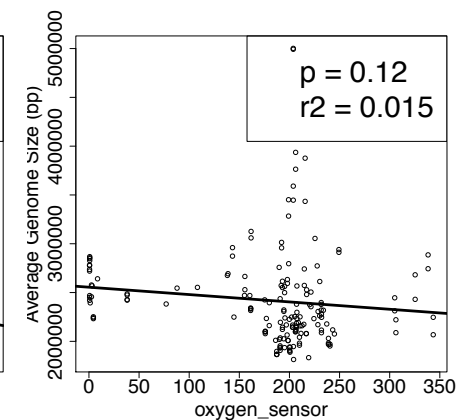
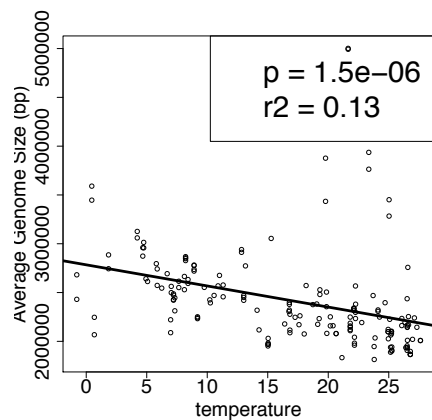
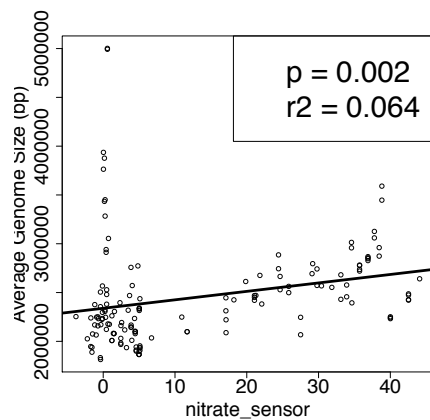
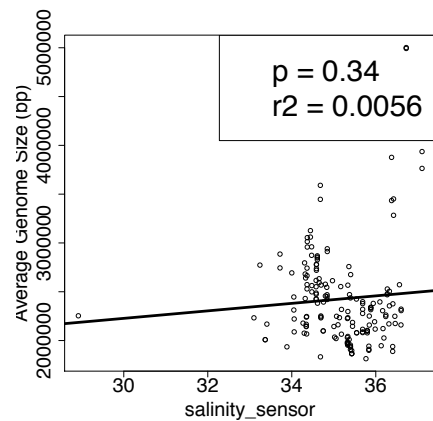
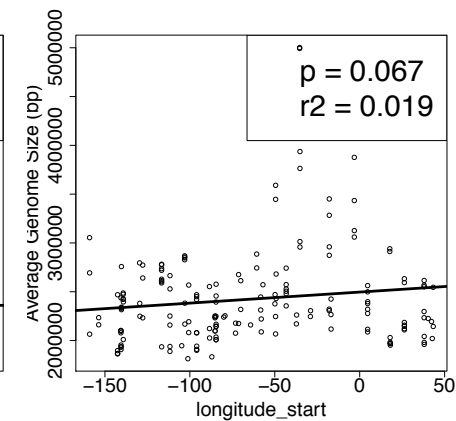
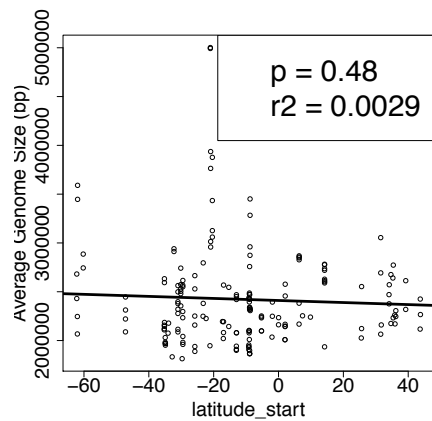
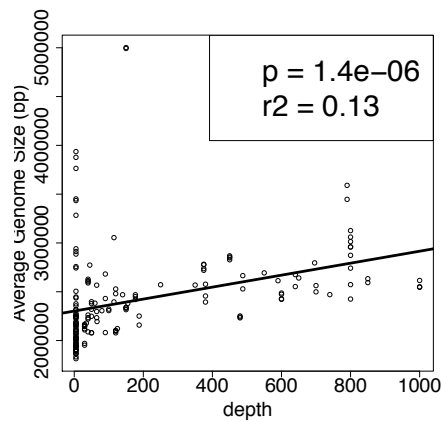






*Conditioned on size fraction 0.22 – 3.0

```
Call:
lm(formula = average_genome_size ~ depth + latitude_start + longitude_start +
    salinity_sensor + nitrate_sensor + temperature + oxygen_sensor +
    chlorophyll_sensor)
```

Residuals:

Min	1Q	Median	3Q	Max
-746914	-251503	-87662	118112	2311283

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-20902.0	1679368.3	-0.012	0.9901	
depth	553.3	267.8	2.066	0.0407	*
latitude_start	-2163.9	1872.8	-1.155	0.2499	
longitude_start	2305.5	933.3	2.470	0.0147	*
salinity_sensor	93180.2	44278.3	2.104	0.0372	*
nitrate_sensor	-11011.8	8981.0	-1.226	0.2223	
temperature	-22821.2	12106.6	-1.885	0.0615	.
oxygen_sensor	-1228.7	829.0	-1.482	0.1406	
chlorophyll_sensor	-44490.9	176446.4	-0.252	0.8013	

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

Residual standard error: 457400 on 137 degrees of freedom
(30 observations deleted due to missingness)
Multiple R-squared: 0.2651, Adjusted R-squared: 0.2222
F-statistic: 6.177 on 8 and 137 DF, p-value: 8.436e-07

*Conditioned on size fraction 0.22 – 3.0