

Oyster Introgression

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Introduction and Methods

This report hypothesises that gene flow is resulting in introgression is occurring between wild and selectively bred oysters that share an estuary, and that this introgression is altering the genome of the selectively bred populations.

Independent variables:

1. Allele frequency in wild oyster populations

Dependent variables:

2. Allele frequency selectively bred oyster populations

The null hypothesis is that there will be no gene flow between wild and selectively bred populations of oysters, and as a result there will be two genetically distinct population clusters shown in the Principal Components Analysis. Assumptions of PCA include multiple variables at continuous levels, a linear relationship between all variables, no significant outliers, sampling adequacy, and adequate correlations suitable for data reduction. A paired t-test was performed to determine whether or not the mean of expected versus observed heterozygosities was significantly different to zero (assumes the differences between pairs are normally distributed). A Bartlett test of homogeneity of variances was also performed (assumes dependent variable is normally distributed) with the null hypothesis being that there is no difference in variances. Observed heterozygosity versus expected heterozygosity per locus was also tested for, as was Hardy-Weinberg equilibrium (no mutation, random mating, no gene flow, infinite population size, and no selection). Expected heterozygosity was plotted as a function of observed heterozygosity.

Results

The null hypothesis is retained. There is no gene flow evident between the two populations. The PCA shows there are two distinct population clusters of oysters, one of selectively bred and one of wild. Populations within these clusters overlap but the two clusters themselves have no overlap. Bartlett's test showed that data follows a normal distribution ($p = 0.5642$, $df = 1$, $K\text{-squared} = 0.333$).

```
##
## Paired t-test
##
## data: div$Hexp and div$Hobs
## t = 30.036, df = 1199, p-value < 2.2e-16
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
## 0.06055909      Inf
## sample estimates:
## mean of the differences
```

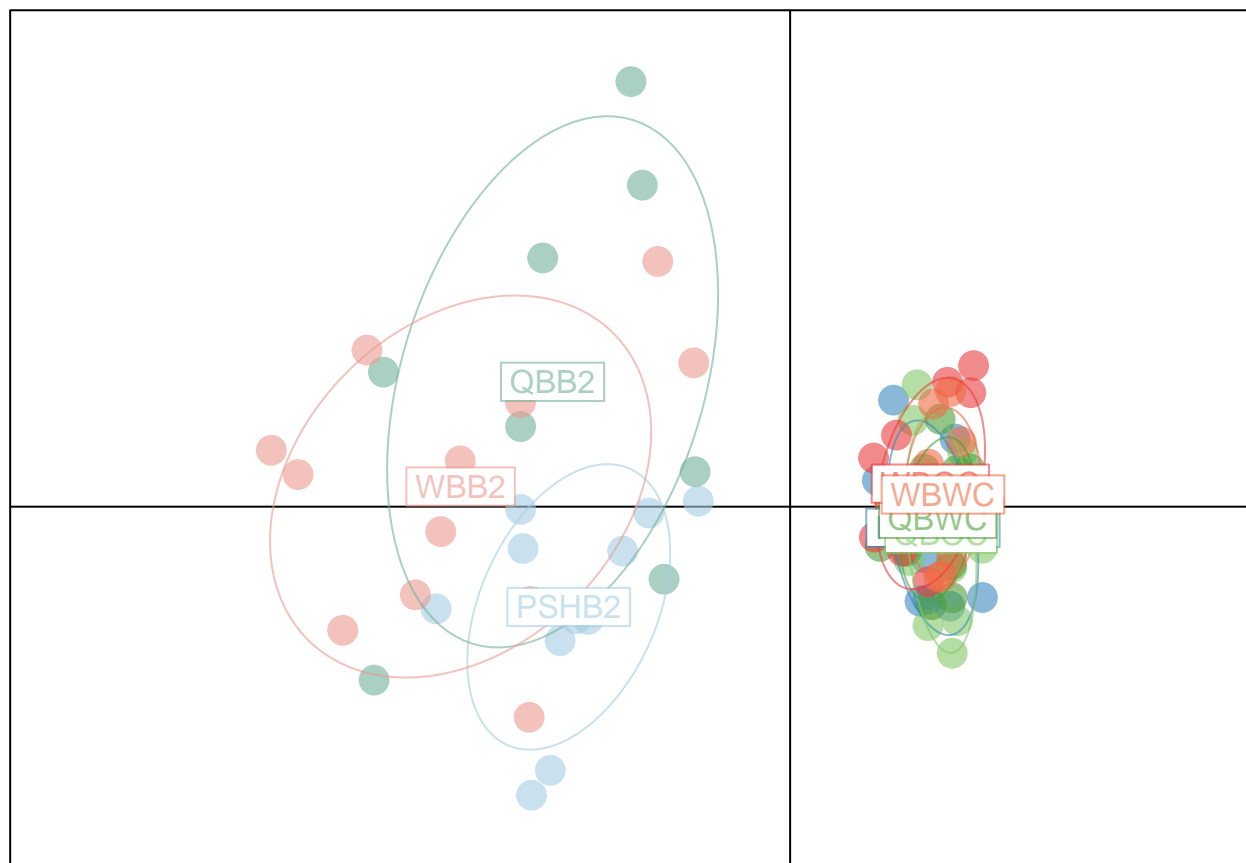
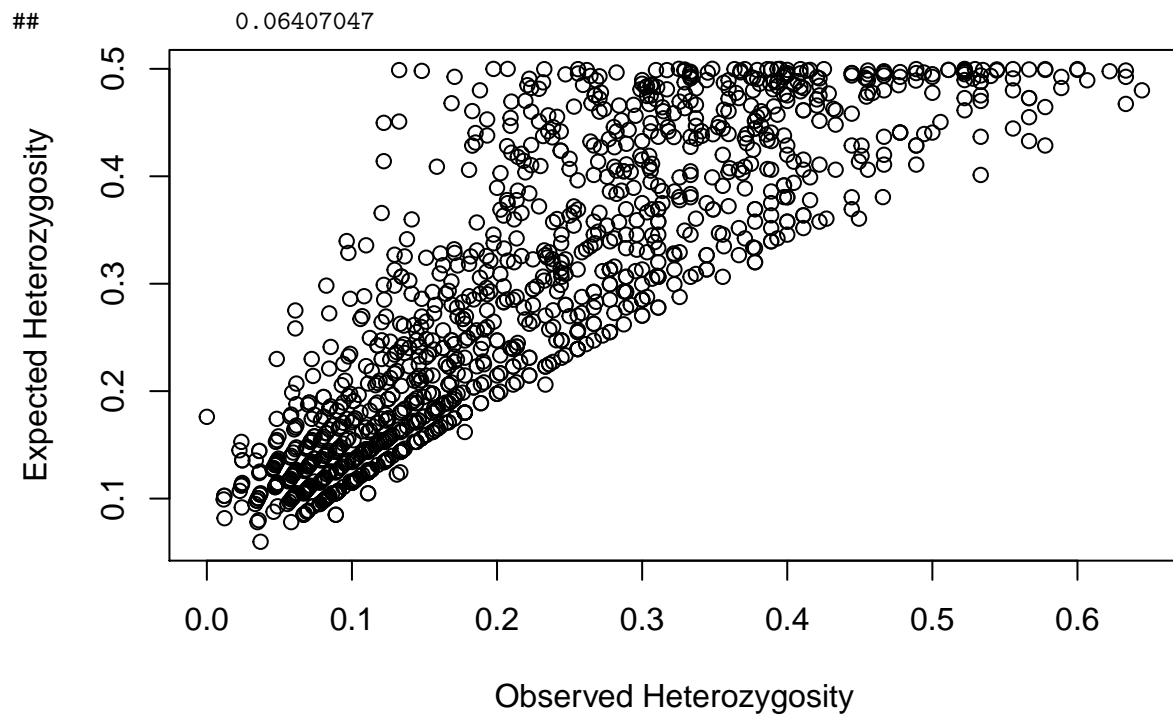


Table 1 Mean and standard deviation of Observed Heterozygosity per population

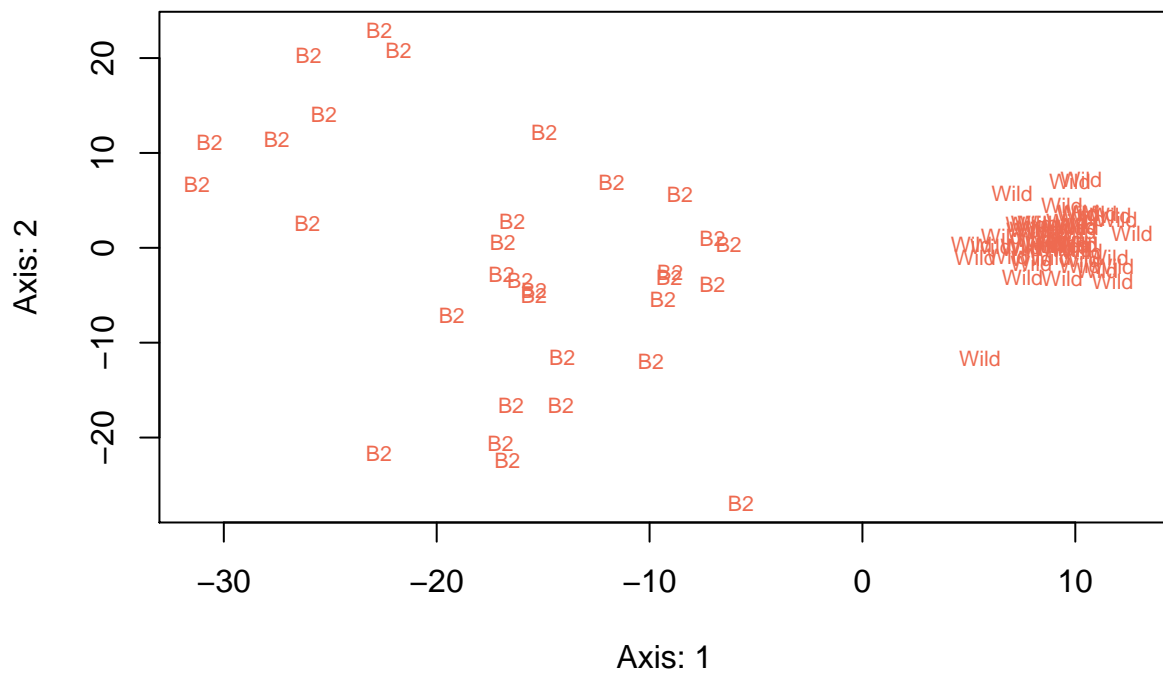
Population	Mean	SD	Population	Mean	SD
PSHB2	0.231	0.197	PSHB2	0.282	0.182
PSHWT	0.203	0.178	PSHWT	0.277	0.182
QBB2	0.263	0.223	QBB2	0.285	0.189
QBOC	0.203	0.169	QBOC	0.278	0.177
QBWC	0.193	0.171	QBWC	0.268	0.180
WBB2	0.235	0.204	WBB2	0.273	0.185
WBOC	0.241	0.196	WBOC	0.278	0.177
WBWC	0.219	0.187	WBWC	0.275	0.176

Table 1: Fis

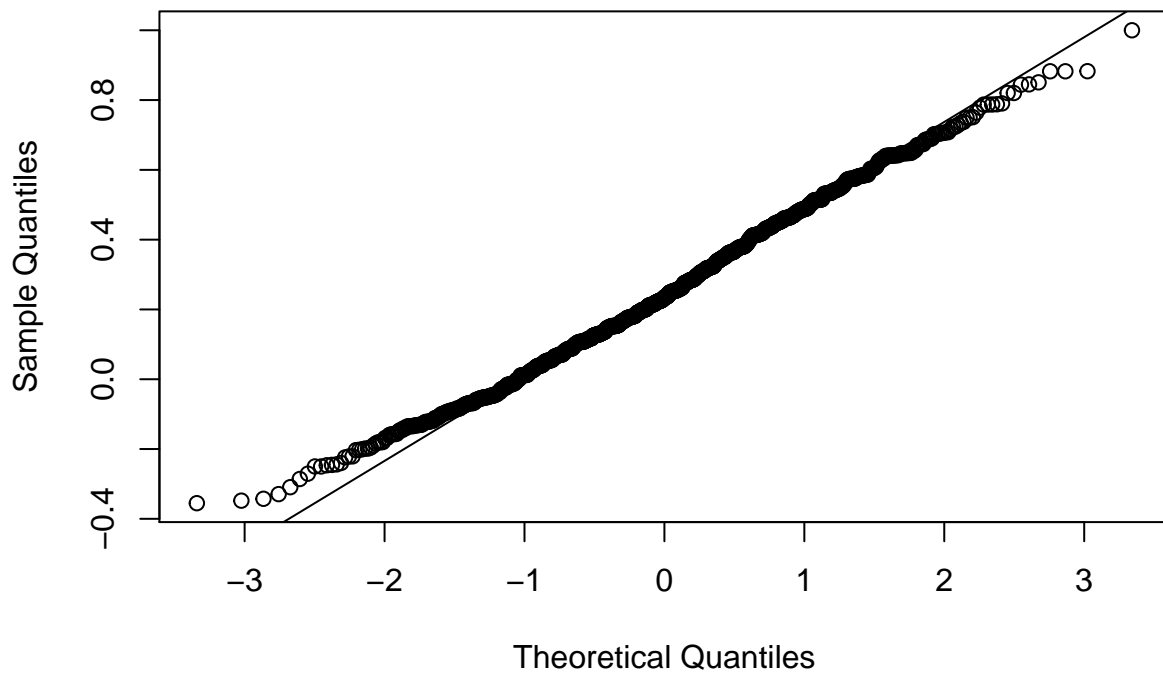
Population	Mean	SD
PSHB2	NaN	NA
PSHWT	NaN	NA
QBB2	NaN	NA
QBOC	NaN	NA
QBWC	NaN	NA
WBB2	NaN	NA
WBOC	NaN	NA
WBWC	NaN	NA

Table 2: Means by cluster

	Ho	Hs	Fis
B2	0.2418813	0.2833992	0.1547038
Wild	0.2125787	0.2766013	0.2501706



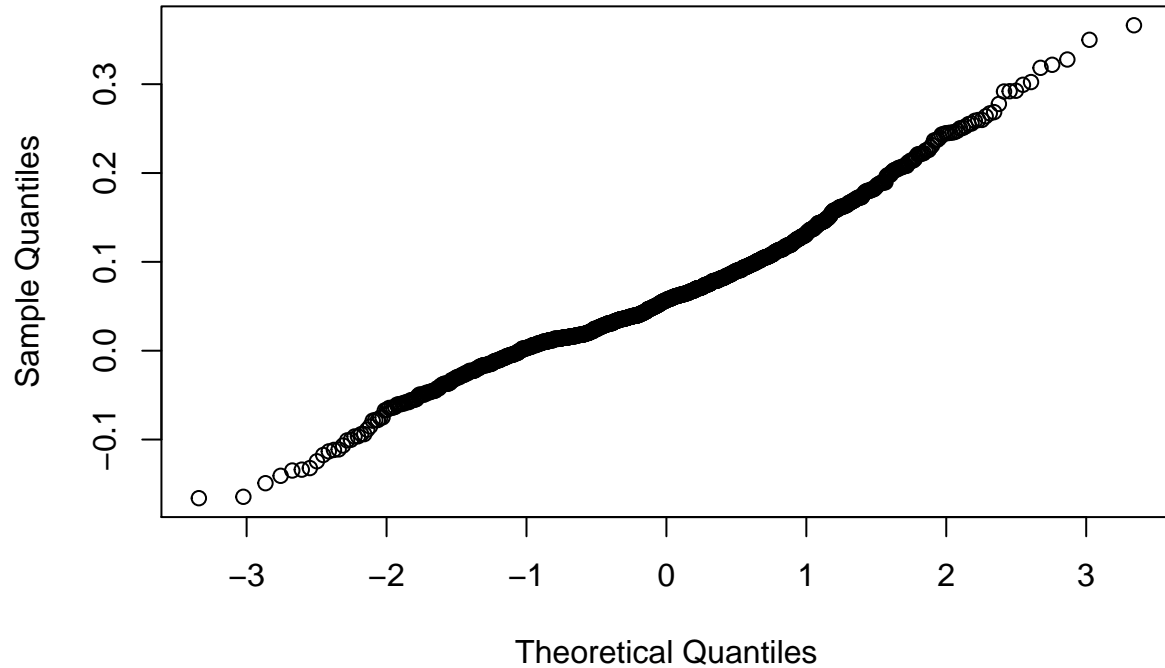
Normal Q-Q Plot



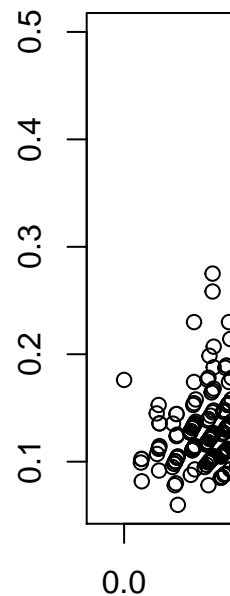
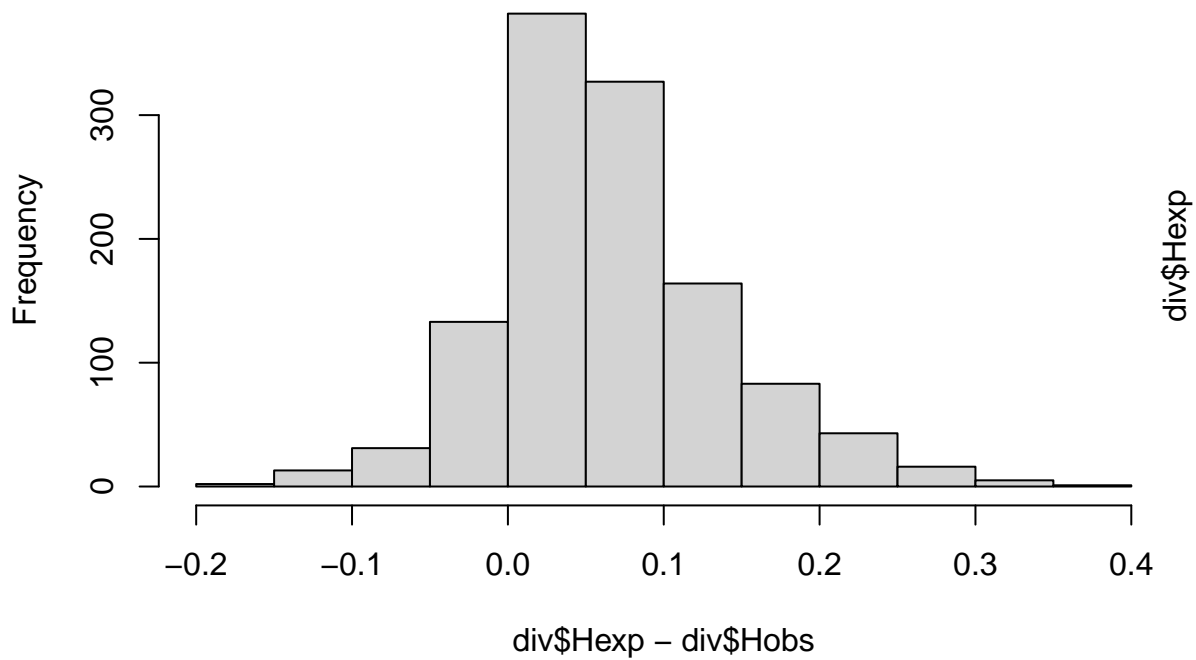
```
##
## One Sample t-test
##
## data: (div$Hexp - div$Hobs)/div$Hexp
## t = 37.449, df = 1199, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.2360068 0.2621024
```

```
## sample estimates:  
## mean of x  
## 0.2490546
```

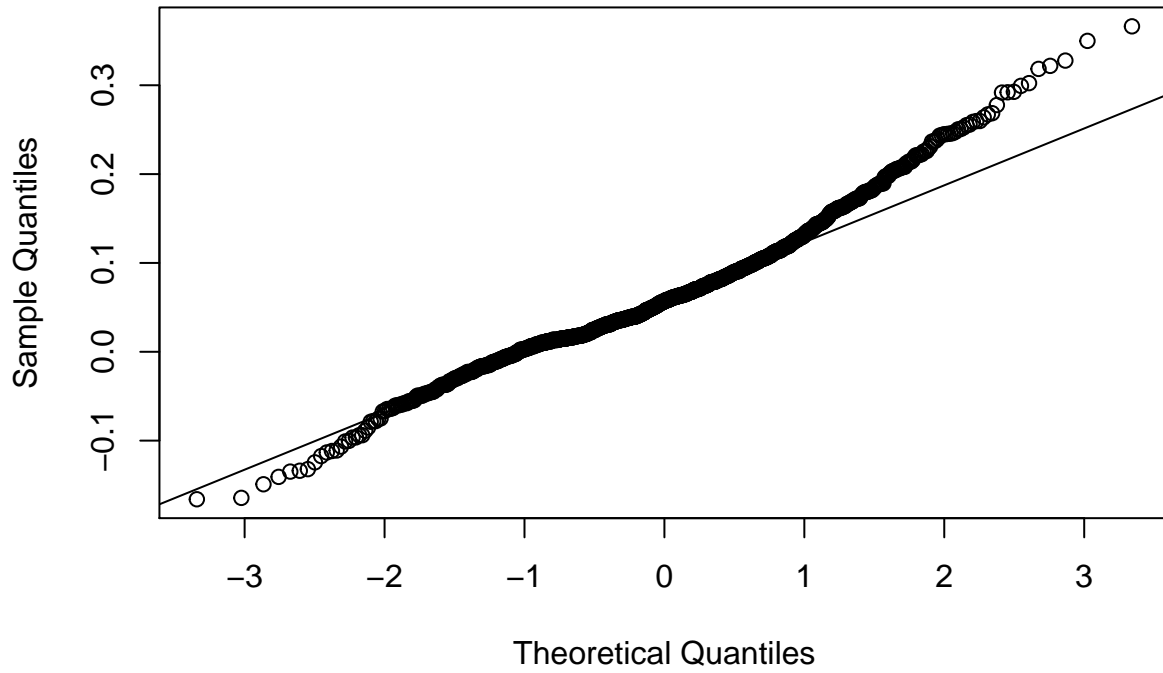
Normal Q-Q Plot



Histogram of $\text{div\$Hexp} - \text{div\$Hobs}$



Normal Q-Q Plot



	PSHB2	PSHWT	QBB2	QBOC	QBWC	WBB2	WBOC	WBWC
PSHB2	0.0000000	0.0665750	0.0417318	0.0651636	0.0661305	0.0379892	0.0631809	0.0665982
PSHWT	0.0665750	0.0000000	0.0701249	0.0333541	0.0339569	0.0804270	0.0343087	0.0341038
QBB2	0.0417318	0.0701249	0.0000000	0.0677433	0.0671852	0.0356512	0.0651010	0.0654191
QBOC	0.0651636	0.0333541	0.0677433	0.0000000	0.0305003	0.0816611	0.0313014	0.0294721
QBWC	0.0661305	0.0339569	0.0671852	0.0305003	0.0000000	0.0821794	0.0330787	0.0297248
WBB2	0.0379892	0.0804270	0.0356512	0.0816611	0.0821794	0.0000000	0.0788351	0.0796010
WBOC	0.0631809	0.0343087	0.0651010	0.0313014	0.0330787	0.0788351	0.0000000	0.0301782
WBWC	0.0665982	0.0341038	0.0654191	0.0294721	0.0297248	0.0796010	0.0301782	0.0000000