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rv370
week-5 Assignment:

```
> bermuda = read.csv("Bermudagrass SNP dataset.csv", header = TRUE, row.names = 1)# complete the
code here
> dim(bermuda)
[1] 8239  132
> #Chi-square test for segregation distortion within each allele freq type:
> chisq_pval_bermuda=c()
> for (i in 1:nrow(bermuda)){
+   hh_sum = sum(bermuda[i,]=="hh" ,na.rm =T) # complete the code here
+   hk_sum = sum(bermuda[i,]=="hk" ,na.rm =T) # complete the code here
+   kk_sum = sum(bermuda[i,]=="kk" ,na.rm =T) # complete the code here
+   observed_geno_freqs =c(c(hh_sum, hk_sum, kk_sum)) # complete the code here
+   chisq_pval_bermuda[i] = chisq.test(observed_geno_freqs, p=c(0.25,0.5,0.25))$p.value# complete the
code here)$p.value
+ }
> # Use plot, hist, table and look at the results...
> # Due on Tuesday midnight..
> plot(chisq_pval_bermuda)
>hist(chisq_pval_bermuda, breaks=20)
> table(chisq_pval_bermuda < 0.0001)

FALSE
 8239
> table(chisq_pval_bermuda < 0.001)

FALSE  TRUE
 7938   301
> table(chisq_pval_bermuda < 0.05)

FALSE  TRUE
 6674  1565
```
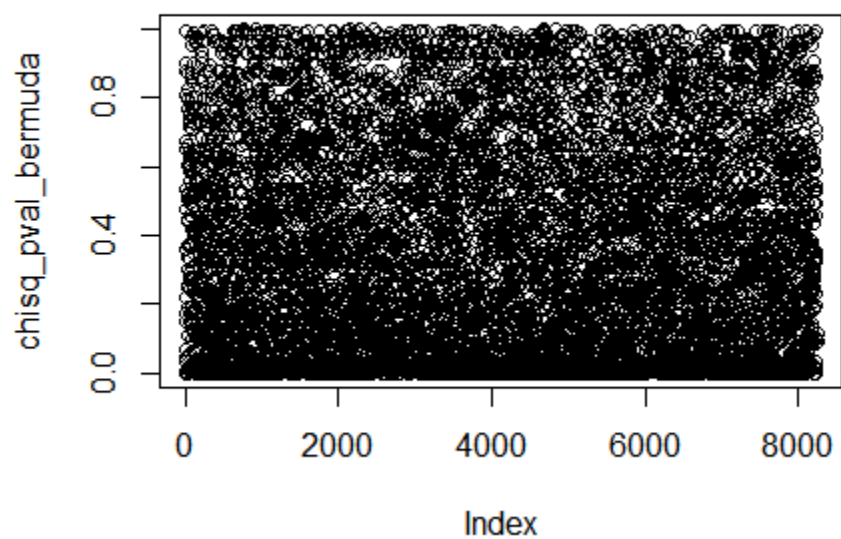
Histogram of chisq_pval_bermuda