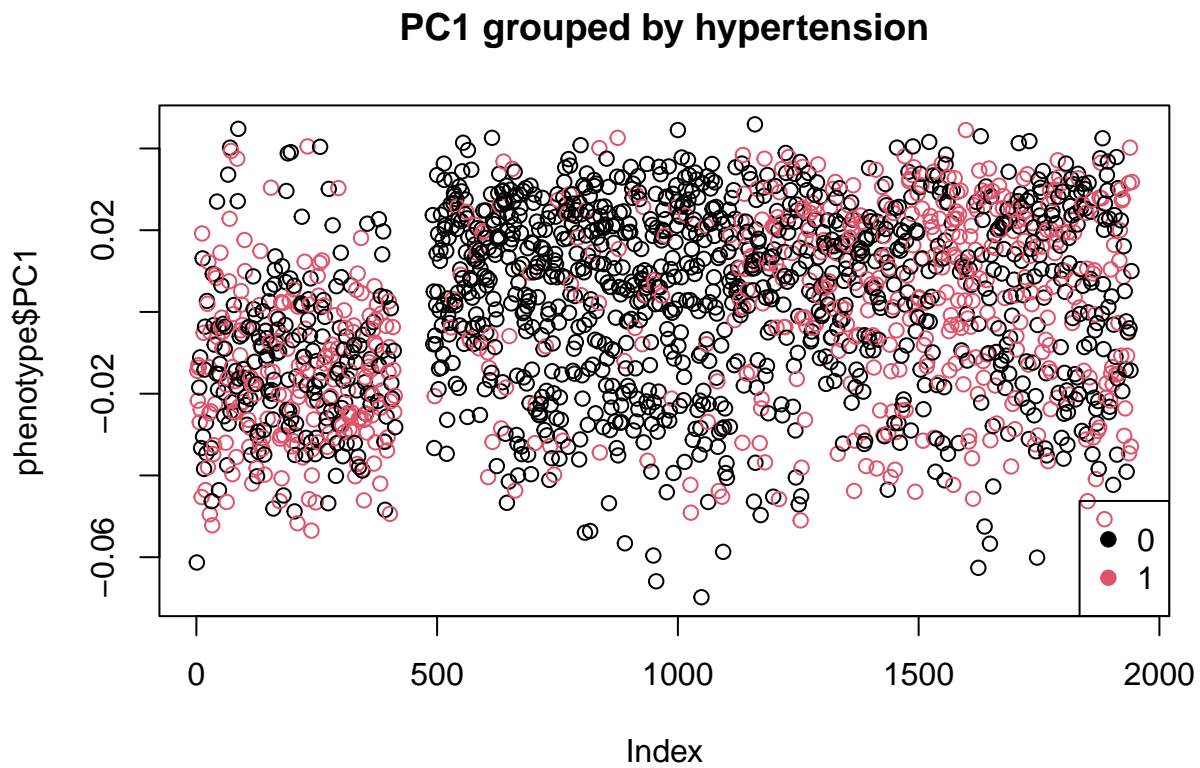


```
#Plotting significant PCs and dichotomous outcomes
```

```
plot(phenotype$PC1,col=factor(phenotype$HTN), main="PC1 grouped by hypertension")
```

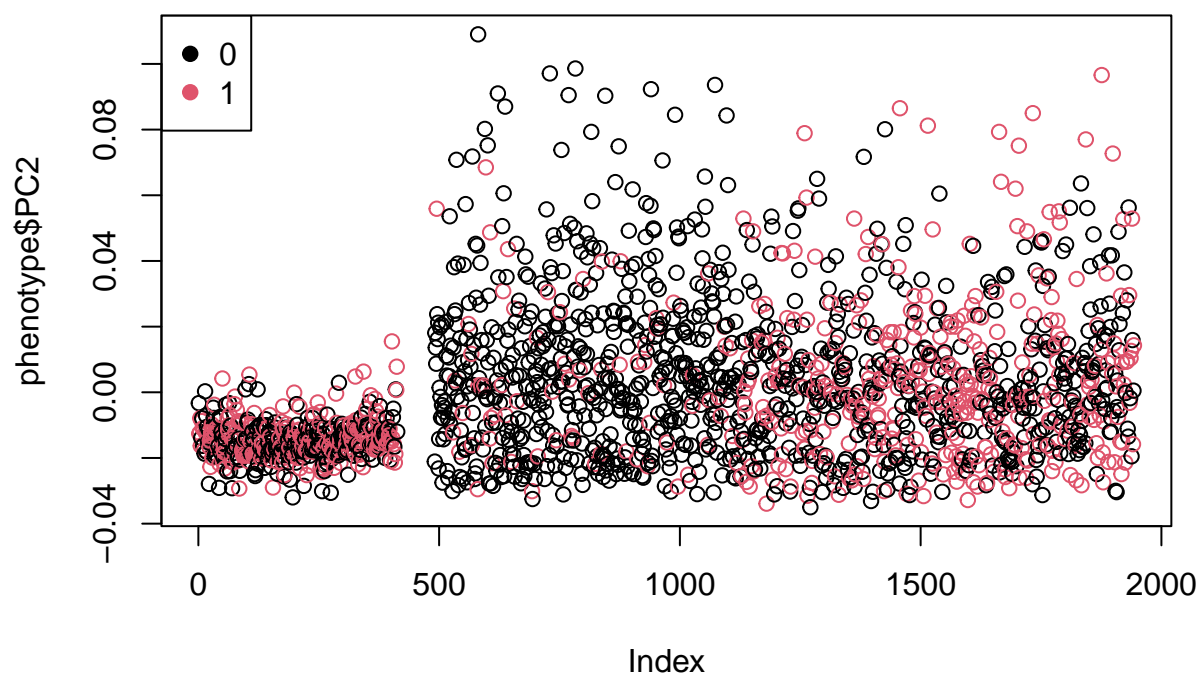
```
legend("bottomright", legend=levels(factor(phenotype$HTN)), pch=19, col=factor(levels(factor(phenotype$HTN))))
```



```
plot(phenotype$PC2, col=factor(phenotype$HTN), main="PC2 grouped by hypertension")
```

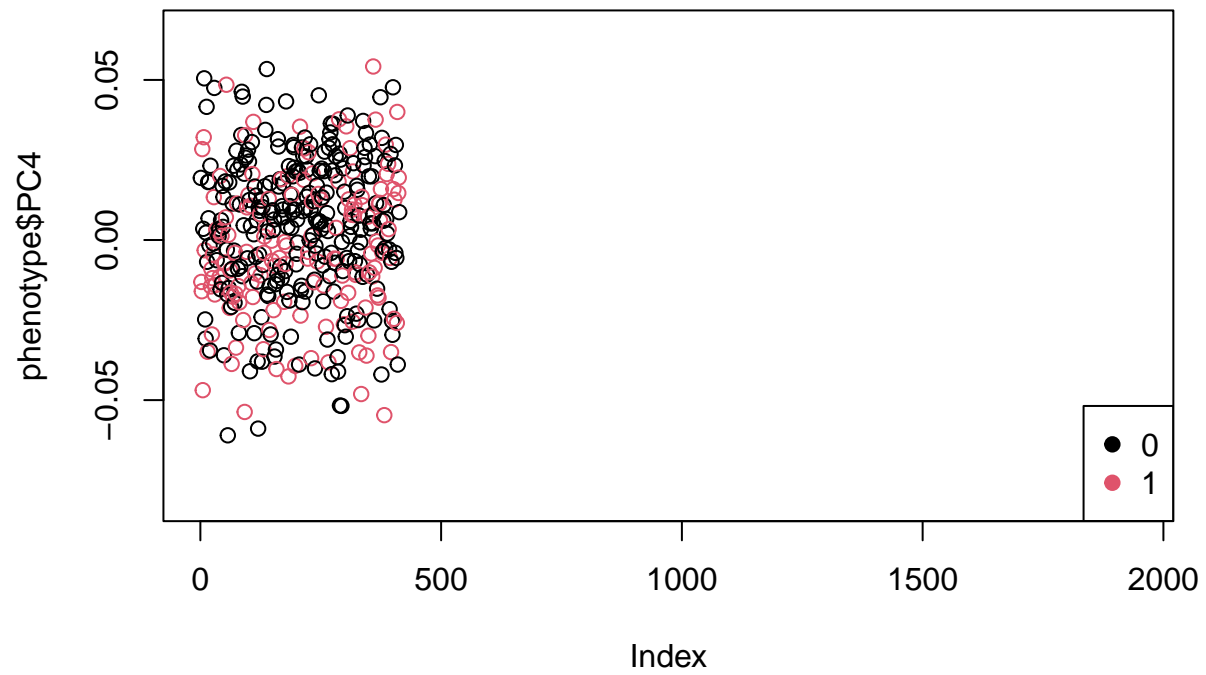
```
legend("topleft", legend=levels(factor(phenotype$HTN)), pch=19, col=factor(levels(factor(phenotype$HTN))))
```

PC2 grouped by hypertension



```
plot(phenotype$PC4, col=factor(phenotype$BPMED), main="PC4 grouped by BPMED")  
legend("bottomright", legend=levels(factor(phenotype$BPMED)), pch=19, col=factor(levels(factor(phenotype$BPMED))))
```

PC4 grouped by BPMED



```
plot(phenotype$PC2, col=factor(phenotype$SEX), main="PC2 grouped by sex")  
legend("topleft", legend=levels(factor(phenotype$SEX)), pch=19, col=factor(levels(factor(phenotype$SEX))
```

