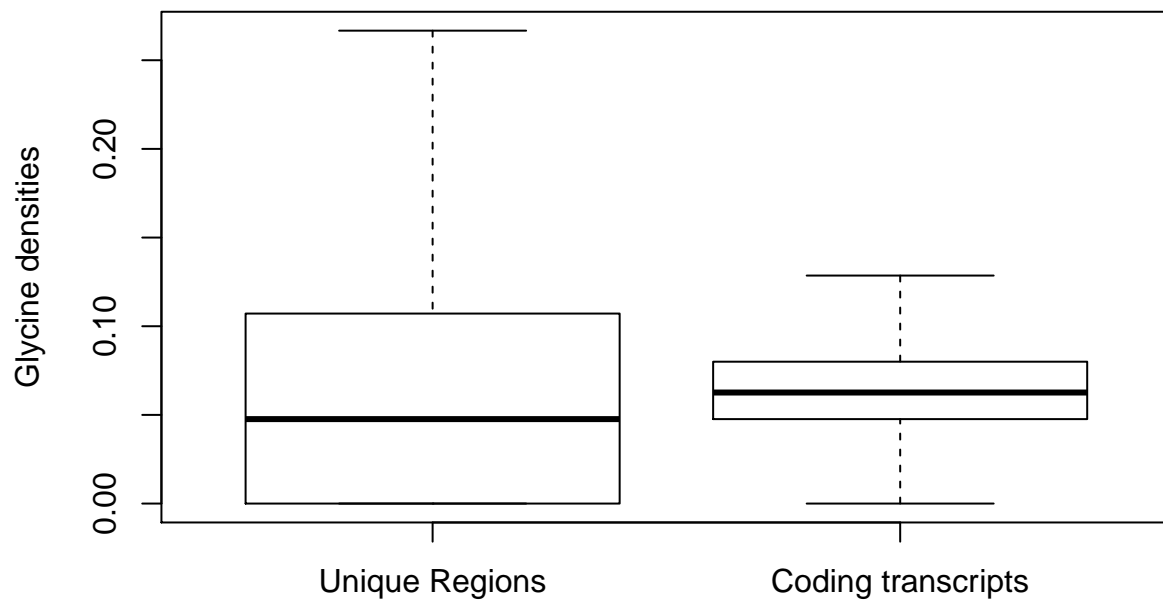


# DensityReport

Human

NMD

## Glycine densities for unique regions and protein coding transcripts



```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: densitiesgly[[1]] and densitiesgly[[2]]
```

```
## t = 5.6255, df = 12913, p-value = 1.888e-08
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

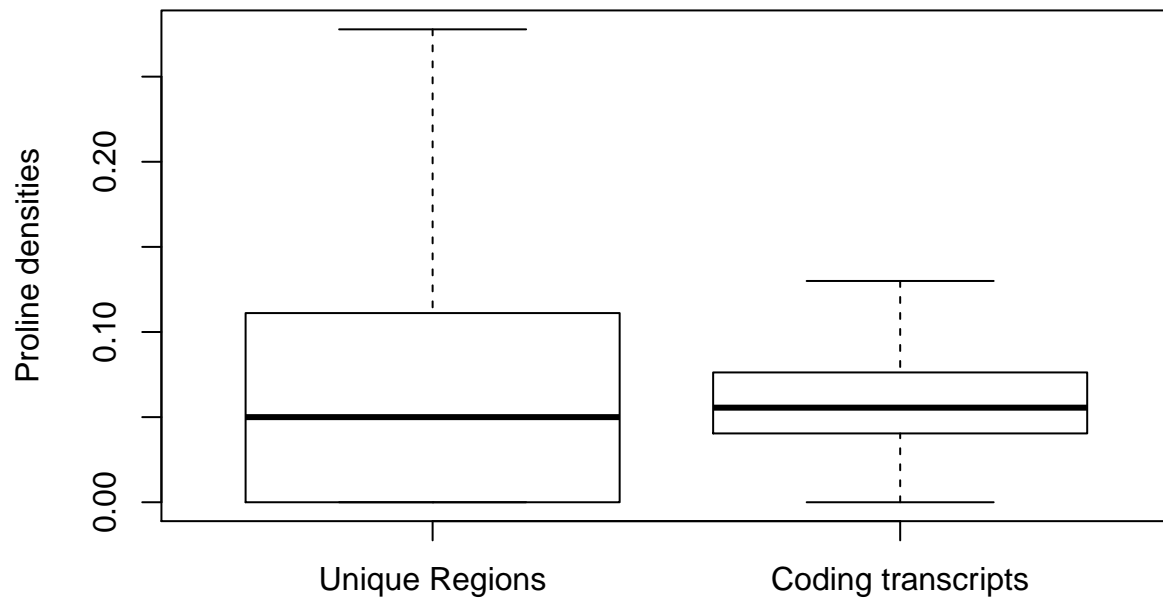
```
## 0.003423380 0.007084866
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.07146637 0.06621225
```

## Proline densities for unique regions and protein coding transcripts

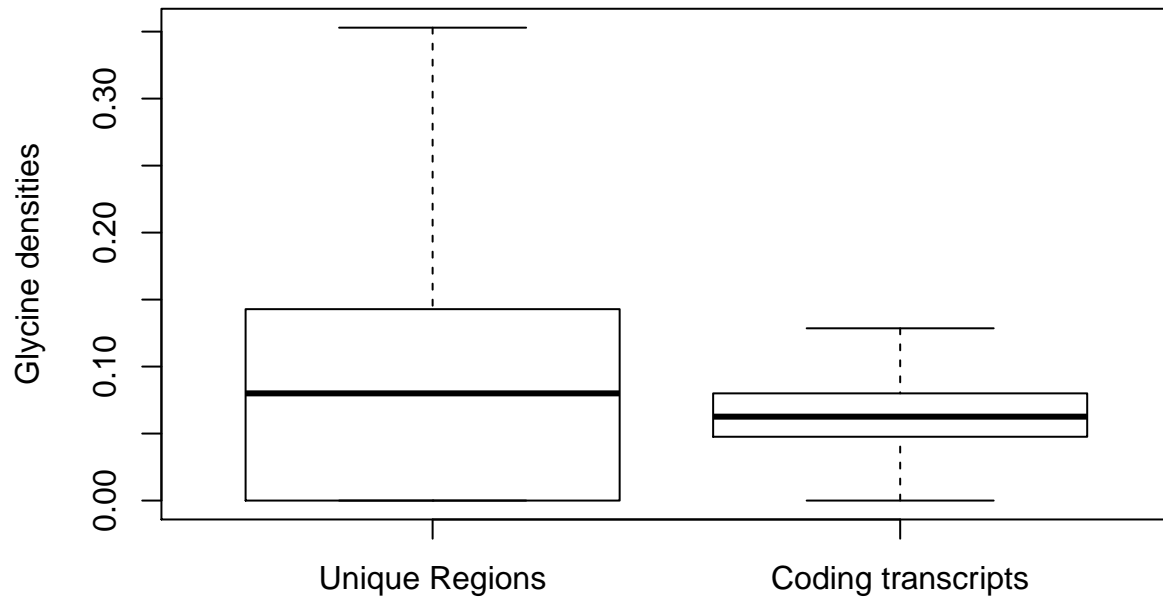


```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##  
## Welch Two Sample t-test  
##  
## data: densitiespro[[1]] and densitiespro[[2]]  
## t = 9.9046, df = 13116, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.006338820 0.009466777  
## sample estimates:  
## mean of x mean of y  
## 0.06966723 0.06176443
```

RI

## Glycine densities for unique regions and protein coding transcripts



```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: densitiesglyRI[[1]] and densitiesglyRI[[2]]
```

```
## t = 28.016, df = 10095, p-value < 2.2e-16
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

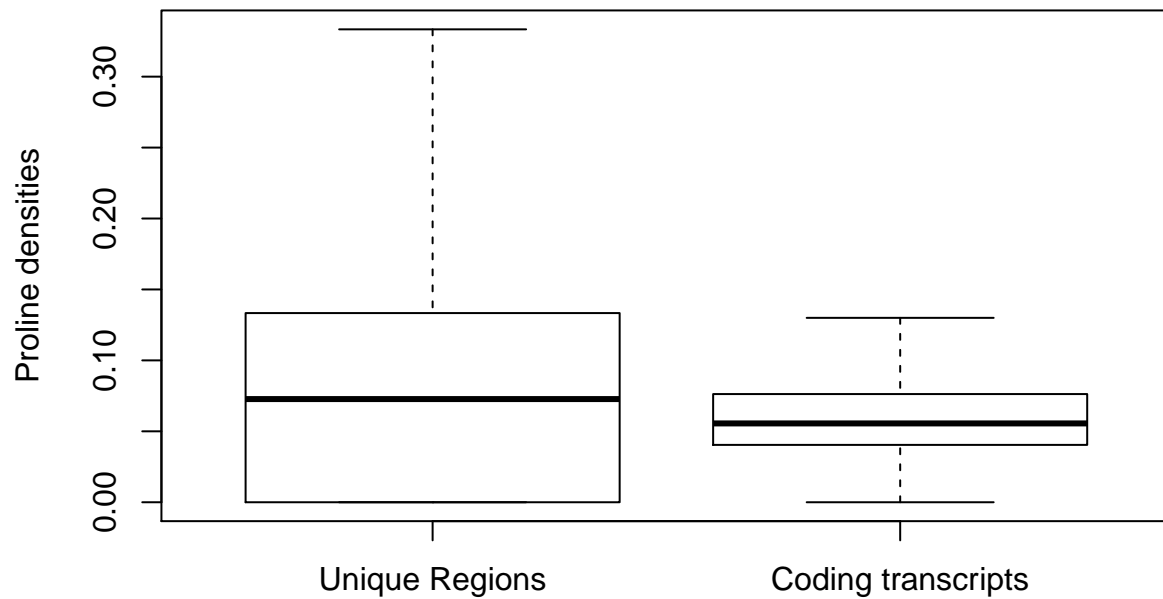
```
## 0.0283012 0.0325595
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.09664260 0.06621225
```

## Proline densities for unique regions and protein coding transcripts



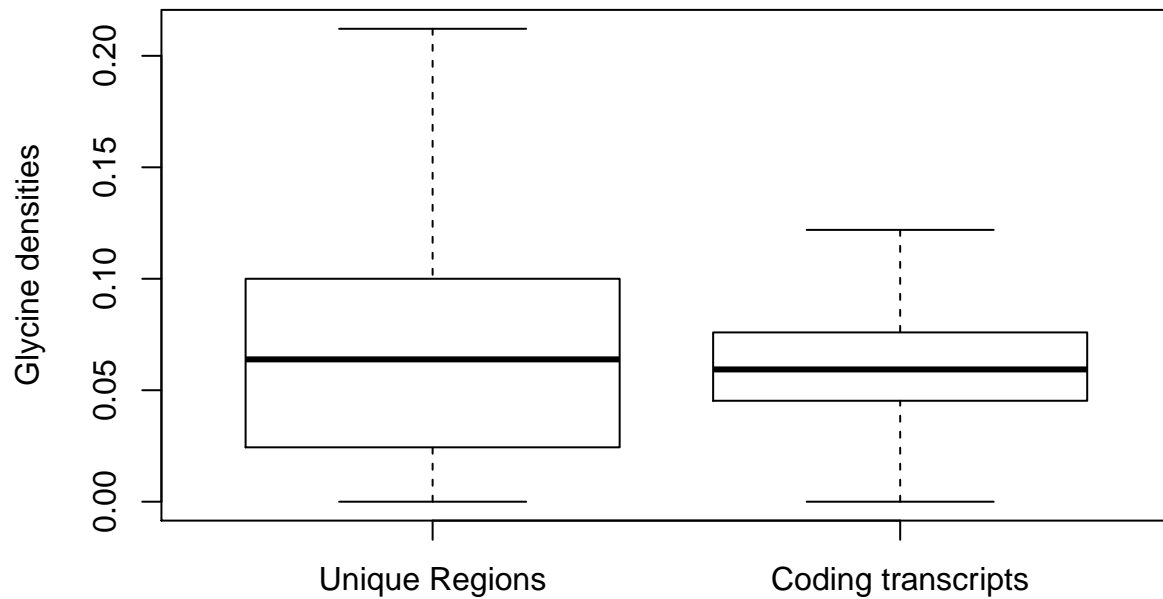
```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##  
## Welch Two Sample t-test  
##  
## data: densitiesproRI[[1]] and densitiesproRI[[2]]  
## t = 26.073, df = 10247, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.02114665 0.02458475  
## sample estimates:  
## mean of x mean of y  
## 0.08463012 0.06176443
```

## Mouse

NMD

### Glycine densities for unique regions and protein coding transcripts



```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: densitiesglyMouse[[1]] and densitiesglyMouse[[2]]
```

```
## t = 7.7434, df = 3053.4, p-value = 1.307e-14
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

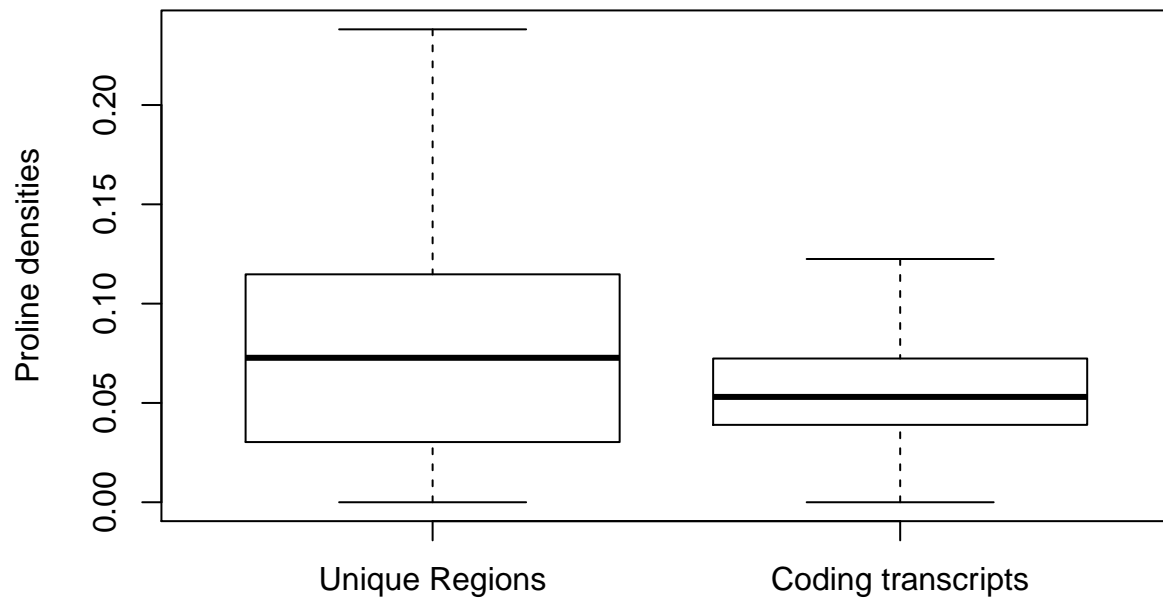
```
## 0.006744476 0.011318220
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.07185273 0.06282138
```

## Proline densities for unique regions and protein coding transcripts

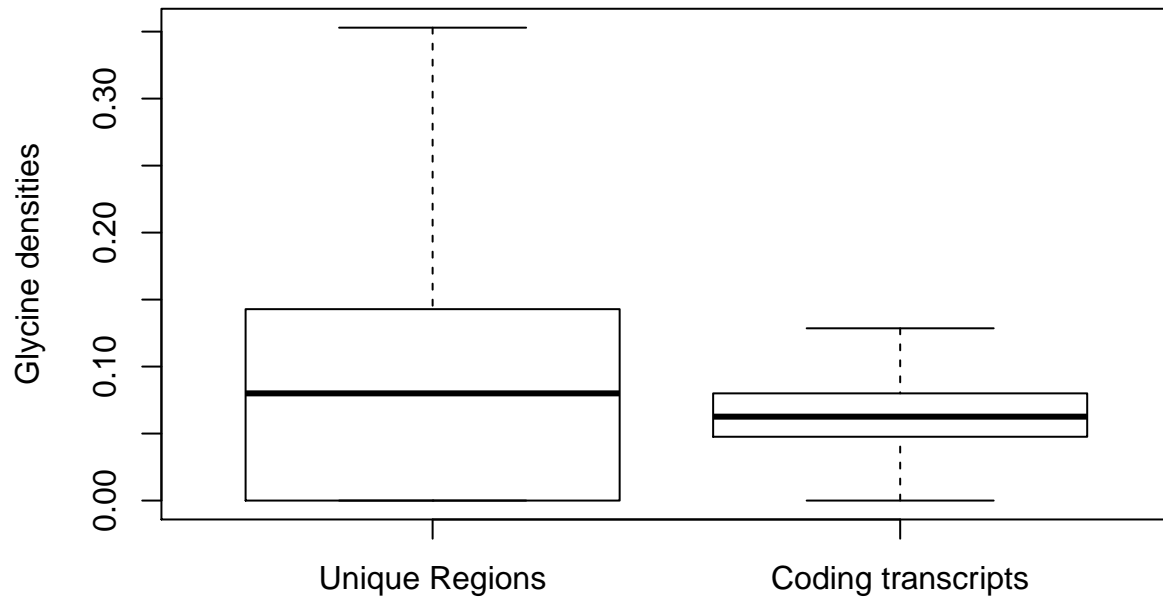


```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##  
## Welch Two Sample t-test  
##  
## data: densitiesproMouse[[1]] and densitiesproMouse[[2]]  
## t = 16.384, df = 3065.7, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.01694731 0.02155502  
## sample estimates:  
## mean of x mean of y  
## 0.07820662 0.05895546
```

RI

## Glycine densities for unique regions and protein coding transcripts



```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: densitiesglyRIMouse[[1]] and densitiesglyRIMouse[[2]]
```

```
## t = 19.638, df = 3838.4, p-value < 2.2e-16
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

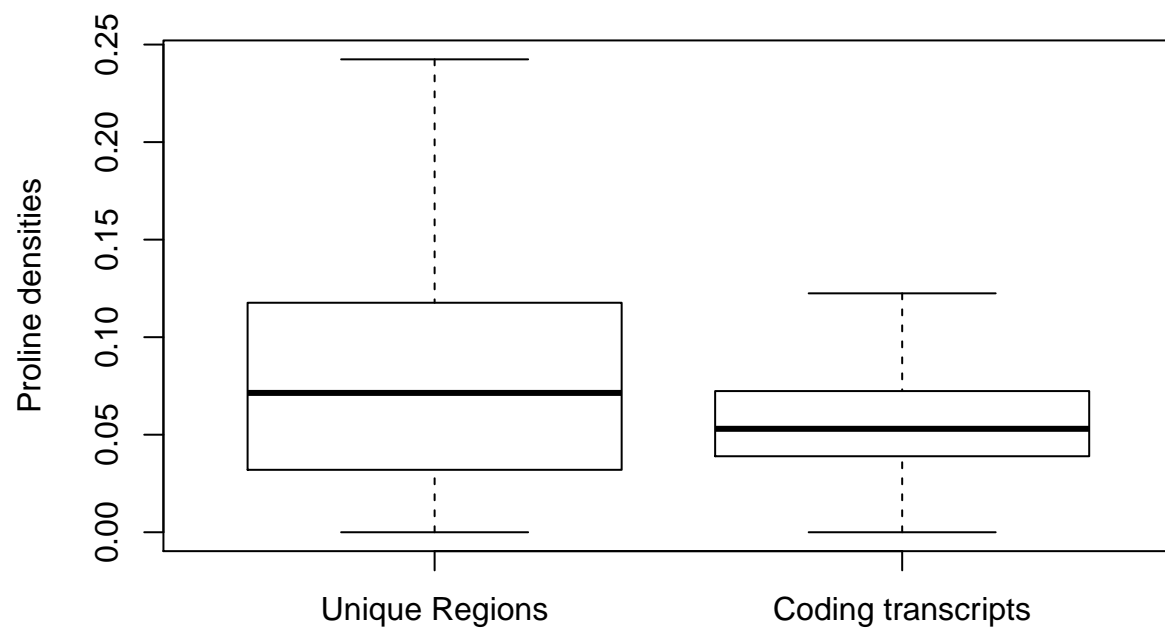
```
## 0.02068703 0.02527578
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.08580278 0.06282138
```

## Proline densities for unique regions and protein coding transcripts



```
## T-test between Unique Protein Regions and coding transcripts:
```

```
##  
## Welch Two Sample t-test  
##  
## data: densitiesproRIMouse[[1]] and densitiesproRIMouse[[2]]  
## t = 19.449, df = 3871.9, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 0.01893630 0.02318204  
## sample estimates:  
## mean of x mean of y  
## 0.08001463 0.05895546
```