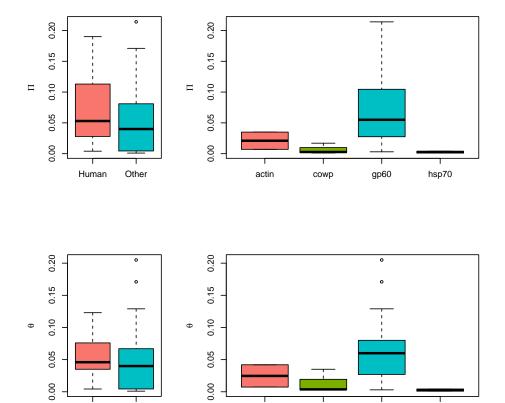
Zoonotic cryptosporidium

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1 Zoonotic - all data

```
> fit <- manova(cbind(Species, Gene, Pi, Theta) ~ Zoonotic, data = Pi_data)
> summary(fit, test = "Pillai")
          Df Pillai approx F num Df den Df Pr(>F)
Zoonotic 1 0.1905
                    1.4709
                                 4
                                       25 0.2409
Residuals 28
> summary.aov(fit)
 Response Species :
           Df Sum Sq Mean Sq F value Pr(>F)
            1 0.025 0.0254 0.0124 0.912
Zoonotic
Residuals
           28 57.175 2.0419
 Response Gene :
           Df Sum Sq Mean Sq F value Pr(>F)
            1 0.0397 0.03968 0.0916 0.7644
Zoonotic
Residuals
            28 12.1270 0.43311
 Response Pi :
                Sum Sq Mean Sq F value Pr(>F)
            1 0.003463 0.0034625 0.9074 0.349
Zoonotic
           28 0.106849 0.0038160
Residuals
 Response Theta:
                Sum Sq
                          Mean Sq F value Pr(>F)
           Df
           1 0.000224 0.00022399 0.0819 0.7769
Zoonotic
           28 0.076598 0.00273564
Residuals
    Gene - all data
2
> fit <- manova(cbind(Species, Pi, Theta) ~ Gene, data = Pi_data)</pre>
> summary(fit, test = "Pillai")
          Df Pillai approx F num Df den Df Pr(>F)
           3 0.33647 1.0948
                                  9
                                        78 0.3765
Gene
Residuals 26
> summary.aov(fit)
```



actin

Figure 1: All data

cowp

gp60

hsp70

```
Response Species :
```

Human

Df Sum Sq Mean Sq F value Pr(>F)

Gene 3 5.722 1.9072 0.9633 0.4249

Residuals 26 51.478 1.9799

Other

Response Pi :

Df Sum Sq Mean Sq F value Pr(>F)

Gene 3 0.023637 0.0078789 2.3635 0.09427 .

Residuals 26 0.086674 0.0033336

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

Response Theta:

Df Sum Sq Mean Sq F value Pr(>F)

Gene 3 0.013931 0.0046436 1.9197 0.1512

Residuals 26 0.062891 0.0024189

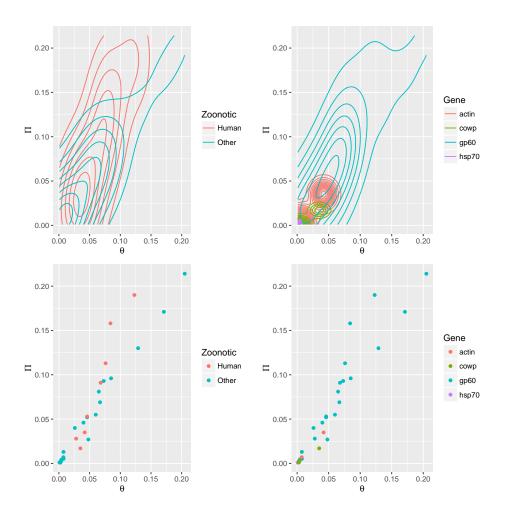


Figure 2: All data diversity density

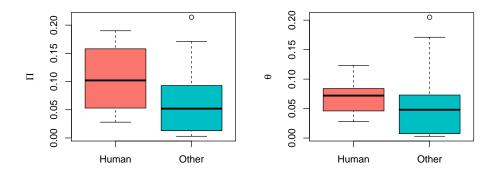


Figure 3: gp60 diversity

3 Zoonotic - gp60 data

```
> fit <- manova(cbind(Species, Pi, Theta) ~ Zoonotic, data = newdata)
> summary(fit, test="Pillai")
          Df Pillai approx F num Df den Df
                                             Pr(>F)
                      5.0216
                                        19 0.009911 **
Zoonotic
          1 0.44224
                                  3
Residuals 21
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
> summary.aov(fit)
 Response Species :
            Df Sum Sq Mean Sq F value Pr(>F)
Zoonotic
            1 0.096 0.09591 0.0392 0.845
            21 51.382 2.44678
Residuals
 Response Pi :
                 Sum Sq
                         Mean Sq F value Pr(>F)
             1 0.007304 0.0073038 1.9459 0.1776
Zoonotic
Residuals
            21 0.078821 0.0037534
 Response Theta:
                 Sum Sq
                           Mean Sq F value Pr(>F)
Zoonotic
             1 0.000406 0.00040604 0.1393 0.7127
            21 0.061203 0.00291443
Residuals
```

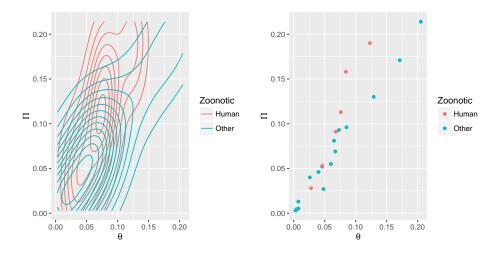


Figure 4: gp60 diversity density