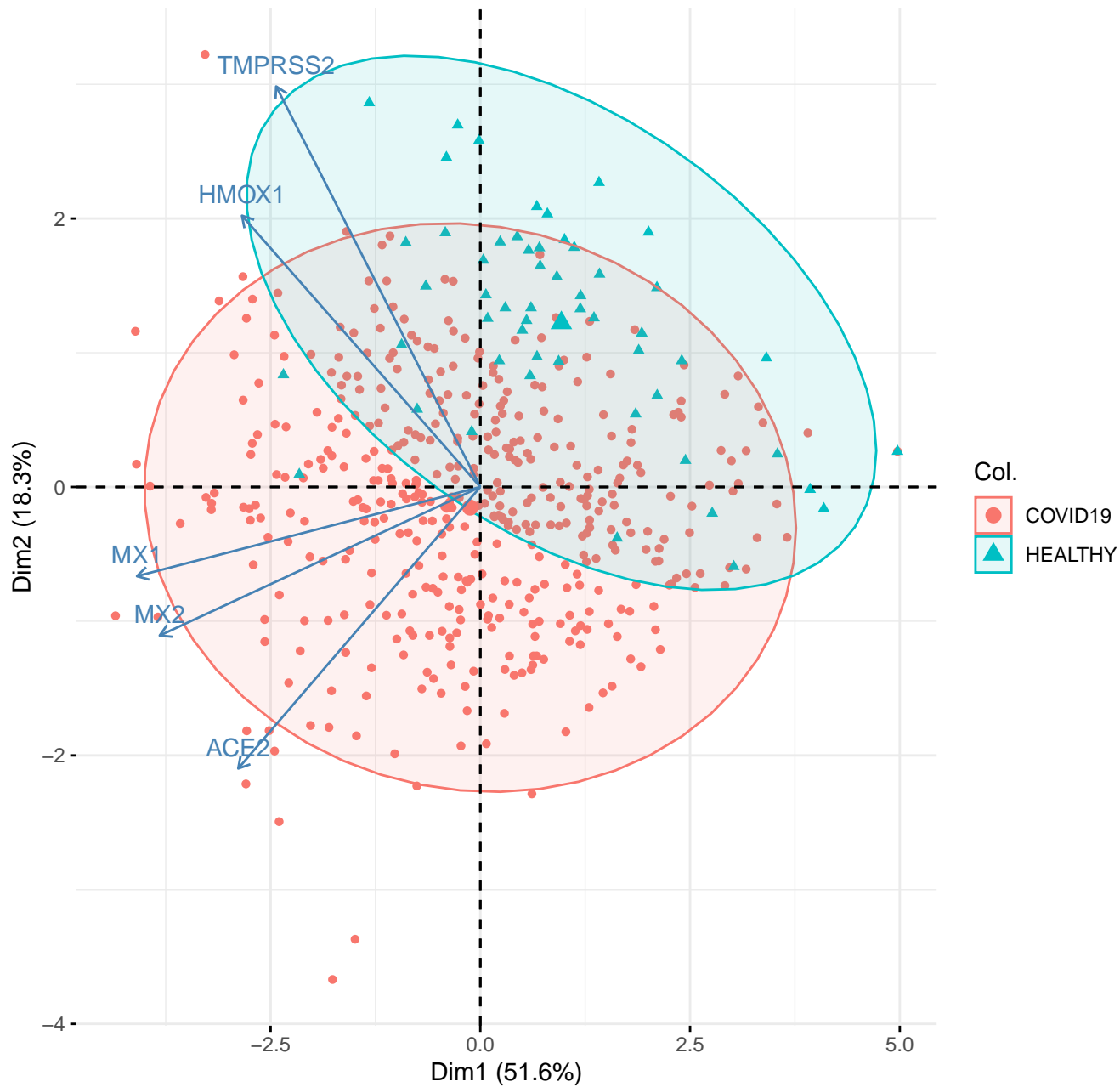
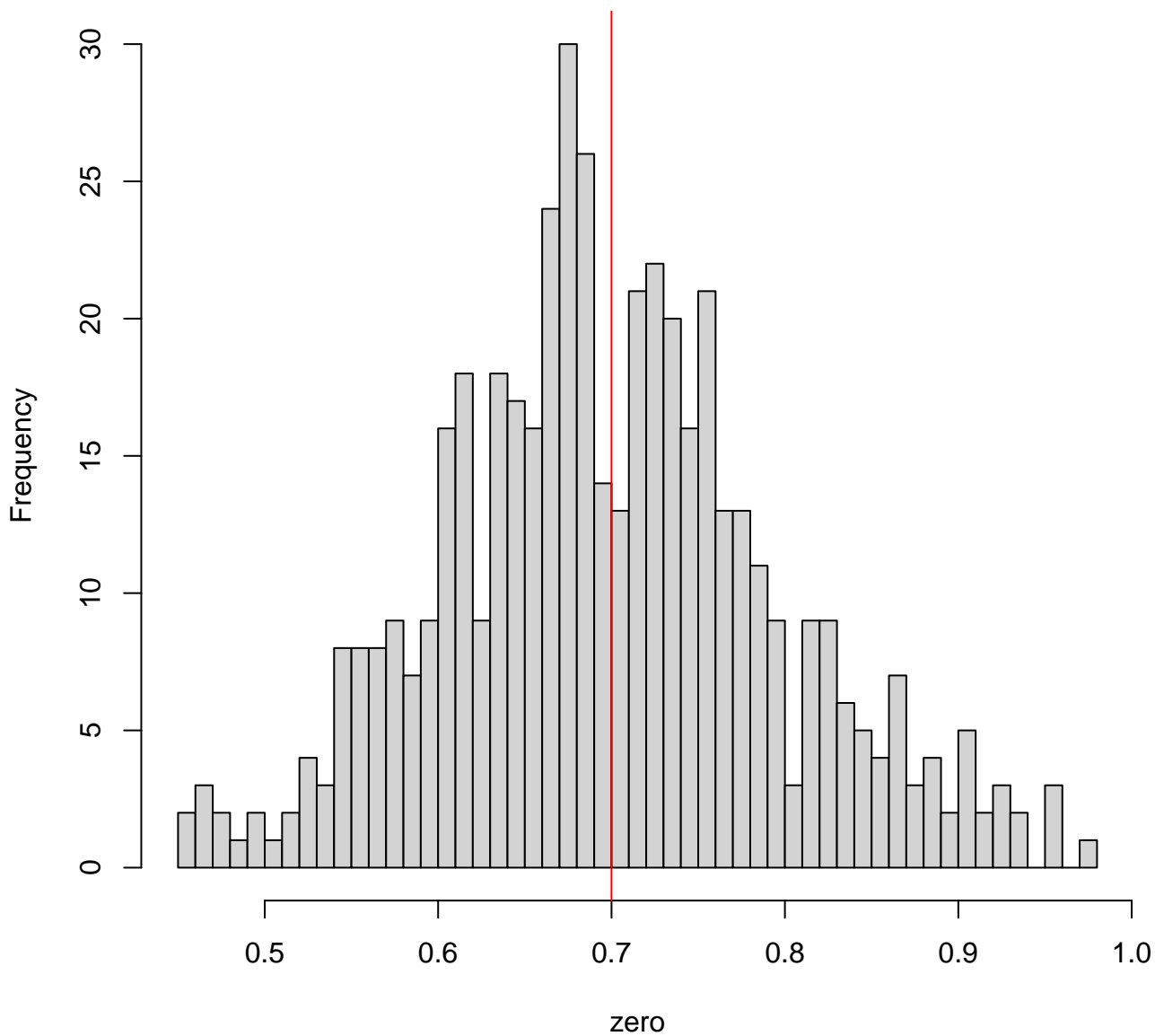
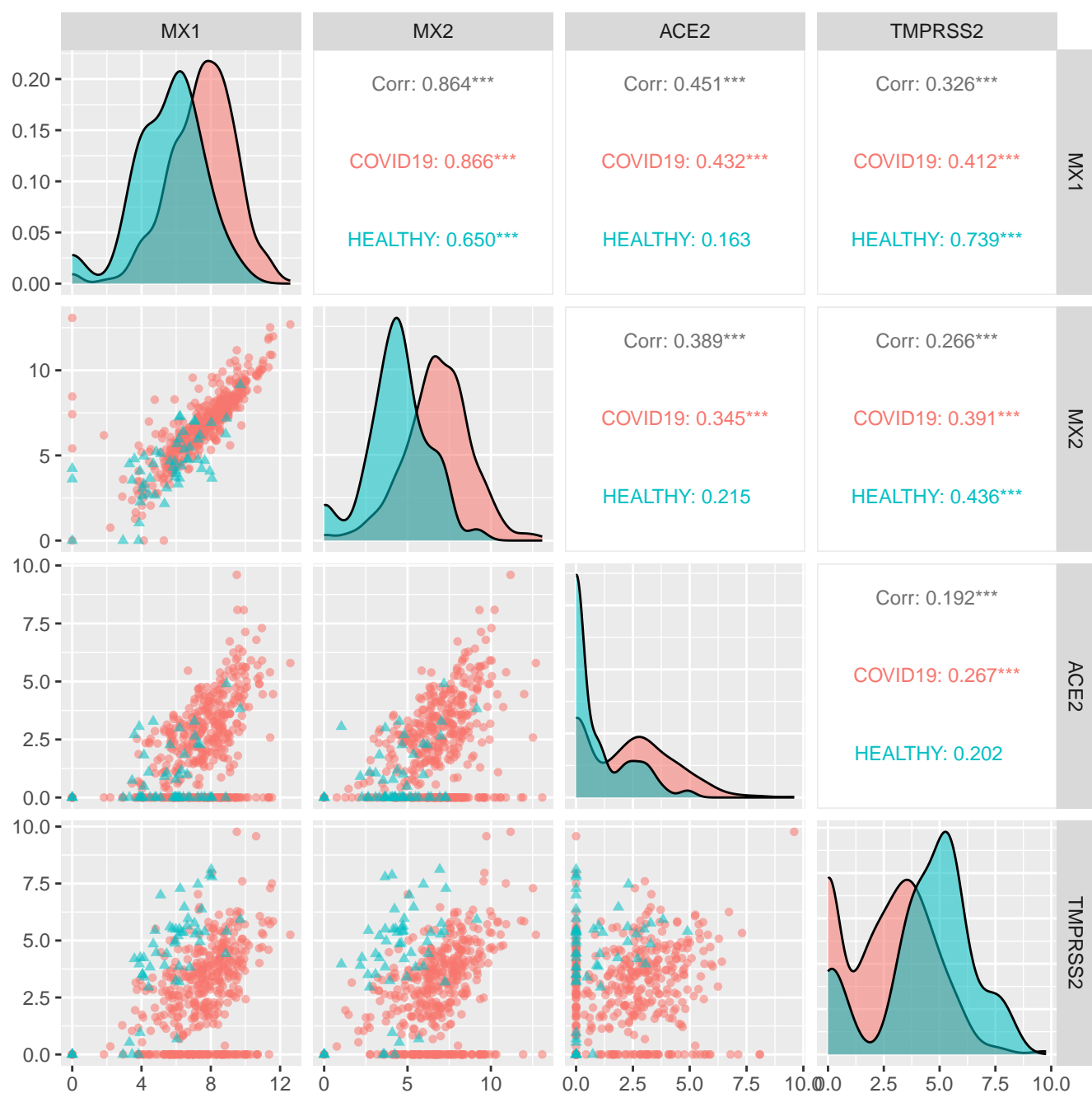


# Principal Component Analysis



**Histogram of zero**





Spearman's rank correlation rho

```
data: unlist(norm_counts[snakemake@config[["target_gene"]], ][which(clindata[[snakemake@config[["disease_s
== snakemake@config[["disease_condition"]]]) and unlist(norm_counts[snakemake@config[["validation_gene'
]][which(clindata[[snakemake@config[["disease_status"]]] == snakemake@config[["disease_condition"]]])
S = 1779766, p-value < 2.2e-16 alternative hypothesis: true rho is not equal to
0 sample estimates: rho 0.8656892
```

Wilcoxon rank sum test with continuity correction

data:   unlist(norm\_counts[snakemake@config[["target\_gene"]],   ]) by clin-  
data[[snakemake@config[["disease\_status"]]]] W = 17802, p-value = 1.651e-10  
alternative hypothesis: true location shift is not equal to 0

Jonckheere-Terpstra test

data:

JT = 30442, p-value = 0.002 alternative hypothesis: decreasing