# Question 5

class = c(1,1,0,0,1,0,0,0,0,0,0,0,0,0,1,0,0,1,1,0) FST = c(-0.006,-0.005,-0.005,-0.002,0.003,0.004,0.006,0.015,0.016,0.016,0.024,0.041,0.044,0.049,0.053,0.058,0.066,0.095,0.116,0.163)

data = data.frame(class,FST) xyz = split(data,data$class) dna = xyz$'0' protein = xyz$'1' hist(dna$FST) hist(protein$FST) a = median(dna$FST) b = median(protein$FST) diff = a – b a b diff boxplot(FST~class) kruskal.test(data$class, data$FST)

x = data$FST

bootmed = apply(matrix(sample(x, rep = TRUE, 10^4\*length(x)), nrow = 10\*4),1,median)

quantile(bootmed,c(0.025,0.975))s

[1] 0.02

[1] 0.028

[1] -0.008

Kruskal-Wallis rank sum test

data: data$class and data$FST

Kruskal-Wallis chi-squared = 16.738, df = 17, p-value = 0.4722

2.5% 97.5%

0.016 0.024

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