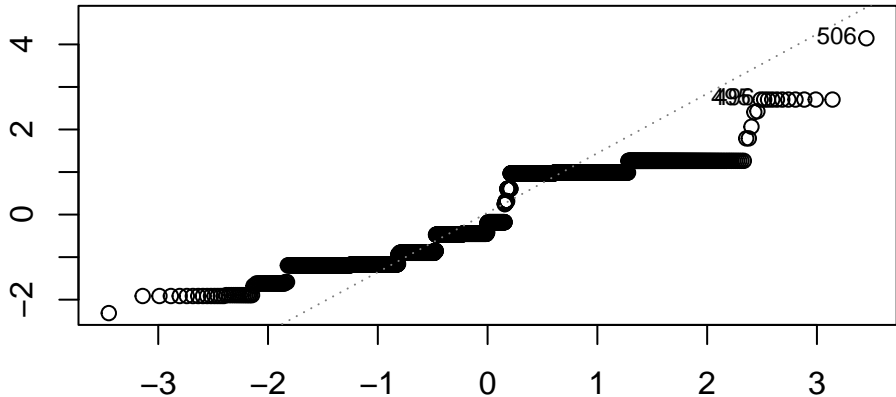


Normal Q-Q

Standardized residuals



Theoretical Quantiles
lm(gene.count ~ category)