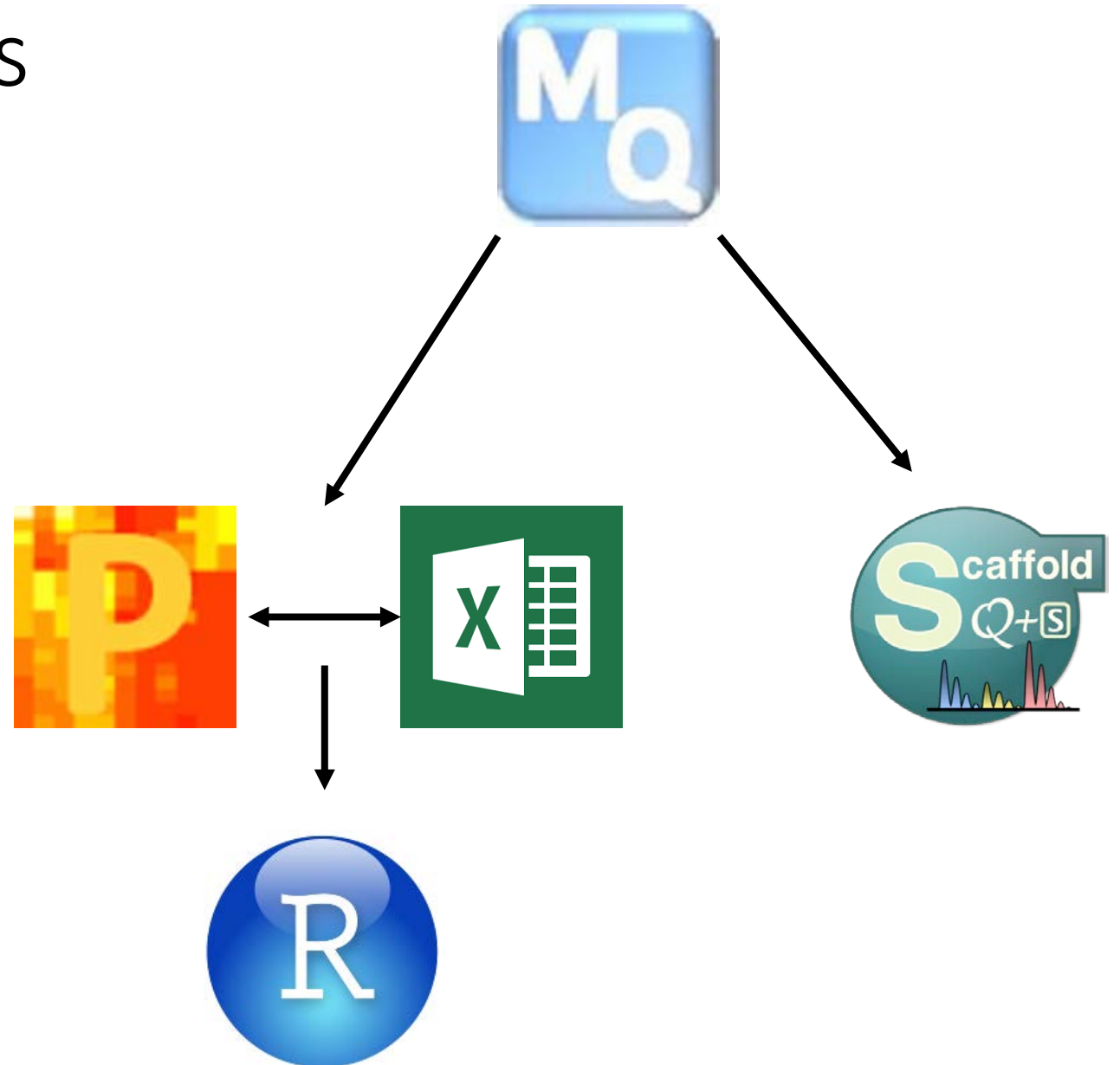


# Bioinformatics for Proteomics

Stephanie Byrum, PhD

# TMT10plex Data Analysis

- Experimental design
- Database search
  - MaxQuant
- Normalization
- Missing Values
- Perseus
- Scaffold Q+S



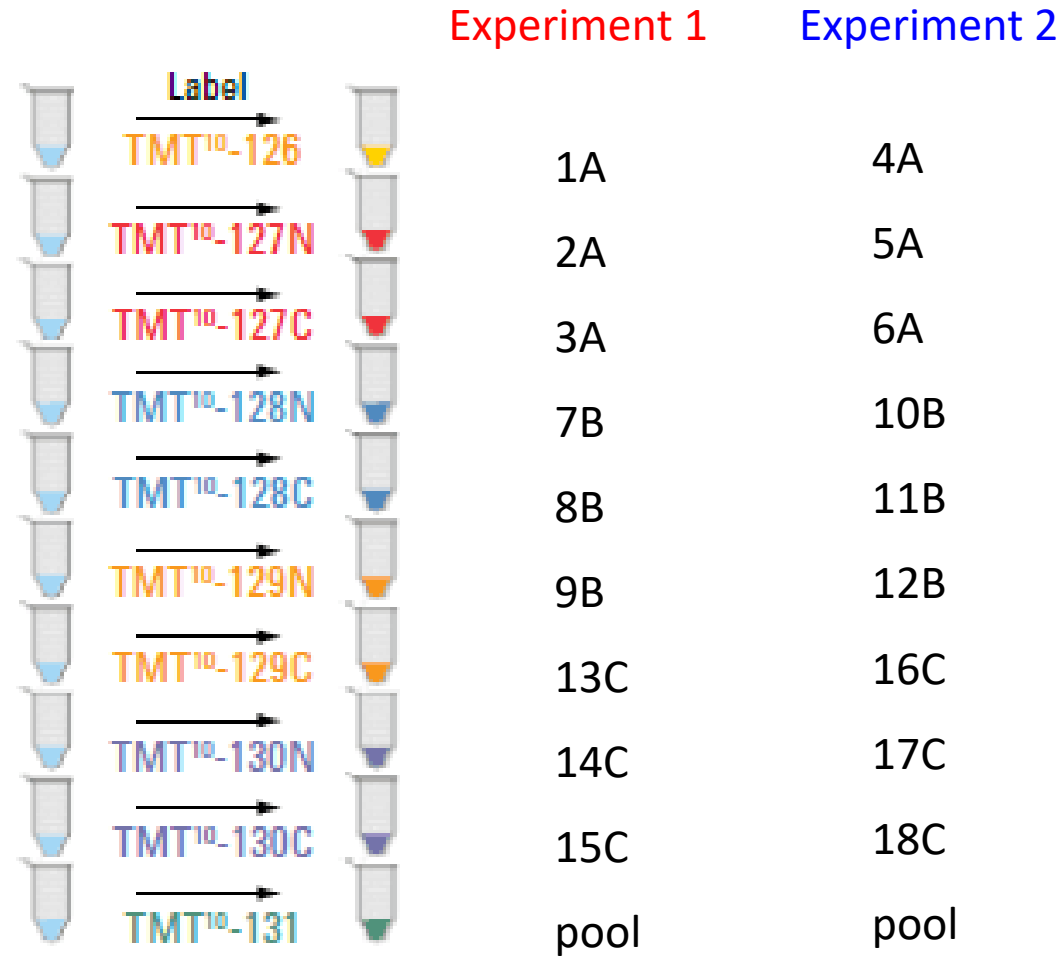
# TMT10plex Sample Mixing

Groups:

**A:** 1, 2, 3, 4, 5, 6

**B:** 7, 8, 9, 10, 11, 12

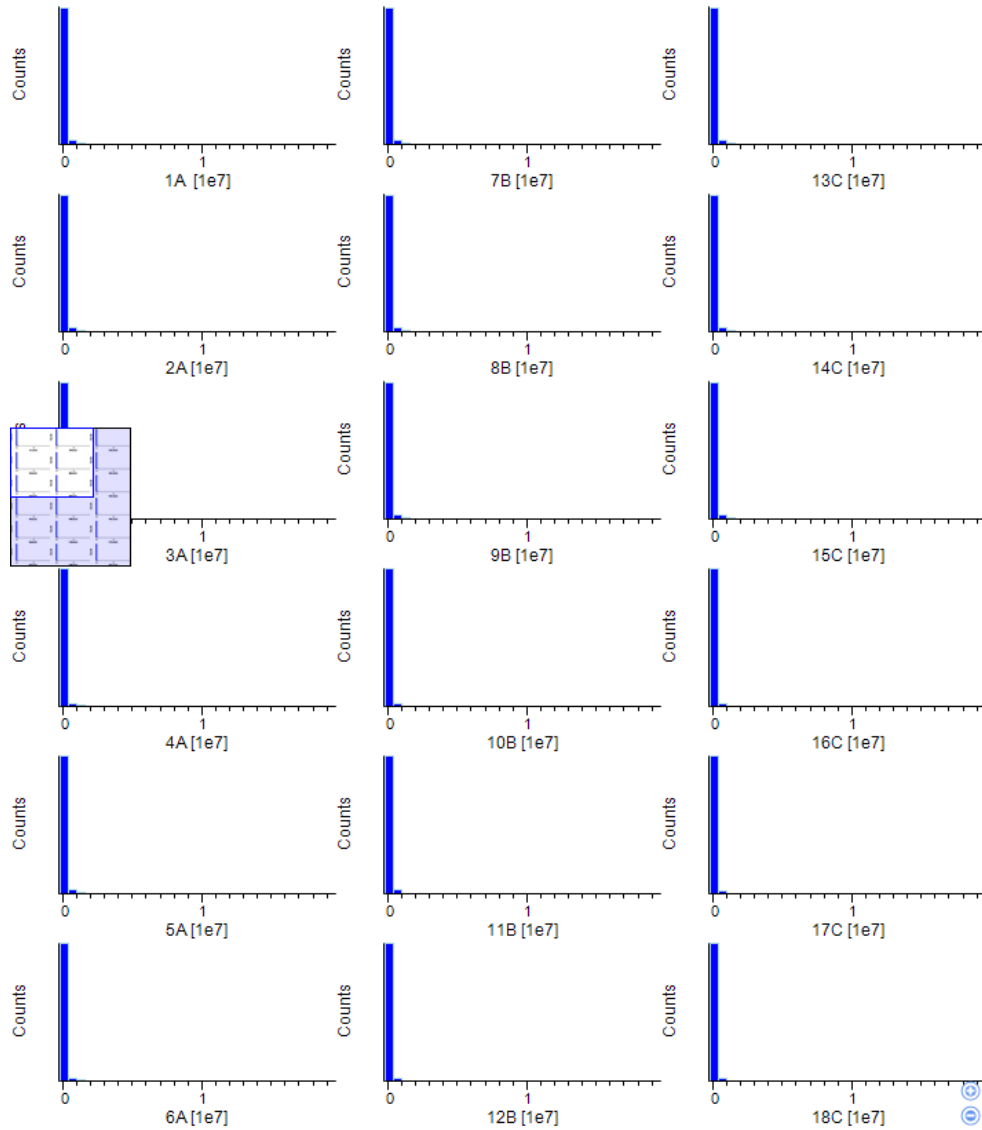
**C:** 13, 14, 15, 16, 17, 18



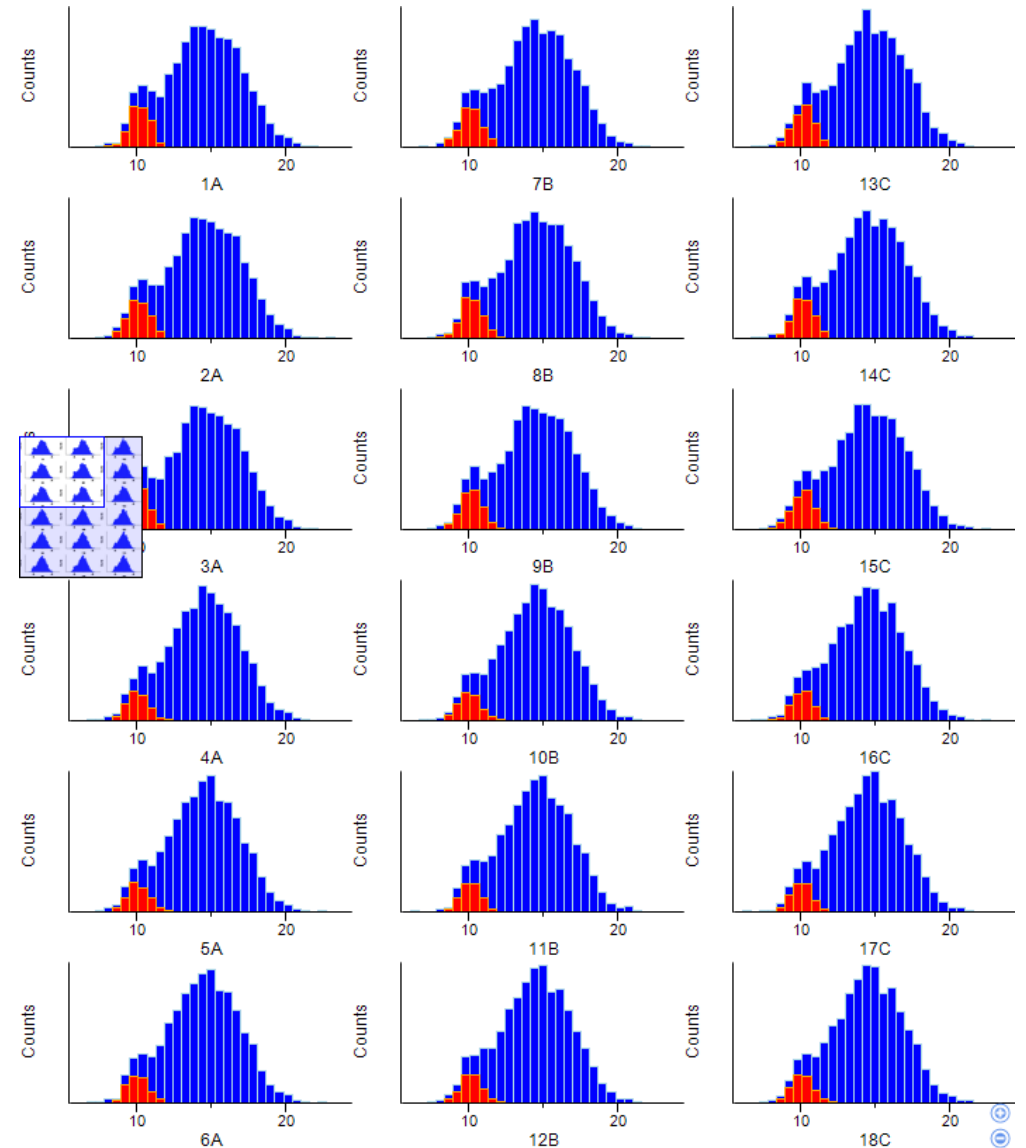


# Perseus- Data Transformation

Before Log2 Transformation

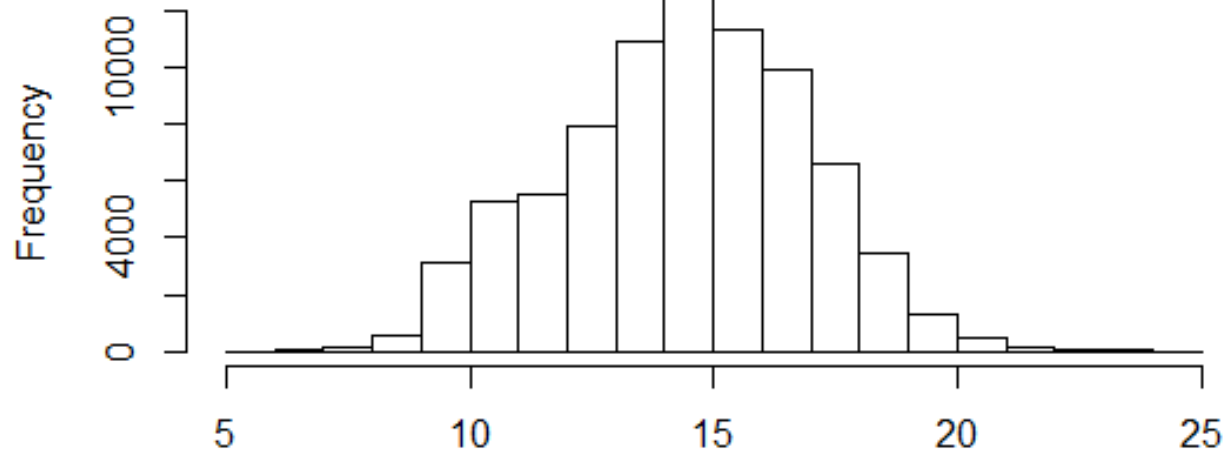


After Log2 Transformation



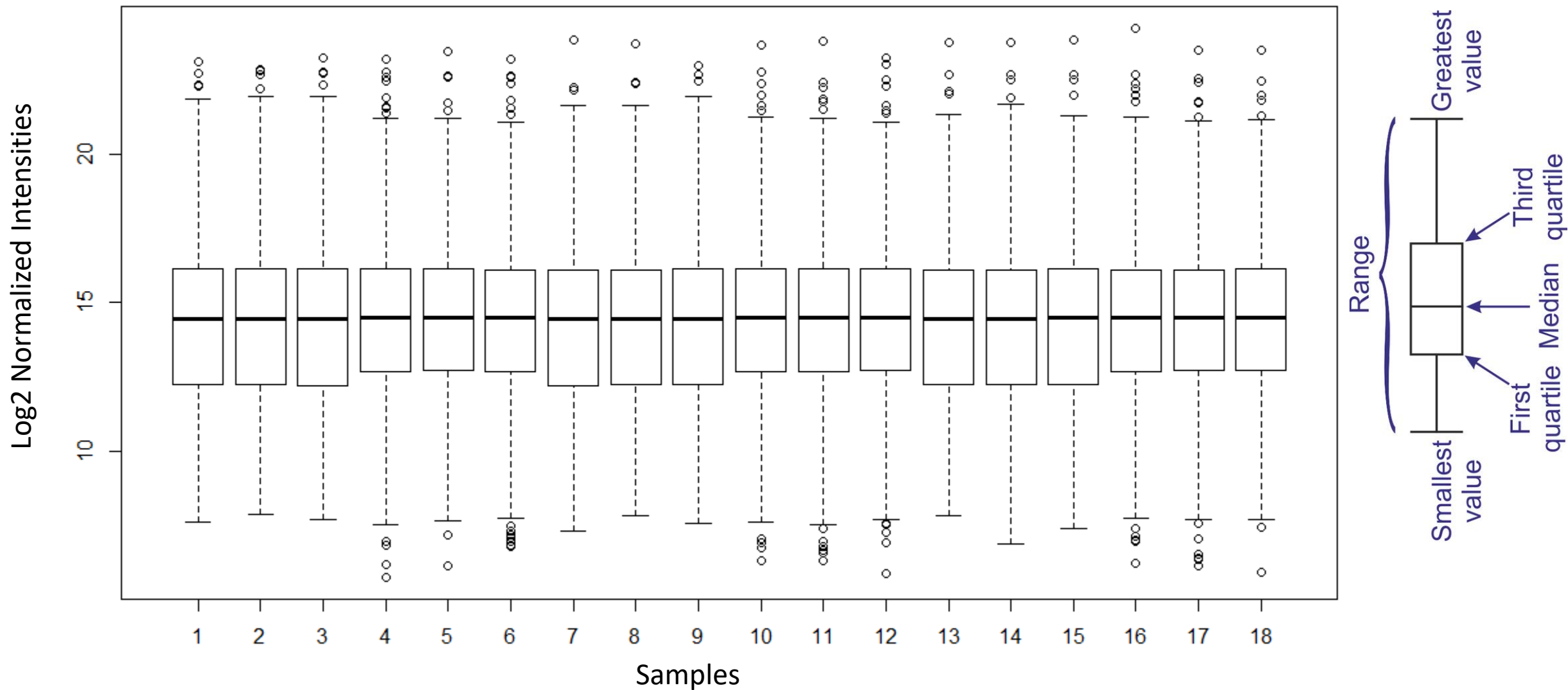


# R Studio – Histogram of Normalized Samples



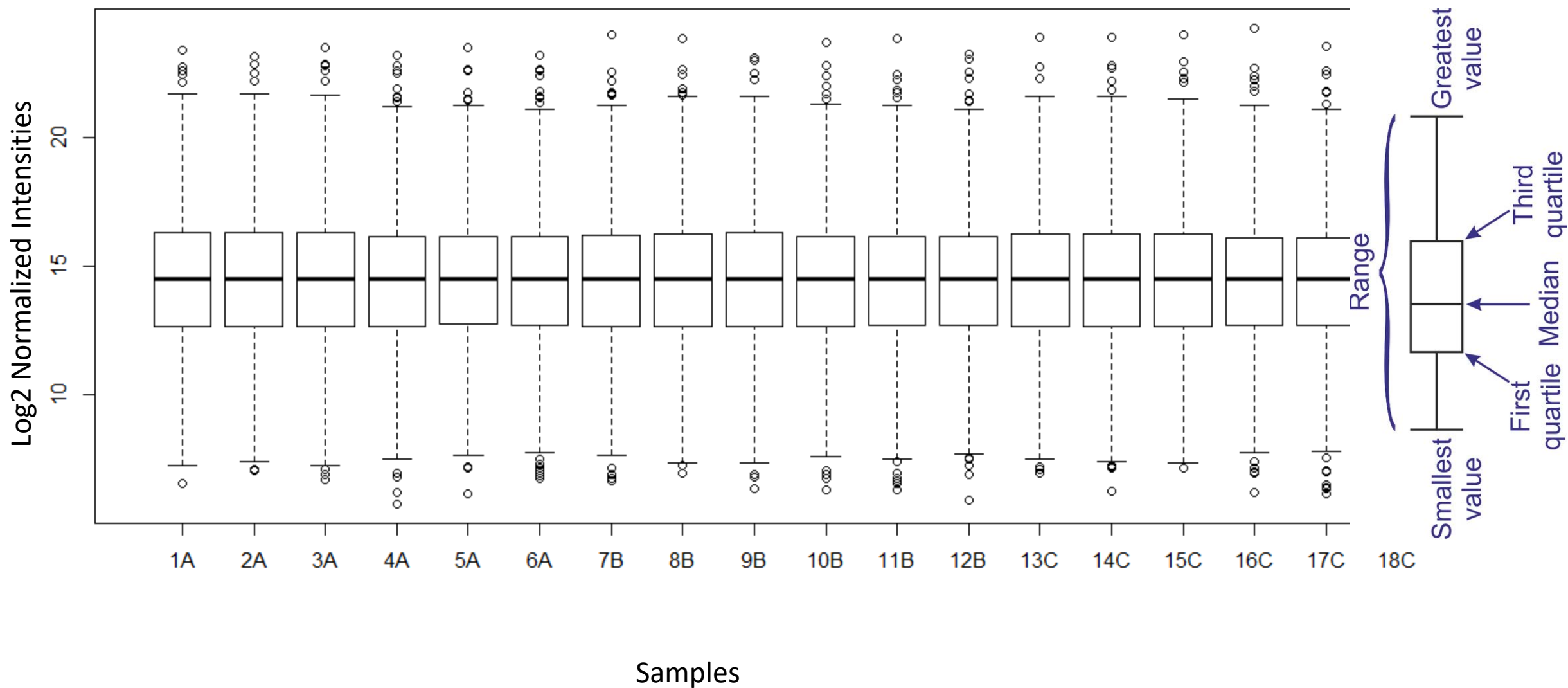


# R Studio – Boxplot of Normalized Samples

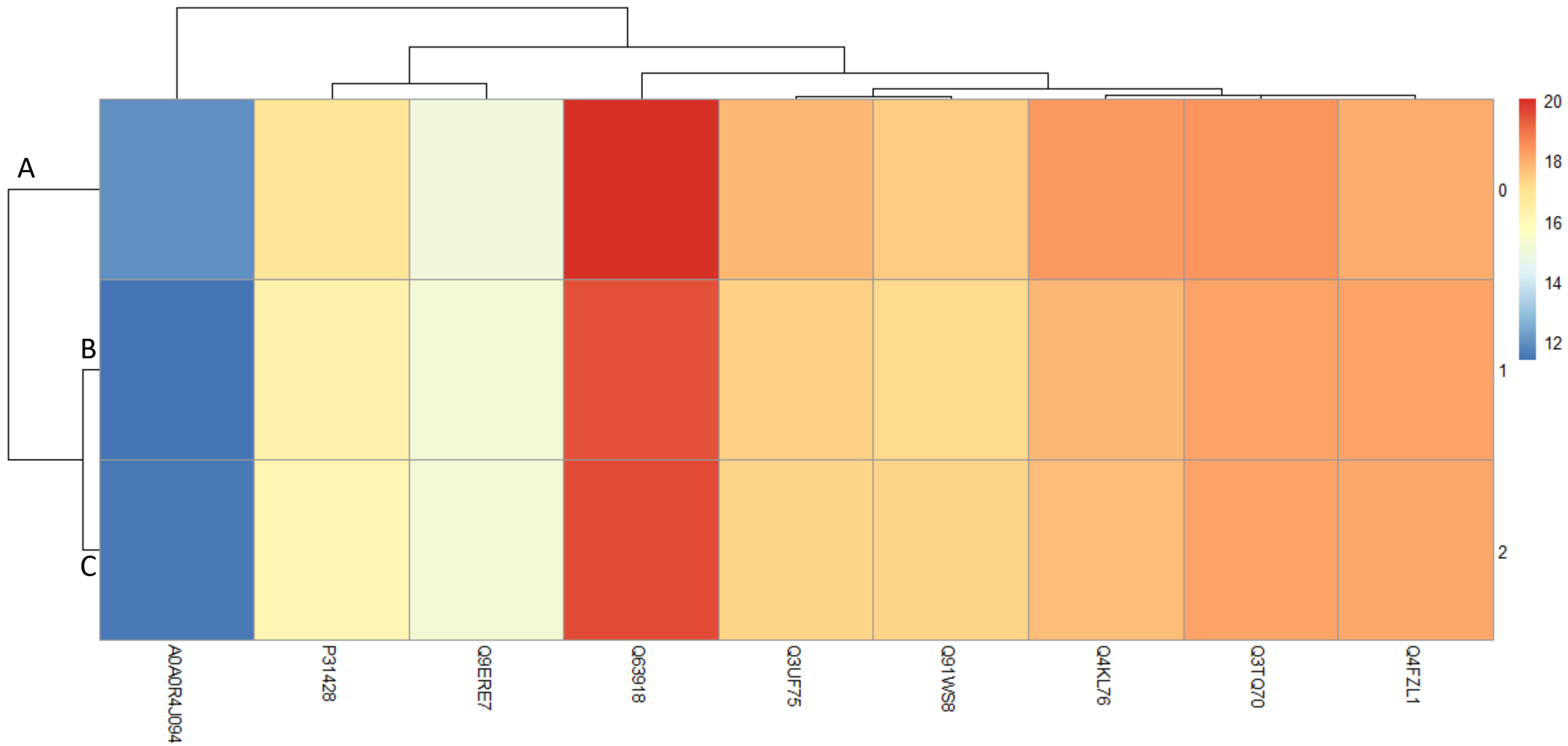




# R Studio – Boxplot of Normalized Samples

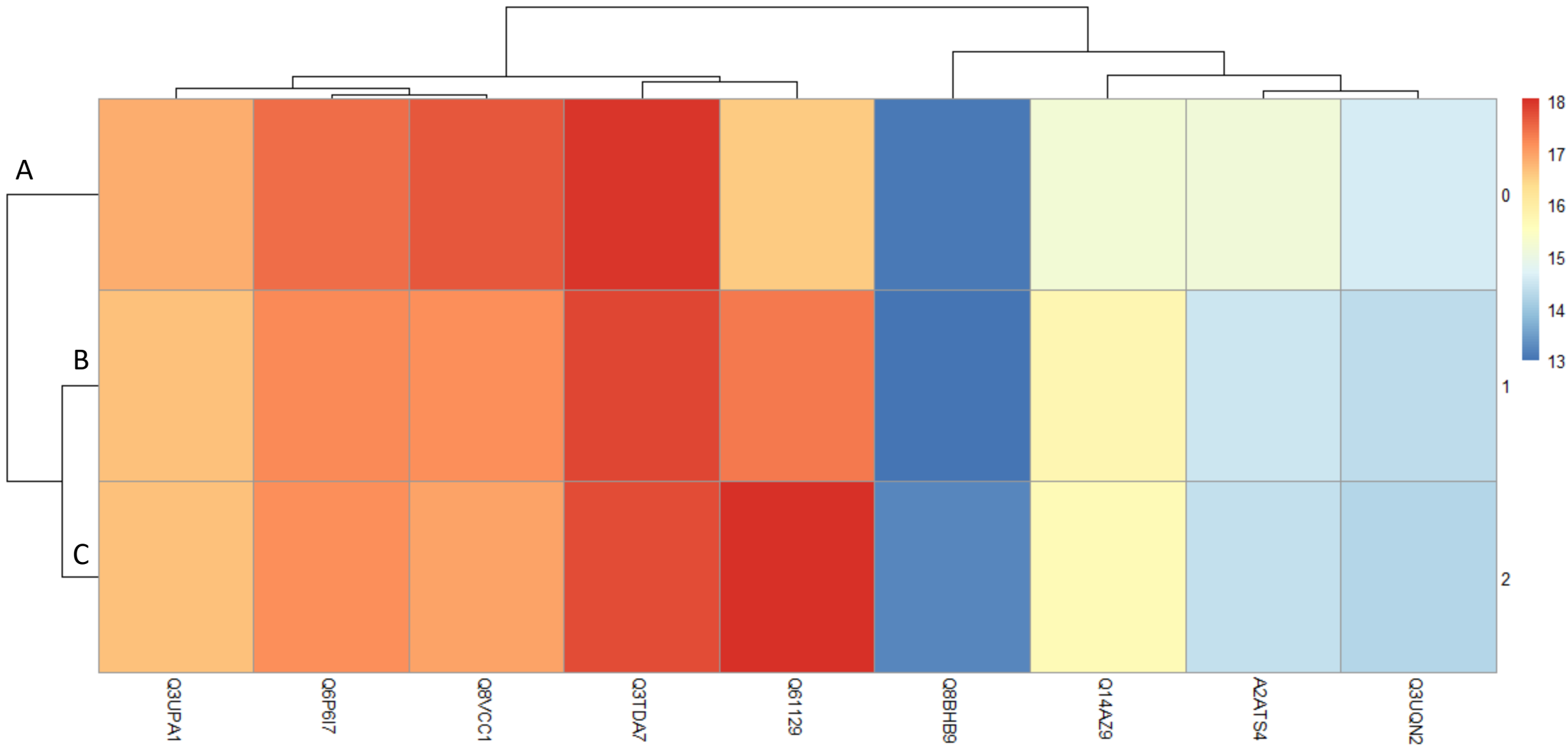


# Group A vs B: H's Stepup method for adjusting Mann-whitney p-values





Group A vs C: H's Stepup method for adjusting Mann-whitney p-values



Group B vs C: H's Stepup method for adjusting Mann-whitney p-values

