

# proteomeR report

08 March, 2017

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This report presents an overview of the proteomeR analysis.

## Summary

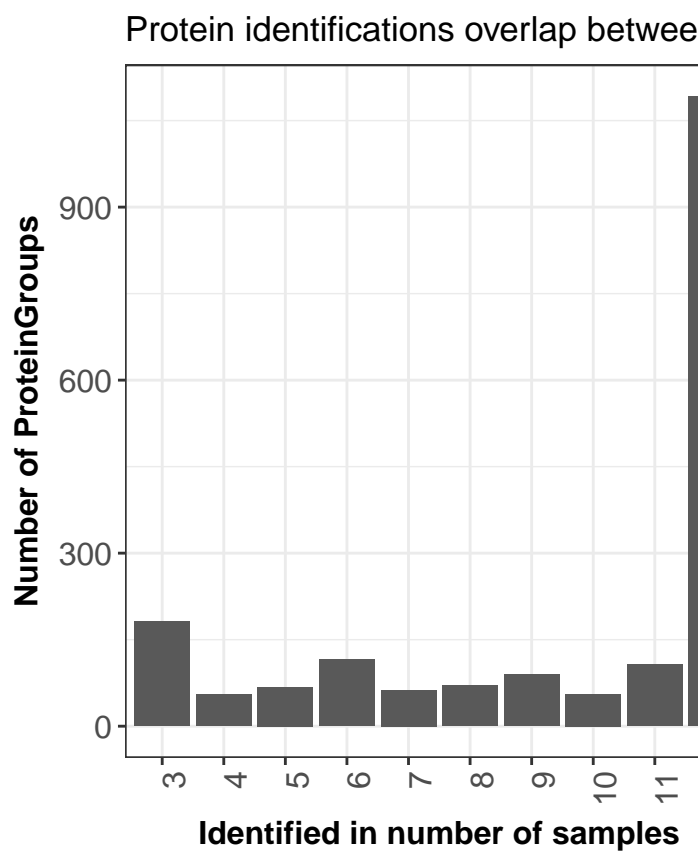
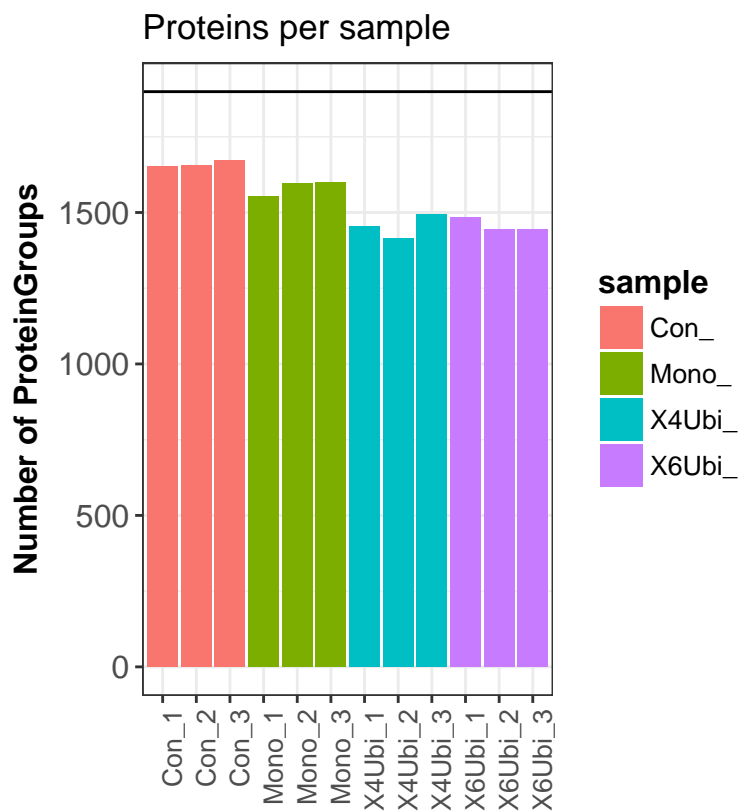
**174 proteins differ significantly between samples.**

Parameters used:

- $p \leq 0.05$
- $lfc \geq 1$

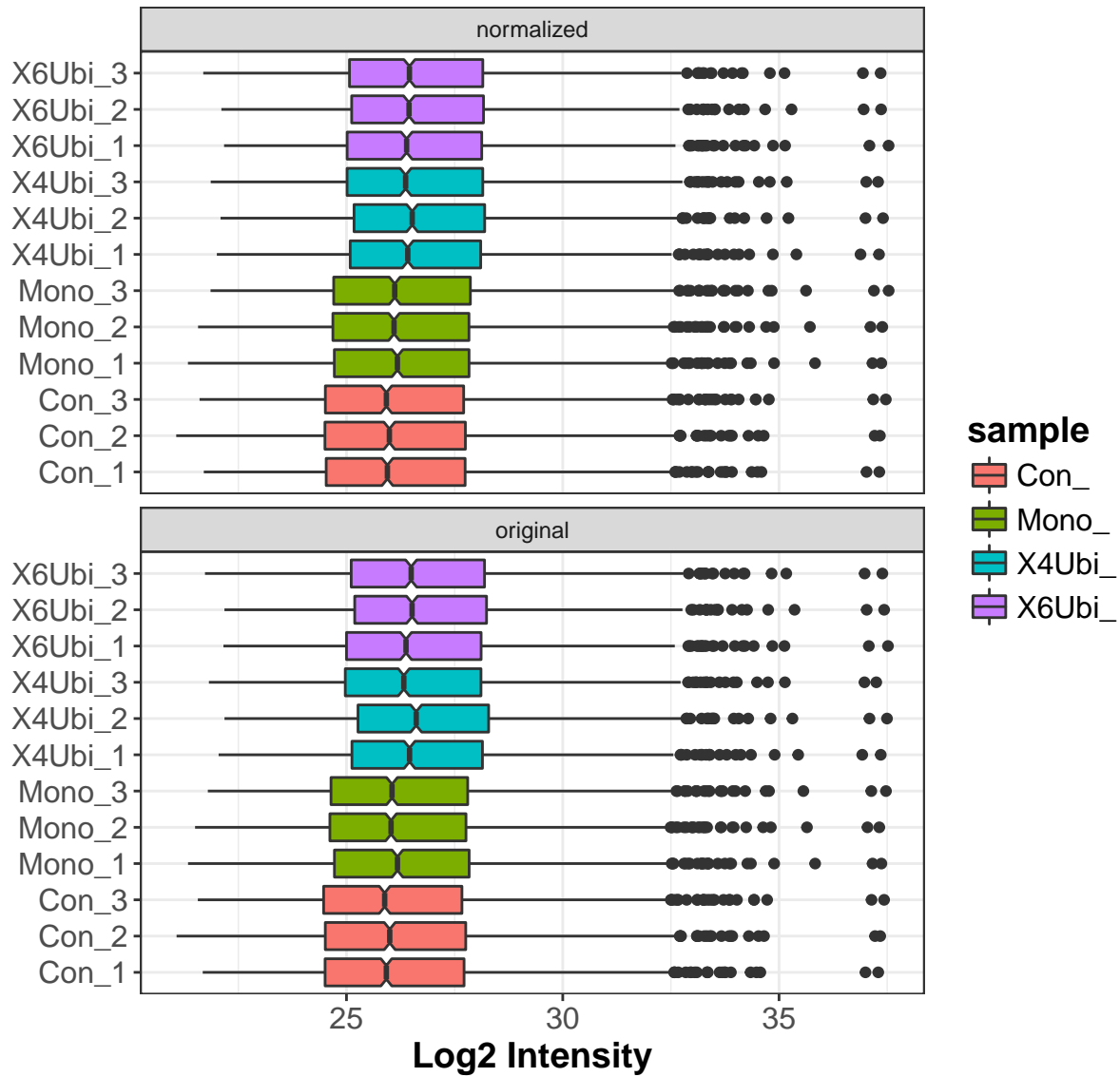
Original file contains 2941 proteins groups, of which 1899 proteins were reproducibly quantified.

In total 12 samples were detected.



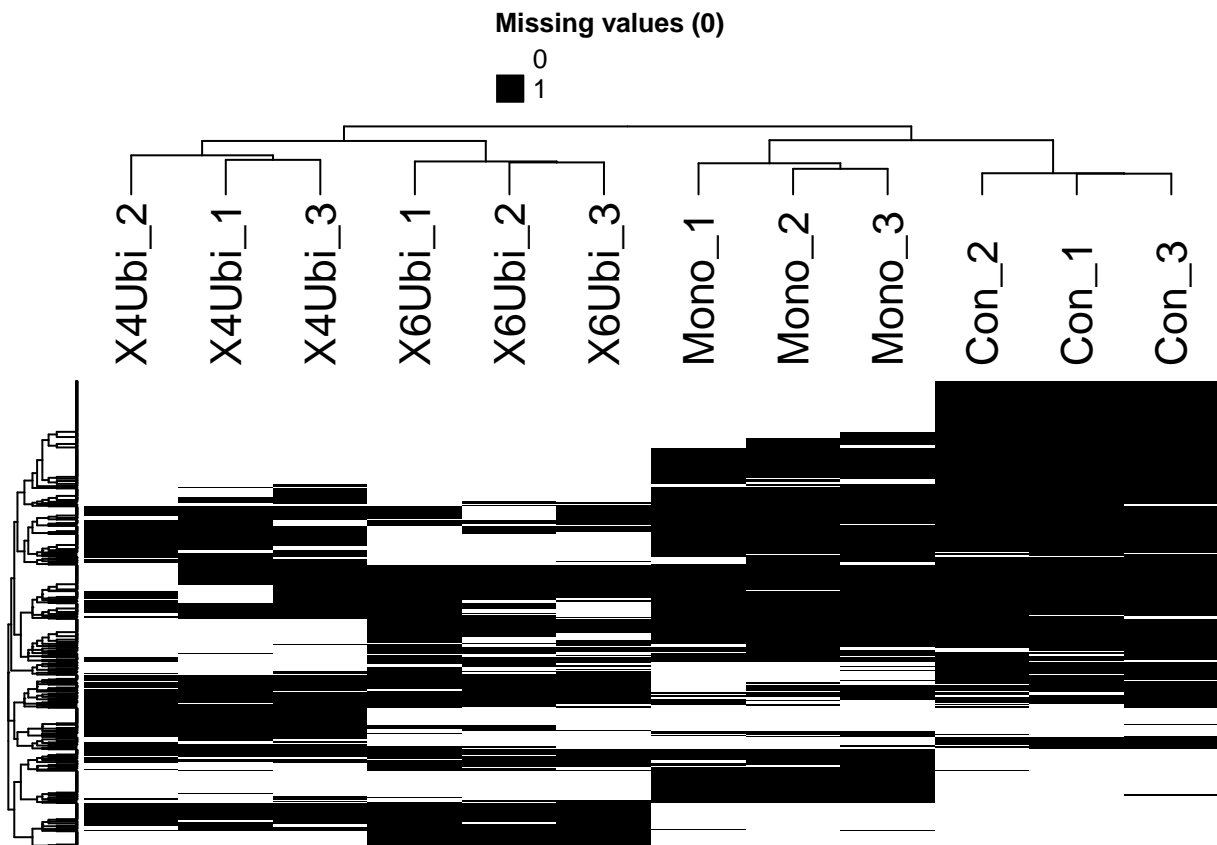
## Normalization

The data was normalized using 'vsn'.



## Missing values

A heatmap of missing values to assess the type of missing data (random or not). If data is randomly missing, use the "knn" option for imputation. If the missing data is biased to certain samples (e.g. controls) which are expected to be devoid of certain proteins, use the "QRILC", "MinProb" or "Perseus" options for imputation.



# Output plots of the data

## Heatmaps

