

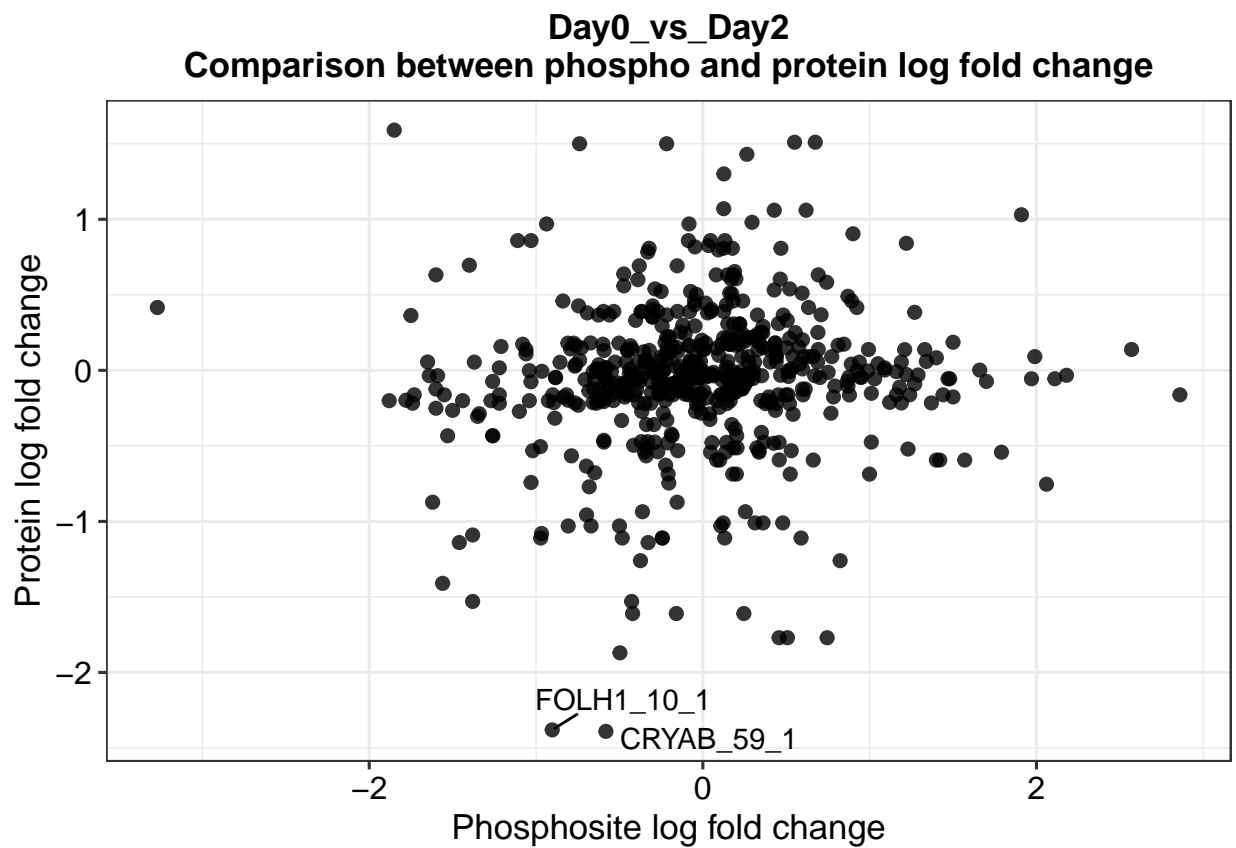
Phospho-Analyst(Comparison) report

14 February, 2022

Quick summary of parameters used:

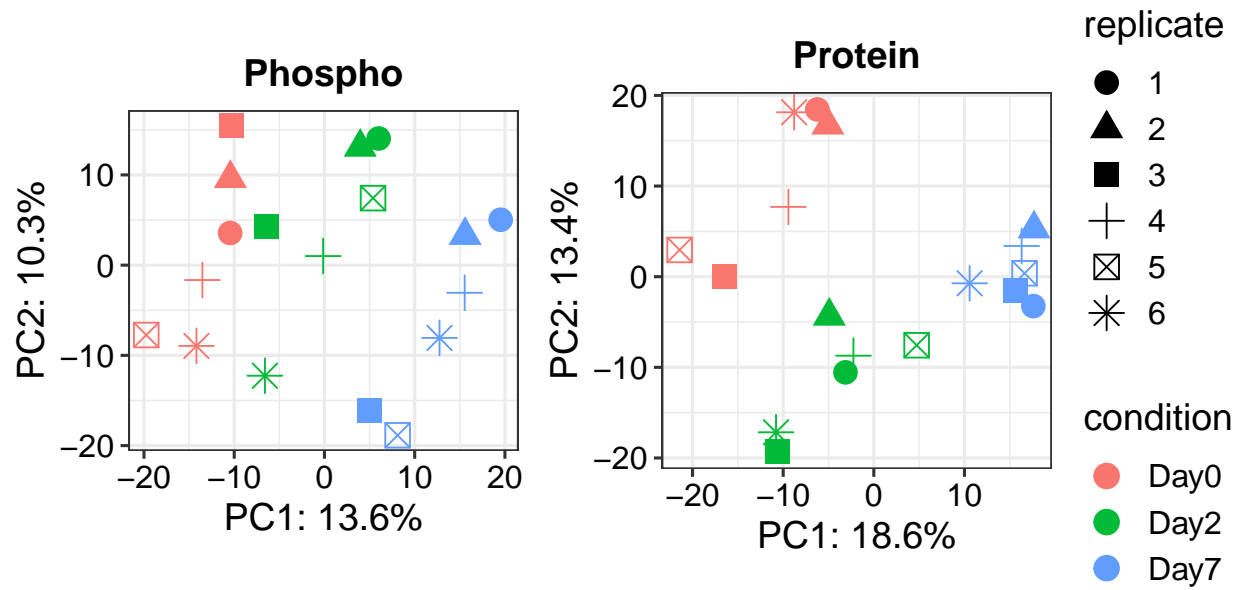
- Selected comparison = Day0_vs_Day2
- Selected gene = AADAT
- Adjusted *p-value* cutoff ≤ 0.05
- Log fold change cutoff ≥ 1

Comparison of phosphosite and proteinGroup log fold change

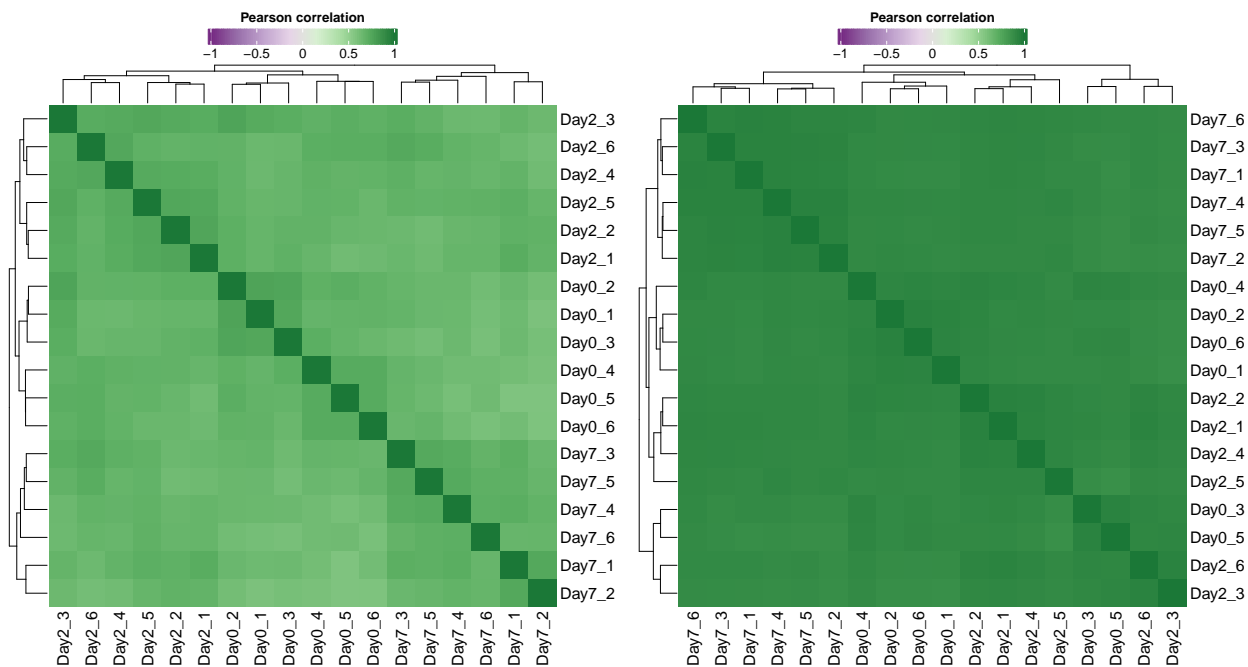


Exploratory Analysis (QC Plots)

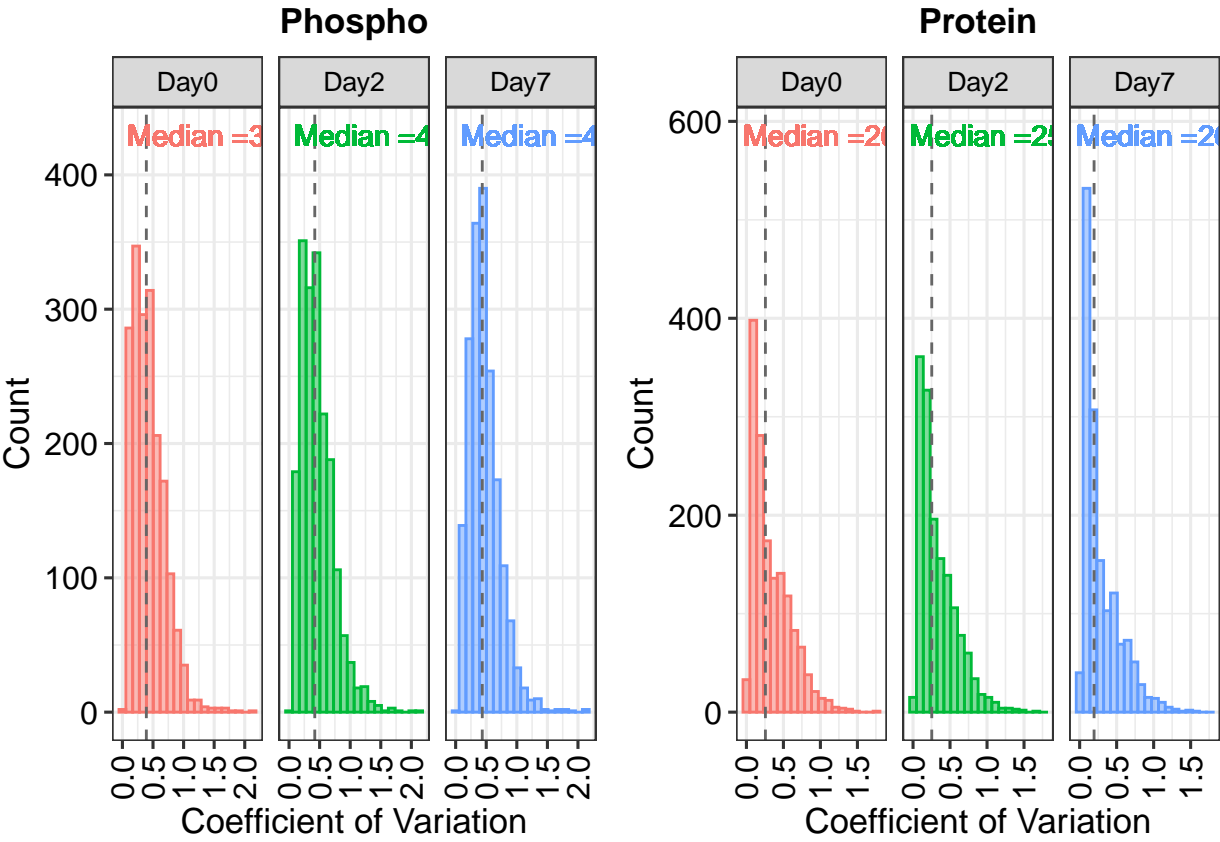
Principle Component Analysis (PCA) plot A plot used the PCA method to emphasize the variation.



Sample Correlation matrix Correlation plot is similar to a heatmap, to visualise the relationship among different samples. The darker the stronger relevance between each sample. (Left: Phospho; Right: Protein)

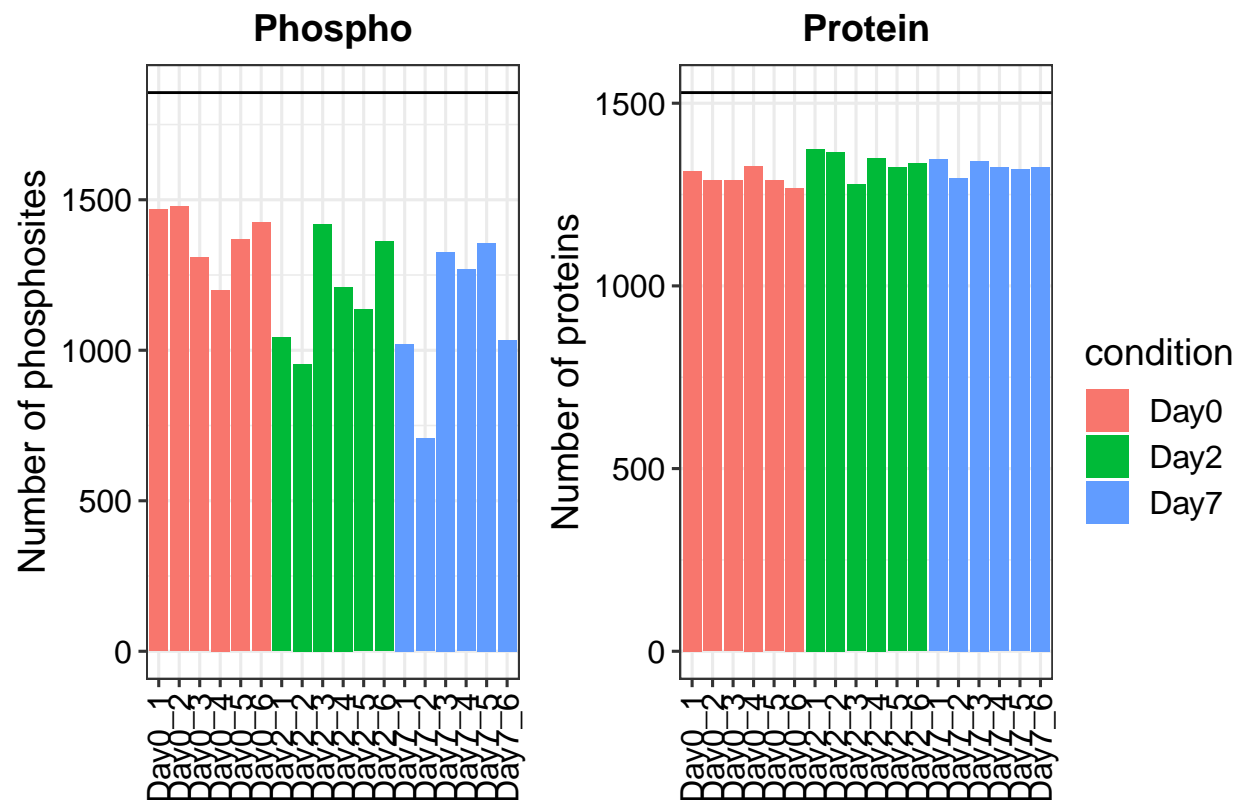


Sample Coefficient of variation (CVs) Also called relative standard deviation (RSD), it is present as a histogram plot, and illustrates the degree of variation relative to the overall mean.

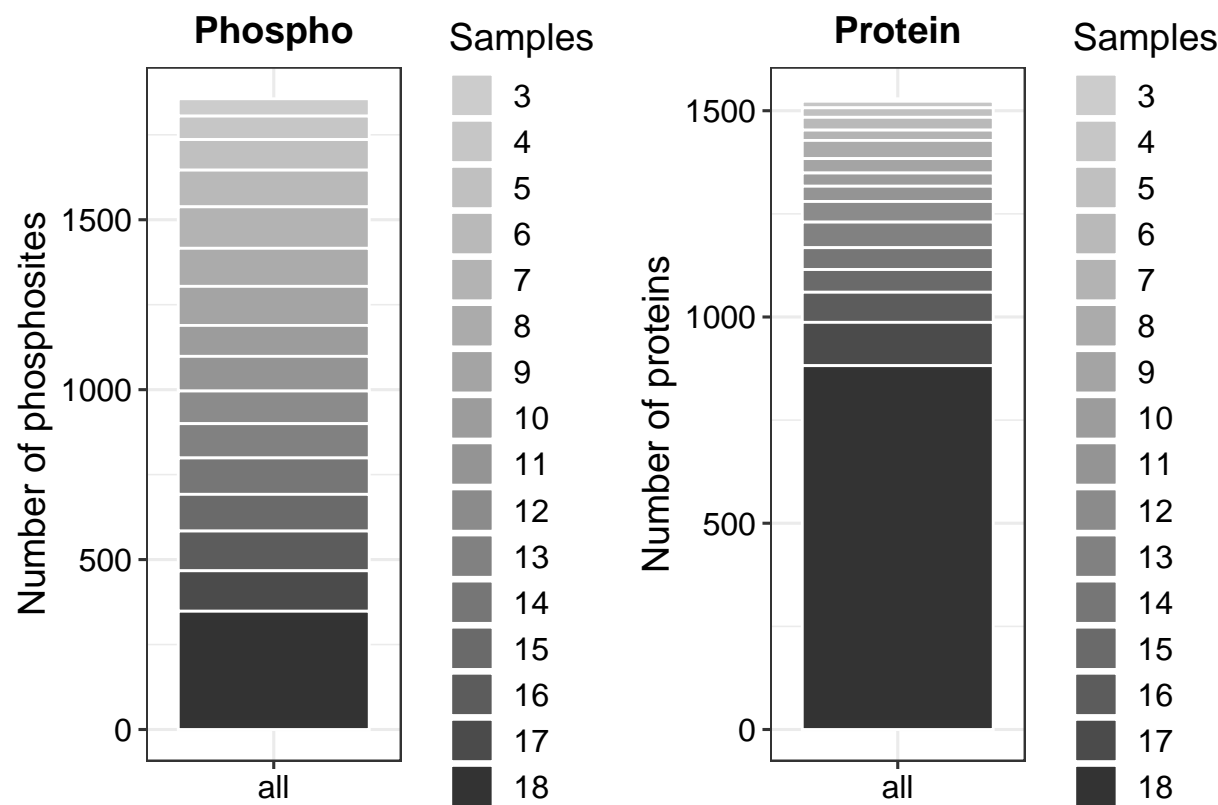


Proteomics Experiment Summary

Phosphosite and Protein quantified per sample (after pre-processing).

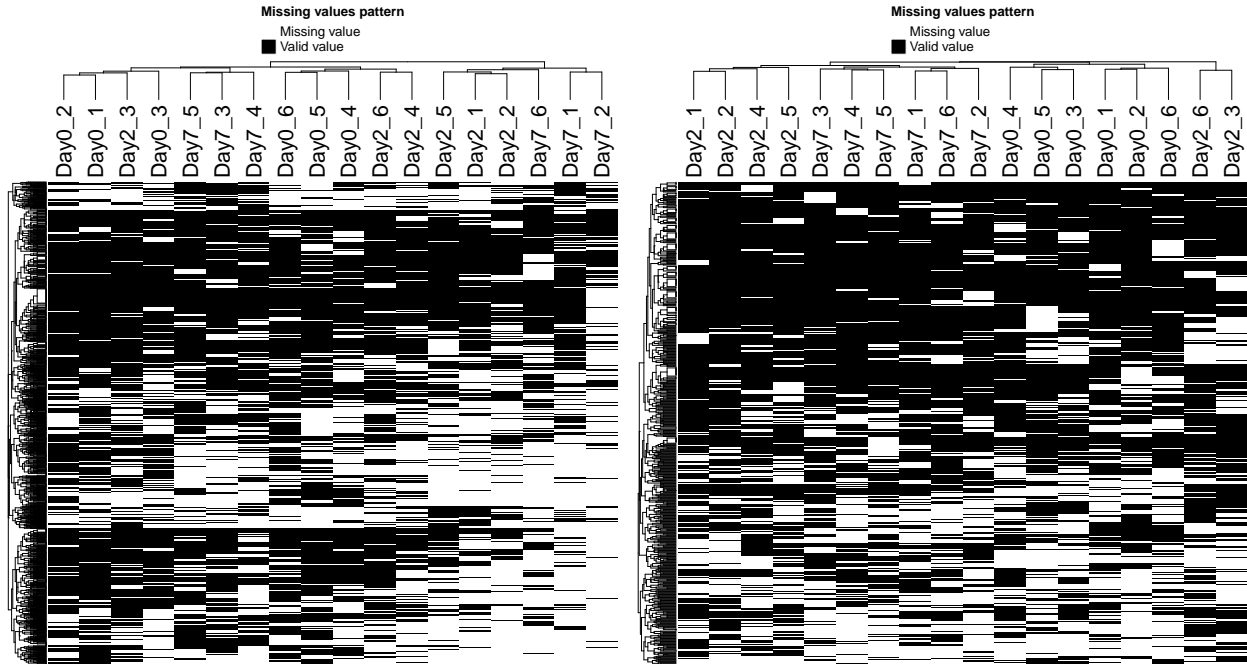


Phosphosite and Protein overlap in all samples.

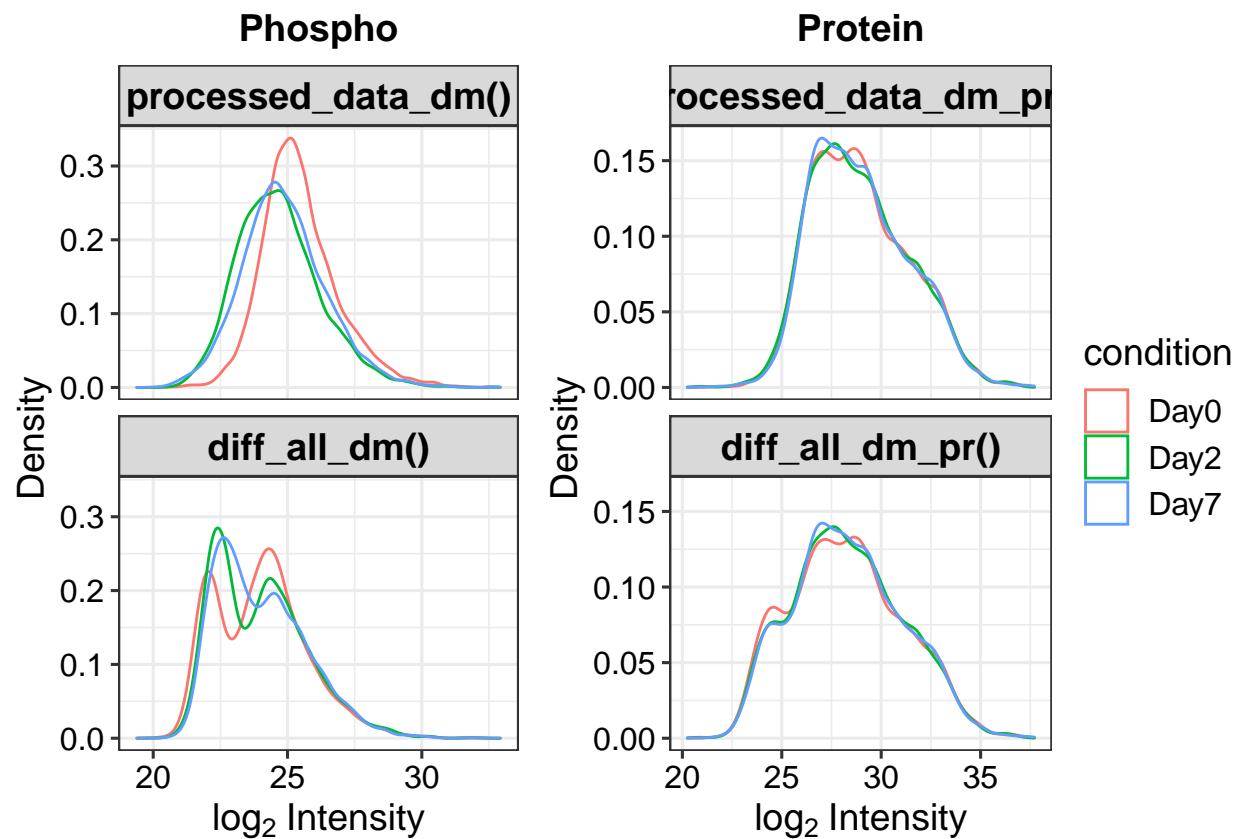


Missing Value handling

Missing value heatmap Heatmaps for phosphosites and proteins with missing value in each dataset. Each row represent a phosphosite/protein with missing value in one or more replicate. Each replicate is clustered based on presence of missing values in the sample. (Left: Phospho; Right: Protein)

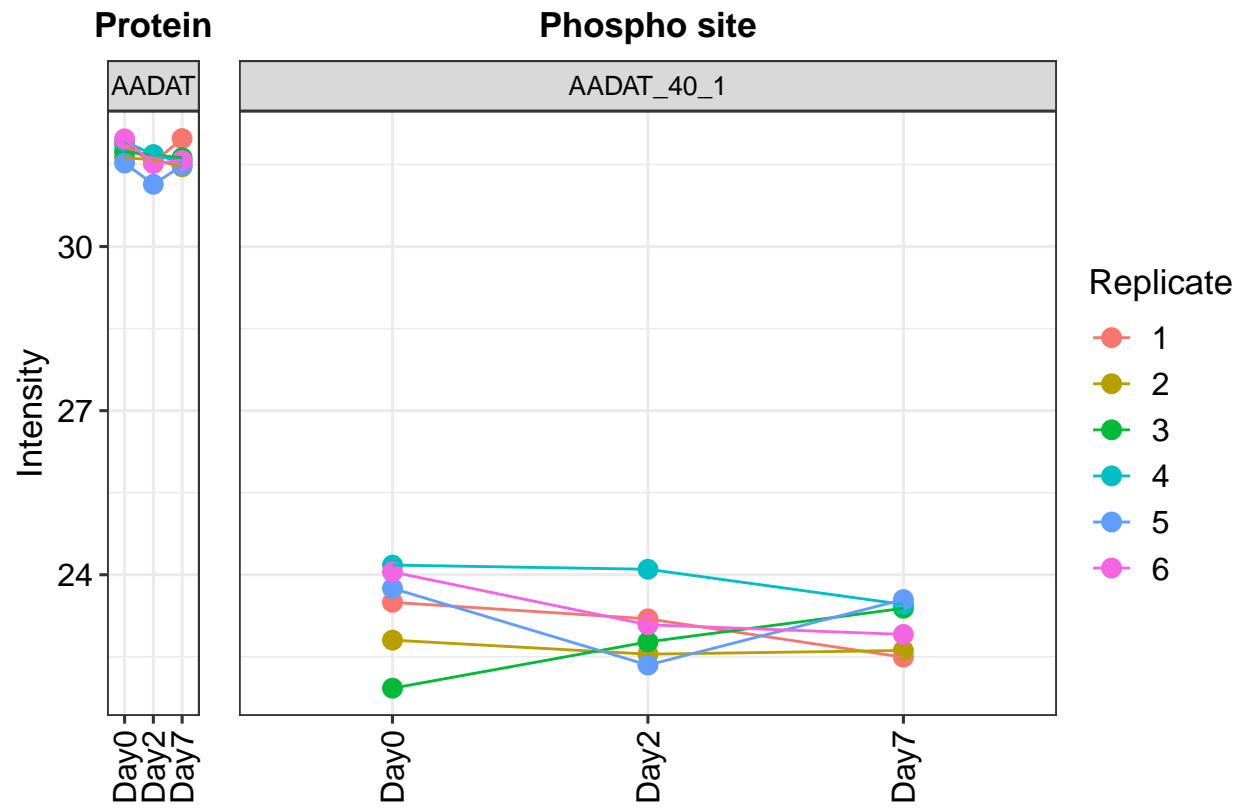


Missing value distribution Phosphosite and Protein expression distribution before and after imputation. The plot showing the effect of imputation on phosphosite and protein expression distribution.



Individual Protein plots

Interaction plot A plot representing the interaction between replicates on protein and its related phosphosite data.



Bubble plot A plot representing the phosphosite intensity values (size of points) of a selected protein group.

