Proteomics RIME-TMT analysis report
Holding: Changes in GRHL2 interactome on Activation

Contents

Introduction

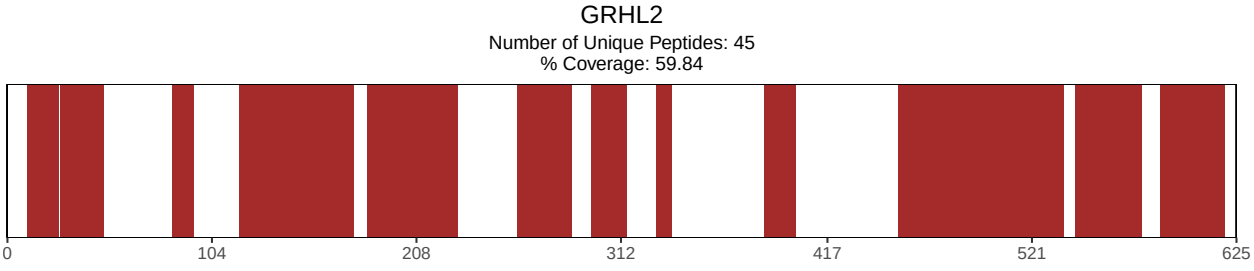
This report provides a summary of the results of your proteomics experiment.

Your experiment has **11** samples. **9032** peptides from **1514** unique proteins were captured in the experiment. Each protein is represented by **1** to **255** peptides, but median number of peptides per protein was **2**.

Raw data QC

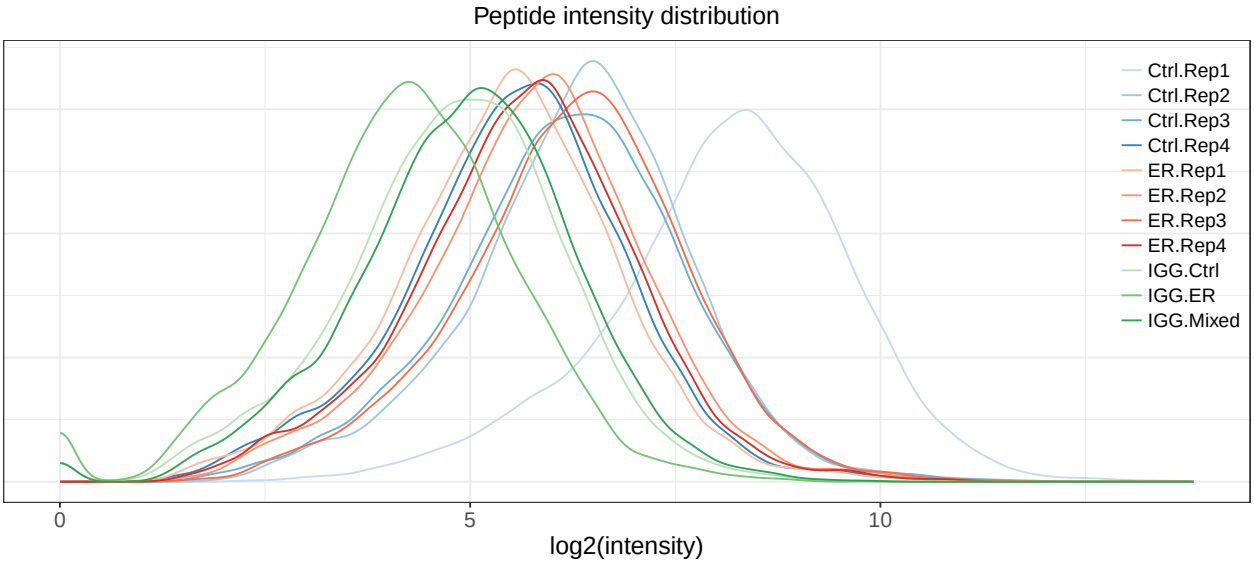
Coverage plot

Figure 1 shows the coverage of the bait protein, GRHL2, in terms of peptides detected.



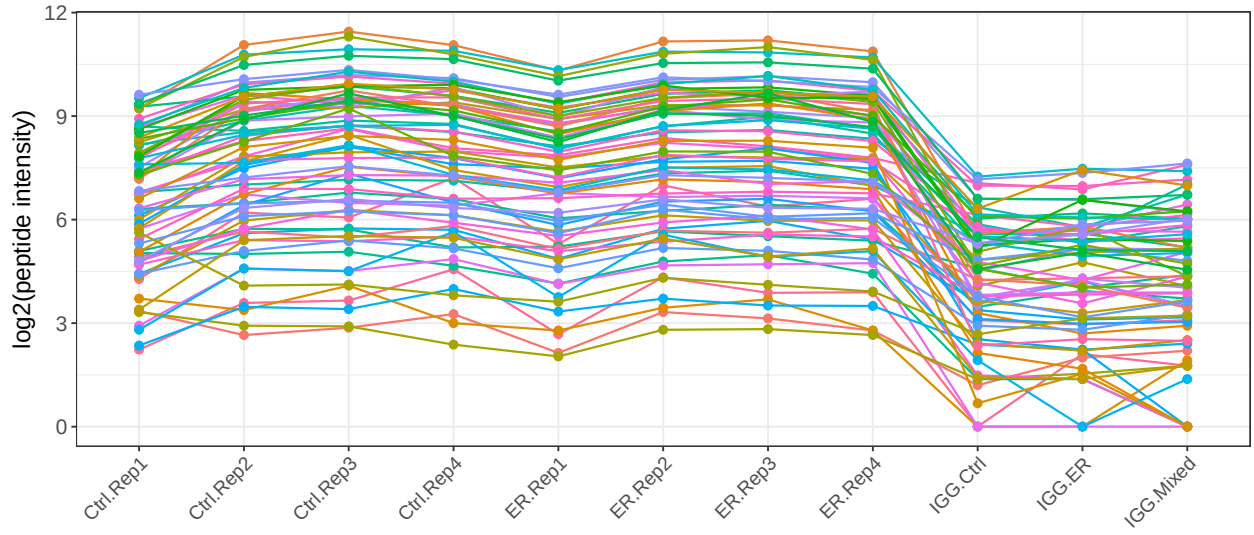
Intensity Plot

Figure 2 shows the distribution of raw peptide intensities for each sample.



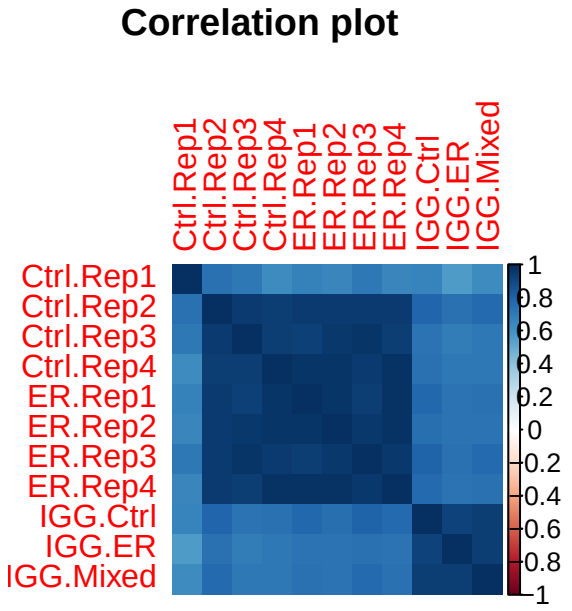
Peptide intensities for GHRL2

Figure 3 shows the raw intensities for each peptide detected for the bait protein GRHL2 in each sample.



Correlation Plot

Figure 4 shows a correlation matrix to visualize the level of linear association of samples within and between groups based on the raw peptide intensities.



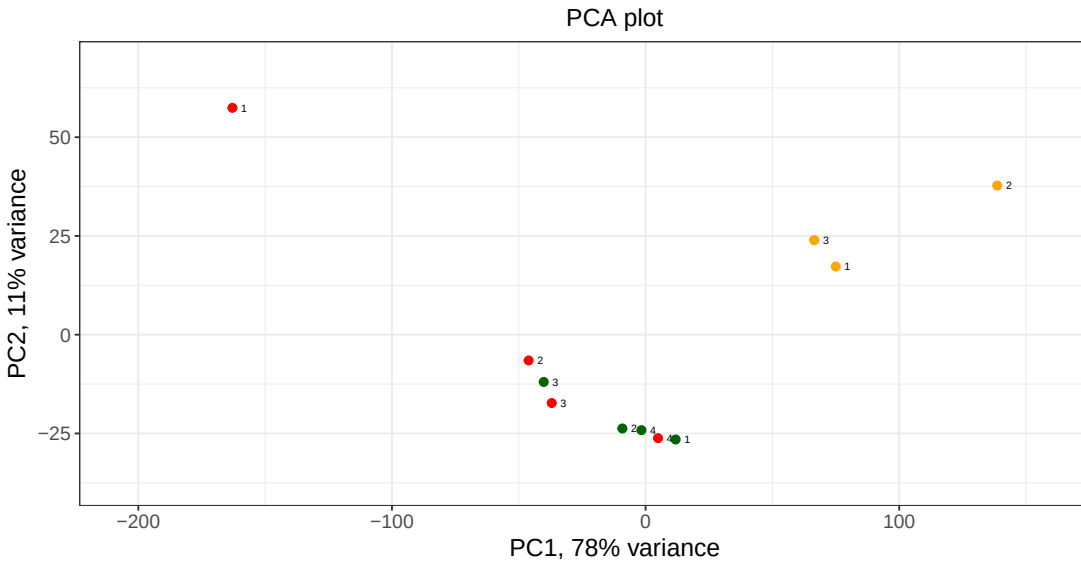
Hierichical clustering dendrogram

Figure 5 shows a dendrogram displaying the hierarchical relationship among samples. The vertical axis shows the dissimilarity (measured by means of the Euclidean distance) between samples: similar samples appear on the same branches. Colors correspond to sample groups.

PCA Plot

Figure 6 shows a visual representation of the scaled loading of the first two dimensions of a principle component analysis of the raw peptide intensities.

List of 1 $ aspect.ratio: num 1 - attr(, *"class")= chr [1:2] "theme" "gg" - attr(*, "complete")= logi FALSE -



attr(*, “validate”)= logi TRUE

QC Conclusion

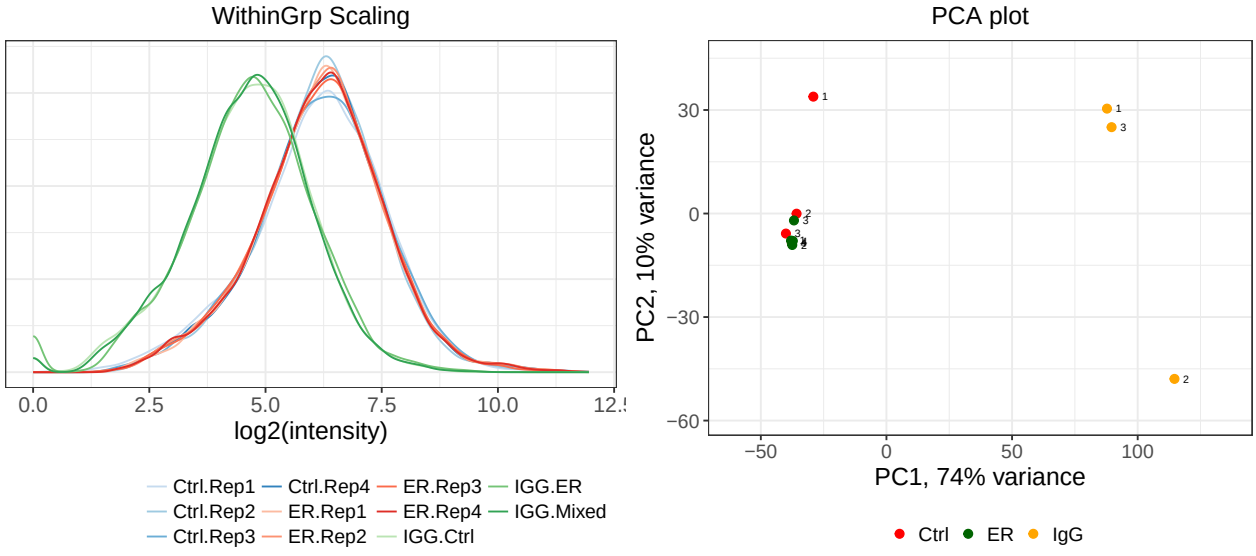
The sample Ctrl rep 1 appears to be an outlier. The differential anlaysis was carried out twice, first with this sample included and then again with the sample excluded.

Full data set analysis

The following section shows the results for analysis of all 8 samples.

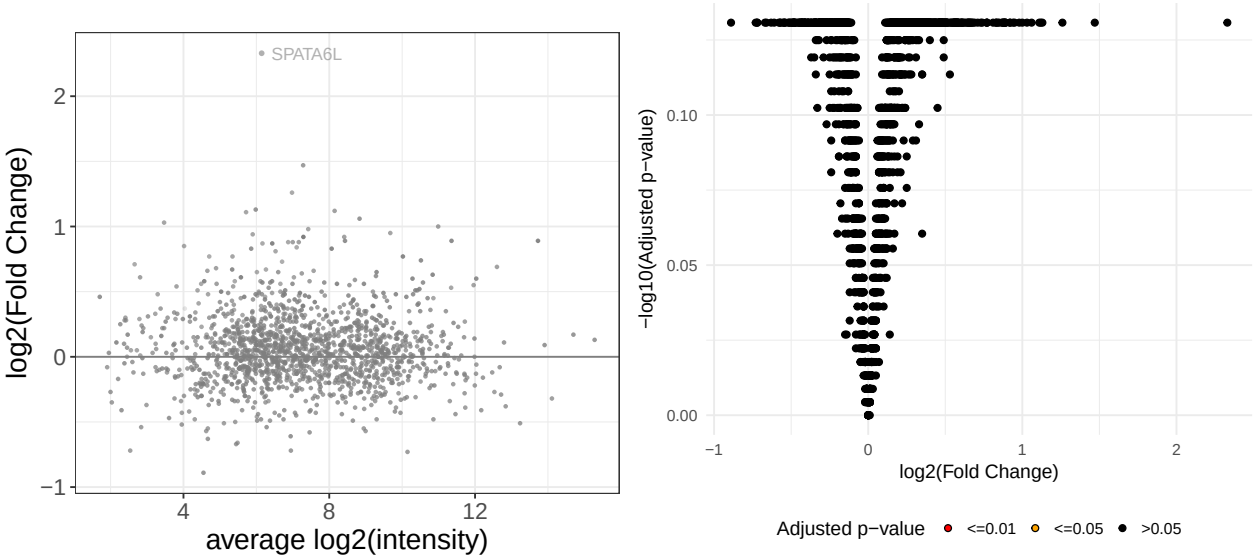
Effect of within group normalisation

Normalisation was carried out using median scaling. The experimental samples and the IgG control samples were normalised separately. Figure 7 show the effects of normalisation on the intensity plots and the principle component analysis.



Differential analysis results

Figure 8 shows differential abundancy results. No proteins were statistically differentially abundant. Figure 7 shows an MA plot and a volcano plot of the differental analysis results.

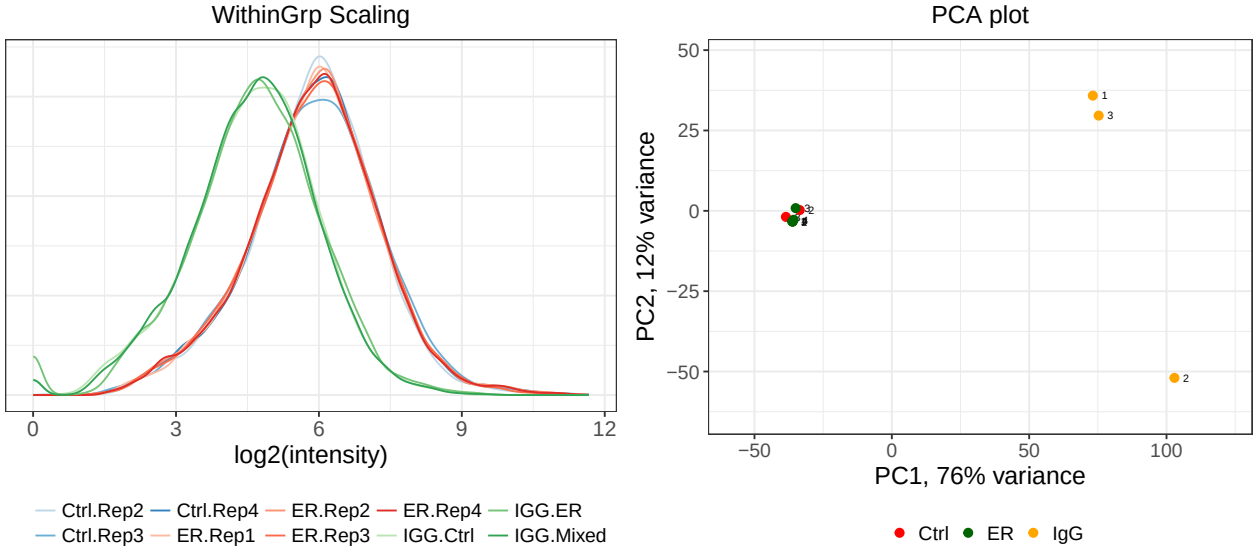


Remove sample Ctrl 1

The following section shows the same analysis, but with the Ctrl rep 1 sample removed

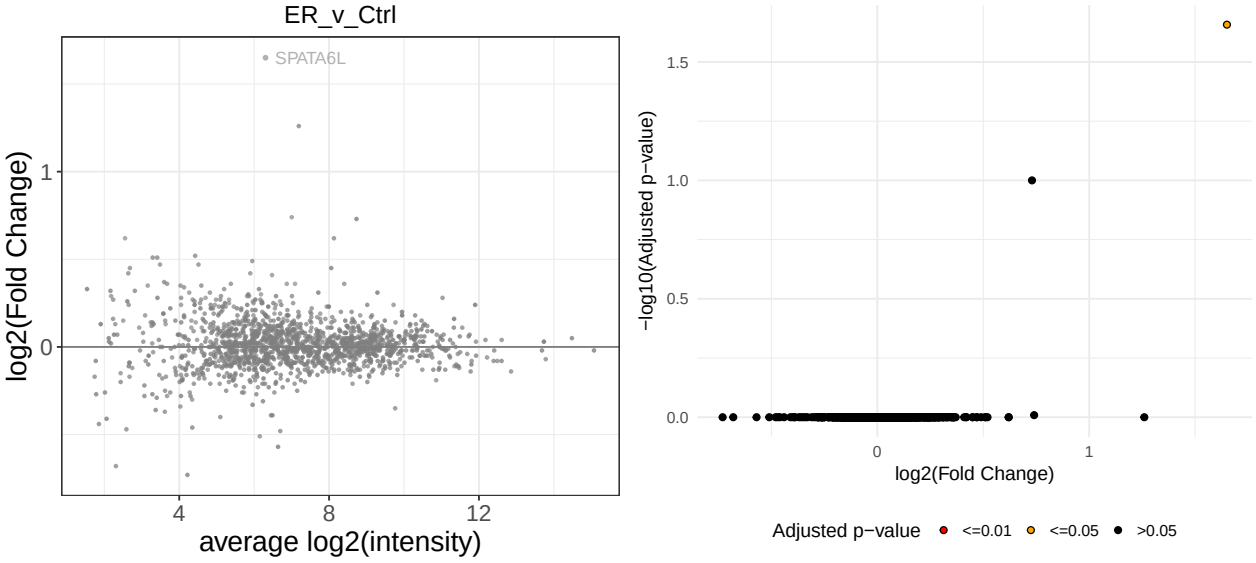
Effect of within group normalisation

Normalisation was carried out using median scaling. The experimental samples and the IgG control samples were normalised separately. Figure 10 show the effects of normalisation on the intensity plots and the principle component analysis.



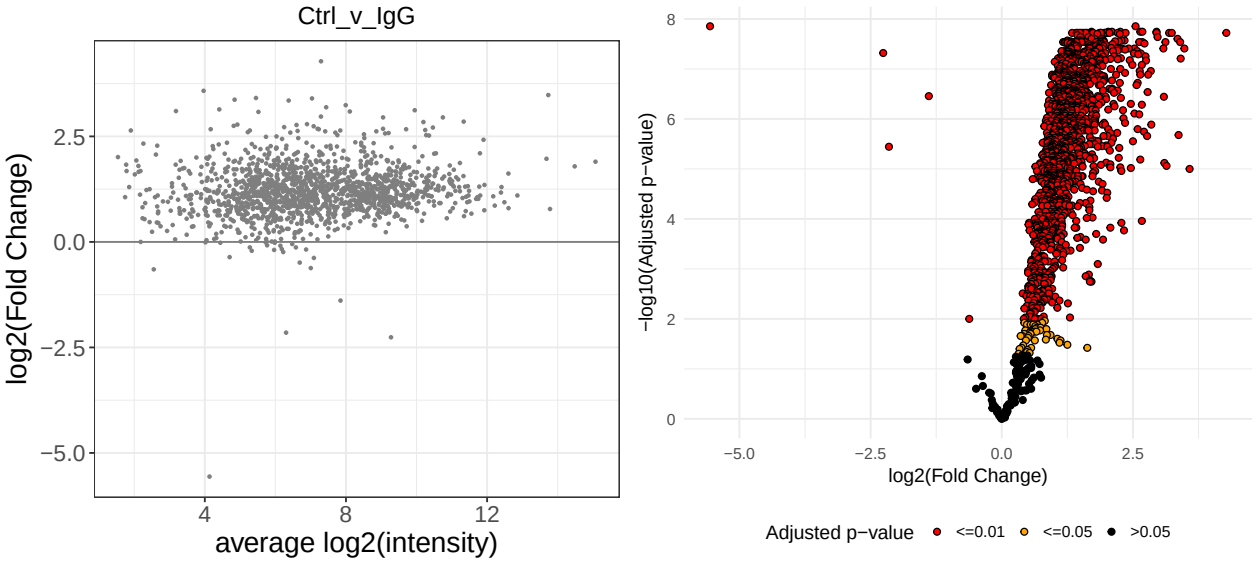
ER - Ctrl

Figure 11 shows differential abundancy results for the contrasts ER_v_Ctrl. Figure 10 shows an MA plot and a volcano plot of the differental analysis results



Ctrl - IgG

Figure 13 shows differential abundancy results for the contrasts Ctrl_v_IgG. Figure 14 shows an MA plot and a volcano plot of the differental analysis results.



ER - IgG

Figure 16 shows differential abundancy results for the contrasts ER_v_IgG. Figure 17 shows an MA plot and a volcano plot of the differental analysis results.