Summary of post-processed MaxQuant output in Expression Atlas

PXDID: PXD001608
Reference: Human Reference Proteome (UniProt, May 2019)
Number of sequences: 95,915
Software: MaxQuant v1.6.3.4

Table 1. Summary

Number of samples	10
Number of identified proteins†	5321
Total number of mapped peptides¶	65527
.... Number of mapped unique peptides§	52349

† The total number of SwissProt proteins (non-isoforms) to which atleast 2 or more peptides from each sample are mapped to.
¶ Sum of peptides that are mapped across all protein groups.
§ The total number of unique peptides associated with the protein group (i.e. these peptides are not shared with another protein group).

Post-processing filters applied:

(i) Remove reverse decoys.

(ii) Remove contaminants.

(iii) Include protein groups that have 2 or more peptides mapped to a protein.

(iv) Include protein groups wherein all protein IDs in the protein group are mapped to an unique Ensembl Gene ID.

Normalisation method:

Fraction Of Total (FOT).
Each protein iBAQ intensity value is scaled to the total amount of signal in a given MS run (column) and transformed to parts per billion (ppb)

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## Warning: Transformation introduced infinite values in continuous y-axis
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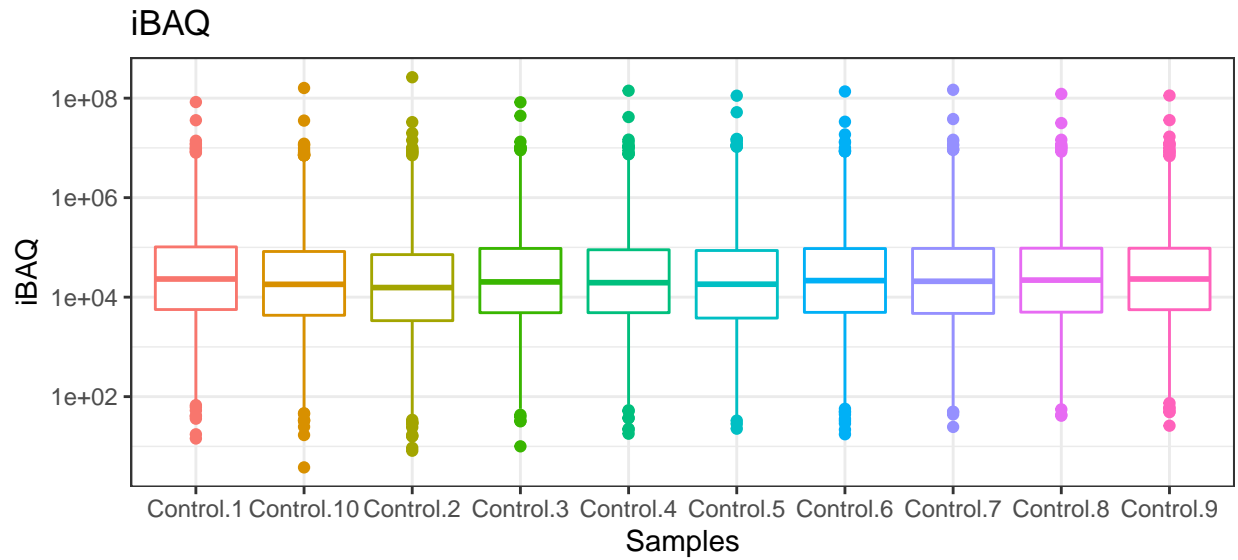
Figure1. Boxplots with distribution of iBAQ values for each sample after FOT normalisation.
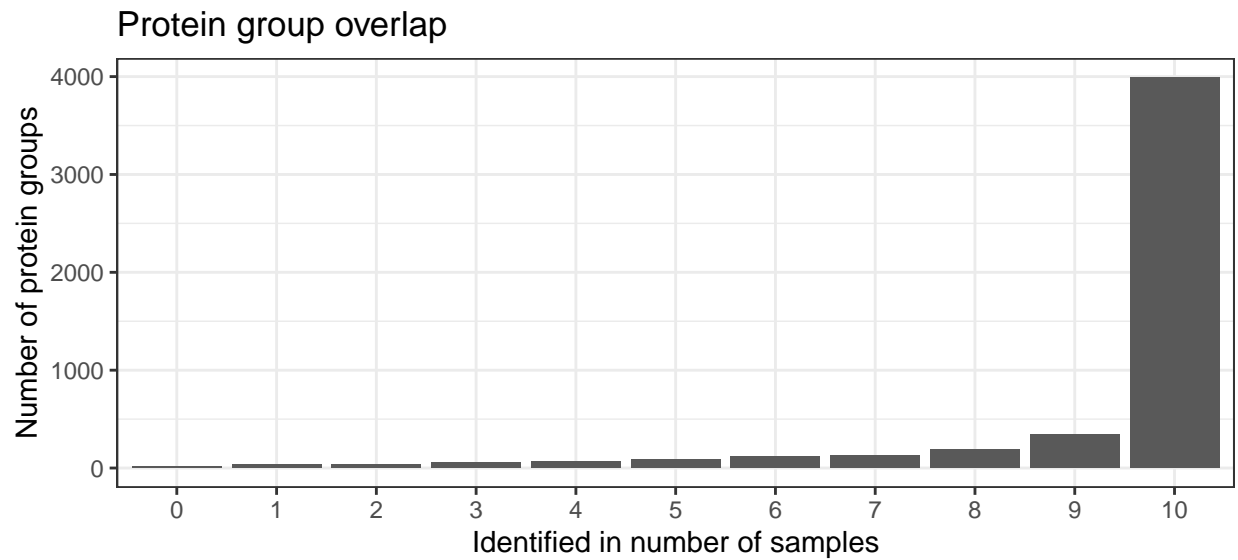

Figure2. Protein overlap. Indicates the number of protein groups that were identified across different samples. Protein groups can have more than one protein.
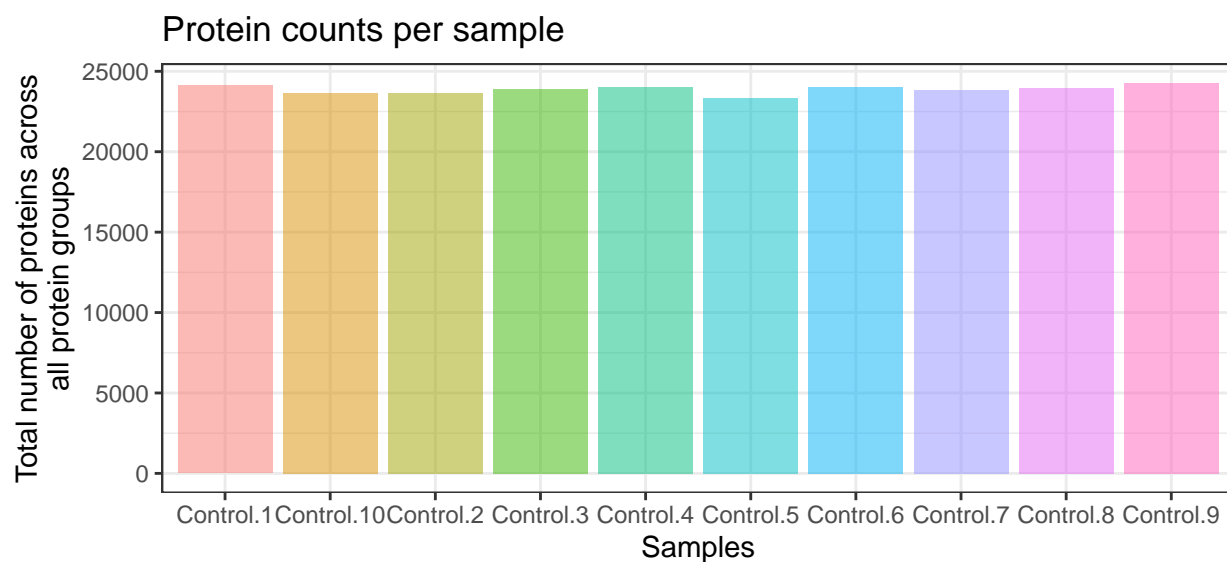
Protein counts per sample

Figure3. Protein counts in each sample. The total number of proteins present across all protein groups to which peptides from each sample are mapped.
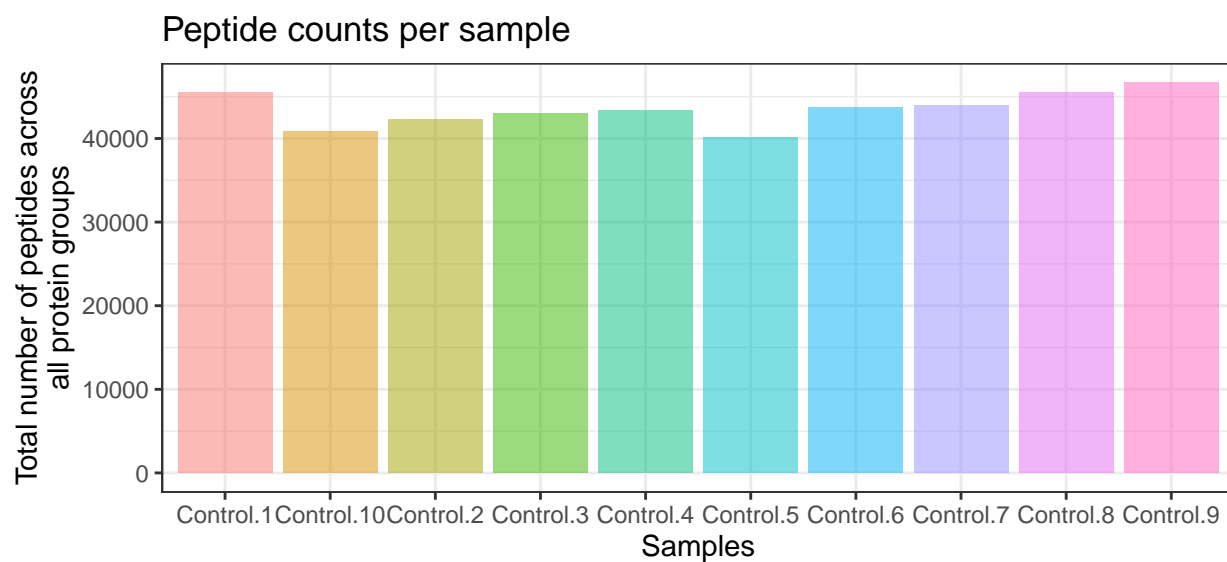
Peptide counts per sample

Figure4. Peptide counts in each sample. The total number of peptides that are mapped across all protein groups from each sample.
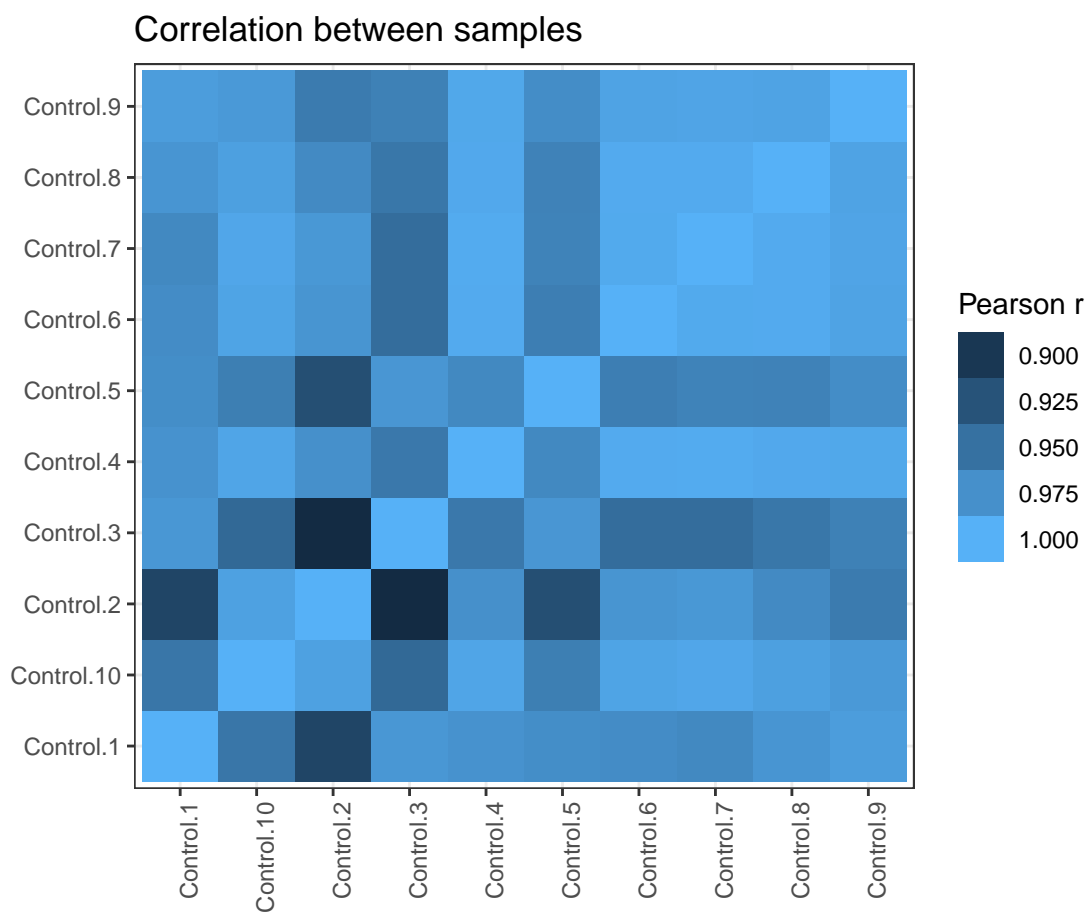
Figure5. Correlation between samples. The pearson correlation between normalised intensities of each sample.