

## Supporting information for:

# Peptide Correlation Analysis (PeCorA) Reveals Differential Proteoform Regulation

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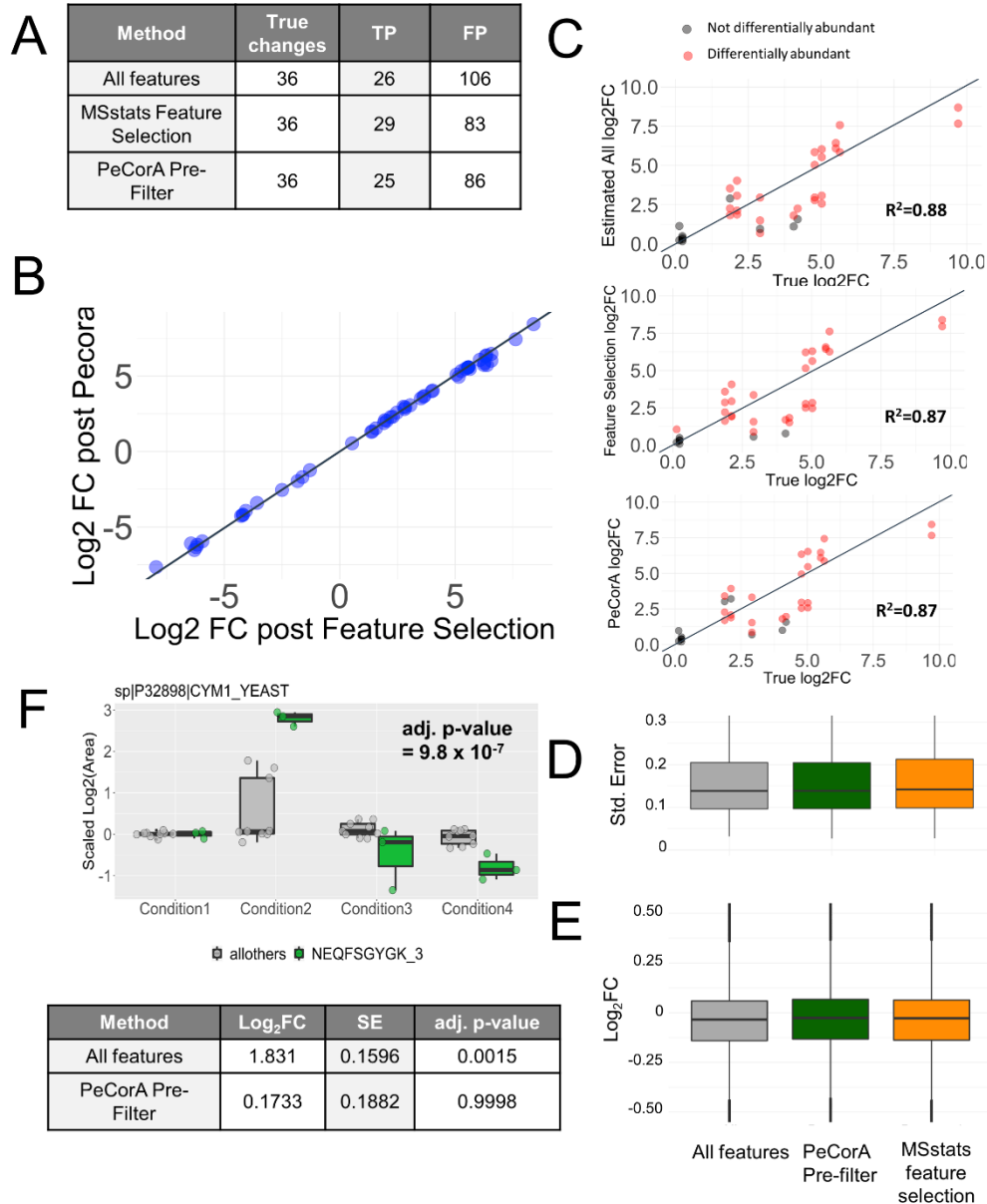
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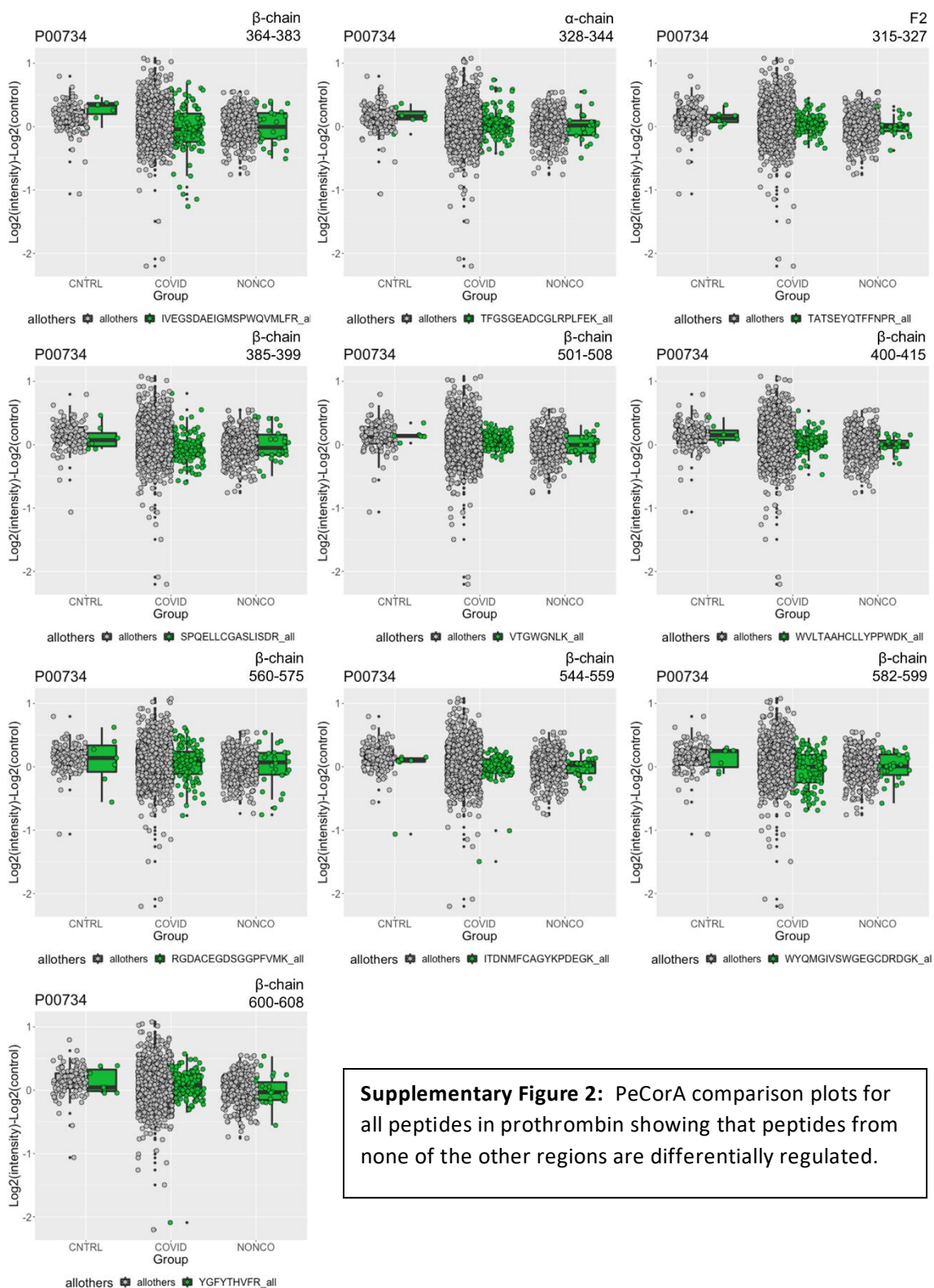
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**Supplementary Figure 1: PeCorA as a peptide filter before protein quantitation using a benchmark dataset.** (A) Summary of the iPRG dataset true positive (TP) and false positive (FP) protein changes detected using all peptide features or the two feature filtration methods. (B) Protein quantities of the 53 significant protein changes (not restricted to spiked-in proteins, FDR<0.01) detected from either of the two feature selection methods shows almost identical performance. PeCorA pre-filtration (y-axis) or MSstats feature selection (x-axis). (C) Regression plots of each method (y-axes) versus the true values based on the amount spiked-in (x-axes). (D) Standard errors and (E) log<sub>2</sub>(fold change) for all protein comparisons between the three methods show that PeCorA pre-filtering performs similar to MSstats feature selection. (F) Example protein P32898 from the iPRG benchmark. PeCorA identifies one outlier feature for that protein (Peptide NEQFSGYGK). Table below: quantification of P32898 by MSstats using all the features or after PeCorA filtration of the poorly quantified feature.



**Supplementary Figure 2:** PeCorA comparison plots for all peptides in prothrombin showing that peptides from none of the other regions are differentially regulated.