

Identification of Inflammatory Proteomics Networks of Toll-like Receptor 4 through Immunoprecipitation-Based Chemical Cross-Linking Proteomics

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Supplementary Figures

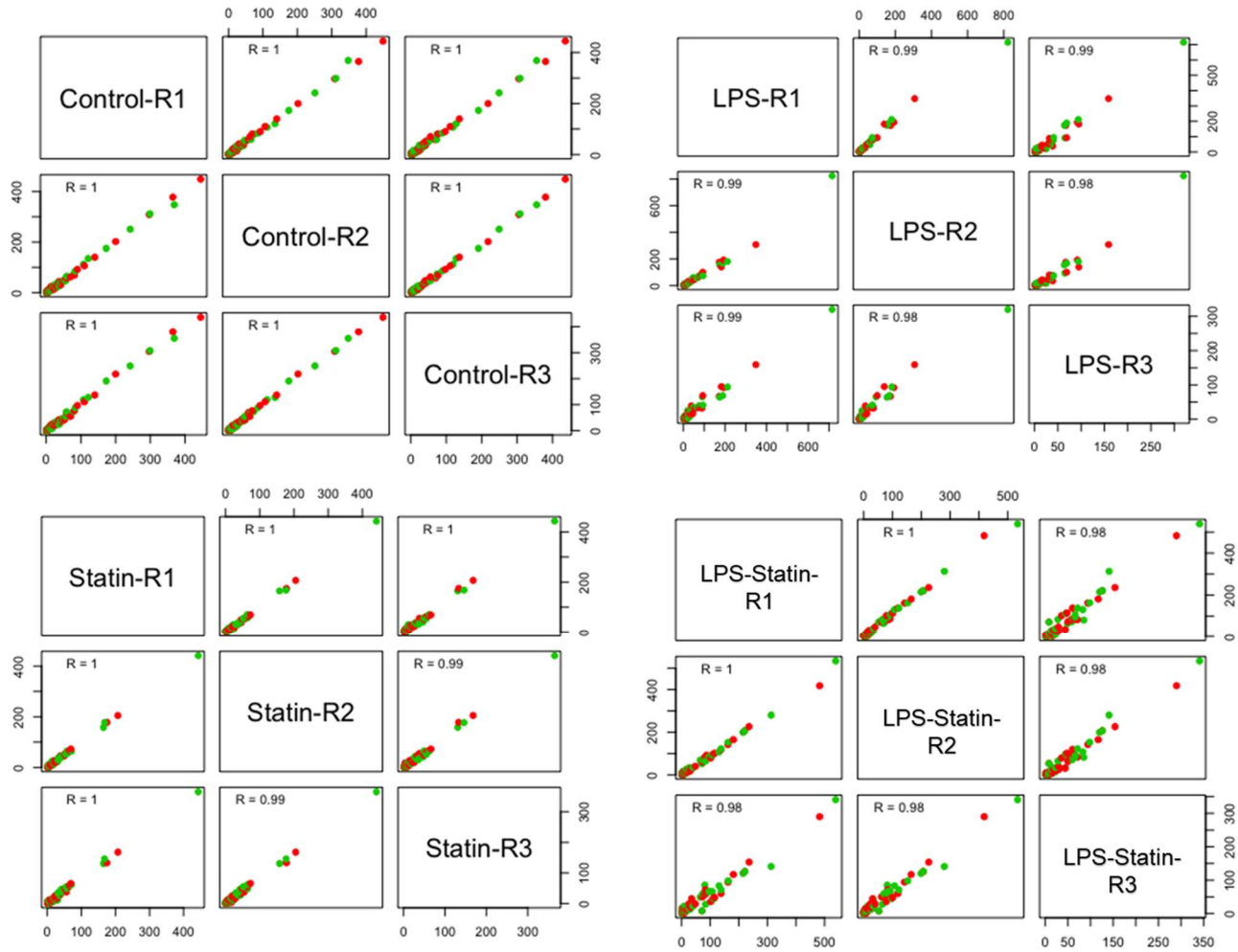


Figure S1. Scatter plots and pairwise correlations among the biological replicates showing significant correlation patterns among replicates of Control sample, LPS, Statin and LPS-Statin treated samples without cross-linker. The PSMs (Peptide Spectral counts) of replicates are plotted against each other across x and y-axis, correspondingly. Every spot symbolizes the abundances of a proteins and corresponds to Pearson's correlation coefficient (R^2) of 1. The scatter plot and pairwise correlation analysis was performed by R package ver. 3.5.3.

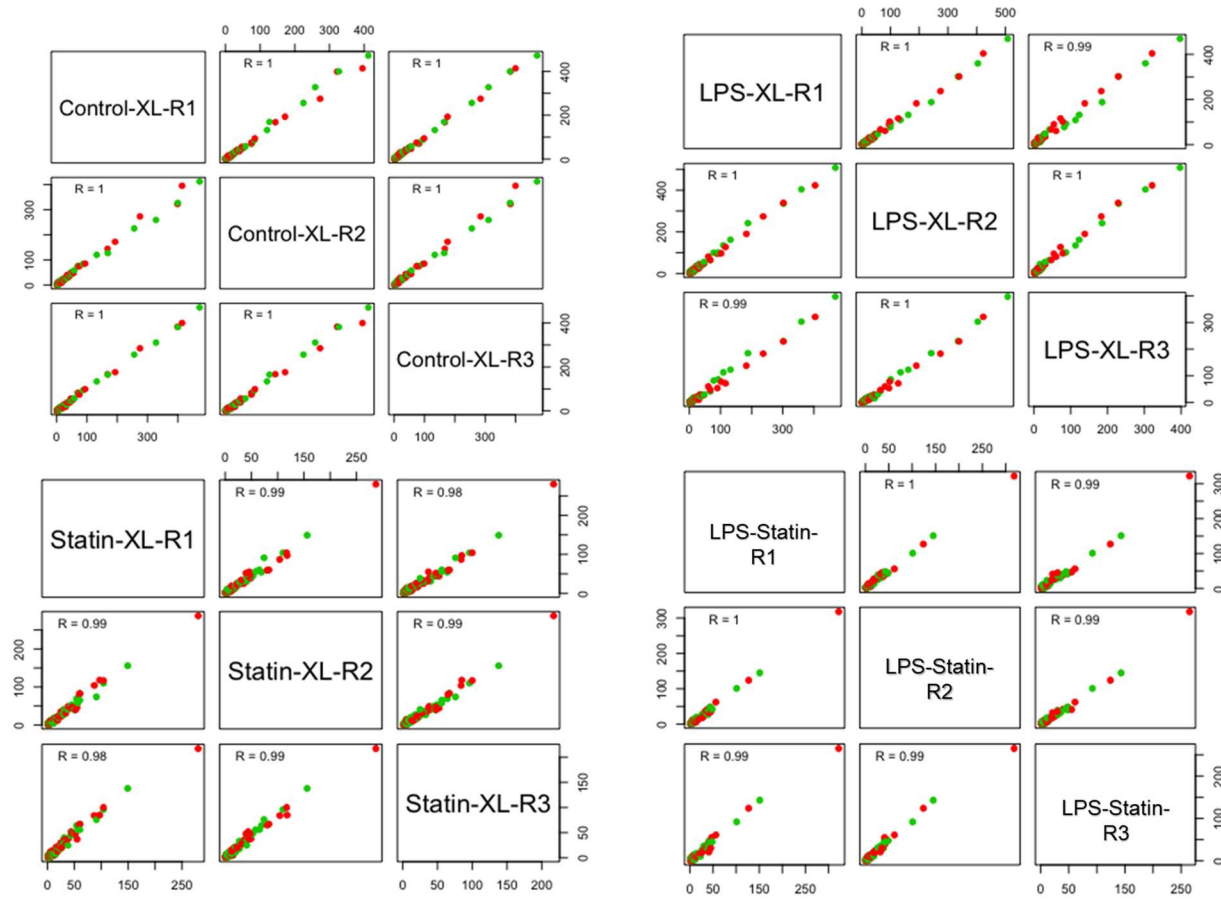


Figure S2. Scatter plots and pairwise correlations among the biological replicates showing significant correlation patterns among replicates of Control sample, LPS, Statin and LPS-Statin treated samples with cross-linker treatment. The PSMs (Peptide Spectral counts) of replicates are plotted against each other across x and y-axis, correspondingly. Every spot symbolizes the abundances of a proteins and corresponds to Pearson's correlation coefficient (R^2) of 1. The scatter plot and pairwise correlation analysis was performed by R package ver. 3.5.3.

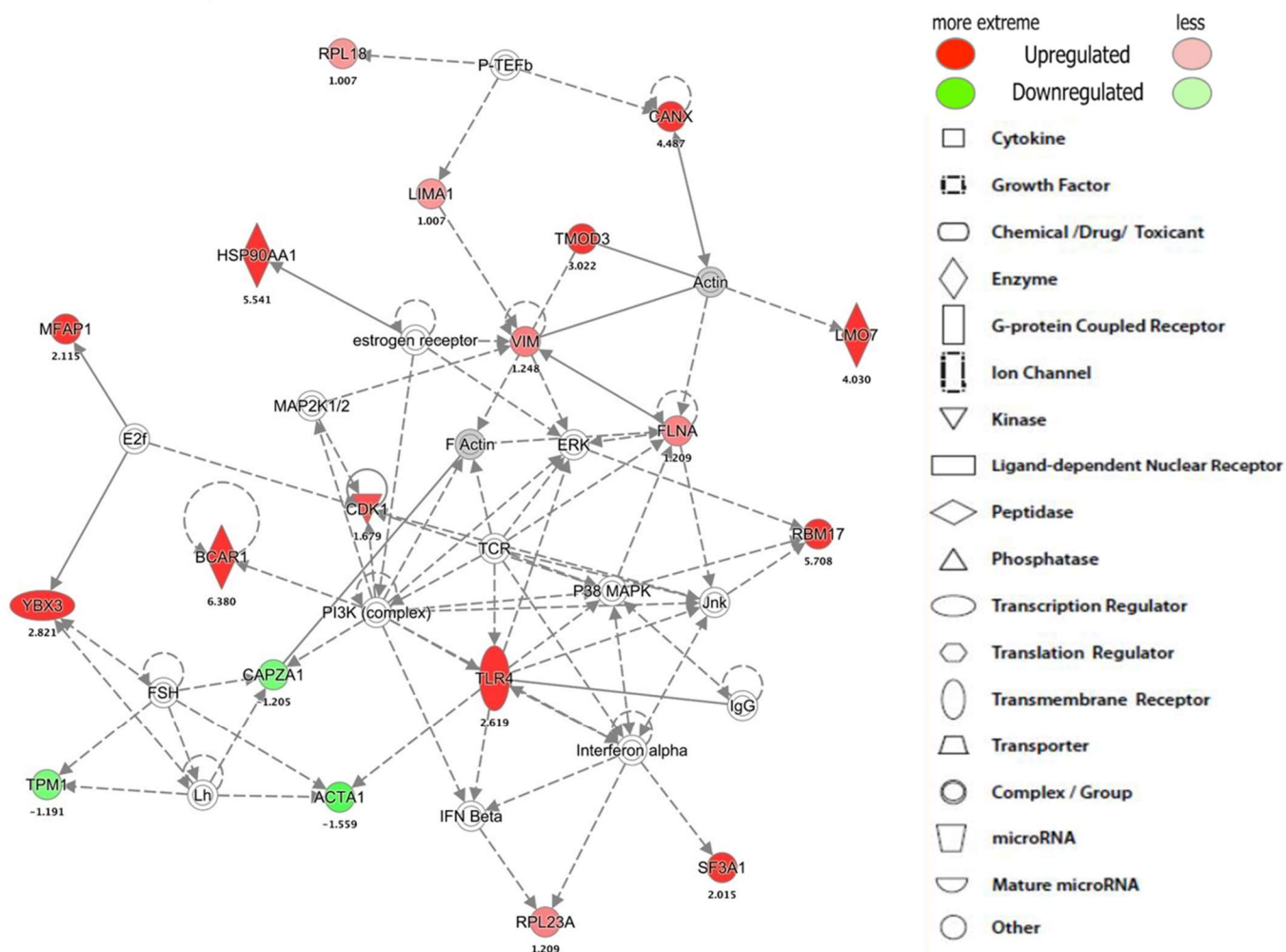


Figure S3. TLR4 targeted protein network with expression profile. The interaction network shown was generated using IPA bioinformatics software upon treatment of LPS in HA-TLR4-HEK293 cells.

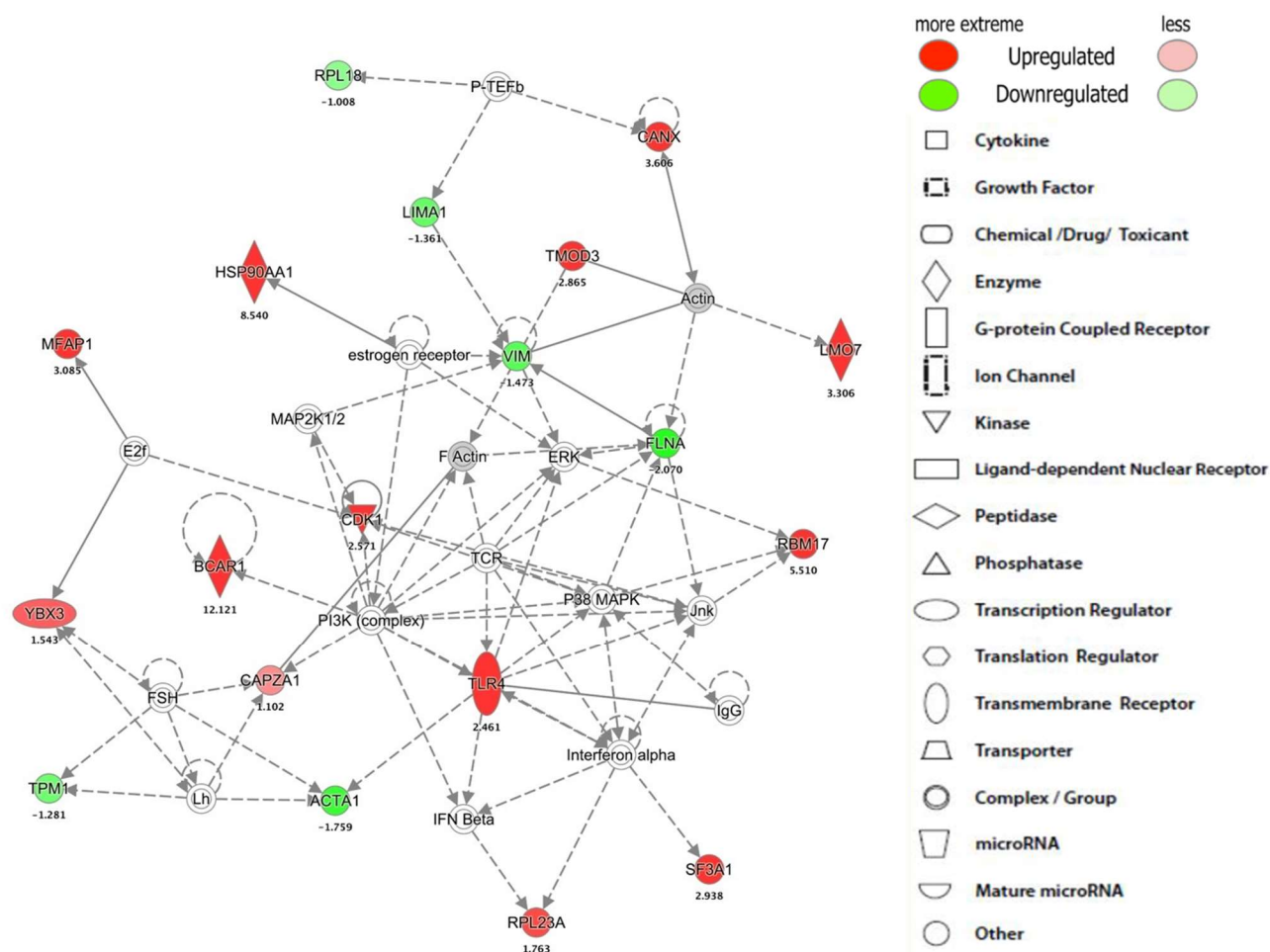


Figure S4. TLR4 targeted protein network with expression profile. The interaction network shown was generated using IPA bioinformatics software upon treatment of LPS-Statin in HA-TLR4-HEK293 cells.

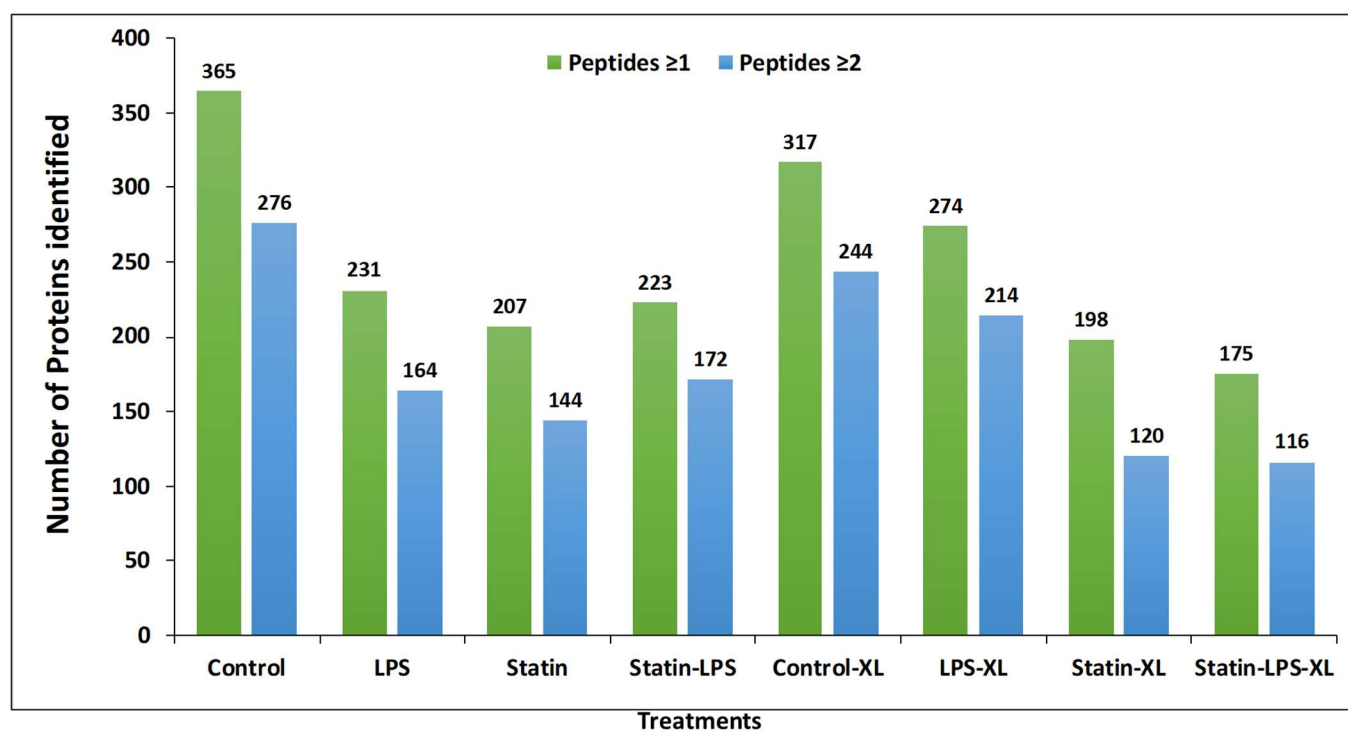


Figure S5. The number of proteins identified with or without cross-linkers across each treatment conditions where at least 1 or 2 peptides identified for each sample.