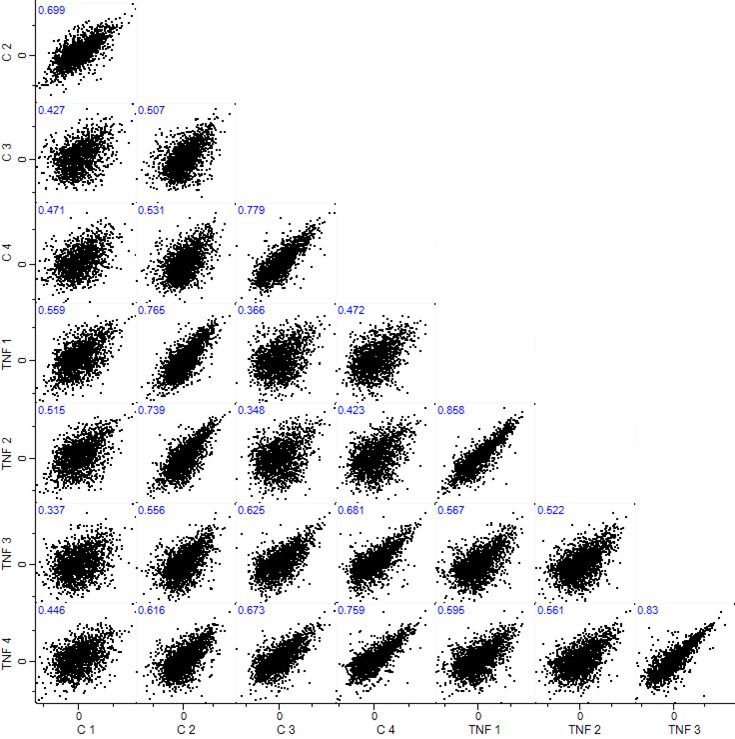
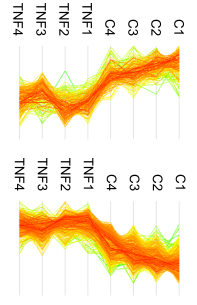
**Supplement**

**A B**

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**Figure S1.** Characterization of the phospho-proteome in TNF long term-exposed cells. Primary human monocytes were incubated ± 400 U/mL TNF for 48 h (n=4) and subsequently analyzed using LC-MS/MS. Following Z-normalization of signal intensities among the 4 different LC-MS/MS assays, a Perseus software-based bioinformatic clustering was performed. **A**. The multi-scatter plot shows the correlation of peptide phosphorylation among different samples. The Pearson correlation coefficient is indicated. **B**. The phosphorylation profile illustrates differences between the phosphorylation levels of detected phospho-sites among TNF long term-incubated samples (TNF1-4) and untreated controls (C1-4), respectively.