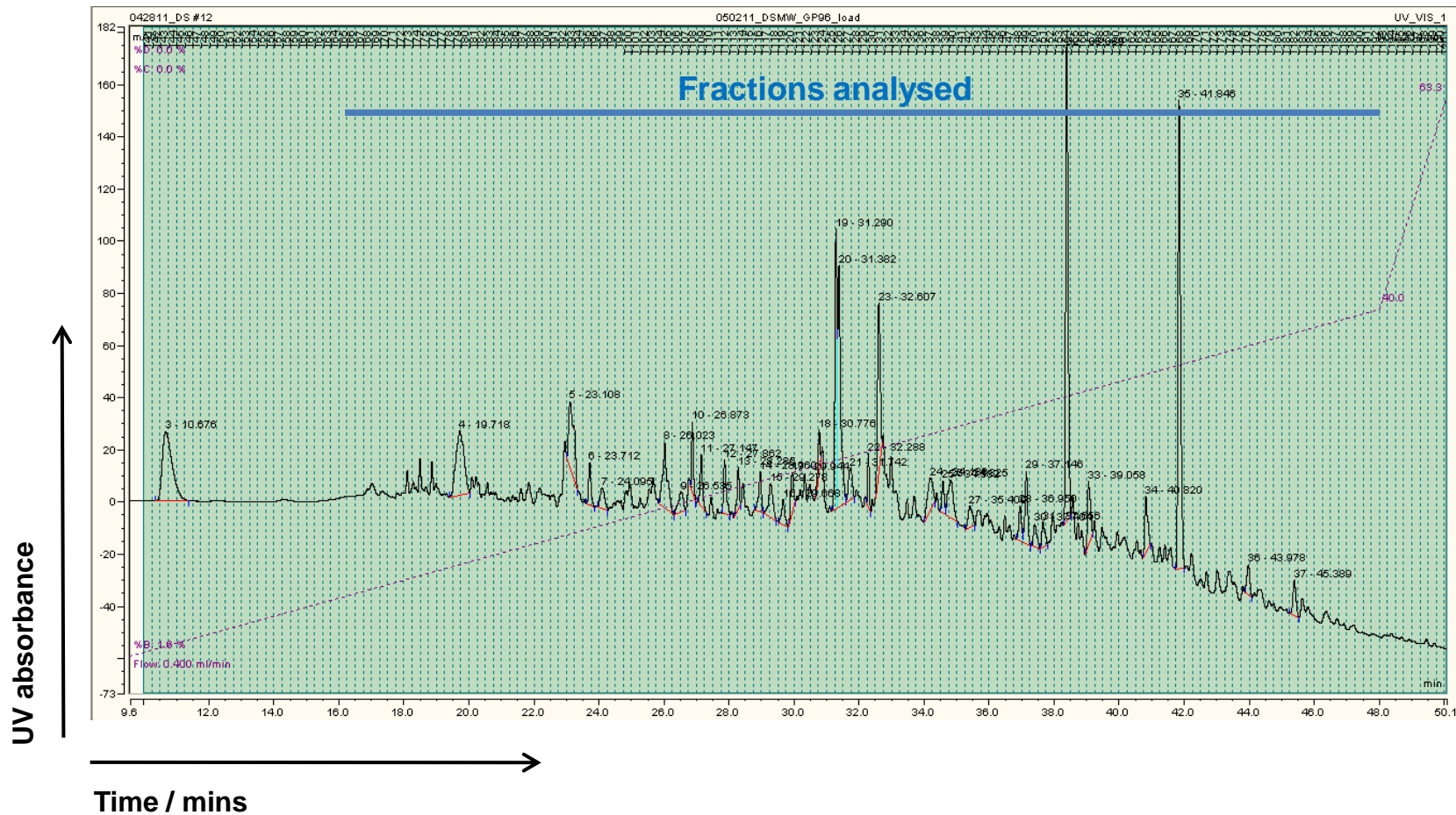
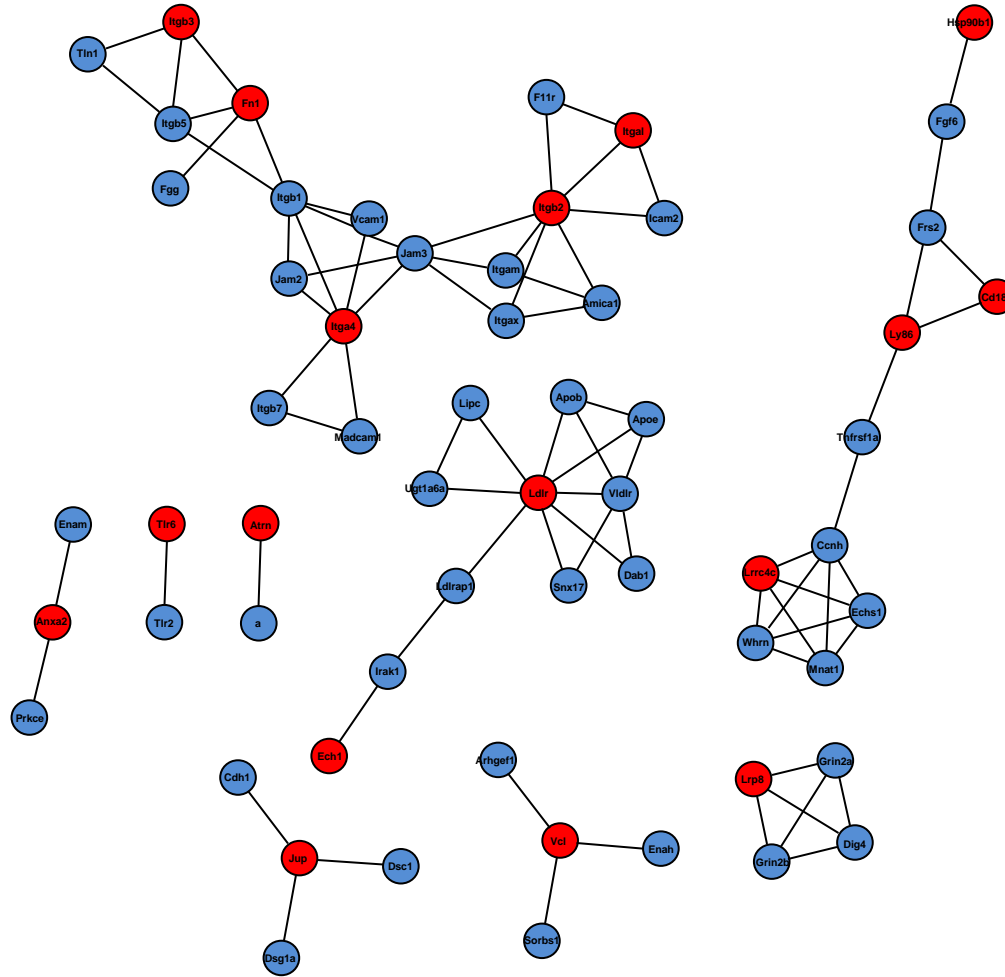


**Figure S1:** UV trace of HpRP-HPLC fractions analysed



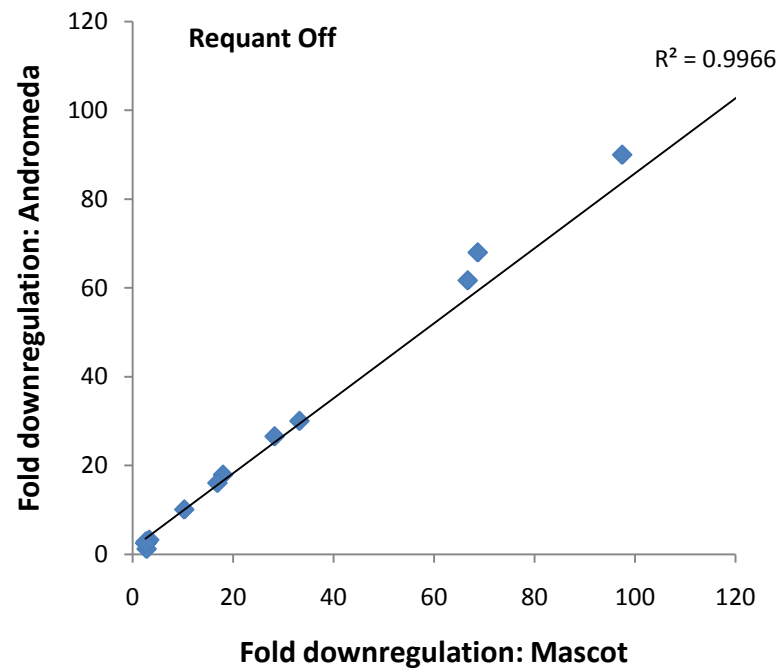
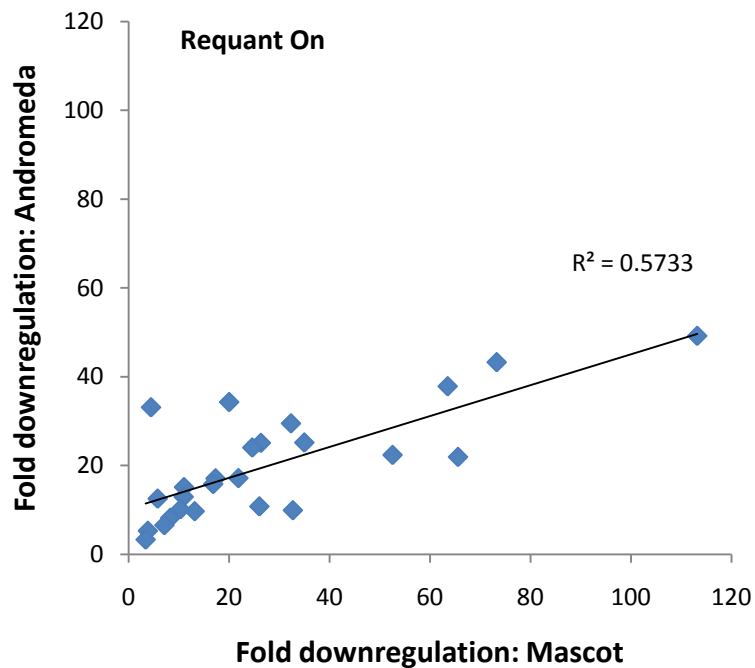
A total of 100 µg of tryptic peptide was subjected to HpRP-HPLC fractionation. Peptides were resolved using a linear 40 min 2-40 % MeCN gradient. Eluting peptides were collected in 15s fractions (dotted vertical lines). Fractions 25 – 152 were analysed.

**Figure S2:** Interactions of proteins down- or up-regulated >3 fold



Cytoscape 2.8.2 was used to search for known interactions of proteins (red circles) that were identified by  $\geq 2$  peptides with a fold downregulation of >3.

**Figure S3:** Comparison of ratios generated by MaxQuant version 1.0.13.13 (using Mascot) and MaxQuant 1.1.1.14 (using Andromeda) with requant on or off



Data is included for all proteins identified in both Mascot and Andromeda by  $\geq 2$  peptides with a fold downregulation of  $>3$ . When we re-processed data with re-quantify turned off, there was much better correspondence between Mascot and Andromeda ratios albeit with a reduced number of quantified proteins.