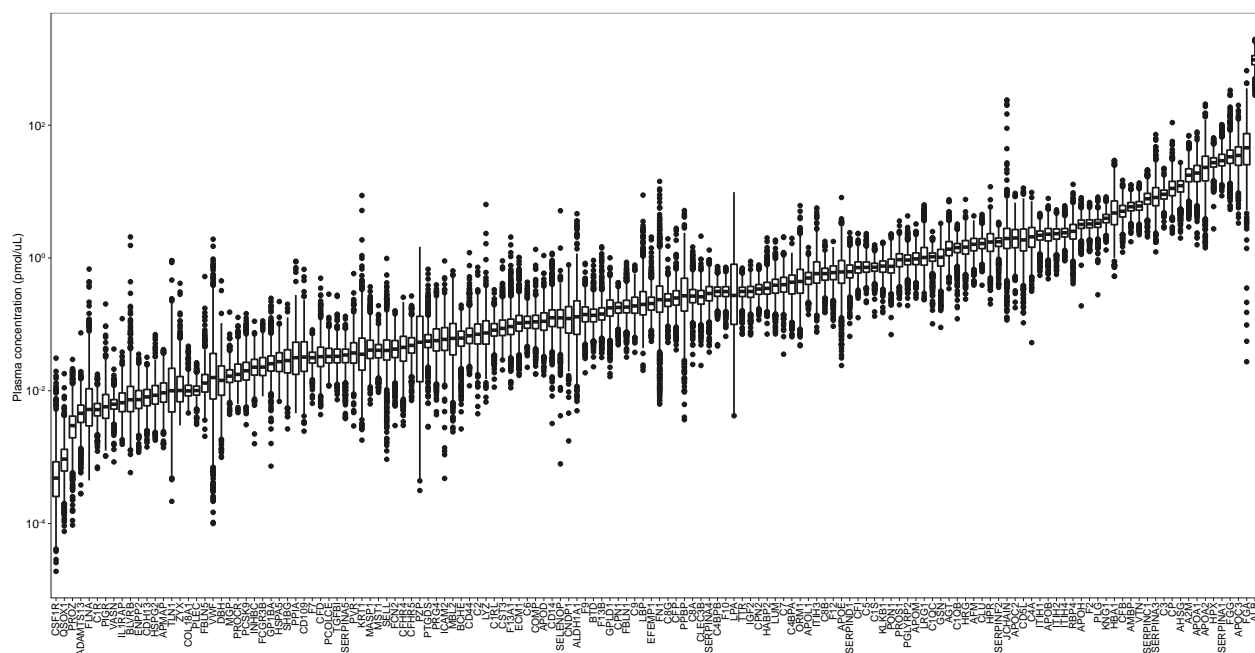**Supplementary Figures**

Figure S1 – *All 146 quantified proteins showing dynamic range over 6 orders of magnitude.*
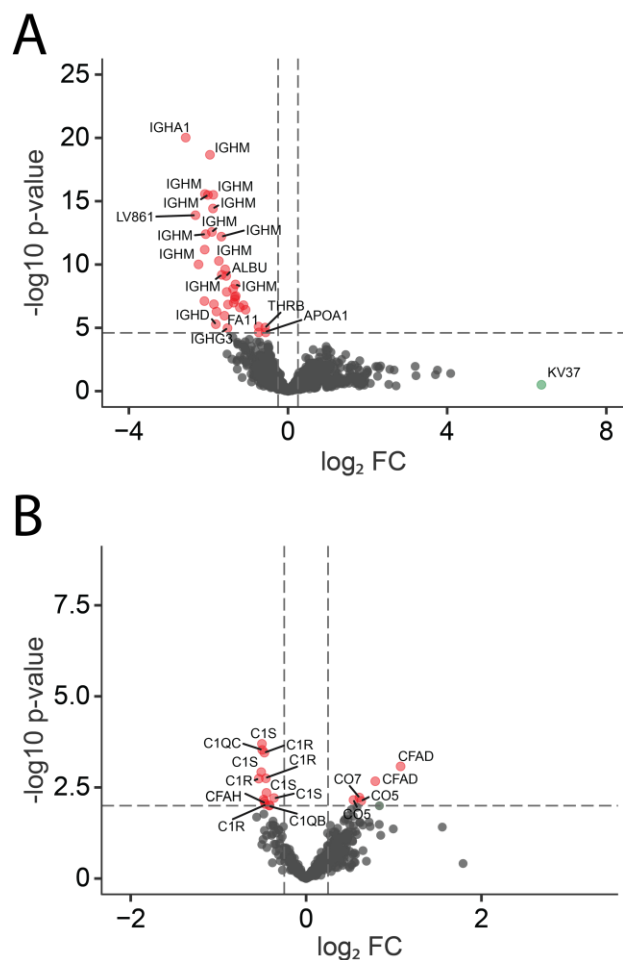

Figure S2 – *Label free quantification data showed protein dysregulation for multiple myeloma compared to all other cancers. A. Confirmed downregulated hallmark proteins for multiple myeloma linked to mainly*

immunoglobulins. B. Complement complex C1 proteins were observed downregulated in label free data, though, less significantly than in absolute quantification data.
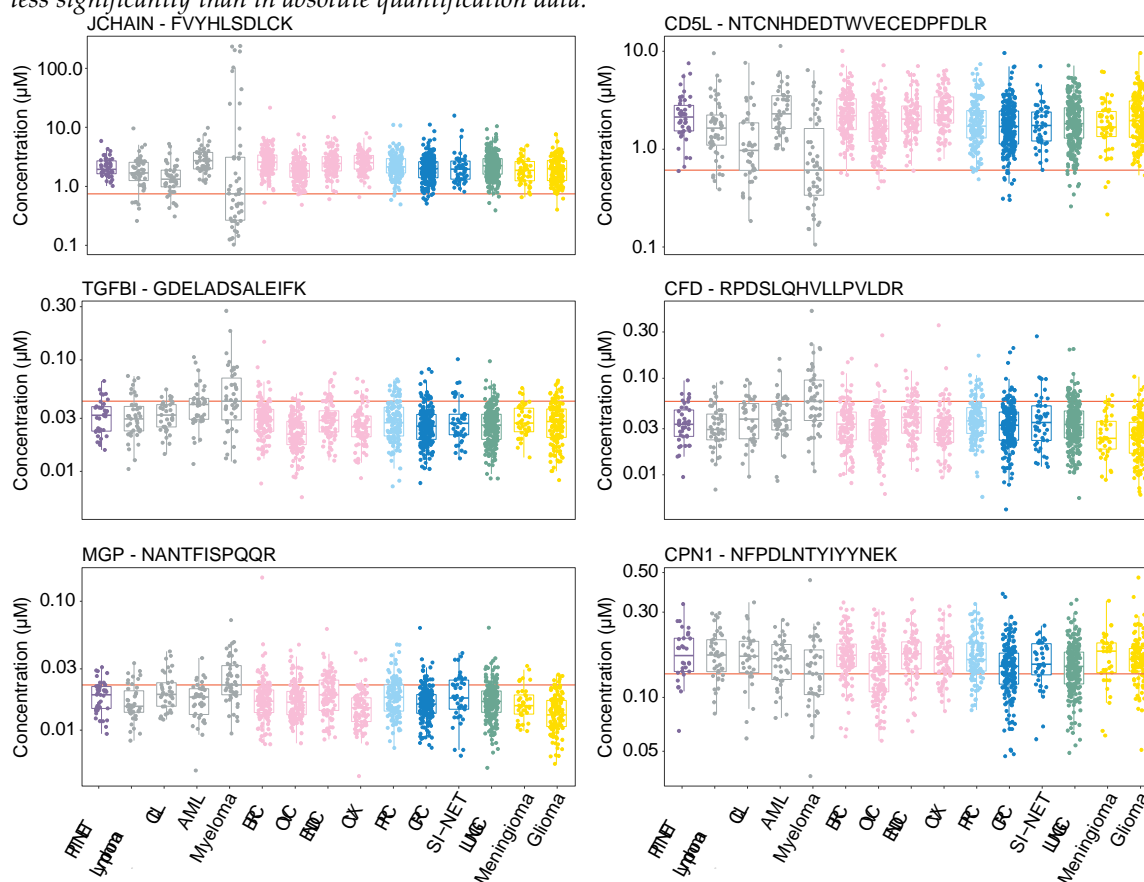

***Figure S3** – Peptides identified as the most important by the random forest models for the classification of multiple myeloma*
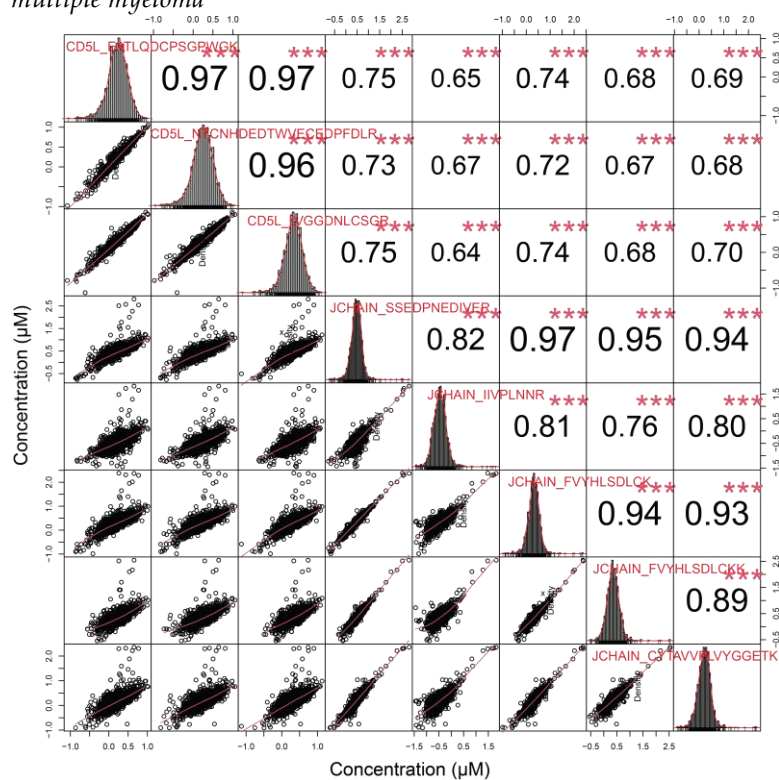

***Figure S4** – Correlation plot between all quantified peptides from CD5L and JCHAIN.*