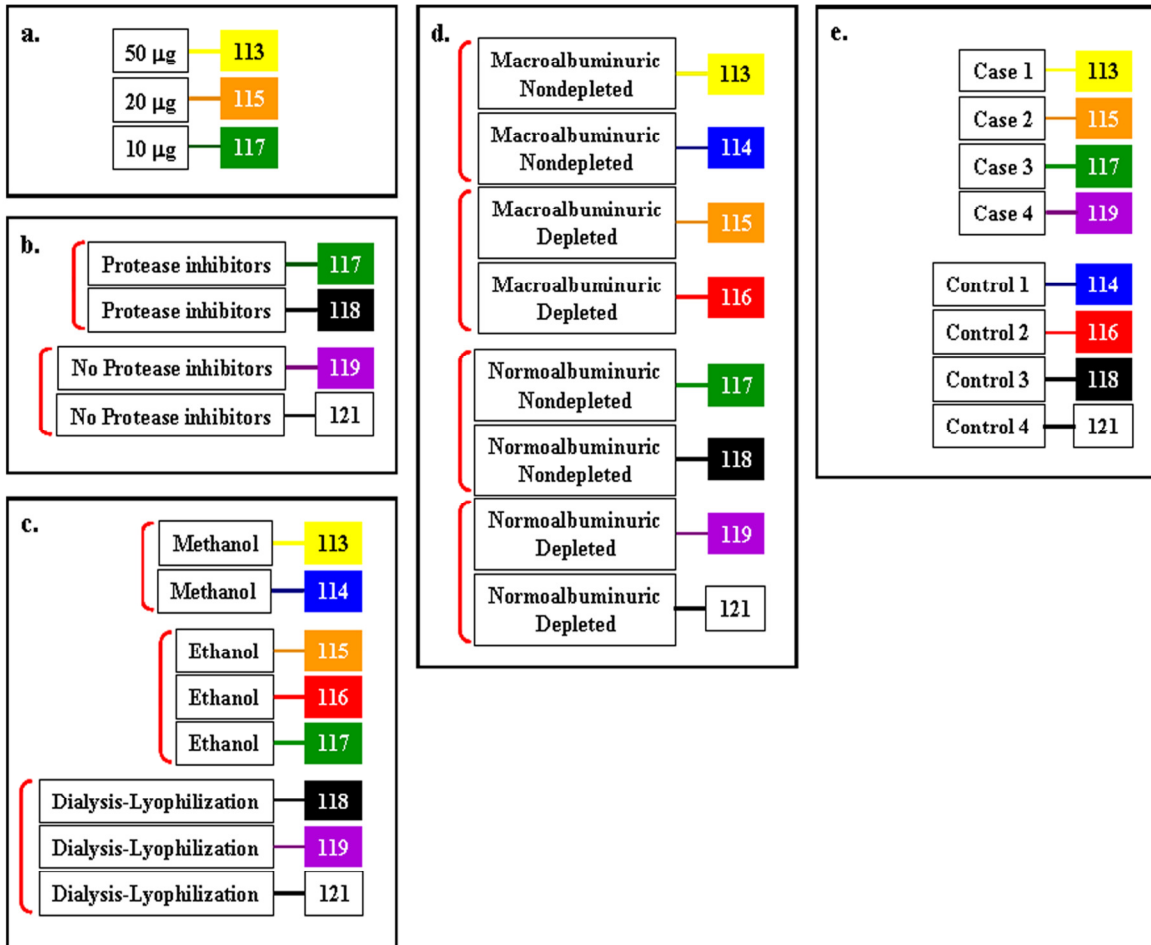


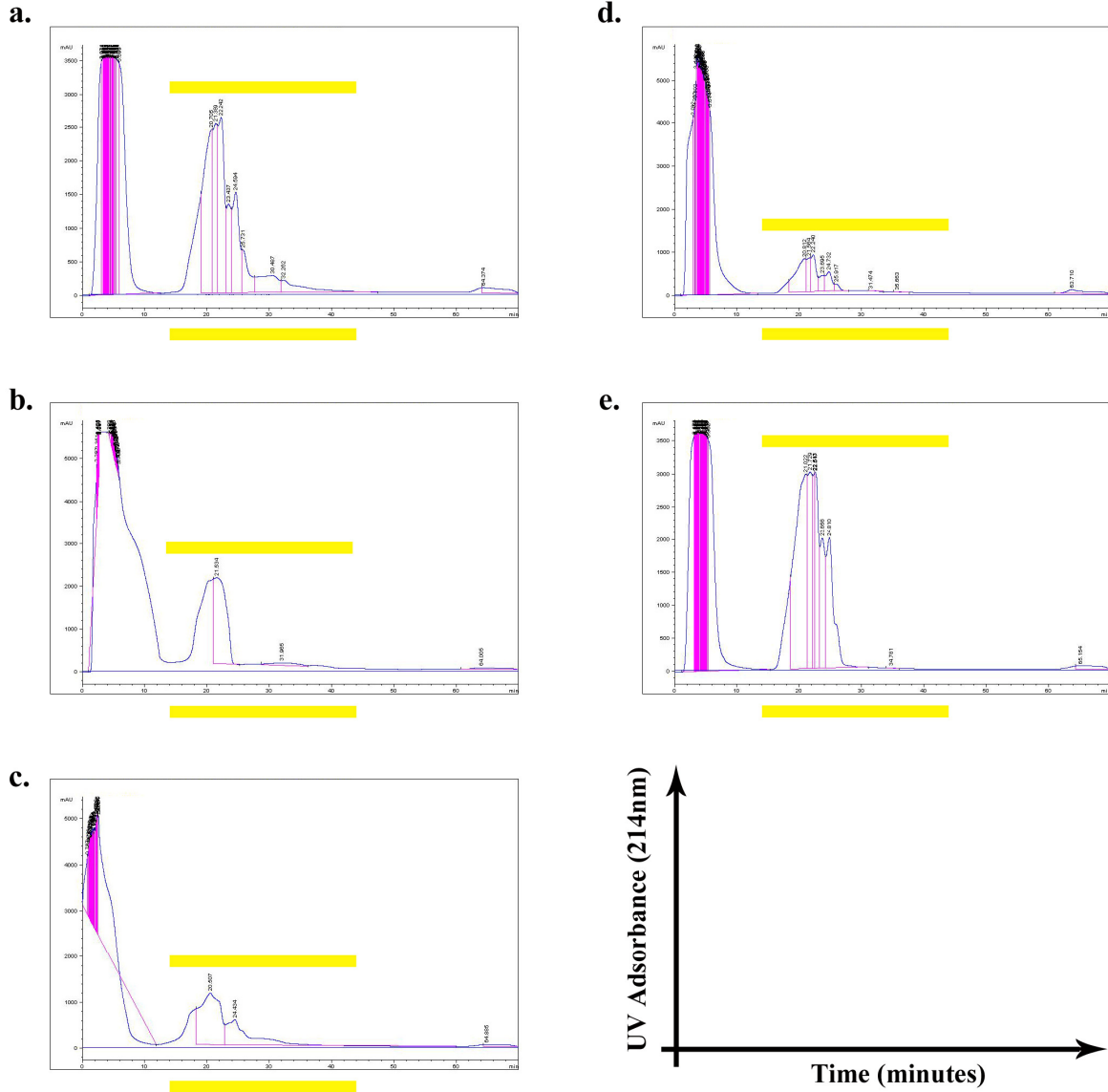
Supplementary Figure 1. BSA standard curve in urine and water

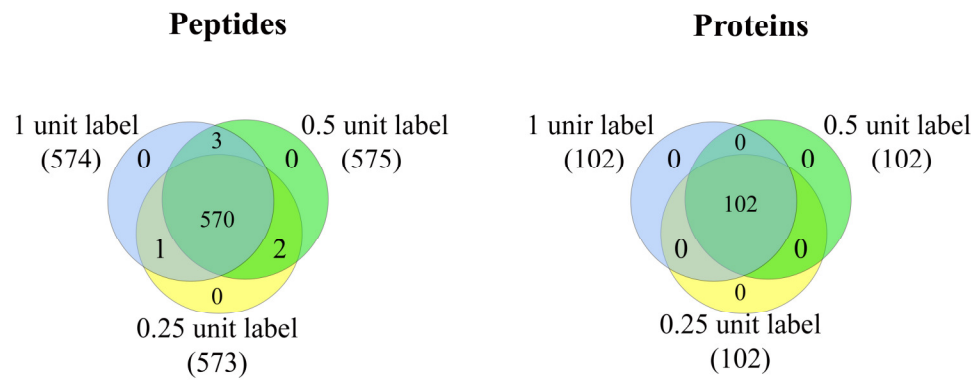
Optimizing a proteomics platform for urine biomarker discovery



Supplementary Figure 2. Sample pooling scheme for Figs 1-5.

# Optimizing a proteomics platform for urine biomarker discovery

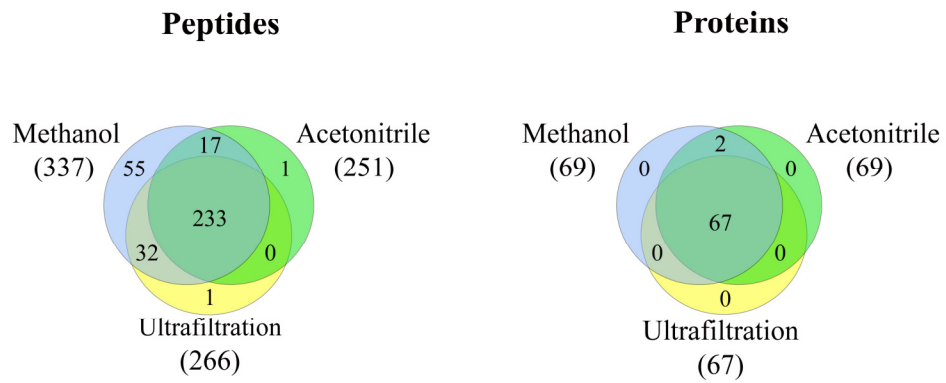




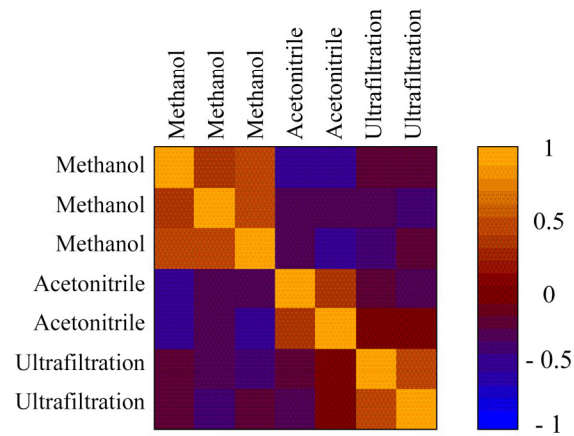
**Supplementary Figure 4. Titration of iTRAQ label**

# Optimizing a proteomics platform for urine biomarker discovery

**a.**



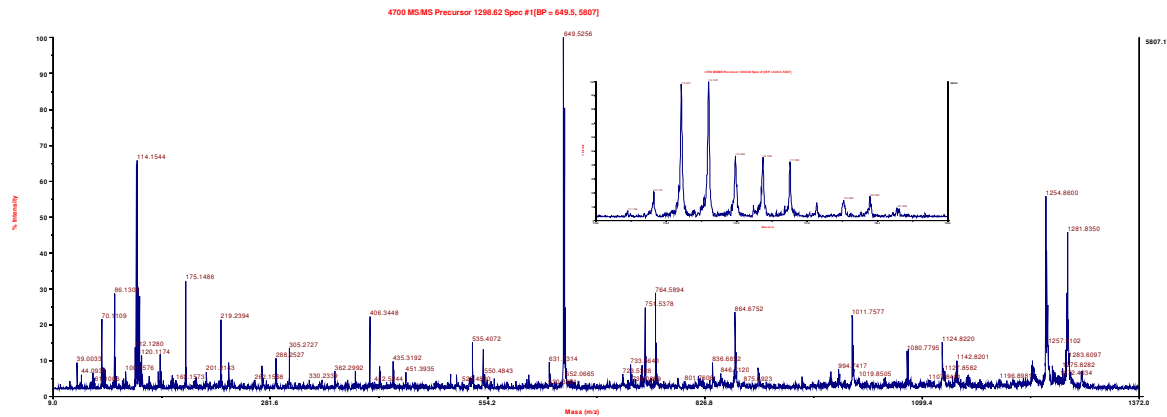
**b.**



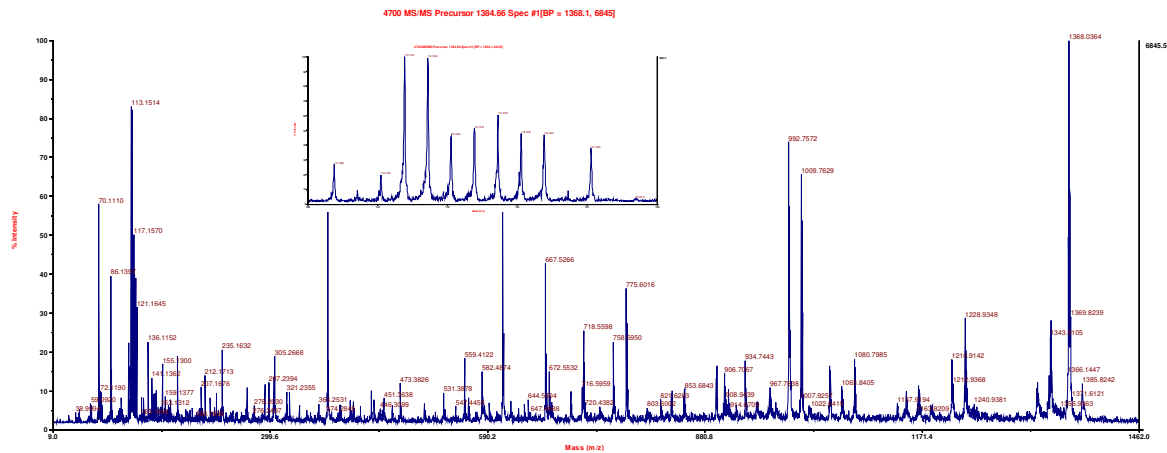
**Supplementray Figure 5. Protein extraction methods**

# Optimizing a proteomics platform for urine biomarker discovery

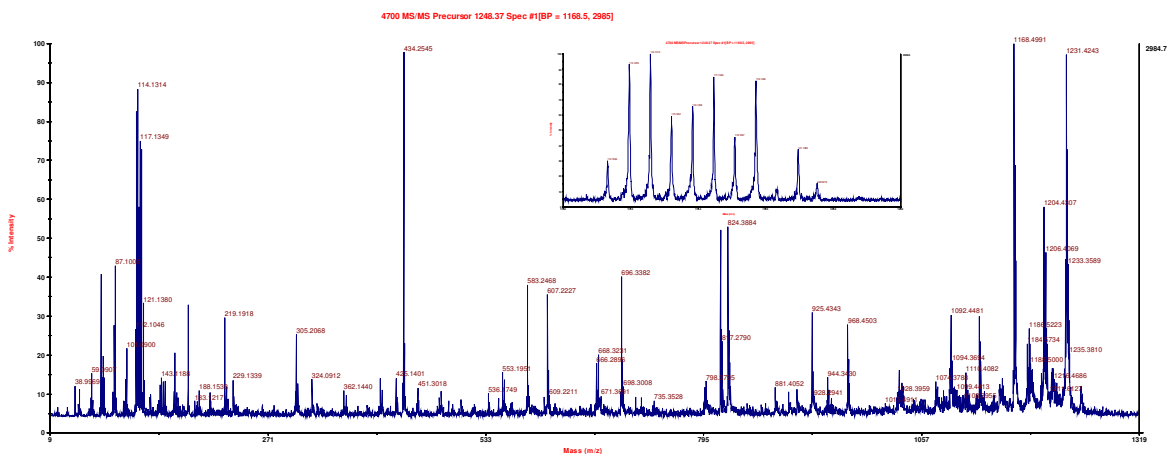
## a. Alpha-1-acid glycoprotein 1 (TEDTIFLR)



## b. Alpha-2-HS-glycoprotein (APHGPGLIYR)



## c. AMBP protein (ECLQTCR)

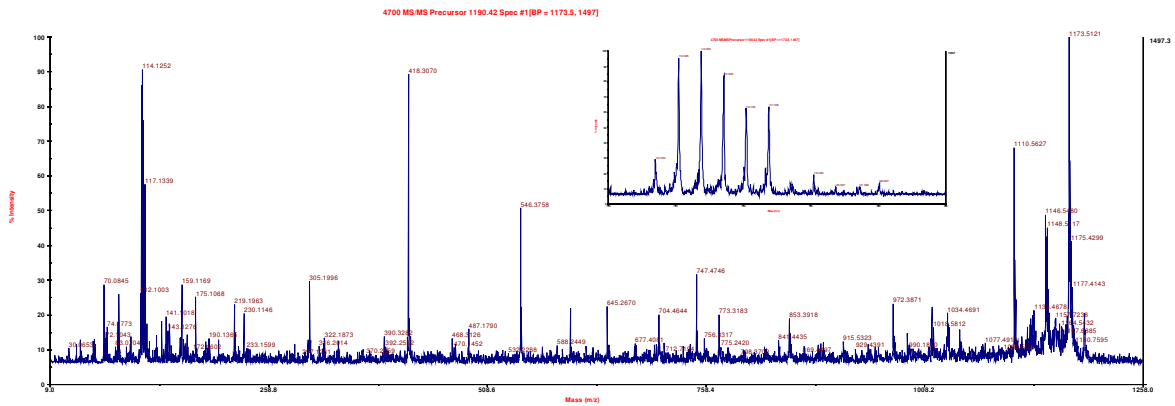


Supplementary Figure 6. Representative Spectra from Figure 5 (a-c)

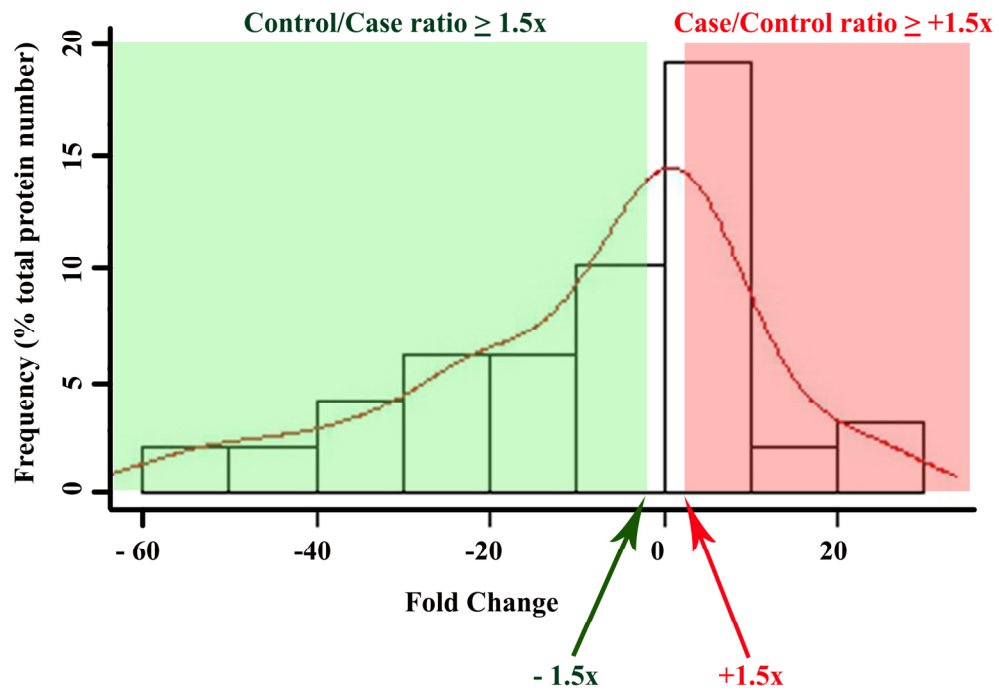


# Optimizing a proteomics platform for urine biomarker discovery

## g. Beta-defensin 1 (IQGTCYR)







Supplementary Figure 7. Distribution of fold-change among the 54 proteins in Pima cases and controls.