

## Figure S2







## Supplemental figure legends

**Figure S1: IHC analysis of mouse tissues.** Images showing protein expression profiles based on five antibodies, immunohistochemical analysis and bright field microscopy. Protein expression is shown in brown and counterstaining in blue. All antibodies were obtained from the Human Protein Atlas project (<u>www.proteinatlas.org</u>). **A.** The antibody, HPA008188, staining PSMA2 shows general, moderate to strong, cytoplasmic staining in all tissues. **B.** and **C.** The antibodies, HPA019527 (B) and HPA20912 (C), staining AMACR both show granular cytoplasmic staining of tubuli in kidney. **D.** The antibody, HPA039482, staining GYS2 shows moderate to strong cytoplasmic staining of hepatocytes in liver and myocytes in skeletal muscle. A weaker luminal staining was observed in small intestine while the remaining tissues were negative. **E.** The antibody, HPA019639, staining CANT1 shows a general cytoplasmic staining of all tissues, with the strongest staining of small intestine.

**Figure S2: Protein identifications across mouse tissue. A.** Plot of the number of identified proteins in each tissue. **B.** Plot of the number of proteins that are common to the specified number of tissues shows that the majority of the proteins are common to all tissues, and only 650 are tissue specific. **C.** Plot of the number of proteins that are exclusively expressed in one tissue.

**Figure S3: Hierarchical clustering of the annotation matrix.** The column dendogram shows the clustering of the tissues and the row dendogram the annotations.

**Figure S4: Comparison of transcriptome and proteome. A**. Hierarchical clustering of the spearman correlations between the RNA-seq data from Mortazavi et al (32) and the MS data. **B-D.** Scatter plots of protein intensities vs. RPKM mRNA data in liver muscle and brain.