Supporting Information

Waanders et al. 10.1073/pnas.0908351106

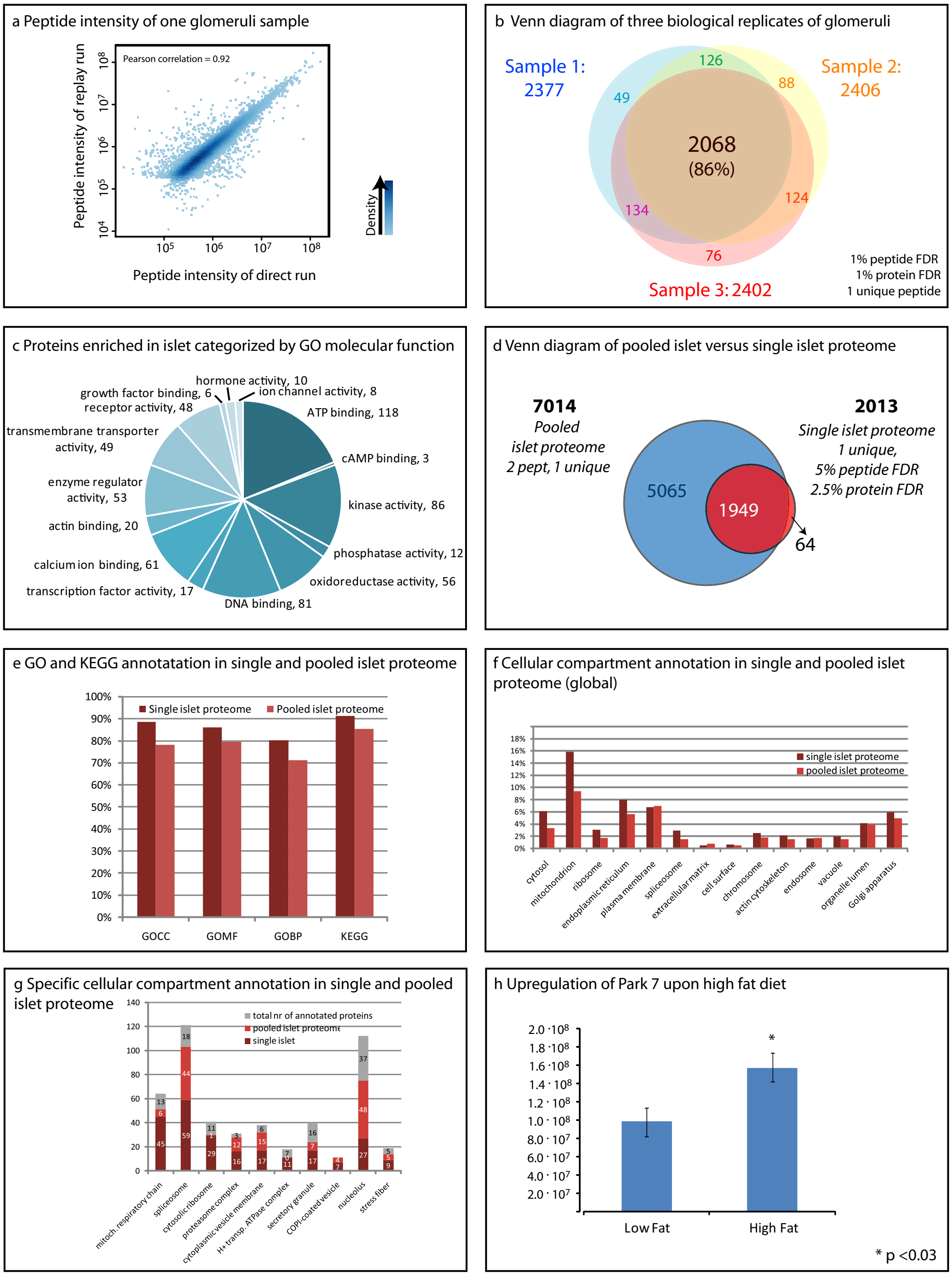

Fig. S1. Fig. S1 as part of Waanders et al. (*A*) Peptide intensity correlation between direct and replay runs (technical replicates) of a glomeruli sample collected by LCM. Pearson correlation coefficient, $R = 0.90$. (*B*) Venn diagram of proteins identified in three individually collected glomeruli samples (biological replicates). (*C*) Annotation of pooled islet dataset by gene ontology-molecular function. (*D*) Venn diagram of pooled islet proteome versus proteins identified in single islets, showing 97% overlap. (*E*) Percentage of identified proteins in single and pooled islet proteome annotated for gene ontology and KEGG. (*f*) Comparison of proteins of different cellular compartments identified in single versus pooled islet proteome. (*G*) Annotation of proteins in single and pooled islet dataset to gene ontology identifiers (cellular compartmentalization) involved in β cell function. (*H*) Up-regulation of Park-7 (DJ-1) upon high-fat diet. Average of two (high-fat) and three (low-fat) experiments, per sample two mice pooled. Mean value +/- SEM.

Other Supporting Information Files

Table S1 (XLS)
Table S2 (XLS)
Table S3 (XLS)
Table S4 (XLS)