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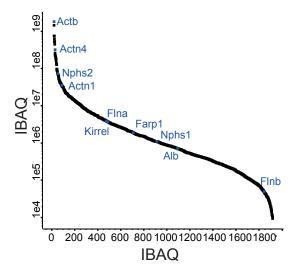
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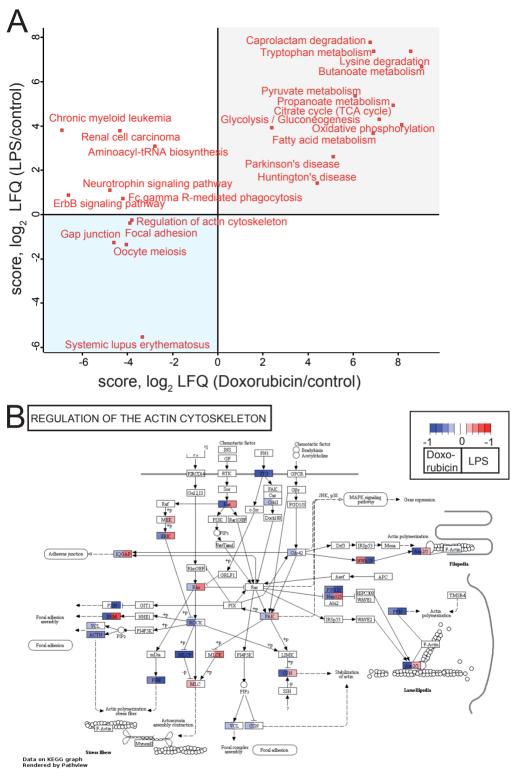
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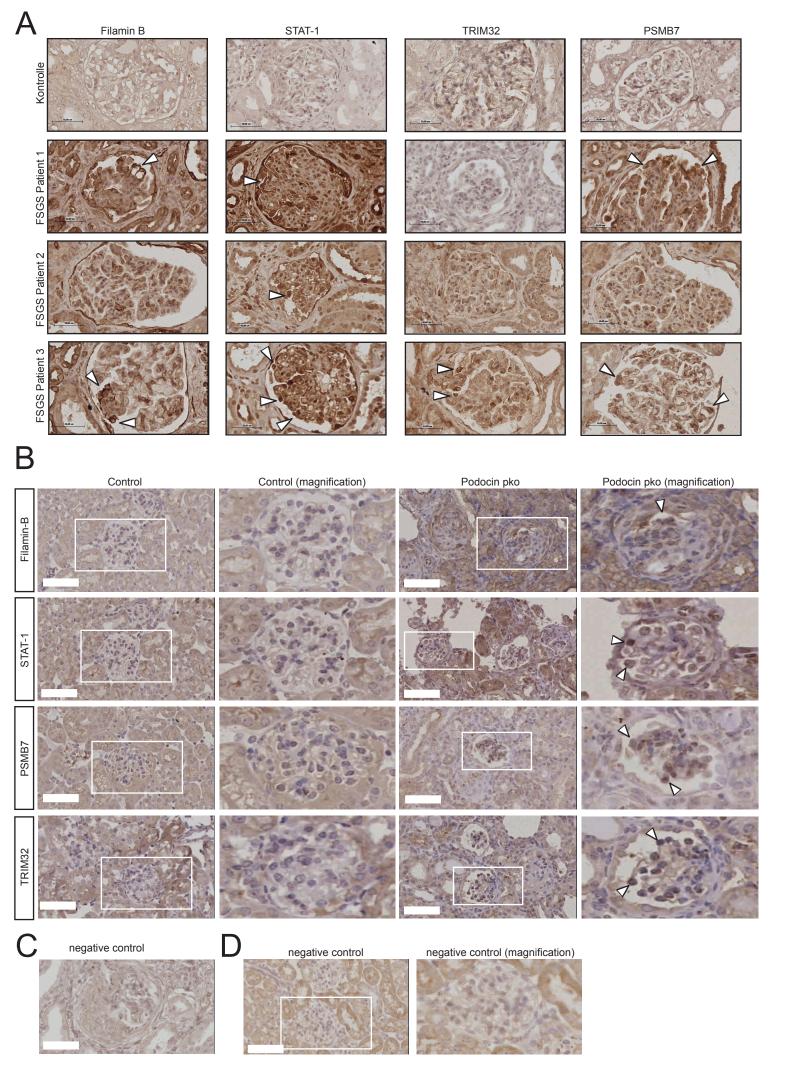
Supplemental Table 4: Proteome data from the LPS study.



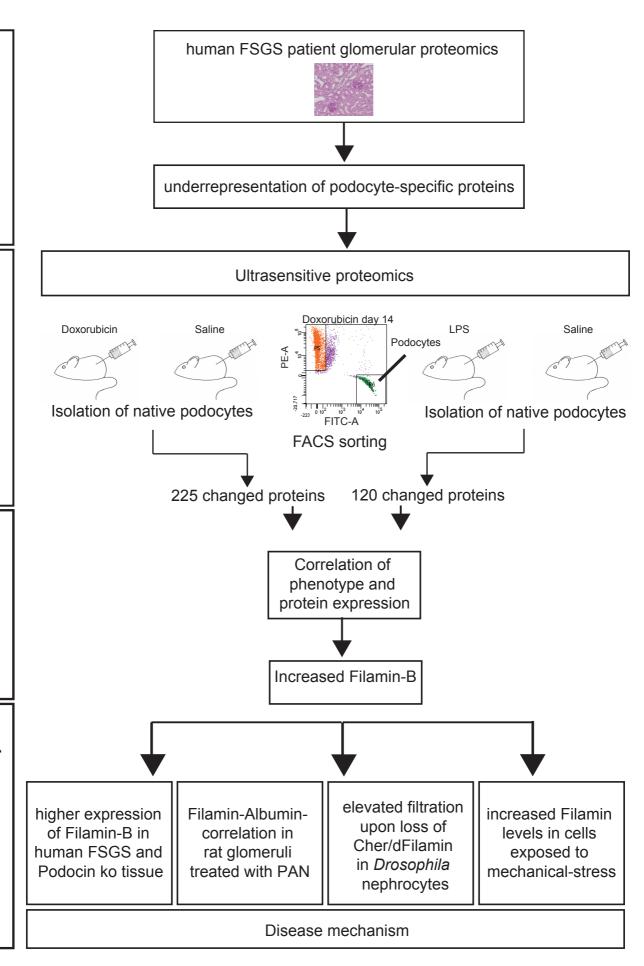
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Supplementary Figure Legends

Supplemental Figure 1: Dynamic range. Protein copy numbers of podocytes isolated from a single mouse. The podocyte protein copy numbers are depicted as log10(iBAQ), a parameter corresponding to protein copy number.

Supplementary Figure 2: Different modes of injury cause an upregulation of metabolic signaling and a down-regulation of actin-cytoskeleton associated pathways. A Comparison of LFQ values of Doxorubicin and LPS treated animals using KEGG pathways revealed an up-regulation of metabolic signaling including citrate cycle, glycolysis and fatty acid metabolism. A common down-regulation was observed for actin-cytoskeleton associated pathways such as gap junctions, focal adhesions and regulation of the actin cytoskeleton. B KEGG pathway analysis revealed differential regulation of actin-cytoskeleton associated proteins in Doxorubicin and LPS treated mice.

Supplemental Figure 3: Immunhistochemistry on human FSGS and Podocin knockout tissue revealed an increased Filamin-B expression A Immunohistochemistry of FSGS patient samples revealed an increased expression of Filamin-B, STAT-1, Trim32 and PSMB7 upon podocyte injury. Scale bar = 50 um. Arrowheads mark positive podocytes. B Immunohistochemistry of kidney tissue from Podocin knockout mice also revealed an increased expression of Filamin-B, STAT-1, TRIM32 and PSMB7 upon podocyte injury. C,D Human and mouse tissue stained without a primary antibody served as negative control. Scale bar = 50 um.

Supplemental Figure 4: Overview of this study demonstrating the applicability of sensitive proteomics for phenotype-proteome correlations.