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**Fig. S1: Clustered heat map of differentially expressed genes in glomeruli of NTN and control groups on day 7, 21 and 42.** Heat maps were constructed using log2 gene expression levels. Statistical analysis on nSolver (NanoString) normalized log2 gene expression levels was based on Limma Package (multi-group comparison), FDR=1%. Time was defined as a continuous covariate in the linear model of the analysis. Red indicates upregulated genes, and green indicates downregulated genes. Dendrograms show the Euclidian distances between samples and genes.