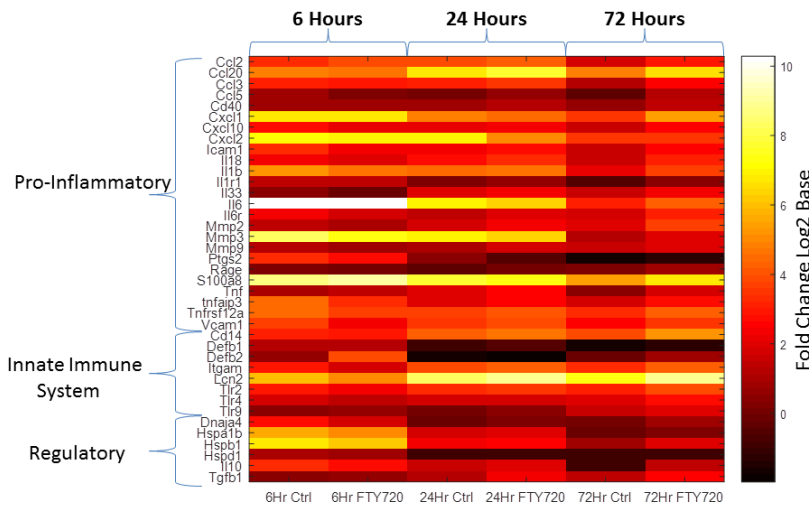


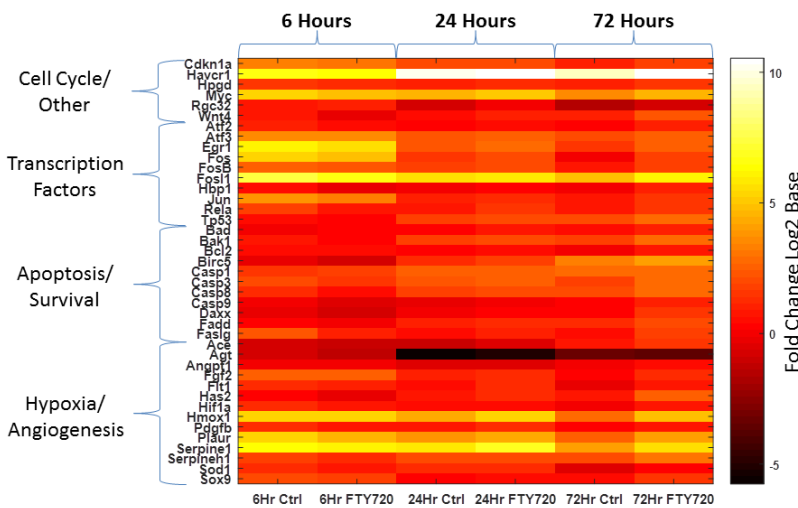
1 **Supplemental Figure S1: Differential expression heat maps from tissue in FTY720-treated versus**
 2 **vehicle control treated rats following renal ischemia.** Tissues collected at 6, 24, and 72 hr point
 3 post IRI were stored in RNALater and subsequently processed for mRNA. cDNA conversion of
 4 1µg of RNA was performed by RT-PCR followed by semi-quantitative real-time PCR for gene
 5 expression analysis using the $2^{-\Delta\Delta CT}$ method. Data was then transposed into a Log₂ Base format
 6 to better display the range of expression observed. A custom low density array panel of genes
 7 relevant to ischemia reperfusion injury was selected for the analysis. For each tissue, gene
 8 expression was quantified relative to naïve control tissue.
 9 **Supplemental Figure S1-A:**

Ischemic Kidney Gene Expression



10

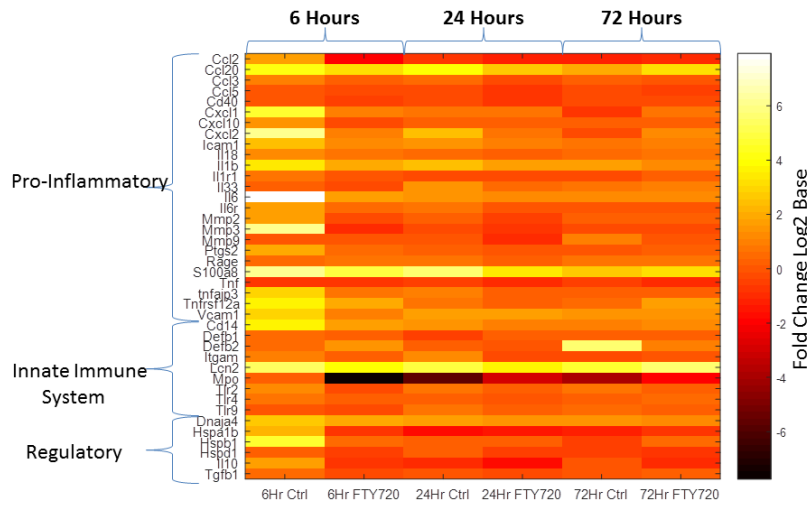
Ischemic Kidney Gene Expression



11

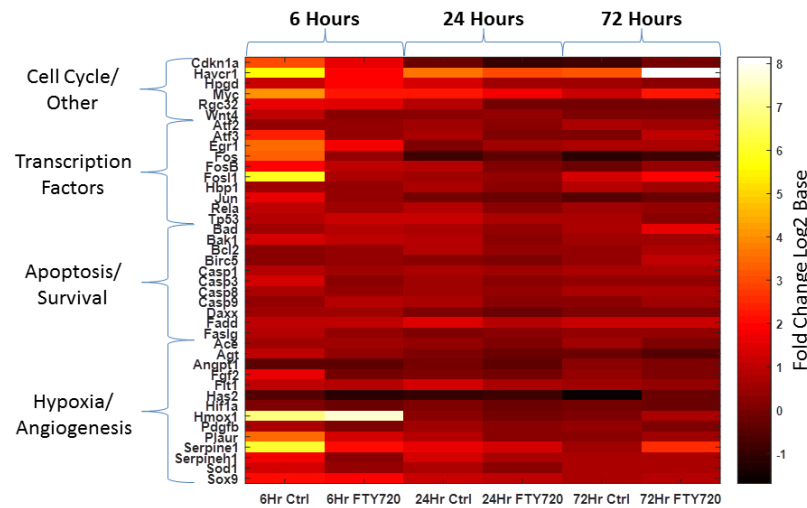
12 Supplemental Figure S1-B:

Normal Kidney Gene Expression



13

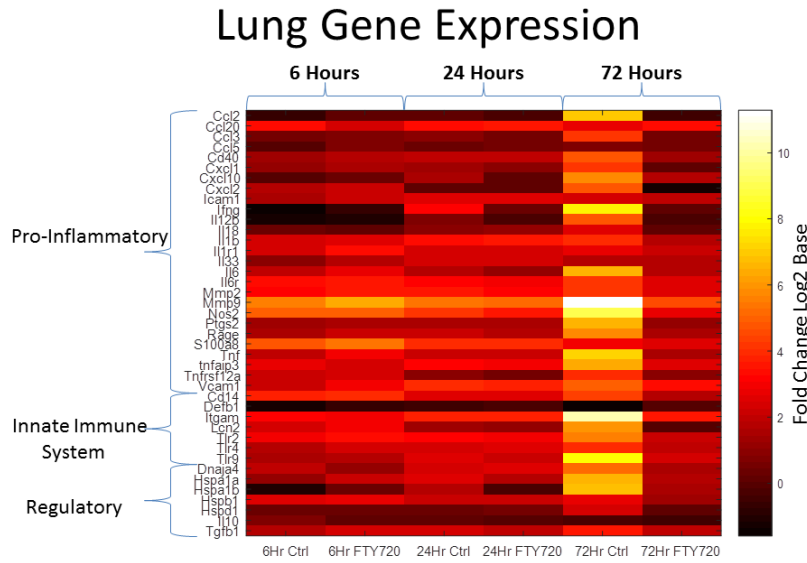
Normal Kidney Gene Expression



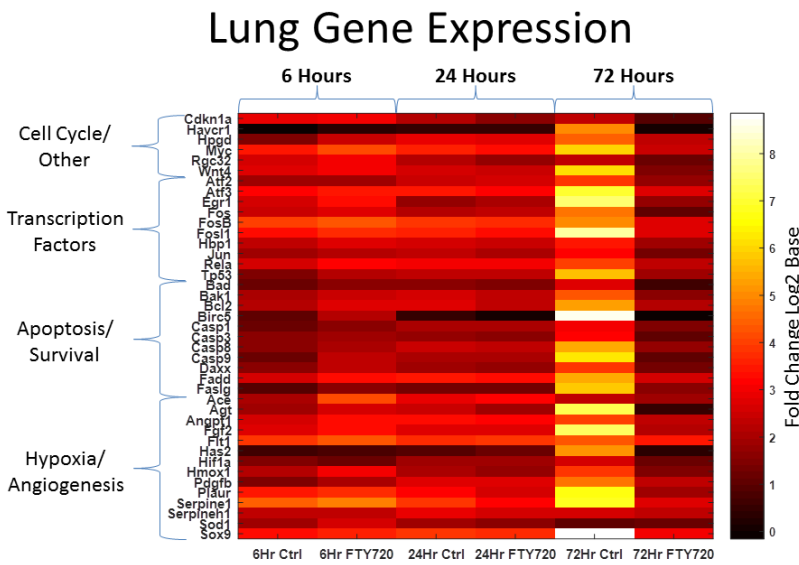
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16 Supplemental Figure S1-C:

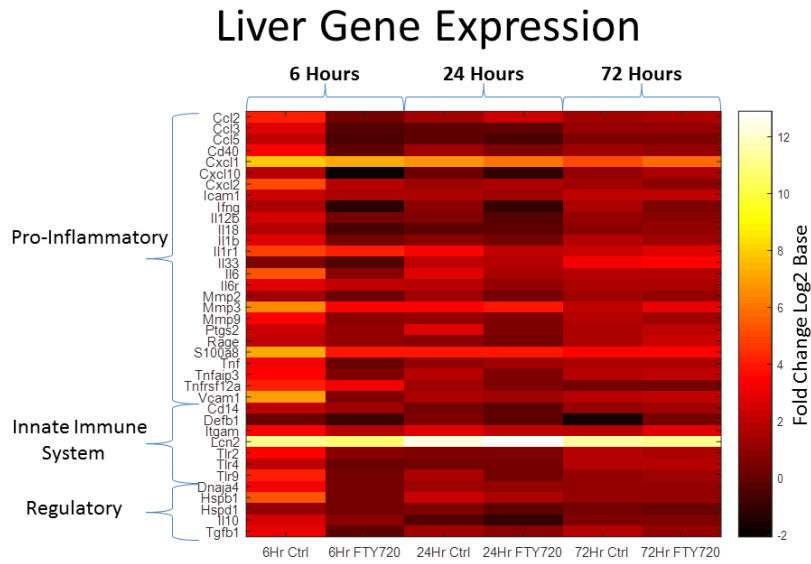


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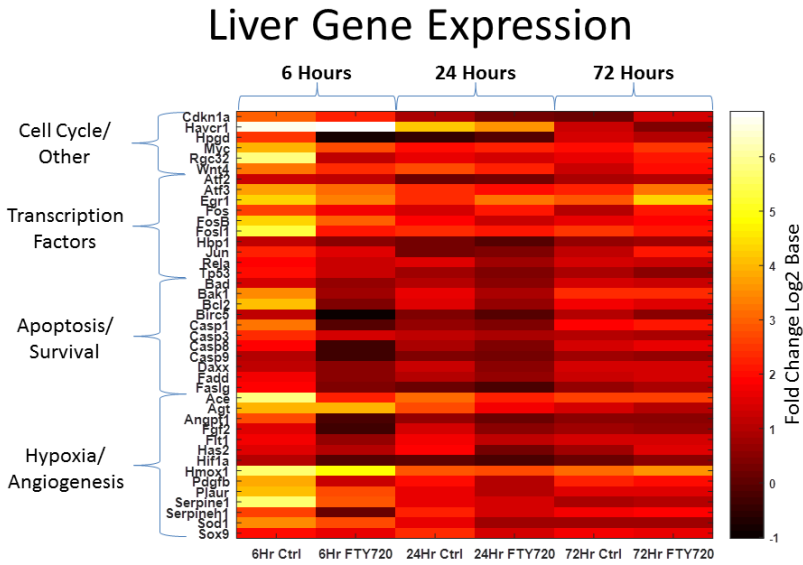


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19 Supplemental Figure S1-D:
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