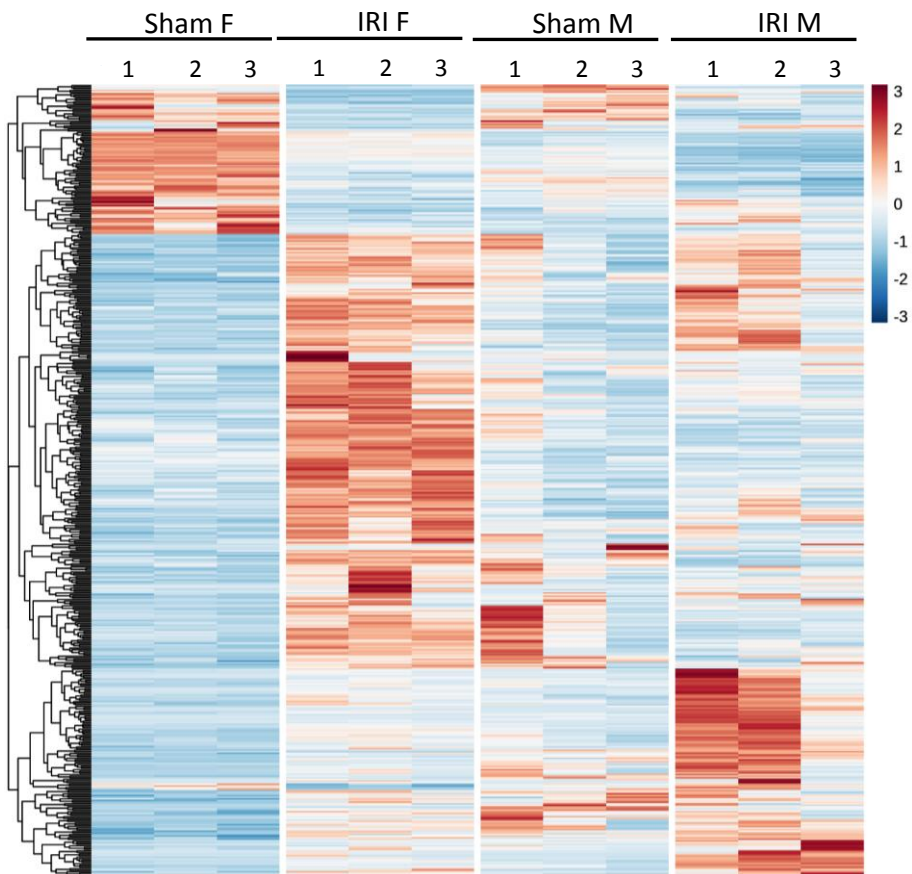
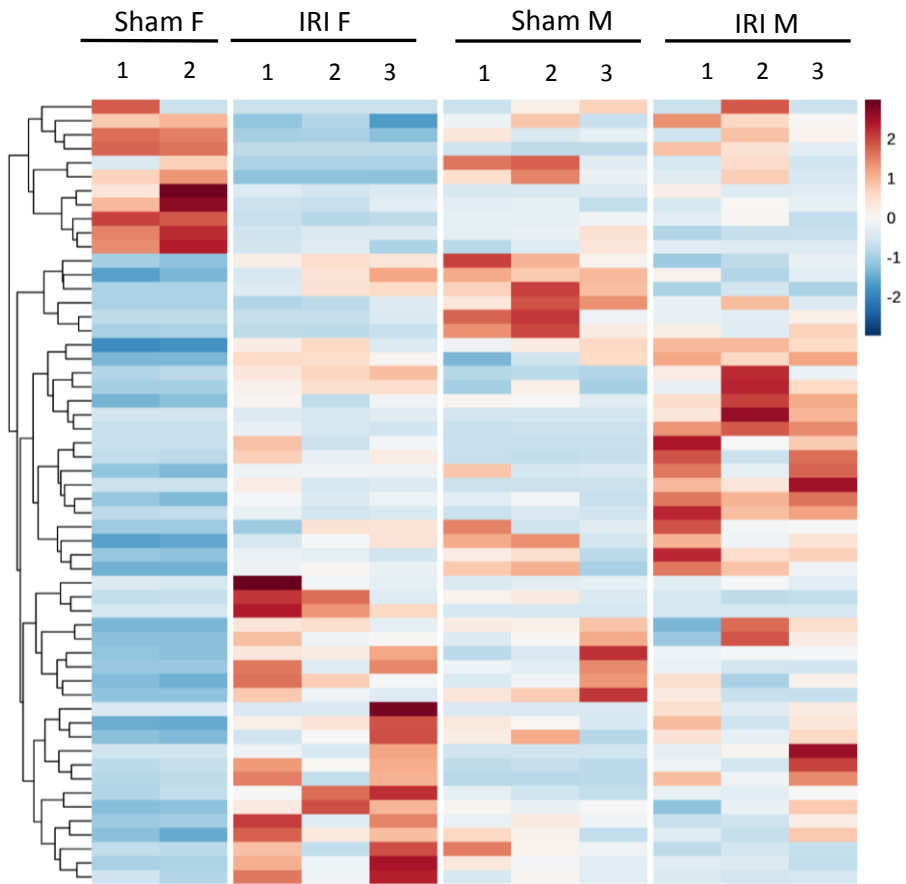


S1. Heat maps for differentially regulated genes (DEGs) from sham male (Sham M) mice compared to sham female (Sham F) mice. A) Heat map for proximal tubular DEGs (1,800 genes). B) Heat map for endothelial cell DEGs (418 genes). Hierarchical clustering of genes indicated at left of each heatmap, and z-score indicated by color; n=3 per group except for sham female endothelial cells (n=2).

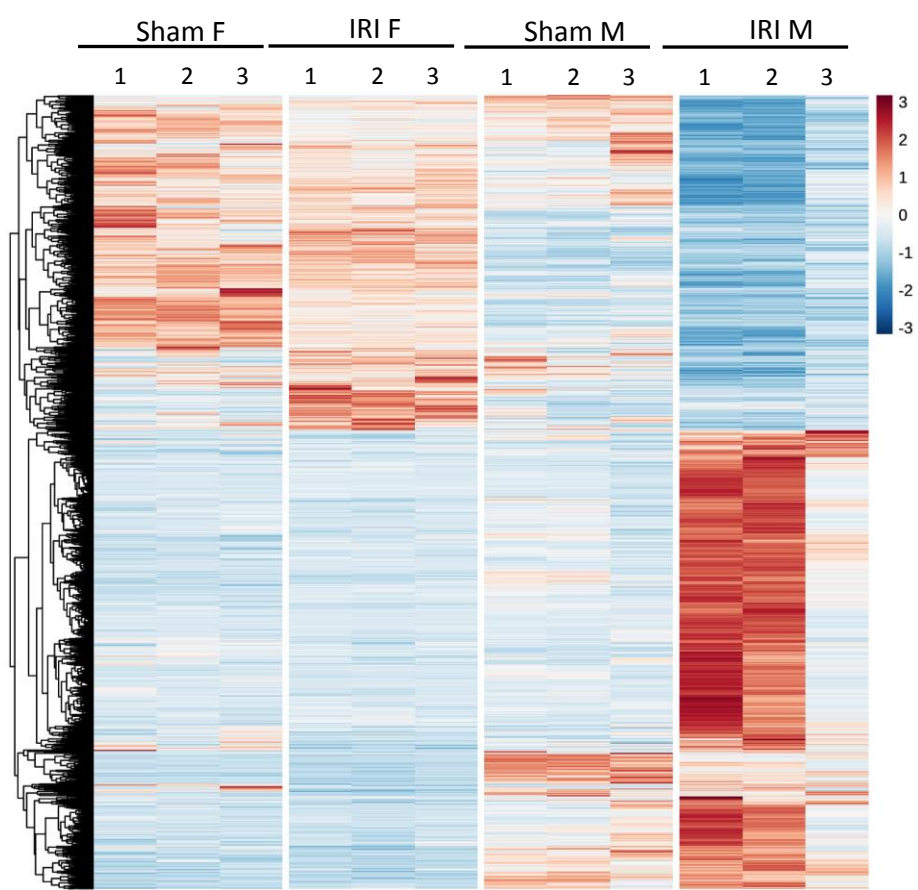


S2. Heat map for 488 differentially regulated genes (DEGs) in IRI female mice (IRI F) compared to sham female mice (Sham F) for proximal tubular cells. Hierarchical clustering of genes indicated at left of each heatmap, and z-score indicated by color; n=3 per group.

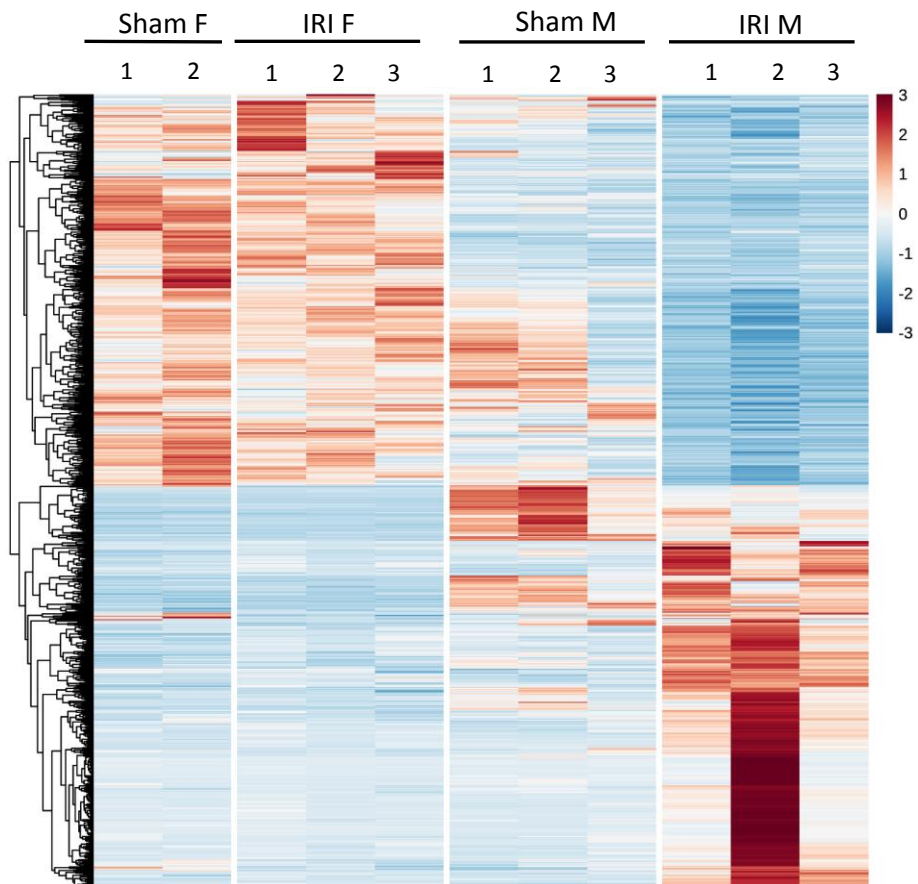


S3. Heat map for 56 differentially regulated genes (DEGs) in endothelial cells from IRI female mice (IRI F) compared to sham female mice (Sham F). Hierarchical clustering of genes indicated at left of each heatmap, and z-score indicated by color; n=3 per group except for sham female endothelial cells (n=2).

A



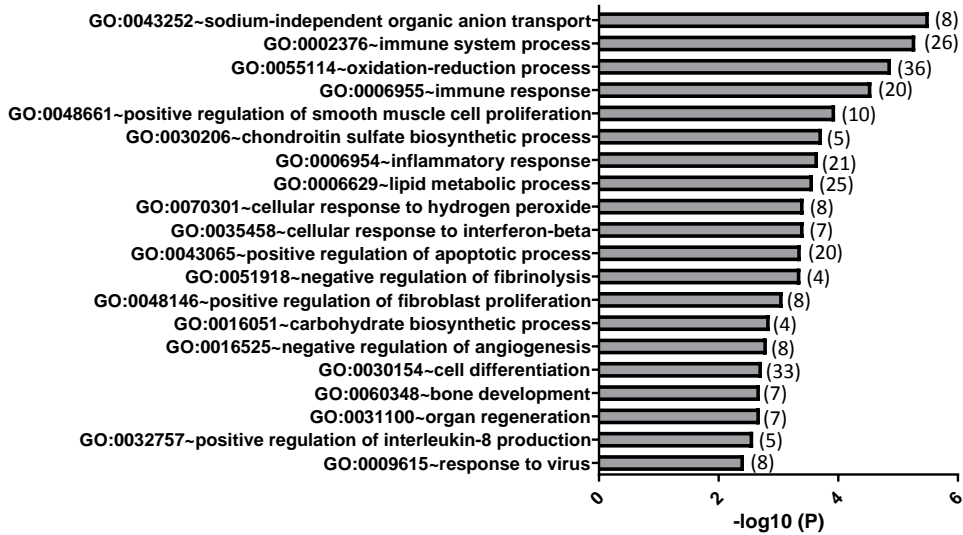
B



S4. Heat maps for differentially regulated genes (DEGs) in IRI male mice (IRI M) compared to IRI female mice (IRI F). A) Heat map for proximal tubular cell DEGs (4,557 genes). B) Heat map for endothelial cell DEGs (992 genes). Hierarchical clustering of genes indicated at left of each heatmap, and z-score indicated by color; n=3 per group except for sham female endothelial cells (n=2).

Sham M. vs F proximal tubules (upregulated)

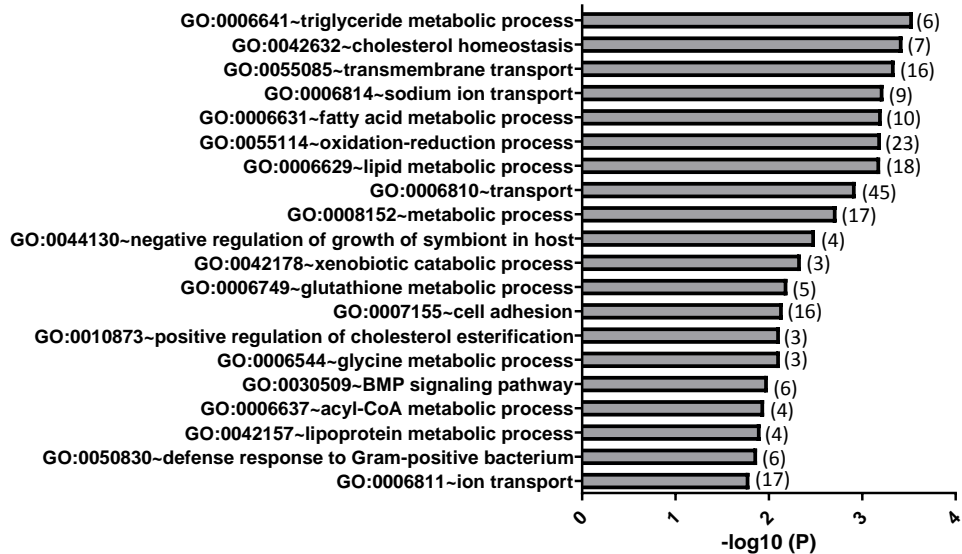
A



Sham M vs F proximal tubules (downregulated)

B

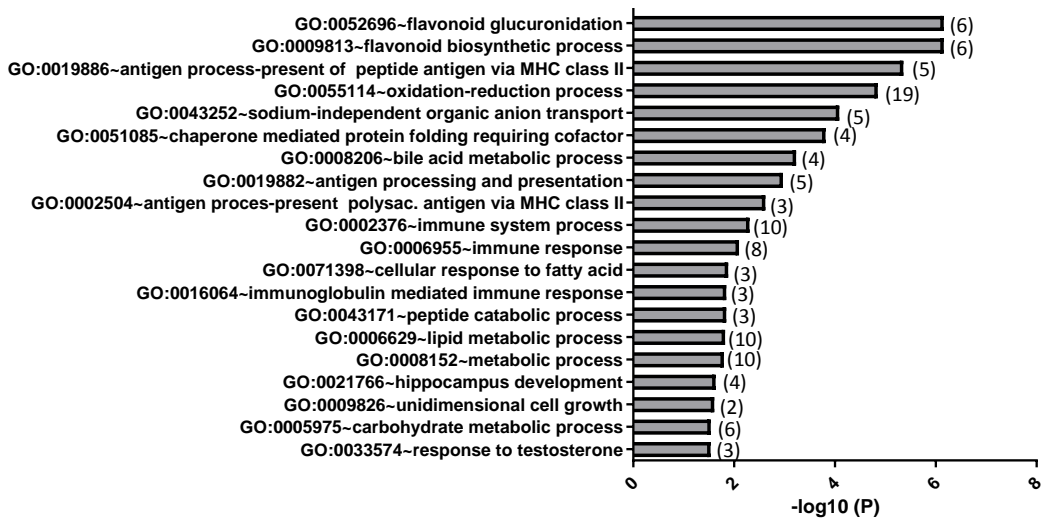
sham male vs female Proximal tubules
downregulated



S5. Gene ontology (GO) analysis for upregulated and downregulated differentially regulated genes (DEGs) in proximal tubular cells from sham male mice compared to sham female mice. A) Top 20 GO codes for upregulated genes from males ranked according to level of significance, with number of genes in each term in parentheses. B) Top 20 GO codes for downregulated genes from males ranked according to level of significance, with number of genes in each term in parentheses.

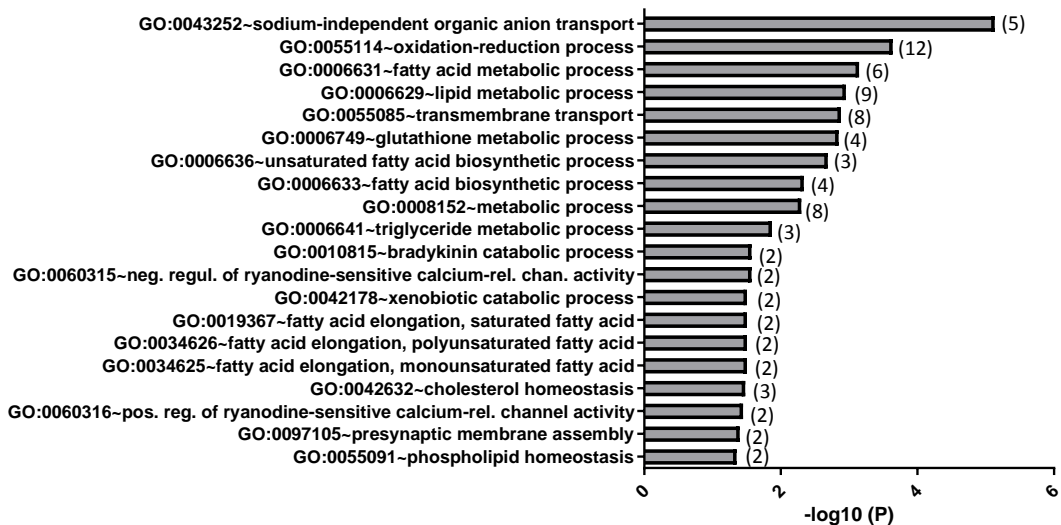
Sham M vs F endothelial cells (upregulated)

A



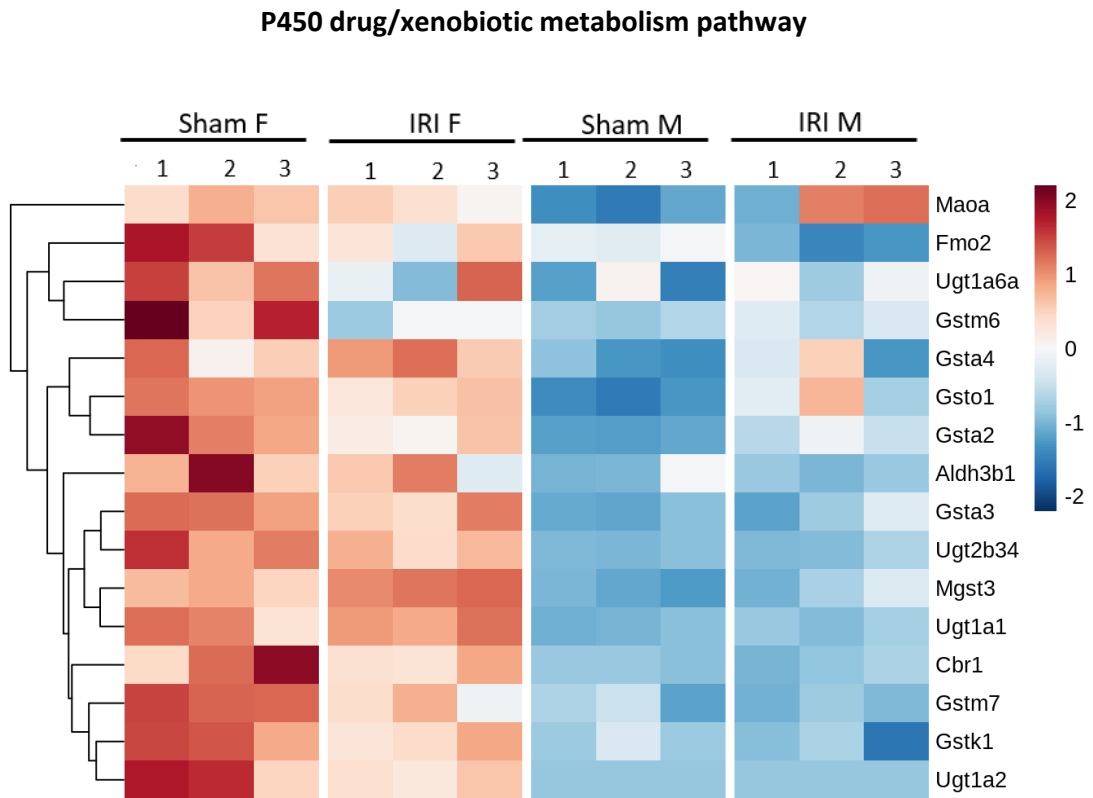
Sham M vs F endothelial cells (downregulated)

B



S6. Gene ontology (GO) analysis for upregulated and downregulated differentially regulated genes

(DEGs) in endothelial cells from sham male mice compared to sham female mice. A) Top 20 GO codes for upregulated genes from males ranked according to level of significance, with number of genes in each term in parentheses. B) Top 20 GO codes for downregulated genes from males ranked according to level of significance, with number of genes in each term in parentheses.



S7. Heat map showing upregulated genes related to the P450 drug/xenobiotic metabolism pathway in sham female proximal tubular cells (Sham F) compared to sham male (Sham M); Differentially regulated genes (DEGs) (16 genes). Hierarchical clustering of genes indicated at left of each heatmap, and z-score indicated by color; n=3 per group.