Supplemental Information for

Transcriptomes of Major Proximal-Tubule Cell-Culture Models

Syed Jalal Khundmiri, Lihe Chen, Eleanor Lederer, Chin-Rang Yang and Mark A. Knepper

Mark A. Knepper, MD, PhD,

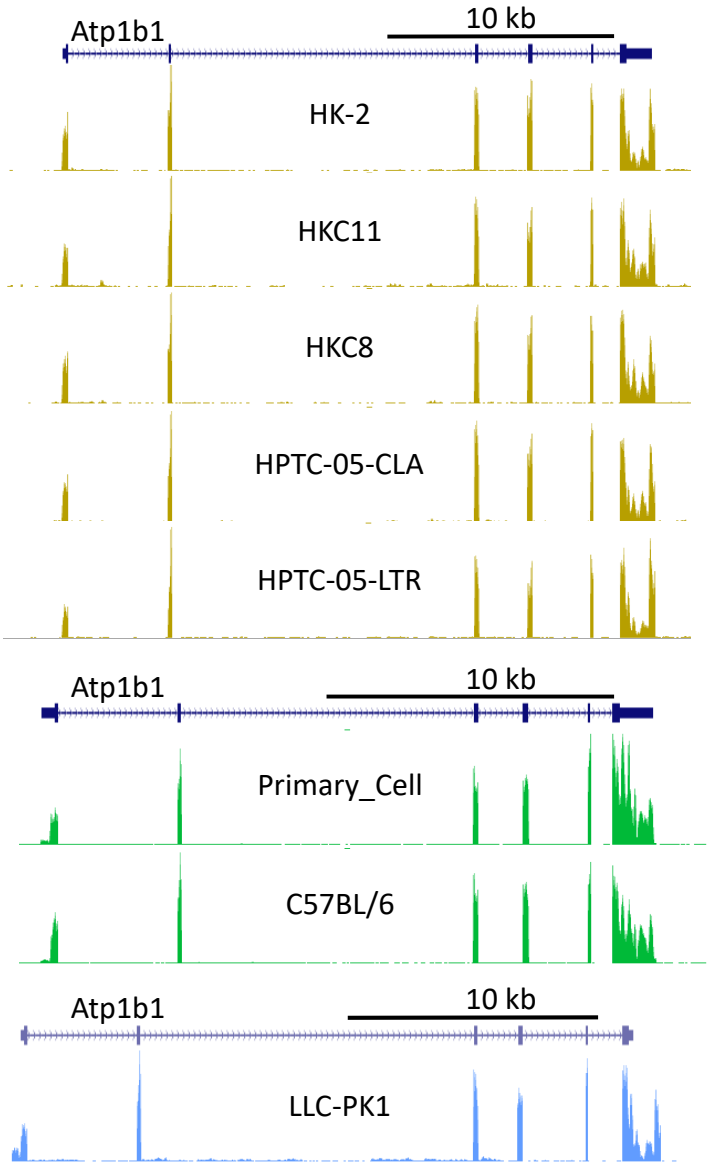
Senior Investigator, Division of Intramural Research, National Heart, Lung, and Blood Institute, NIH, Bethesda, MD 20892-1603

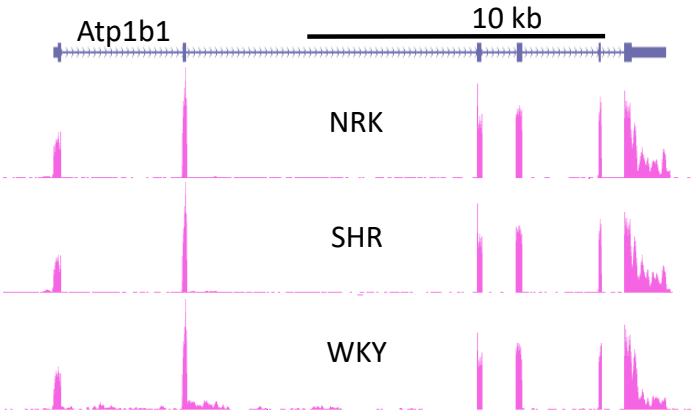
Email: knepperm@nhlbi.nih.gov

This PDF file includes:

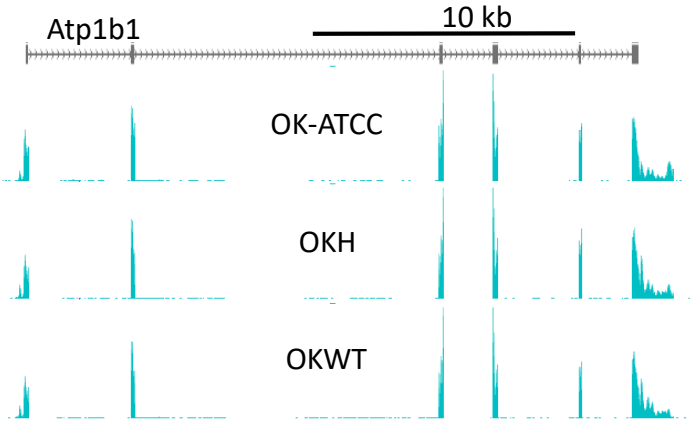
Supplemental Figures 1 to 2

Supplemental Tables 1 to 4

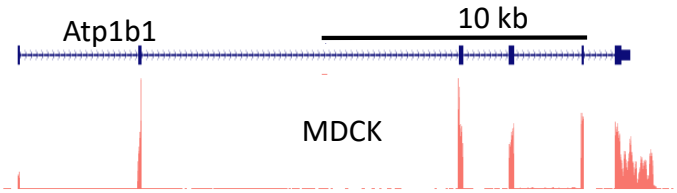

Atp1b1
10 kb
HK-2
HKC11
HKC8
HPTC-05-CLA
HPTC-05-LTR


Atp1b1
10 kb
NRK
SHR
WKY

Atp1b1
10 kb
Primary_Cell
C57BL/6


Atp1b1
10 kb
OK-ATCC
OKH
OKWT

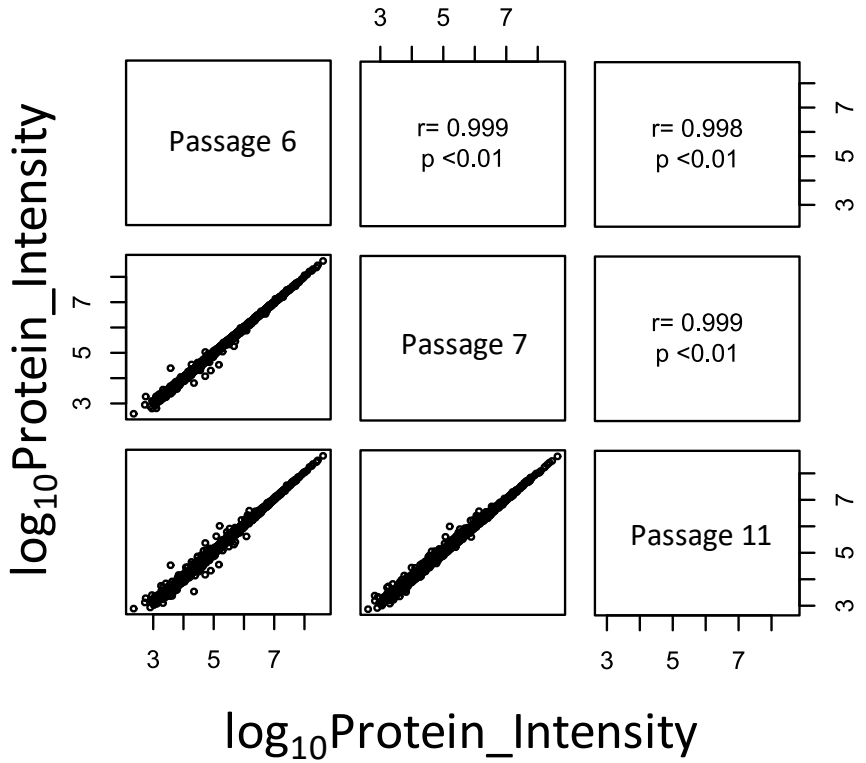
Atp1b1
10 kb
LLC-PK1


Atp1b1
10 kb
MDCK

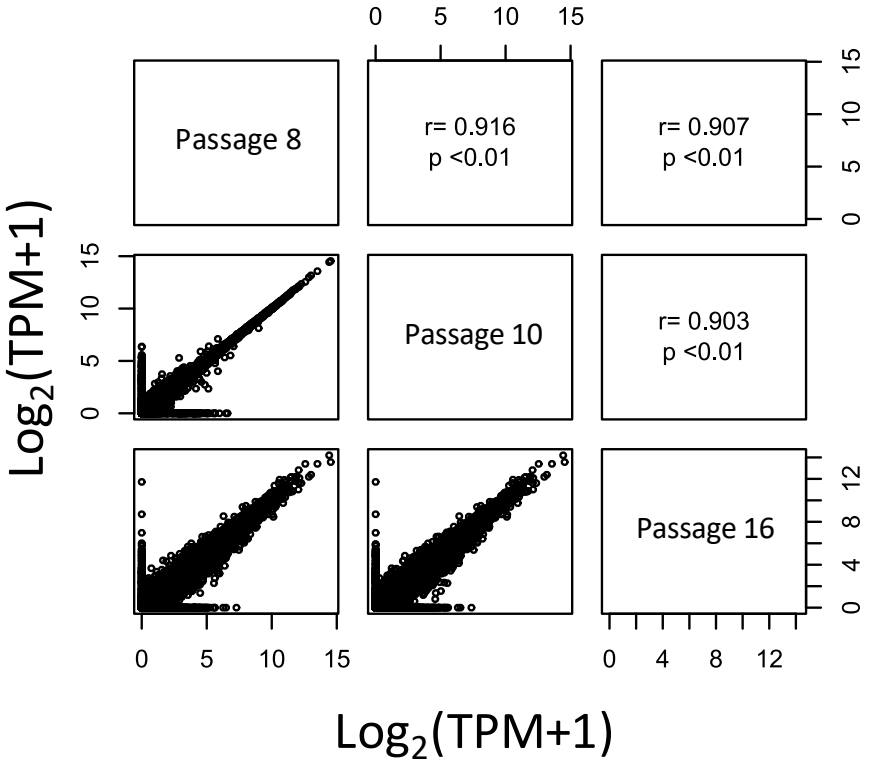
Supplemental Figure Legends

Supplemental Figure 1. Quality control of RNA-Seq data. Visualization of mapped read distributions along gene body of Atp1b1 across different cell lines. The tracks shown are on auto scale. Map of exon/intron organization of Atp1b1 gene was shown on top of individual subpanel (exons were shown as thick rectangles and introns as lines connecting the exons). The 5' to 3' gene direction of mouse and rat was flipped to match the directions of other species in the figure. Colors indicate animal species: green, mouse; brown, human; magenta, rat; light blue, opossum; dark blue, pig; red, dog.

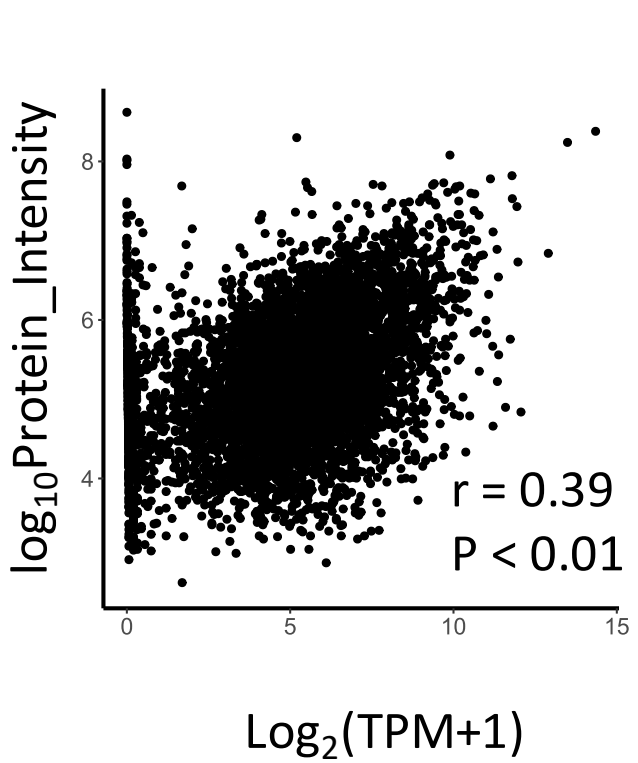
A


NRK-52E Proteome correlation
Passage 6
r= 0.999
p <0.01
r= 0.998
p <0.01
Passage 7
r= 0.999
p <0.01
Passage 11
log10Protein_Intensity
log10Protein_Intensity

B


NRK-52E Transcriptome correlation
Passage 8
r= 0.916
p <0.01
r= 0.907
p <0.01
Passage 10
r= 0.903
p <0.01
Passage 16
Log2(TPM+1)
Log2(TPM+1)

C


Transcriptome/Proteome correlation
r = 0.39
P < 0.01
log10Protein_Intensity
Log2(TPM+1)

Supplemental Figure 2. Transcriptome and proteome correlations among NRK-52E passages. High correlation coefficients were observed among NRK-52E passages at the proteome (A) and transcriptome (B) level. The protein intensities are log10 transformed and plotted. The TPM values are log2 transformed and plotted. (C) Correlation between mean NRK-52E transcriptome and proteome.

Supplemental Table 1. Percent expression of native proximal tubule transcripts in cell lines and native mouse tissues.

Supplemental Table 2. Cell line expression of transcripts corresponding to recognized genetic diseases of the proximal tubule.

Supplemental Table 3. Quantification of protein expression in NRK-52E cell line and whole rat kidney tissue.

Supplemental Table 4. Quantification of proximal tubule-specific proteins in NRK-52E cell line.