Supplementary Figure S3

A

Frequency of detection in Control Late (%)

Gatm, Slc5a2, Slc5a12, Cd36, Ly6e, Pigr, Apoc3, Defb19, Fabp5

log2FC Contro Late vs Control Early

B

Control Early | Control Late | KO Early | KO Late

Apoc3

Defb19

C

L2FC KO Late vs KO Early

Apoc3, Ly6e, Cd36, Pigr, Fabp5, Defb19, Slc5a2, Slc5a12, Gatm

L2FC KO Early vs Control Early

D

PT Markers

Enrichment Score

NES = -1.76
$p = 4.6 \times 10^{-8}$

E

Maf   *Pax8*

Expression

PT   PT like   PT   PT like

F

tdTomato-positive cells expressing *Mki67* (%)

p = 0.0191
p = 0.0134
p = 0.0191
p = 0.0255
p = 0.0161

PT S1 | PT S2 | PT S3 | PT Class A | PT Class B | PT like

G

CD45-positive foci per sq.mm tissue

p = 0.0303

Control Late | KO Late

H

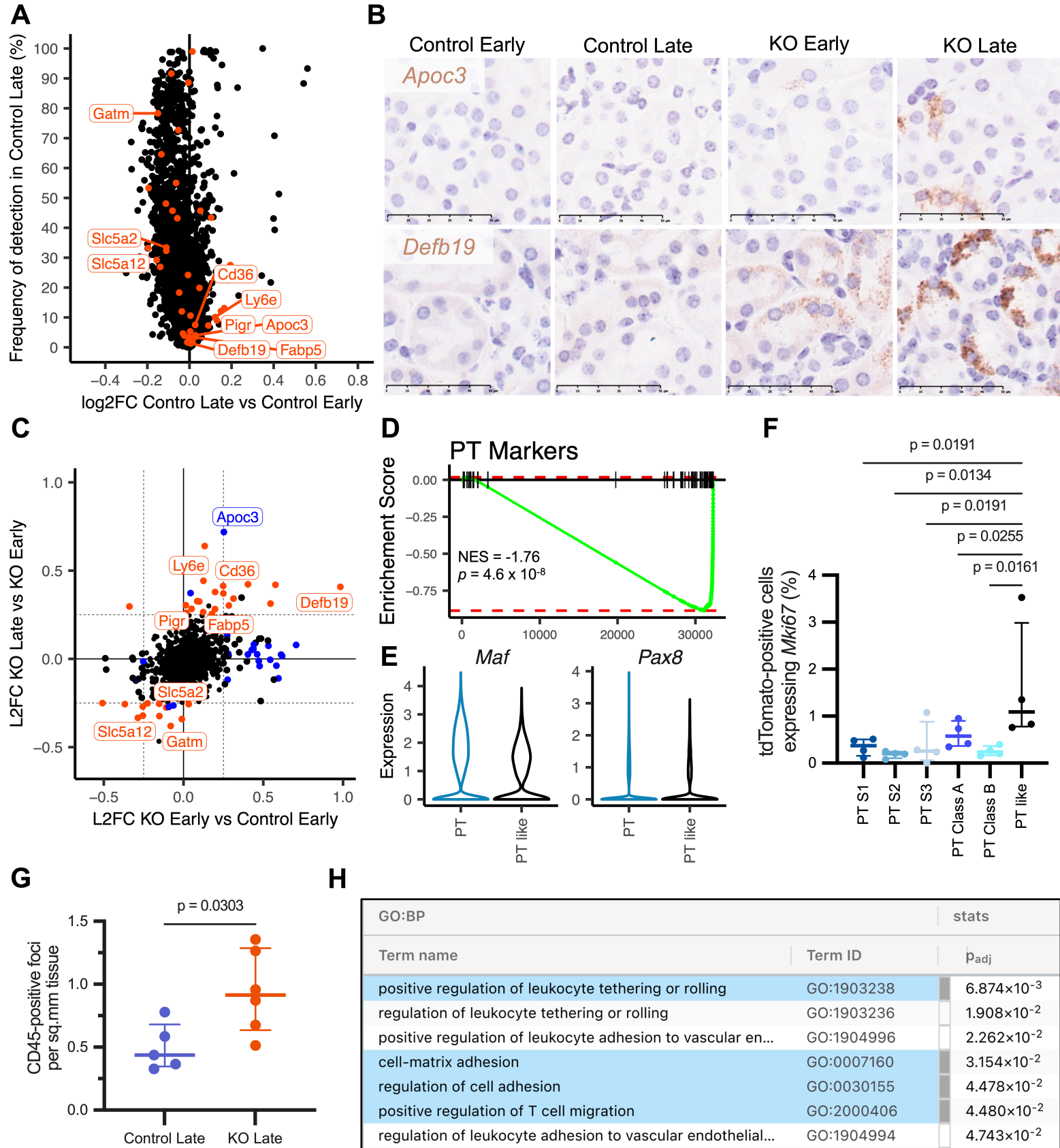| GO:BP		stats
Term name	Term ID	p_{adj}
positive regulation of leukocyte tethering or rolling	GO:1903238	6.874×10^{-3}
regulation of leukocyte tethering or rolling	GO:1903236	1.908×10^{-2}
positive regulation of leukocyte adhesion to vascular en...	GO:1904996	2.262×10^{-2}
cell-matrix adhesion	GO:0007160	3.154×10^{-2}
regulation of cell adhesion	GO:0030155	4.478×10^{-2}
positive regulation of T cell migration	GO:2000406	4.480×10^{-2}
regulation of leukocyte adhesion to vascular endothelial...	GO:1904994	4.743×10^{-2}

Supplementary Figure S3: *Vhl*-null cells specifically undergo time-dependent alterations in gene expression. **(A)** Scatter plot depicting frequency of expression in tdTomato-positive cells from Control mice at the late timepoint against log$_2$-fold change (log2FC) between cells from Control mice at the late *versus* early timepoints for all genes. Genes specifically regulated over time in *Vhl*-null cells (orange; from Fig 5C). Genes explicitly mentioned in the main text are labelled. **(B)** Representative *in situ* RNA hybridization for *Apoc3* (top) and *Defb19* (bottom) mRNA in kidneys from Control and KO mice harvested at the early and late timepoints (at least n = 2F, 1M per timepoint for both transcripts). Scale bar denotes 50 μm; 40x magnification. **(C)** Scatter plot depicting log$_2$-fold change (L2FC) in *Vhl*-null cells over time against log$_2$-fold change early after *Vhl* inactivation for all genes. Genes regulated over time (orange). HIF target genes (blue). Genes explicitly mentioned in the main text are labelled. **(D)** Gene set enrichment plot depicting downregulation of PT marker genes in PT-like cells compared to PT cells at the late timepoint. NES = Normalized Enrichment Score. p value adjusted by Bonferroni correction for multiple testing. **(E)** Violin plots depicting expression of *Maf* and *Pax8* in *Vhl*-null PT or PT like cells at the late timepoint. **(F)** Proportion of tdTomato-positive cells of any PT identity that express *Mki67* from kidneys of KO mice harvested at the late timepoint (n = 2F, 2M). Pairwise comparisons by one-way ANOVA with Holm-Šídák correction. **(G)** Number of foci of leukocytes observed per mm^2 of renal cortex and outer medulla in Control (n = 1F, 4M) and KO (n = 6M) mice harvested at the late timepoint. Pairwise comparison by Mann-Whitney test. **(H)** Significantly enriched Gene Ontology terms for genes upregulated over time in tdTomato-negative macrophages in KO samples. Results from gProfiler. **(F, G)** Median and inter-quartile range plotted.