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Supplemental information

Protective role for kidney *TREM2^{high}* macrophages in obesity- and diabetes-induced kidney injury

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Supplementary Figure Legends

Supplementary Figure 1. Phenotypic characterization of mouse DKD models

(A) Assessment of podocytes in glomeruli from patients with and without DKD using *in situ* HCR with probes complementary to podocin (*NPHS2*; red) and synaptopodin (*SYNPO*; green). *LRP2* (megalin; cyan) delineates the proximal convoluted tubules (DAPI; blue); scale bar 50 μm. Podocytes were quantified in three independent fields of view for each of the DKD and non-DKD samples.

(B) Quantification of podocytes by *in situ* HCR in patients with and without DKD. Mean podocyte percentage: 26.2% +/- 1.74% in non-DKD versus 18.1% +/- 0.27% in DKD, **p<0.01 (unpaired Student's t-test).

(C) Phenotypic characterization of the HFD-fed mice including serum creatinine concentration and albuminuria quantification, *p<0.05, **p<0.01, ***p<0.001. Serum creatinine chow (n = 32), HFD (n = 37), p<0.0001; urine albumin for chow (n = 57) and HFD (n = 106).

(D) Light and transmission electron microscopic examination of kidney tissue from chow and HFD-fed mice.

(C-L) Metabolic profile of chow- and HFD-fed mice: body weight (E), glucose tolerance test (F), insulin tolerance test (G), and plasma levels of insulin (H), adiponectin (I) and leptin (J). Body fat percentage (K, plasma cholesterol level (L), triglyceride level (M) and bone mineral density (N) are also shown. Chow (n = 33); HFD (n = 39); Mean +/- S.E.M. *p<0.05, ***p<0.001.

(M-N) Glucose (O) and insulin (P) tolerance tests in 5- and 10-week-old BTBR *wt/wt* and *ob/ob* mice, respectively. BTBR *wt/wt* 5wk n= 9; *ob/ob* 5wk n = 9; BTBR *wt/wt* 10wk n= 9; *ob/ob* 10wk n = 9; Mean +/- S.E.M.

(O-Q) Measurement of renal parameters in 5- and 10-week-old BTBR *ob/ob* mice; 24h urinary albumin (Q), blood urea nitrogen (BUN, R)) and serum creatinine (S). Mean +/- S.E.M. ***p<0.001

(T) Plasma total cholesterol levels in 5- and 10-week-old BTBR mice. Mean +/- S.E.M. ***p<0.001.

(L) Transmission electron microscopy of kidney tissue from 10-week-old BTBR *wt/wt* and *ob/ob* mice.

Supplementary Figure 2. DKD in mouse and human kidney tissue at single cell resolution

(A, B) UMAP plots of the cell populations identified in nephrectomy specimens from patients (A) with DKD (N=3) and (B) without DKD (N=9). Individual populations are represented by distinct colors.

(C, D) UMAP plots of cells recovered from the kidneys of (C) HFD- and (D) chow-fed mice (N=4 in each condition). Individual populations are represented by distinct colors.

(E, F) UMAP plots of cell populations identified in the kidneys of 5-week-old BTBR (E) *ob/ob* and BTBR (F) *wt/wt* mice. (N=5 in each condition) Individual populations are represented by distinct colors.

(G, H) UMAP plots of cell populations identified in the kidneys of 10-week-old BTBR (G) *ob/ob* and BTBR (H) *wt/wt* mice (N=3 in each condition). Individual populations are represented by distinct colors.

(I-L) Number of differentially expressed genes (FDR < 5%) by cell class for the mouse models (Wilcoxon-rank-sum test): human data (I, Poisson mixed-effects model, FDR<0.1), HFD (J), BTBR 5wk (K), and BTBR 10wk (L).

(M-P) UpSet plots representing shared and unique signatures among the human and mouse DKD data in the (M) DCT, (N) TAL, (O) podocyte and (P) mesangial cells. The set size represents the total number of differentially expressed genes in DKD. The intersection size represents the number of genes in the intersection of the sets represented by the black dots connected by the line segment. In podocytes and mesangial cells, the transcriptional response to disease varied between mouse and human, both in terms of the specific genes affected and the direction of the effect.

Supplementary Figure 3. Changes in podocyte, mesangial and Proximal Convoluted Tubular (PCT) cell DKD-related gene expression

(A) Boxplots showing normalized gene expression of *Col4a3* in podocytes from mouse models. From left to right: BTBR *wt/wt*, and BTBR *ob/ob* 5 wk, 10wk, and chow-fed, HFD mouse models.

(B) Representative *in situ* HCR images and quantification of *Col4a3* expression in podocytes of 10-week-old BTBR *wt/wt* (mean 0.24 +/- SEM 0.02; n=3) and BTBR *ob/ob* (mean 0.46 +/- SEM 0.02; n=3) mice. Scale bars 50μm. **p < 0.01, unpaired Student's t-test.

(C) Boxplots showing normalized gene expression of *Col4a2* in mesangial cells from DKD mouse models. From left to right: BTBR *wt/wt*, and BTBR *ob/ob* 5 wk, 10wk, and chow-fed, HFD mouse models.
(D) Representative *in situ* HCR images and quantification of *Col4a2* in mesangial cells of 10-week-old BTBR *wt/wt* (mean 0.72 +/- SEM 0.02; n=5) and *ob/ob* (mean 1.77 +/- SEM 0.09; n=5) mice. Scale bars 50 μm. ***p < 0.001, unpaired Student's t-test.
(E-G) Boxplots showing normalized gene expression of *Pck1* (E), *Lrp2*(F), *Gsta2*(G) in proximal convoluted tubule cells from DKD mouse models. From left to right: BTBR *wt/wt*, and BTBR *ob/ob* 5 wk, 10wk, and chow-fed, HFD mouse models.
(H) (left) Immunofluorescent staining of Pck1 (red) in kidney tissue from chow- and HFD-fed mice. (right) Quantification of Pck1 immunofluorescence in kidneys from chow- (mean 7.28 +/- SEM 0.25; n = 5) and HFD-fed mice (mean 10.06 +/- SEM 1.09; n = 5); ** p<0.01, FU, fluorescence units. Scale bars 50 μm.
(I) (left) *In situ* HCR for expression of *Lrp2* (green), *Pck1* (red), *Gsta1/2* (cyan) in kidneys from 10-week-old BTBR *wt/wt* and BTBR *ob/ob* mice.
(middle) Quantification of *Pck1* expression in 10-week-old BTBR *wt/wt* (n=4) and BTBR *ob/ob* (n=4) mice by *in situ* HCR; *p<0.05, unpaired Student's t-test. RFU, relative fluorescence units.
(right) Quantification of *Gsta1/2* expression in 10-week-old BTBR *wt/wt* mice (mean 1.82 +/- SEM 0.08; n=4) and BTBR *ob/ob* mice (mean 12.37 +/- SEM 1.75; n=4) by *in situ* HCR; *** p <-.001, unpaired Student's t-test. RFU, relative fluorescent units.

Supplementary Figure 4. Macrophage cell populations present in the kidneys of the HFD and BTBR mice and validation in the UK cohort

(A) UMAP visualization of resident MΦ pan-marker and subset specific marker genes in the kidney meta-atlas.
(B) Dot plot visualization of marker genes (columns) from *LYVE1* macrophages in the heart (PMID: 32971526) distinguishing myeloid subsets (rows). Size of the dots represent the proportion of cells in each subset (columns) expressing the gene (rows). Color of the dots represents the normalized average expression in units of log(TPX+1).
(C) UMAP visualization of myeloid cells in the KPMP scRNA-seq dataset (N=45).
(D) Heatmap visualization of cluster specific marker genes. Cluster 5 was enriched for the *TREM2* program.
(E) UMAP visualization of *TREM2*^{high} macrophages in healthy donors and patients with hypertensive chronic kidney disease (H-CKD) or diabetic kidney disease (DKD)
(F) Heatmap showing DE genes characterizing kidney resident and infiltrating macrophage populations in the two mouse models (HFD and BTBR) and time points (5- and 10-week-old BTBR).
(G) UMAP plots of MΦ cell populations identified in the kidneys of 5-week-old BTBR *wt/wt* and BTBR *ob/ob* mice. Individual populations are represented by distinct colors.
(H) Heatmap showing canonical and data-derived DE genes used for immune cell cluster annotation in chow- and HFD-fed mice.
(I) Heatmap showing canonical and data-derived DE genes used for 5-week-old BTBR *wt/wt* and BTBR *ob/ob* mouse kidney immune cell cluster annotation.
(J) Heatmap showing canonical and data-derived DE genes used for immune cell cluster annotation in 10-week-old BTBR *wt/wt* and BTBR *ob/ob* mice.
(K) Comparison of macrophage populations between mouse strains to show shared and unique populations. Comparisons were performed by training a classifier on the HFD model macrophages and predicting labels on the 5-week-old BTBR macrophage data.
(L) Correlation between BMI (20-60) and TREM2^{+} macrophages % of CD163^{+} cells/ROI with the outlier included. ROI; region of interest. R = 0.34; p = 0.02.
(M) Correlation between BMI (20-60) and TREM2^{+} macrophages % of CD163^{+} cells/ROI with the outlier excluded. ROI; region of interest. R = 0.32; p = 0.03.
(N) Dotpot visualization of *Trem2* expression among all kidney cell types in the HFD model of DKD. The size of the dots represents the proportion of cell in the cell type (rows, Y-axis) that express the gene and the color represents average gene expression in units log(TPX+1).

Supplementary Figure 5. HFD-treatment induced podocyte foot process effacement and tubular cell mitochondrial injury in *Trem2*$^{-/-}$ mice.

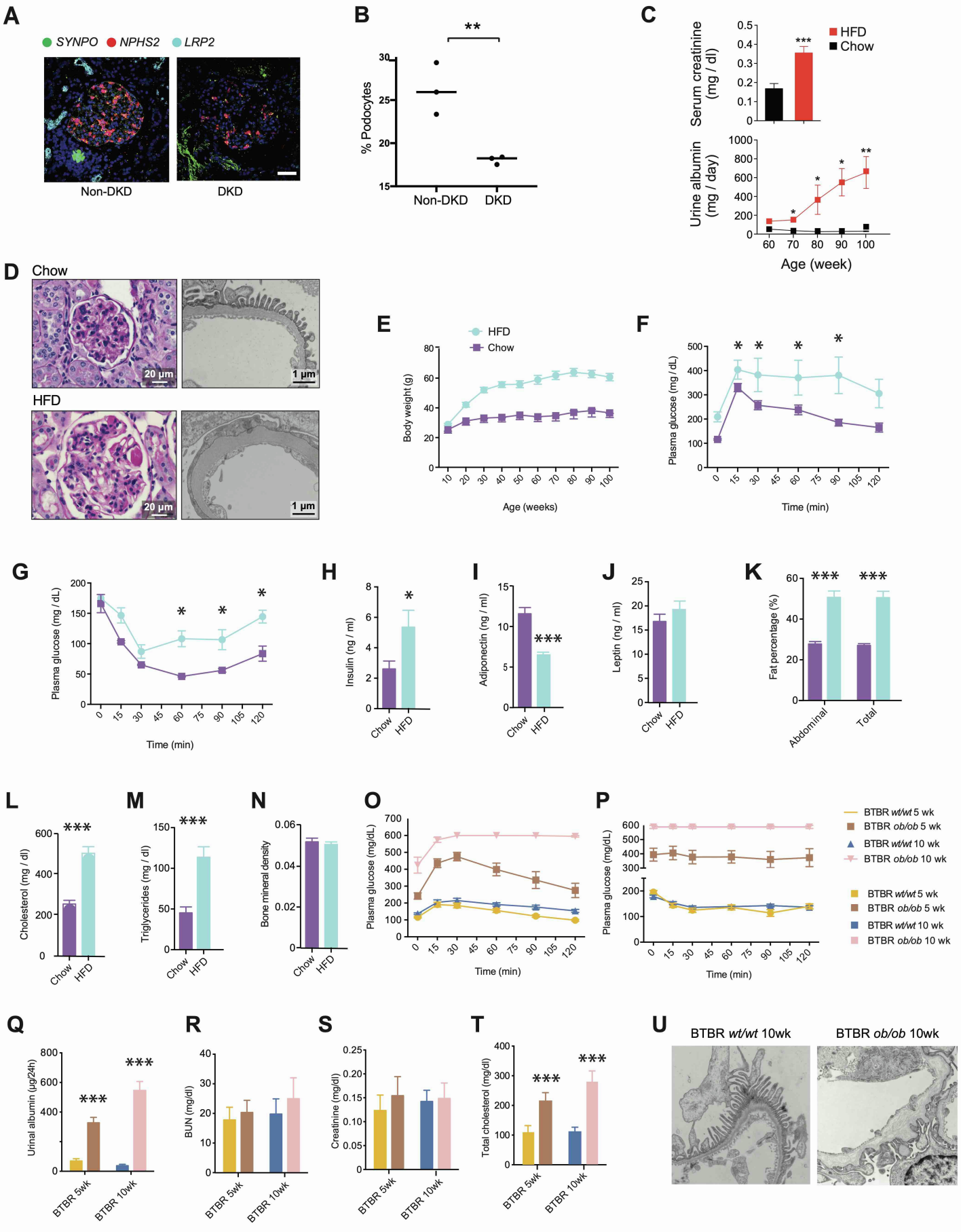
(**A**) CRISPR-cas9 knockout strategy for *Trem2*$^{-/-}$ mice.

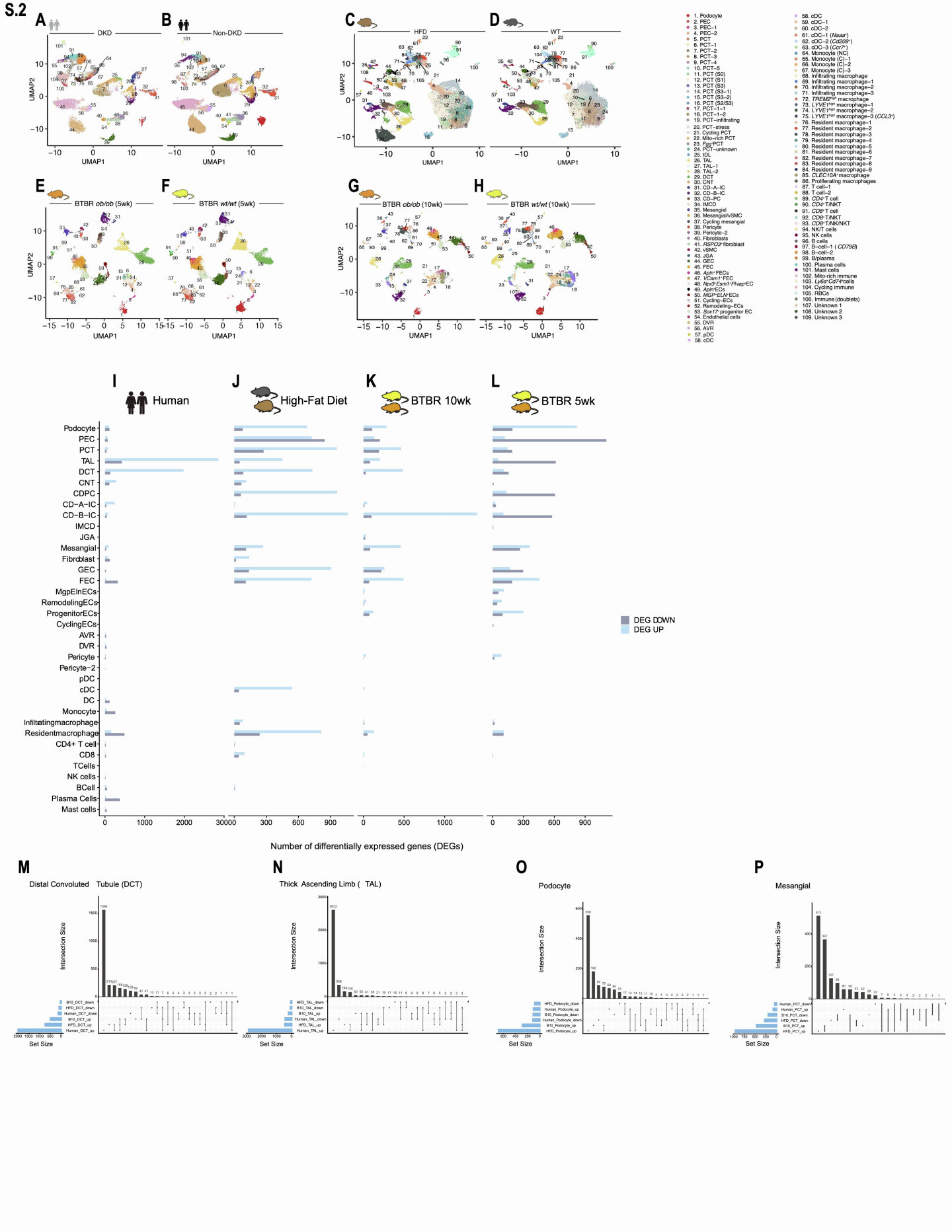
(**B**) PCR validation of Trem2 gene in WT and *Trem2*$^{-/-}$ mice. Primer set 1 and 2 for amplification of KO and WT regions, respectively.

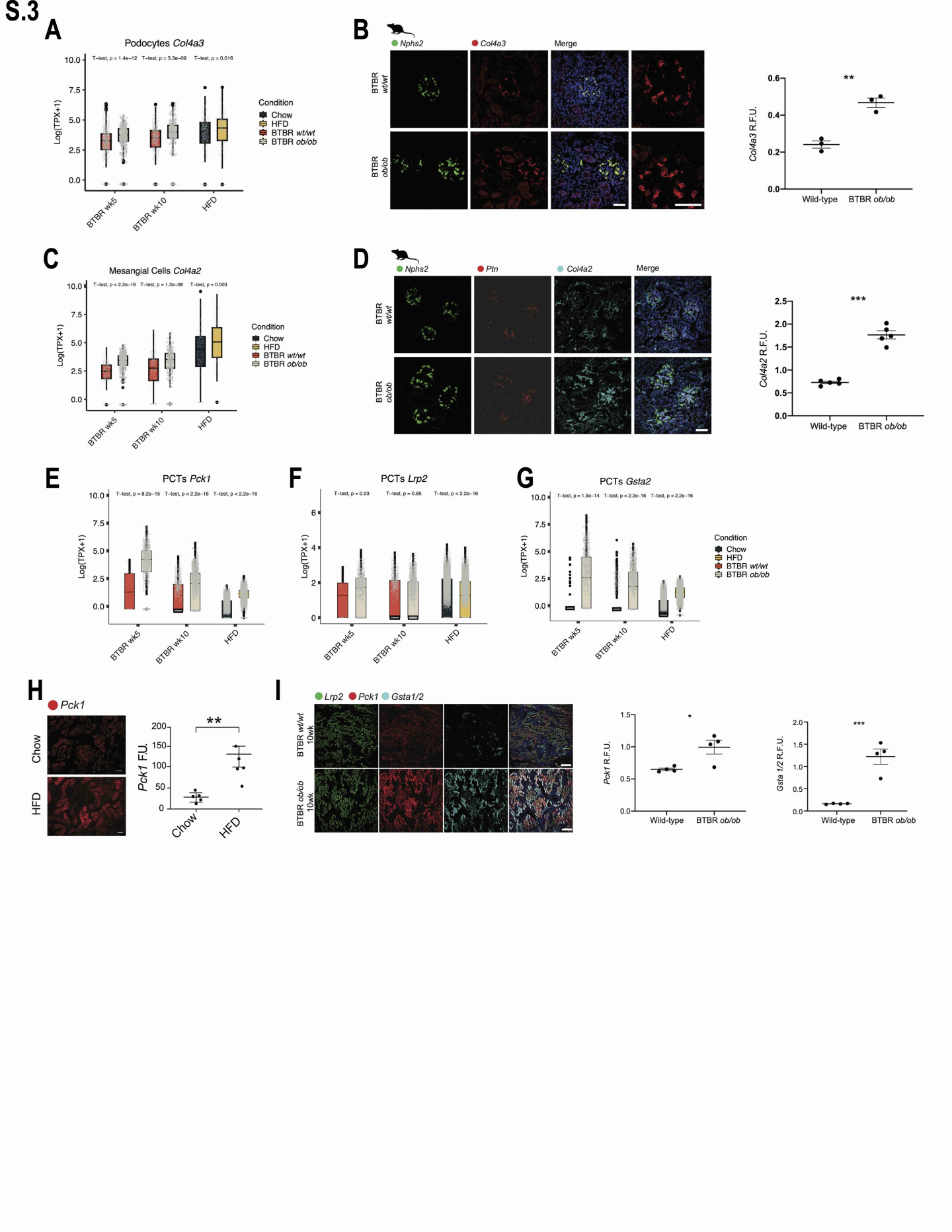
(**C**) Glucose tolerance test of WT chow, WT HFD, *Trem2*$^{-/-}$ chow, and *Trem2*$^{-/-}$ HFD mice.

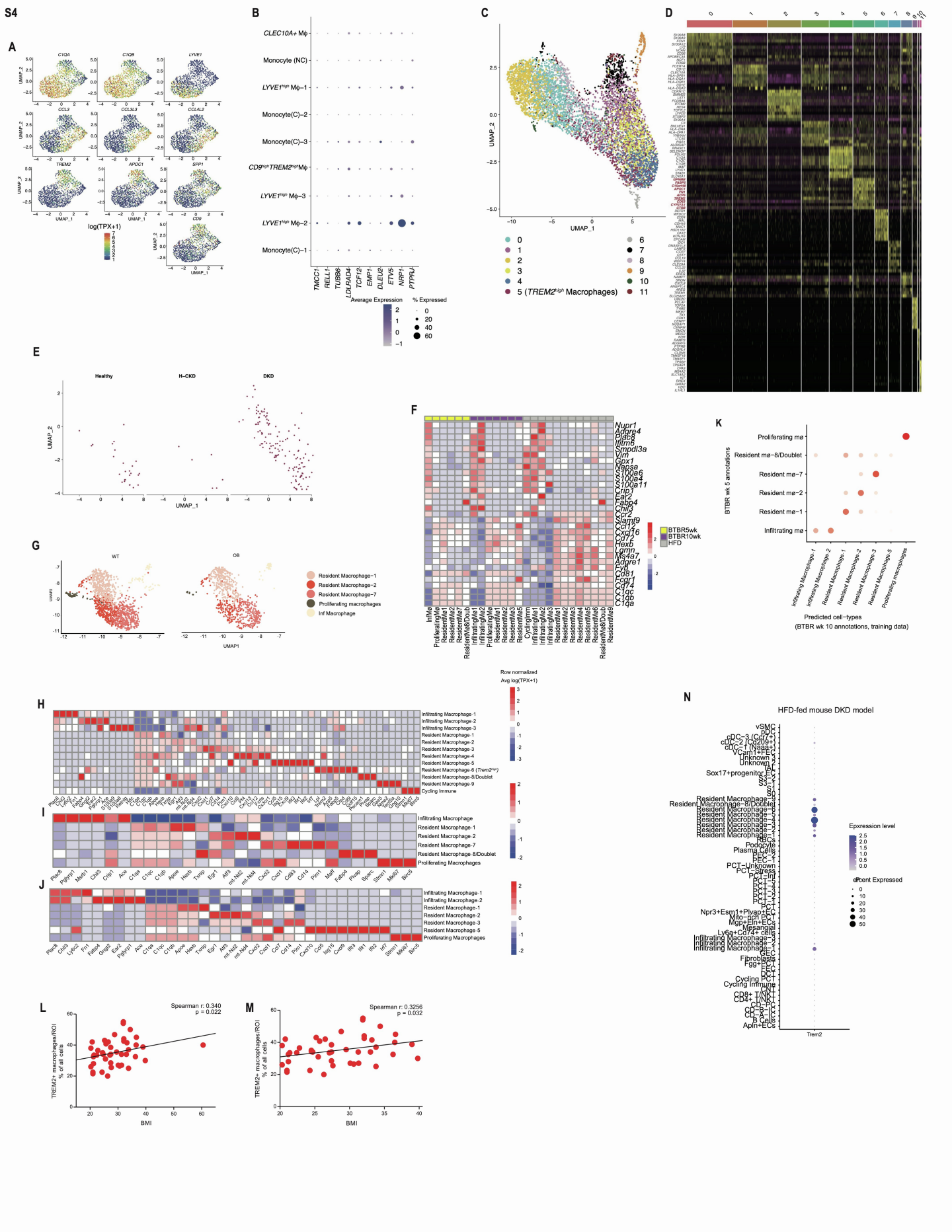
(**D-G**) Histograms of changes in body weight gain (D), serum glucose (E), triacylglycerol (F), and cholesterol levels (G) in WT and Trem2-/- HFD mice treated with chow and HFD. **P < 0.01, ***P < 0.001, ****P < 0.0001. Mean ± S.E.M.

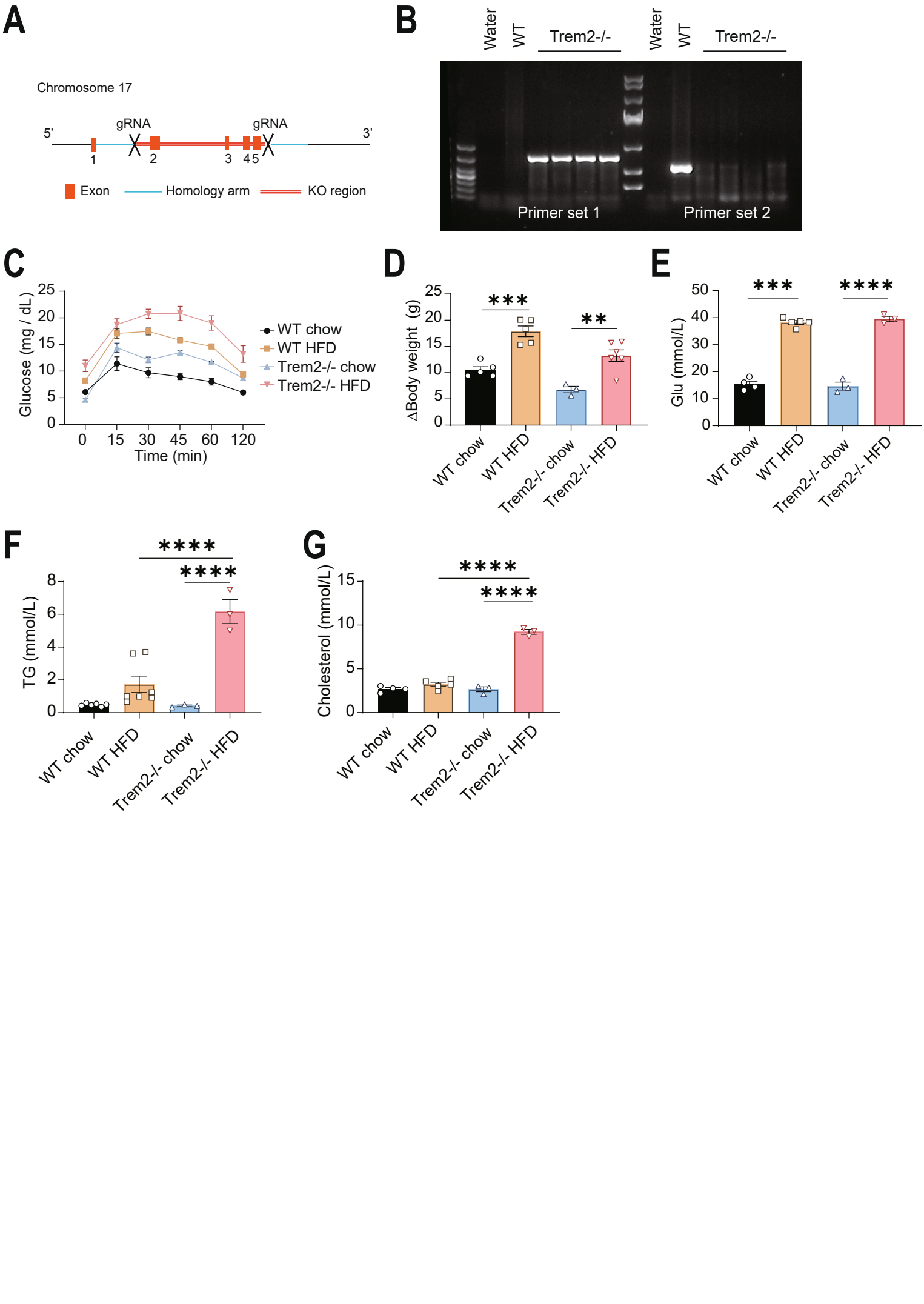
S1


A
SYNPO NPHS2 LRP2
Non-DKD
DKD
B
% Podocytes
Non-DKD
DKD
C
Serum creatinine (mg / dl)
HFD
Chow
Urine albumin (mg / day)
Age (week)
D
Chow
HFD
20 μm
1 μm
E
HFD
Chow
Body weight (g)
Age (weeks)
F
Plasma glucose (mg / dL)
Time (min)
G
Plasma glucose (mg / dL)
Time (min)
H
Insulin (ng / ml)
I
Adiponectin (ng / ml)
J
Leptin (ng / ml)
K
Fat percentage (%)
Abdominal
Total
L
Cholesterol (mg / dl)
M
Triglycerides (mg / dl)
N
Bone mineral density
O
Plasma glucose (mg/dL)
Time (min)
P
Plasma glucose (mg/dL)
Time (min)
BTBR wt/wt 5 wk
BTBR ob/ob 5 wk
BTBR wt/wt 10 wk
BTBR ob/ob 10 wk
Q
Urinal albumin (μg/24h)
BTBR 5wk
BTBR 10wk
R
BUN (mg/dl)
S
Creatinine (mg/dl)
T
Total cholesterol (mg/dl)
U
BTBR wt/wt 10wk
BTBR ob/ob 10wk


S.2
A
DKD
B
Non-DKD
C
HFD
D
WT
E
BTBR ob/ob (5wk)
F
BTBR wt/wt (5wk)
G
BTBR ob/ob (10wk)
H
BTBR wt/wt (10wk)
UMAP1
UMAP2
1. Podocyte
2. PEC
3. PEC–1
4. PEC–2
5. PCT
6. PCT–1
7. PCT–2
8. PCT–3
9. PCT–4
10. PCT–5
11. PCT (S0)
12. PCT (S1)
13. PCT (S3)
14. PCT (S3–1)
15. PCT (S3–2)
16. PCT (S2/S3)
17. PCT–1–1
18. PCT–1–2
19. PCT–infiltrating
20. PCT–stress
21. Cycling PCT
22. Mito–rich PCT
23. Fbp1+PCT
24. PCT–unknown
25. tDL
26. TAL
27. TAL–1
28. TAL–2
29. DCT
30. CNT
31. CD–A–IC
32. CD–B–IC
33. CD–PC
34. IMCD
35. Mesangial
36. Mesangial/vSMC
37. Cycling mesangial
38. Pericyte
39. Pericyte–2
40. Fibroblasts
41. RSPO3+ fibroblast
42. vSMC
43. JGA
44. GEC
45. FEC
46. Aplnr+FECs
47. Vcam1+FEC
48. Npr3+Esm1+Plvap+EC
49. Aplnr+ECs
50. MGP+ELN+ECs
51. Cycling–ECs
52. Remodeling–ECs
53. Sox17+ progenitor EC
54. Endothelial cells
55. DVR
56. AVR
57. pDC
58. cDC
58. cDC
59. cDC–1
60. cDC–2
61. cDC–1 (Naaa+)
62. cDC–2 (Cd209+)
63. cDC–3 (Cor7+)
64. Monocyte (NC)
65. Monocyte (C)–1
66. Monocyte (C)–2
67. Monocyte (C)–3
68. Infiltrating macrophage
69. Infiltrating macrophage–1
70. Infiltrating macrophage–2
71. Infiltrating macrophage–3
72. TREM2hi macrophage
73. LYVE1hi macrophage–1
74. LYVE1hi macrophage–2
75. LYVE1hi macrophage–3 (CCL3+)
76. Resident macrophage–1
77. Resident macrophage–2
78. Resident macrophage–3
79. Resident macrophage–4
80. Resident macrophage–5
81. Resident macrophage–6
82. Resident macrophage–7
83. Resident macrophage–8
84. Resident macrophage–9
85. CLEC10A+ macrophage
86. Proliferating macrophages
87. T cell–1
88. T cell–2
89. CD4+T cell
90. CD4+ T/NKT
91. CD8+T cell
92. CD8+T/NKT
93. CD8+T/NK/NKT
94. NK/T cells
95. NK cells
96. B cells
97. B–cell–1 (CD79B)
98. B–cell–2
99. B/plasma
100. Plasma cells
101. Mast cells
102. Mito–rich immune
103. Ly6a+Cd74+cells
104. Cycling immune
105. RBCs
106. Immune (doublets)
107. Unknown 1
108. Unknown 2
109. Unknown 3
I
Human
J
High-Fat Diet
K
BTBR 10wk
L
BTBR 5wk
Podocyte
PEC
PCT
TAL
DCT
CNT
CDPC
CD–A–IC
CD–B–IC
IMCD
JGA
Mesangial
Fibroblast
GEC
FEC
MgpElnECs
RemodelingECs
ProgenitorECs
CyclingECs
AVR
DVR
Pericyte
Pericyte–2
pDC
cDC
DC
Monocyte
Infiltratingmacrophage
Residentmacrophage
CD4+ T cell
CD8
TCells
NK cells
BCell
Plasma Cells
Mast cells
DEG DOWN
DEG UP
Number of differentially expressed genes (DEGs)
M
Distal Convoluted Tubule (DCT)
N
Thick Ascending Limb (TAL)
O
Podocyte
P
Mesangial
Intersection Size
Set Size
B10_DCT_down
HFD_DCT_down
Human_DCT_down
B10_DCT_up
HFD_DCT_up
Human_DCT_up
B10_TAL_down
HFD_TAL_down
Human_TAL_down
B10_TAL_up
HFD_TAL_up
Human_TAL_up
B10_Podocyte_down
HFD_Podocyte_down
Human_Podocyte_down
B10_Podocyte_up
HFD_Podocyte_up
Human_Podocyte_up
B10_PCT_down
HFD_PCT_down
Human_PCT_down
B10_PCT_up
HFD_PCT_up
Human_PCT_up


S.3
A
Podocytes Col4a3
T−test, p = 1.4e−12
T−test, p = 5.3e−09
T−test, p = 0.016
Log(TPX+1)
Condition
Chow
HFD
BTBR wt/wt
BTBR ob/ob
BTBR wk5
BTBR wk10
HFD
B
Nphs2
Col4a3
Merge
BTBR wt/wt
BTBR ob/ob
Col4a3 R.F.U.
**
Wild-type
BTBR ob/ob
C
Mesangial Cells Col4a2
T−test, p < 2.2e−16
T−test, p = 1.2e−08
T−test, p = 0.003
D
Nphs2
Ptn
Col4a2
Merge
Col4a2 R.F.U.
***
E
PCTs Pck1
T−test, p = 8.2e−15
T−test, p < 2.2e−16
T−test, p < 2.2e−16
F
PCTs Lrp2
T−test, p = 0.03
T−test, p = 0.85
T−test, p < 2.2e−16
G
PCTs Gsta2
T−test, p = 1.9e−14
T−test, p < 2.2e−16
T−test, p < 2.2e−16
H
Pck1
Chow
HFD
Pck1 F.U.
**
I
Lrp2
Pck1
Gsta1/2
BTBR wt/wt 10wk
BTBR ob/ob 10wk
Pck1 R.F.U.
*
Gsta 1/2 R.F.U.
***


S4
A
C1QA
C1QB
LYVE1
CCL3
CCL3L3
CCL4L2
TREM2
APOC1
SPP1
CD9
UMAP_1
UMAP_2
log(TPX+1)
B
CLEC10A+ Mϕ
Monocyte (NC)
LYVE1high Mϕ–1
Monocyte(C)–2
Monocyte(C)–3
CD9highTREM2high Mϕ
LYVE1high Mϕ–3
LYVE1high Mϕ–2
Monocyte(C)–1
TMCC1
RELL1
TUBB6
LDLRAD4
TCF12
EMP1
DLE2
ETV5
NRP1
PTPRJ
Average Expression
% Expressed
C
UMAP_1
UMAP_2
0
1
2
3
4
5 (TREM2high Macrophages)
6
7
8
9
10
11
D
E
Healthy
H–CKD
DKD
UMAP_1
UMAP_2
F
Nupr1
Adgre4
Plac8
Ifitm6
Smpdl3a
Vim
Gpx1
Napsa
S100a6
S100a4
S100a11
Crip1
Ear2
Fabp4
Chil3
Ccr2
Slamf9
Ccr12
Cxcl16
Cd72
Hexb
Lgmn
Ms4a7
Adgre1
Fyb
Cd81
Fcgr1
Cd74
C1qc
C1qb
C1qa
BTBR5wk
BTBR10wk
HFD
G
WT
OB
UMAP1
UMAP2
Resident Macrophage−1
Resident Macrophage−2
Resident Macrophage−7
Proliferating macrophages
Inf Macrophage
K
BTBR wk 5 annotations
Proliferating mø
Resident mø−8/Doublet
Resident mø−7
Resident mø−2
Resident mø−1
Infiltrating mø
Infiltrating Macrophage-1
Infiltrating Macrophage-2
Resident Macrophage-1
Resident Macrophage-2
Resident Macrophage-3
Resident Macrophage-5
Proliferating macrophages
Predicted cell−types
(BTBR wk 10 annotations, training data)
H
Row normalized
Avg log(TPX+1)
Infiltrating Macrophage-1
Infiltrating Macrophage-2
Infiltrating Macrophage-3
Resident Macrophage-1
Resident Macrophage-2
Resident Macrophage-3
Resident Macrophage-4
Resident Macrophage-5
Resident Macrophage-6 (Trem2hi)
Resident Macrophage-8/Doublet
Resident Macrophage-9
Cycling Immune
I
Infiltrating Macrophage
Resident Macrophage-1
Resident Macrophage-2
Resident Macrophage-7
Resident Macrophage-8/Doublet
Proliferating Macrophages
J
Infiltrating Macrophage-1
Infiltrating Macrophage-2
Resident Macrophage-1
Resident Macrophage-2
Resident Macrophage-3
Resident Macrophage-5
Proliferating Macrophages
N
HFD-fed mouse DKD model
vSMC
PVC
cDC−3 (Cd72+)
cDC−2 (Cd209+)
cDC−1 (Naaa+)
VCan1+FEC
Unknown 3
Unknown 2
TAL
Sox17+progenitor EC
S3−1
S3−2
S2
S1
Resident Macrophage-9
Resident Macrophage-8/Doublet
Resident Macrophage-6
Resident Macrophage-5
Resident Macrophage-2
Resident Macrophage-3
Resident Macrophage-4
Resident Macrophage-1
RBCs
Podocyte
Plasma Cells
PEC−2
PEC−1
PCT−Unknown
PCT−Stress
PCT−Inf1
PCT−5
PCT−4
PCT−3
PCT−2
PCT−1
PCT
Npr3+Esm1+Plvap+EC
Mito−high PCT
Mgp+Eln+ECs
Mesangial
Ly6a+Cd74+ cells
Infiltrating Macrophage-3
Infiltrating Macrophage-2
Infiltrating Macrophage-1
GEC
Fibroblasts
Fgg+EC
EEC
DCT
Cycling PCT
Cycling Immune
CNT
CD8+ T/NKT
CD4+ T/NKT
CD−TC
CD−B−IC
CD−A−IC
B Cells
Apln+ECs
Trem2
Expression level
Percent Expressed
L
Spearman r: 0.340
p = 0.022
TREM2+ macrophages/ROI
% of all cells
BMI
M
Spearman r: 0.3256
p = 0.032
TREM2+ macrophages/ROI
% of all cells
BMI


A
Chromosome 17
5'
gRNA
gRNA
3'
1
2
3
45
Exon
Homology arm
KO region
B
Water
WT
Trem2-/-
Water
WT
Trem2-/-
Primer set 1
Primer set 2
C
Glucose (mg / dL)
Time (min)
WT chow
WT HFD
Trem2-/- chow
Trem2-/- HFD
D
ΔBody weight (g)
***
**
WT chow
WT HFD
Trem2-/- chow
Trem2-/- HFD
E
Glu (mmol/L)
***
****
WT chow
WT HFD
Trem2-/- chow
Trem2-/- HFD
F
TG (mmol/L)
****
****
WT chow
WT HFD
Trem2-/- chow
Trem2-/- HFD
G
Cholesterol (mmol/L)
****
****
WT chow
WT HFD
Trem2-/- chow
Trem2-/- HFD

Supplementary Table 7 Main demographic and clinical characteristics of kidney donors, relevant to Figures 3H, I

	All N=45	**Healthy (A) N=16**	**HTN (B) N=8**	**P value A vs B**	**Obese (C) N=13**	**P value A vs C**	**Diabetic (D) N=8**	**P value A vs D**
Male, n (%)	29 (64)	9 (56)	5 (62)	1	9 (69)	0.70	6 (75)	0.65
Age, median (IQR) –years	62 (49-70)	46 (22-63)	67 (61-76)	**0.021**	61 (58-69)	**0.035**	69 (58-72)	0.10
Cause of death, n (%)								
Cerebral event	30 (66)	7 (44)	6 (75)	0.21	10 (77)	0.12	7 (87)	0.07
Cardiorespiratory	10 (22)	5 (31)	2 (25)	1	2 (15)	0.41	1 (13)	0.62
Trauma	4 (9)	3 (19)	0	0.53	1 (8)	0.60	0	0.52
Other	1 (2)	1 (6)	0	1	0	1	0	1
sCr at retrieval, median (IQR) – µM/L	72 (59-88)	73 (59-96)	57 (51-70)	0.11	75 (67-85)	0.83	85 (78-97)	0.35
eGFR at retrieval, median (IQR) – mL/min/1.73 m^2	95 (88-111)	94 (78-112)	99 (90-112)	0.58	98 (78-111)	0.88	96 (90-101)	0.95
Arterial hypertension, n (%)	23 (51)	0	8 (100)	**<0.001**	10 (77)	**<0.001**	6 (75)	**<0.001**
Treatment, n (%)								
RAAS inhibitors	12/23 (52)	--	4 (50)	--	4/10 (40)	--	4/6 (66)	--
Calcium channel blockers	7/23 (30)	--	2 (25)	--	3/10 (30)	--	2/6 (33)	--
Other	7/23 (30)	--	3 (37)	--	1/10 (10)	--	3/6 (50)	--
None/diet	6/23 (26)	--	2 (25)	--	4/10 (40)	--	2/6 (33)	--
BMI, median (IQR)	27 (24-32)	25 (23-27)	24 (23-27)	0.83	34 (32-36)	**<0.001**	32 (28-34)	**0.012**
BMI ≥30, n (%)	19 (42)	0	0	1	13 (100)	**<0.001**	6 (75)	**<0.001**
Diabetes, n (%)	8 (18)	0	0	1	0	1	8 (100)	**<0.001**
Treatment, n (%)								
Insulin	0	--	--	--	--	--	0	--
Metformin	4/8 (50)	--	--	--	--	--	4 (50)	--
SGLT2i	0	--	--	--	--	--	0	--
Other	1/8 (12)	--	--	--	--	--	1 (12)	--
None/diet	4/8 (50)	--	--	--	--	--	4 (50)	--

BMI, body mass index; HTN, hypertensive; IQR, interquartile range; sCr, serum creatinine

RAAS inhibitors include angiotensine converting enzyme inhibitors and angiotensine II receptor blockers