

Figure S 1. Confocal images from PGFP mice made diabetic with multiple low doses of STZ. FPs are not effaced. Images are typical of 3 STZ diabetic mice. Scale bars indicate the magnification.

Figure S2. Staining for osteopontin (A) and complement component C3 (B) increases in OVE-GFP podocytes and in other diabetic kidney cells. Most OVE-GFP podocytes (lower row in A) have osteopontin staining, indicated by yellow/orange color in the Merge panel. C3 positive OVE-GFP podocytes (lower row in B) are less frequent and are pointed out with arrowheads. The scale bars for A panels = 30 μ m. The scale bars for B panels = 10 μ m.

Table S1: 40 most upregulated genes in OVE-GFP podocytes

Table S2: 40 most downregulated genes in diabetic OVE podocytes

Movies S1-3. 3D movies of a normal glomerulus (Movie S1) and two diabetic glomeruli (Movies S2 and S3).

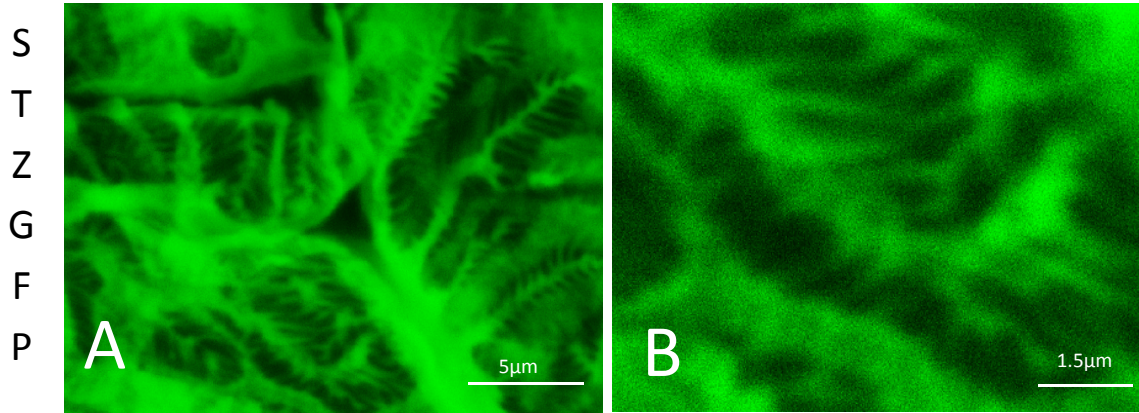


Figure S1

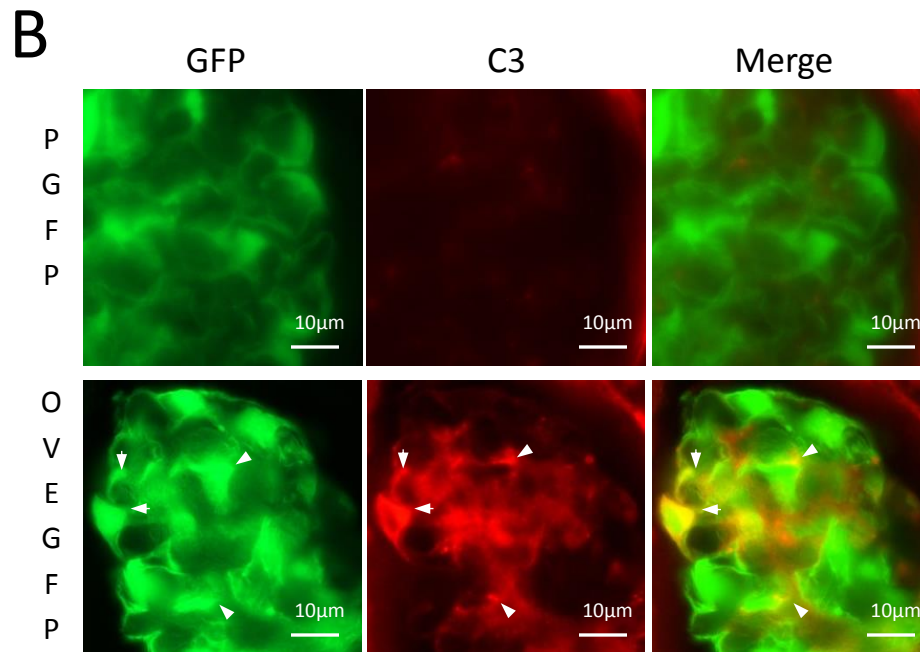
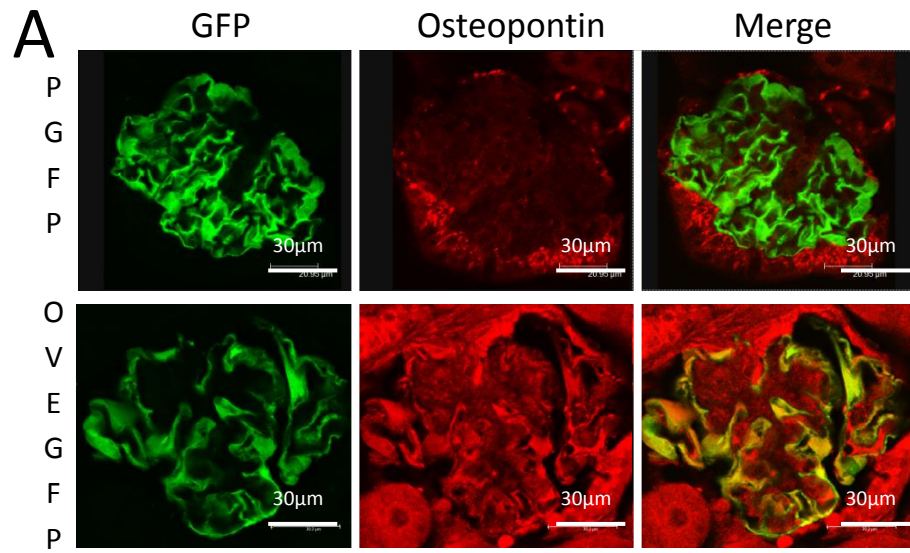


Figure S2

Table S1: 40 most upregulated genes in OVE-GFP podocytes

Gene Title	Gene Symbol	OVE/FVB	P value
lipocalin 2	Lcn2	26.8	0.042
solute carrier family 7 , member 12	Slc7a12	18.8	0.015
complement component 1, q subcomponent, beta polypeptide	C1qb	16.1	0.017
cytochrome P450, family 4, subfamily a, polypeptide 14	---	11.2	0.045
complement component 3	C3	10.8	0.049
ribonucleotide reductase M2	Rrm2	10.4	0.002
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	10.4	0.009
aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1	9.3	0.009
neurofilament, light polypeptide	Nefl	9.2	0.027
aquaporin 4	Aqp4	8.8	0.005
clusterin /// similar to clusterin	Clu	8.6	0.003
early growth response 2	Egr2	8.4	0.044
glutathione S-transferase omega 1	Gsto1	8.3	0.025
ATPase, H+ transporting, lysosomal V0 subunit D2	Atp6v0d2	7.9	0.011
Cytochrome P450, family 4, subfamily a, polypeptide 10	Cyp4a10	7.1	0.015
keratin 18	Krt1-18	7.0	0.029
keratin 8	Krt2-8	6.8	0.011
secretogranin V	Sgne1	6.6	0.004
cathepsin S	Ctss	6.4	0.031
neurofilament, medium polypeptide	---	6.2	0.014
predicted gene 8126 /// predicted gene 8267 ///	1700049E17Rik	5.9	0.010
WAP four-disulfide core domain 2	Wfdc2	5.7	0.012
RIKEN cDNA 1600029D21 gene	1600029D21Rik	5.6	0.021
chemokine (C-X-C motif) ligand 1	---	5.4	0.048
FXFD domain-containing ion transport regulator 4	Fxyd4	5.4	0.003
ras homolog gene family, member U	Rhou	5.3	0.024
metallothionein 2	Mt2	5.3	0.014
prostaglandin-endoperoxide synthase 2	Ptgs2	5.2	0.025
sema domain, immunoglobulin domain (Ig), short basic domain	Sema3c	5.1	0.001
mucoilin 3	---	5.0	0.000
histocompatibility 2, class II antigen A, alpha	H2-Aa	4.9	0.009
predicted gene 7325	LOC433110	4.9	0.012
apolipoprotein B	Apob	4.9	0.022
osteoglycin	Ogn	4.6	0.049
S100 calcium binding protein G	S100g	4.5	0.020
defensin beta 1	Defb1	4.5	0.006
metallothionein 1	---	4.5	0.043
solute carrier family 26, member 4	Slc26a4	4.4	0.022
solute carrier organic anion transporter family, member 4a1	Slco4a1	4.4	0.0002
receptor-interacting serine-threonine kinase 4	Ripk4	4.4	0.029

Table S2: 40 most downregulated genes in diabetic OVE podocytes

Gene Title	Gene Symbol	OVE/FVB	P value
solute carrier organic anion transporter family, 1a1	Slco1a1	0.05	0.019
kidney androgen regulated protein	Kap	0.10	0.022
solute carrier family 7, member 13	Slc7a13	0.12	0.035
SRY-box containing gene 8	Sox8	0.15	0.005
indolethylamine N-methyltransferase	Inmt	0.23	0.029
cytochrome P450, family 2, subfamily j, polypeptide 13	Cyp2j13	0.24	0.025
expressed sequence AI594671	AI594671	0.24	0.004
RIKEN cDNA 2900078I11 gene	2900078I11Rik	0.24	0.001
RIKEN cDNA 5330409N07 gene	5330409N07Rik	0.26	0.002
CKLF-like MARVEL transmembrane domain containing 7	Cklfsf7	0.27	0.001
calcium channel, voltage-dependent, alpha 2/delta subunit 2	Cacna2d2	0.28	0.001
---	2810040C05Rik	0.29	0.001
BTB (POZ) domain containing 11	Btbd11	0.29	0.033
acyl-CoA synthetase long-chain family member 6	Acsl6	0.30	0.000
---	Glcci1	0.31	0.006
ChaC, cation transport regulator-like 1 (E. coli)	1810008K03Rik	0.31	0.001
neuropeptide Y receptor Y1	Npy1r	0.33	0.006
neuropilin 1	Nrp1	0.34	0.020
---	B130020M22Rik	0.34	0.004
aspartoacylase (aminoacylase) 3	Acy3	0.35	0.034
---	Phtf1	0.35	0.014
---	Csf1r	0.36	0.008
spermatogenesis associated, serine-rich 2-like	A230104H11Rik	0.36	0.000
RIKEN cDNA 5730405O12 gene	5730405O12Rik	0.36	0.006
RIKEN cDNA E430022K19 gene	E430022K19Rik	0.36	0.000
---	Als2cr19	0.36	0.005
---	Nup88	0.37	0.037
phosphodiesterase 10A	Pde10a	0.37	0.019
---	Cbfa2t2h	0.37	0.008
gap junction protein, alpha 3	---	0.37	0.001
RIKEN cDNA 6330575P09 gene	6330575P09Rik	0.37	0.004
---	Mtx2	0.38	0.040
solute carrier family 2 (facilitated glucose transporter)10	Slc2a10	0.38	0.029
RIKEN cDNA 8030447M02 gene	8030447M02Rik	0.38	0.000
tribbles homolog 3 (Drosophila)	Trib3	0.38	0.003
sorting nexin 31	4631426E05Rik	0.38	0.006
Rho guanine nucleotide exchange factor (GEF) 15	Arhgef15	0.38	0.009
src-like adaptor	Sla	0.39	0.000
Solute carrier family 12, member 6	9530023I19Rik	0.39	0.038
GA repeat binding protein, beta 2	A430024B14Rik	0.40	0.030