

Mouse Models of Diabetic Nephropathy

***Mount Sinai / Jefferson /
Einstein / Minnesota***

Erwin Böttinger, PI

Kumar Sharma, Co-PI

Group Members

- *Mount Sinai: Phenotyping, Molecular Pathology & Validation*
 - Erwin Bottinger (PI)
 - Sandhya Xavier (Fellow)
 - Liping Yu, Technician
- *Albert Einstein: Strain Generation & Characterization*
 - Maureen Charron (Co-Investigator)
 - Scott Henderson, Technician
 - Katalin Susztak, Co-Investigator
- *Thomas Jefferson: Experimental Diabetes, HPLC Core, Phenotyping*
 - Kumar Sharma (Co-PI)
 - Steve Dunn, Technician and Core Manager
 - Kevin Williams, (Co-Investigator)
 - Peter McCue, Pathology
- *U Minnesota: Phenotyping (Morphometry)*
 - Michael Steffes, Consultant

Progress Report

- *Strain Generation*

Katalin Susztak (AECOM)/Erwin Bottinger (MSSM)

- **gGT-CD36 tg > NO EXPRESSION in 11 lines screened**
- **Alternate strategy: sglt2l-CD36 tg > 9 Founders**

- *Experimental Models*

Bottinger (MSSM)

completed

- db/db C57BLKS longitudinal, standardized phenotyping
- Ins2-Akita longitudinal, standardized phenotyping
- flk-1 RAGEtg with low dose STZ to 28 wks
- Cd2ap+/- with STZ to 28 wks
- Db/db and Ins2-Akita (glomerular RNA profiles - molecular phenotyping: up to 28 wk-of-age)

ongoing

- **flk-1 RAGEtg x Ins2-Akita CD1xB6 > 24 wk-of-age phenotyping**
- **Cd2ap+/- x Ins2-Akita 129xB6 > 24 wk-of-age phenotyping**

Kumar Sharma (TJU)

Manuscript in preparation

- **Decorin knockout with low dose STZ**

- *Phenotyping Cores*

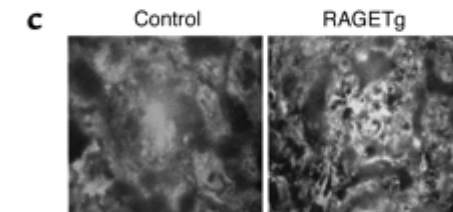
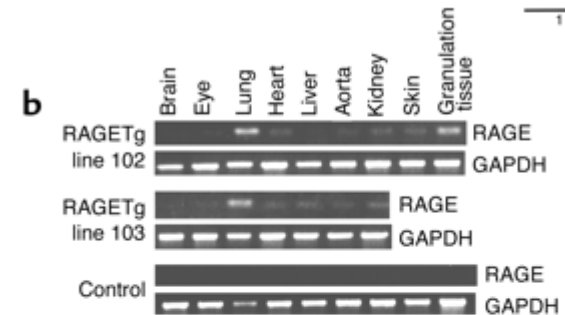
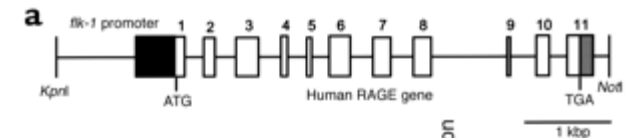
HPLC creatinine... Kumar Sharma/Steve Dunn (TJU)

Genomics.... Erwin Bottinger (MSSM)

Ins2Akita x flk-RAGE tg

Development and prevention of advanced diabetic nephropathy in RAGE-overexpressing mice

Yasuhiko Yamamoto and Hiroshi Yamamoto;
J Clin Invest, 2001



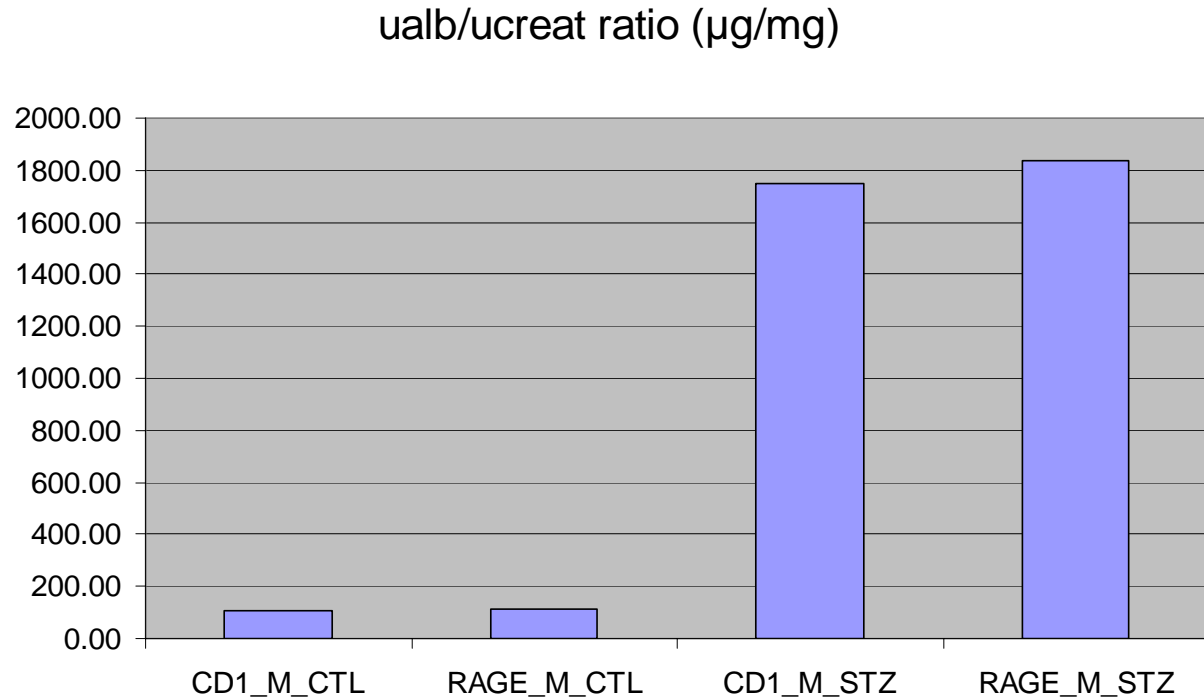
DIABETES INDUCTION

inducible nitric oxide synthase
(iNOS) under the control of the
insulin promoter (iNOSTg)

Low Dose STZ in flk-RAGE tg [CD1-tg(Kdr-Ager)]

Experimental Design

- Female and Male mice
- CD1 inbred
- STZ 8 wk
- Sac 20 wk



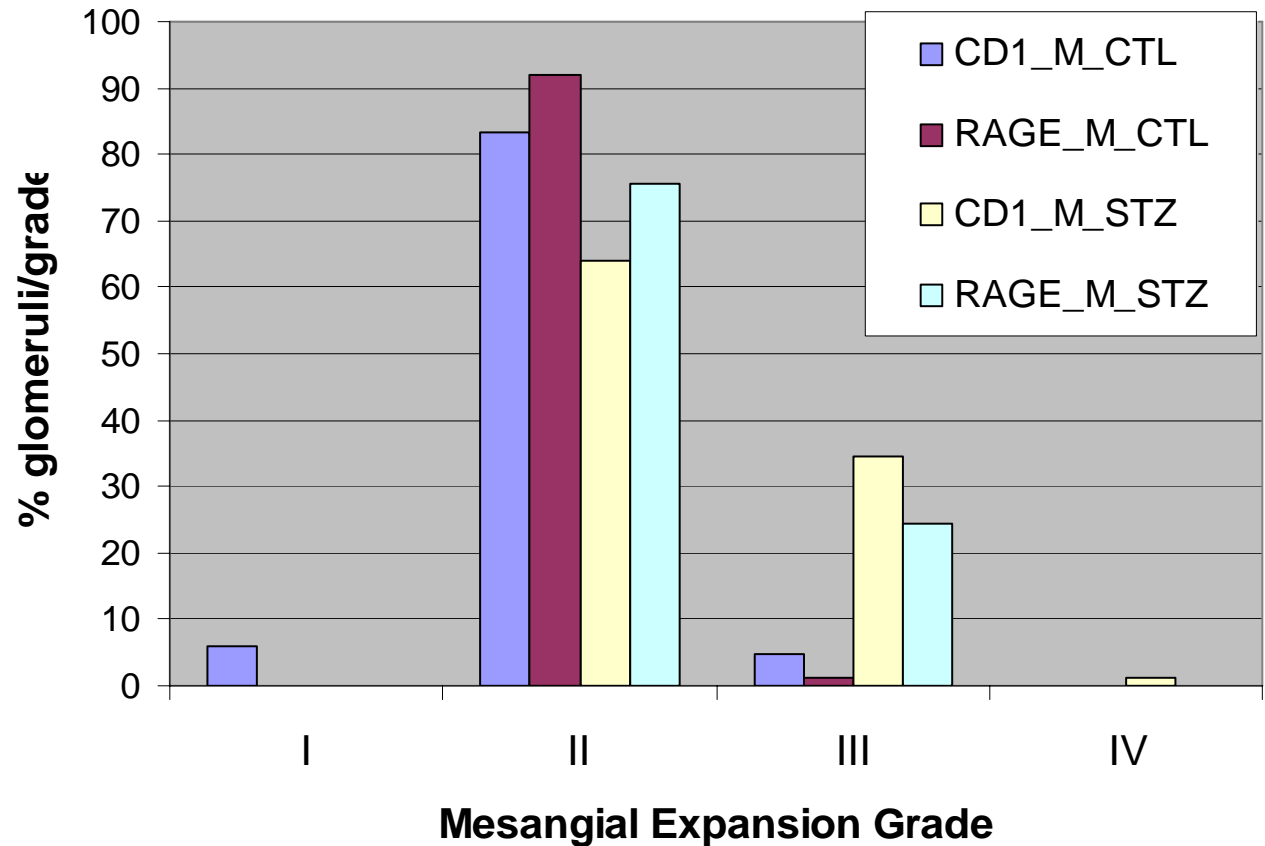
Low Dose STZ in flk-RAGE tg [CD1-tg(Kdr-Ager)]

Experimental Design

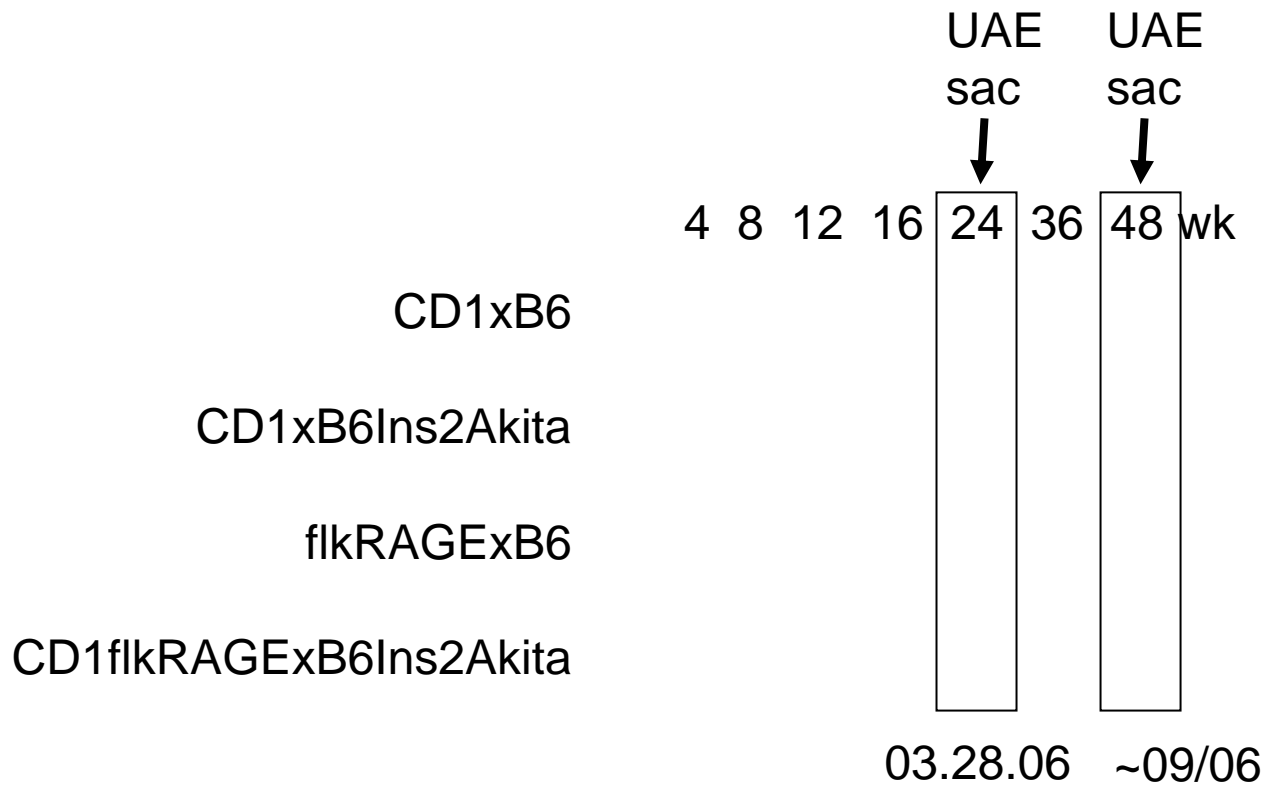
- Male mice
- CD1 inbred
- STZ 8 wk
- Sac 20 wk

Pathology Report

- No nodular lesion
- No tub.int. lesions
- No vascular lesions



Ins2Akita x flk-RAGE tg



Decorin and diabetic nephropathy

- **Background:** Decorin is a small proteoglycan that inhibits TGF- β via direct binding to active TGF- β . Decorin is stimulated in human mesangial cells by high glucose and stimulated in several mouse models of diabetic kidney disease.
- **Hypothesis:** Decorin protects against diabetic kidney disease.
- **Back-cross *Dcn* KO allele onto the C57BL/6J background; induce STZ diabetes in male littermates with different *Dcn* gene doses**
 - Albuminuria
 - Creatinine clearance by HPLC
 - Histologic parameters of diabetic nephropathy

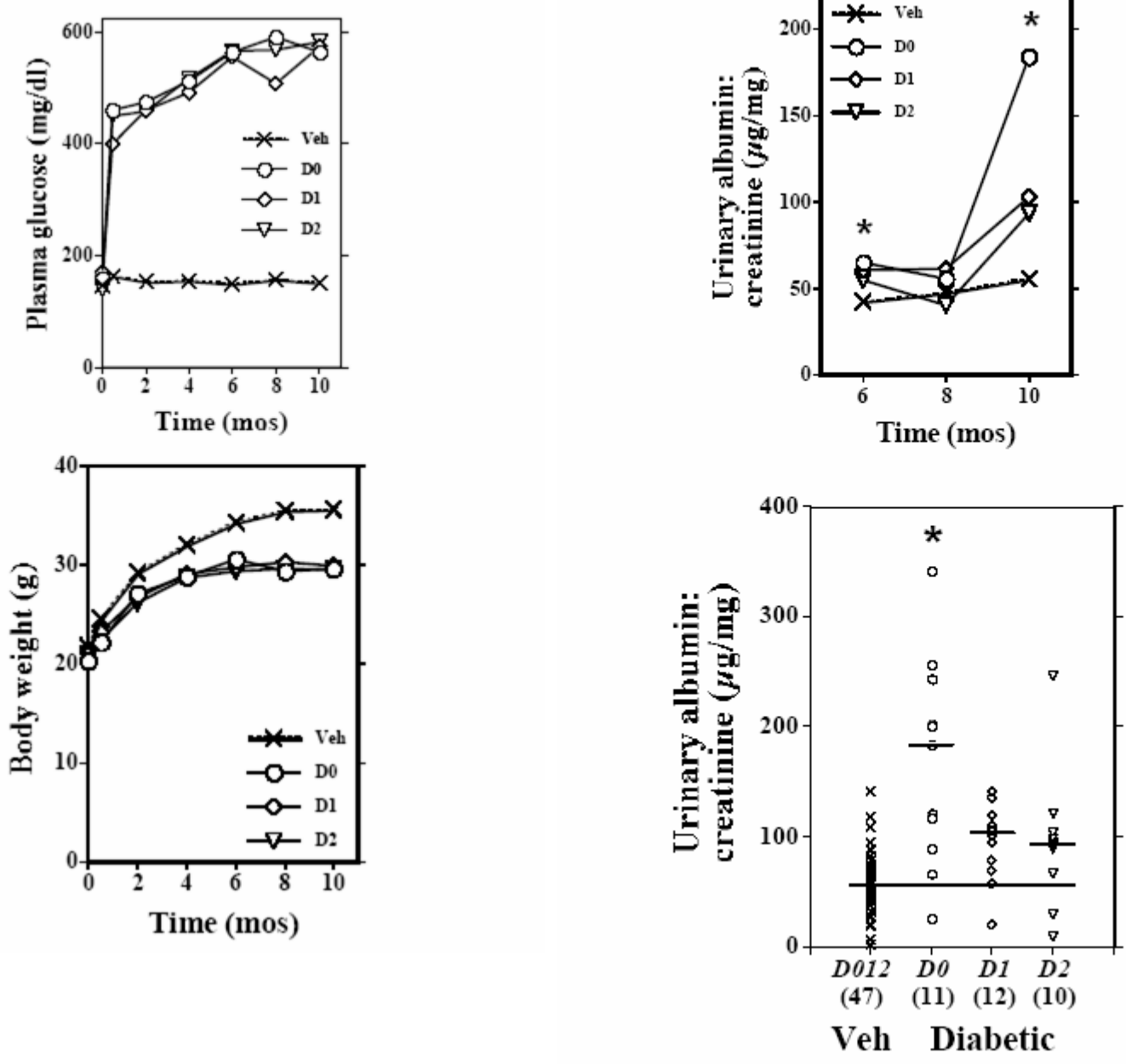
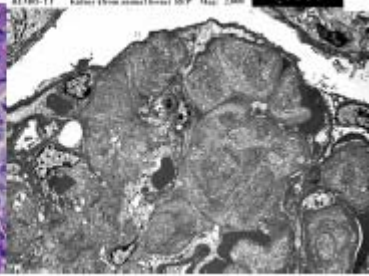
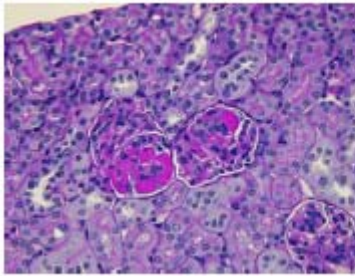
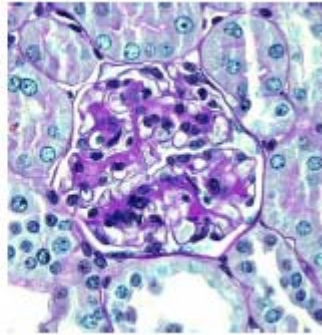
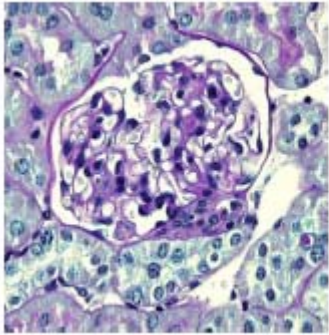
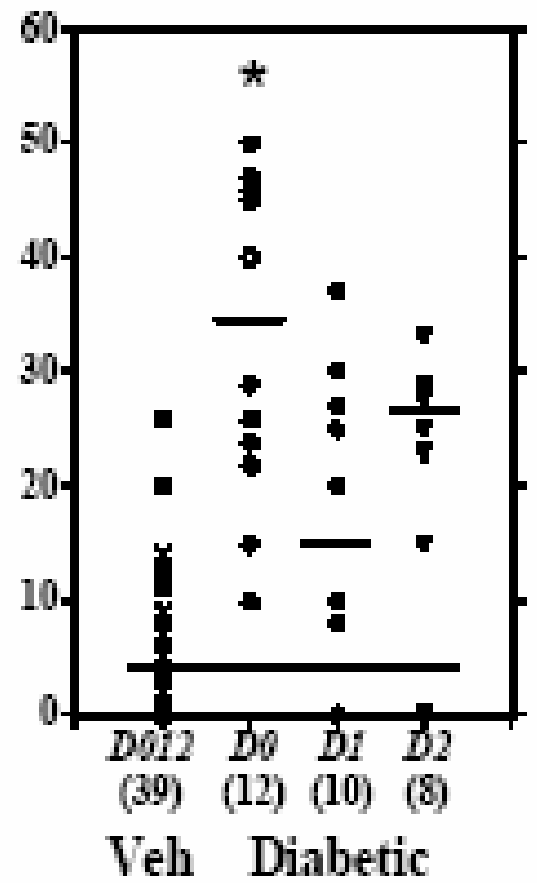


Figure 2

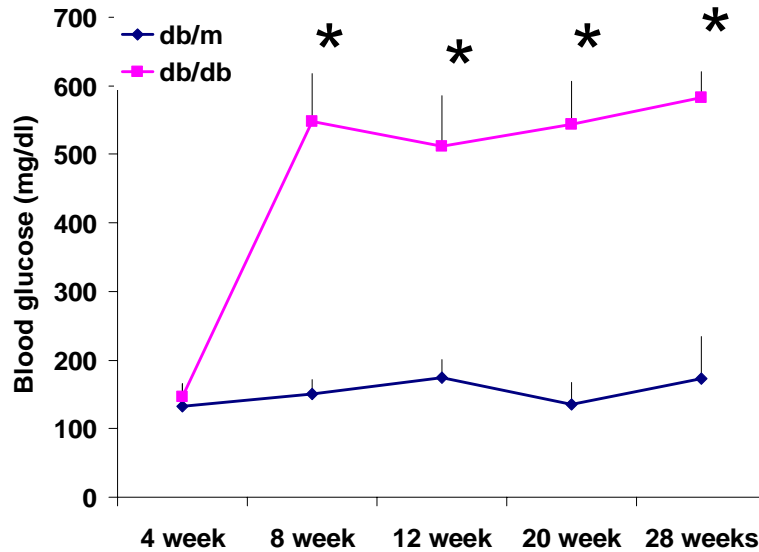


Glomeruli with advanced matrix scores per 50 per mouse

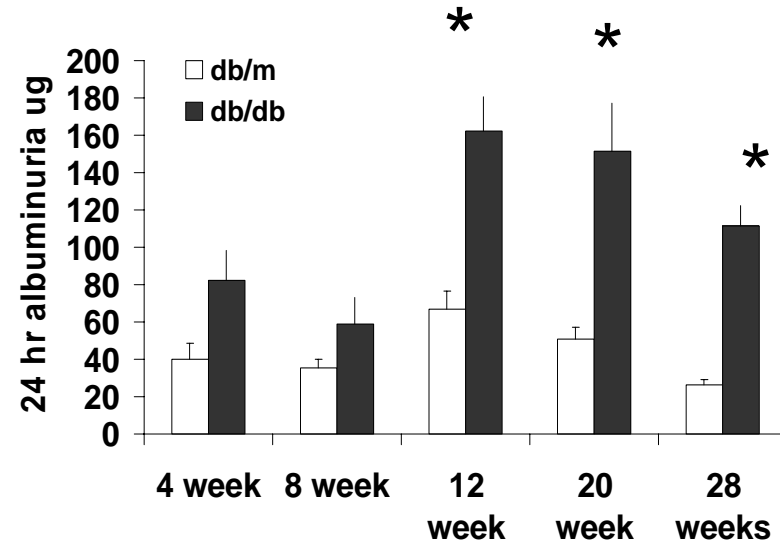


db/db C57BLKS/J Molecular Phenotyping

Blood Glucose (BG)



Urinary Albumin Excretion (UAE)



Glomerular and tubular RNA preparations



MOE430 whole genome profiling

Experiments:

	db/db	db/m		Akita	B6
4 weeks	4	5	4-5 weeks	1	3
8 weeks	10	7	10 weeks	3	0
12 weeks	3	3	18-20 weeks	5	2
20 weeks	4	4	28 weeks	2	2

Unique genes: 14097

Filtering: Genes whose median expression value cross experiments < 2 are excluded from analysis.

SAM and GoMiner are used to identify differentially expressed genes and pathways.

Cutoff for selecting differentially expressed genes: $FDR \leq 0.05$

Cutoff for selecting enriched GO category: $FDR \leq 0.01$

Experiment	Differentially expressed genes
db/db 8, 12&20 weeks and Akita all vs db/db 4 weeks and db/m all and B6 all (All diabetic vs all non-diabetic)	2691
db/db 20 weeks vs db/db 4, 8&12 weeks and db/m all	2641
db/db 12&20 weeks vs db/db 4&8 weeks and db/m all	2132
db/db 8, 12&20 weeks vs db/db 4 weeks and db/m all (Diabetic vs non-diabetic)	1550
db/db 12&20 weeks vs db/m 12&20 weeks	1195
db/db 8&12 weeks vs db/m 8&12 weeks	697
db/db 8 weeks vs db/m 8 weeks	402
db/db 8&12 weeks vs db/db 4&20 weeks and db/m all	350
db/db 20 weeks vs db/m 20 weeks	231
Akita all vs B6 all (Diabetic vs non-diabetic)	220
Akita 18-20&28 weeks vs B6 18-20&28 weeks	23
db/db 12 weeks vs db/m 12 weeks	18
Akita 4-5&10 weeks vs B6 4-5 weeks	6

Gene Set Enrichment Analysis (Diabetic vs Non-diabetic for db/db & db/m)

Top leading pathways (up-regulated in diabetic): Total 453 pathways (genesets) analyzed

GeneSet/Pathway	SIZE	SOURCE
MAP00350_Tyrosine_metabolism	23	GenMAPP
calcineurinPathway	19	Increased intracellular calcium activates the phosphatase calcineurin in differentiating keratinocytes.
erkPathway	26	Cell growth is promoted by Ras activation of the anti-apoptotic p44/42 MAP kinase pathway.
inflamPathway	25	BioCarta
dcPathway	21	Dendritic cells internalize and present antigen, after which they migrate to lymphocyte-rich tissues and induce T and B cell differentiation.
intrinsicPathway	22	BioCarta
MAP00280_Valine_leucine_and_isoleucine_degradation	25	GenMAPP
MAP00260_Glycine_serine_and_threonine_metabolism	15	GenMAPP
fmlppathway	36	The fMLP receptor is a G-protein coupled receptor in neutrophils that recognizes formylated bacterial peptides and activates NADPH oxidase.
MAP00310_Lysine_degradation	15	GenMAPP
ST_G_alpha_i_Pathway	31	Signalling Transduction KE
CR_TRANSPORT_OF_VESICLES	20	PNAS_2015
MAP00030_Pentose_phosphate_pathway	15	GenMAPP
P53_UP	31	Kannan_et_al_2001
mef2dPathway	16	BioCarta
MAP00330_Arginine_and_proline_metabolism	32	GenMAPP
cell_adhesion	144	The attachment of a cell, either to another cell or to the extracellular matrix, via cell adhesion molecules.
MAP00071_Fatty_acid_metabolism	26	GenMAPP
MAP00590_Prostaglandin_and_leukotriene_metabolism	15	GenMAPP

Experiments:

**db/db 8, 12&20 weeks (diabetic) vs
db/db 4 weeks and db/m 4, 8, 12&20 weeks (non-diabetic)**

Selected GO categories:

GO:0044255_cellular_lipid_metabolism

GO:0006629_lipid_metabolism

GO:0008610_lipid_biosynthesis

GO:0006694_steroid_biosynthesis

GO:0006986_response_to_unfolded_protein

GO:0016125_sterol_metabolism

GO:0016126_sterol_biosynthesis

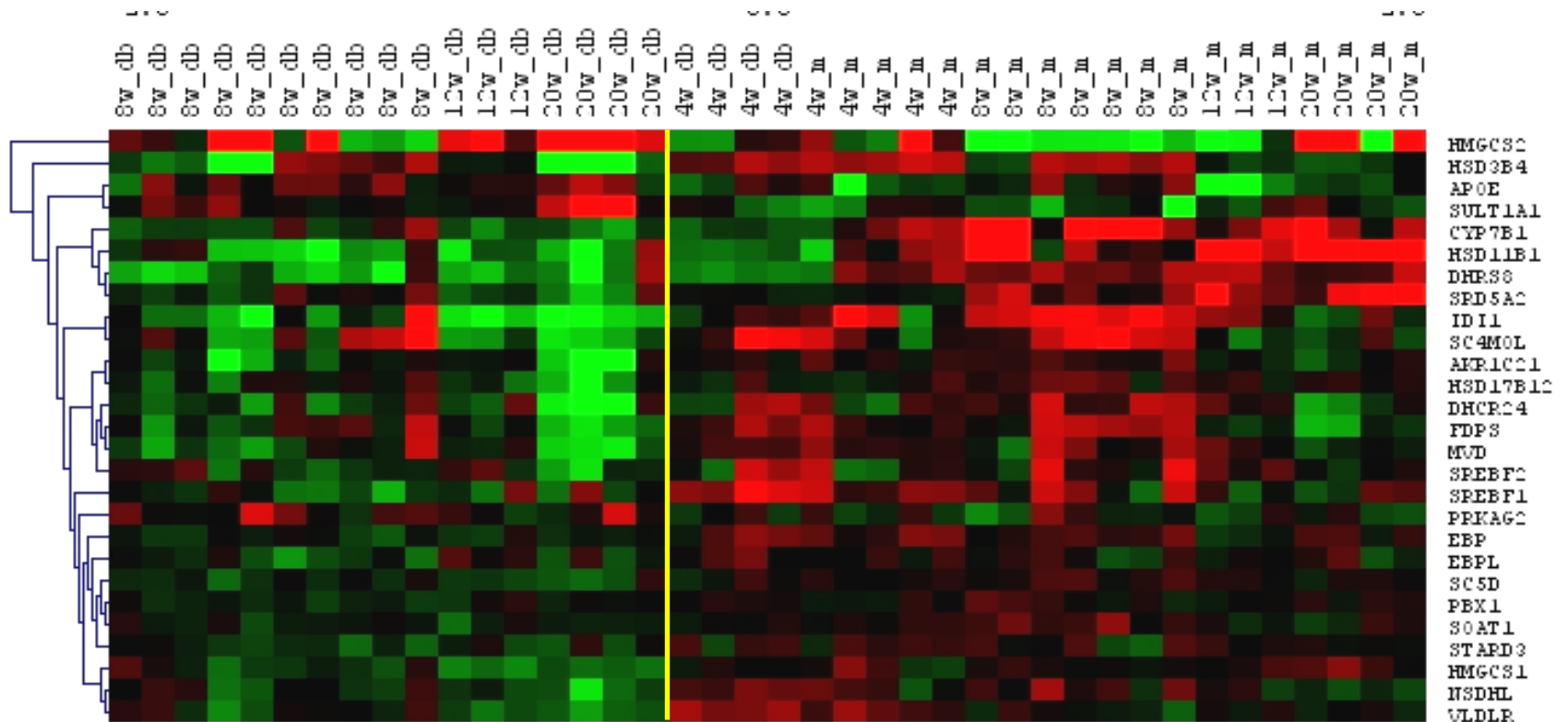
GO:0008202_steroid_metabolism

GO:0006631_fatty_acid_metabolism

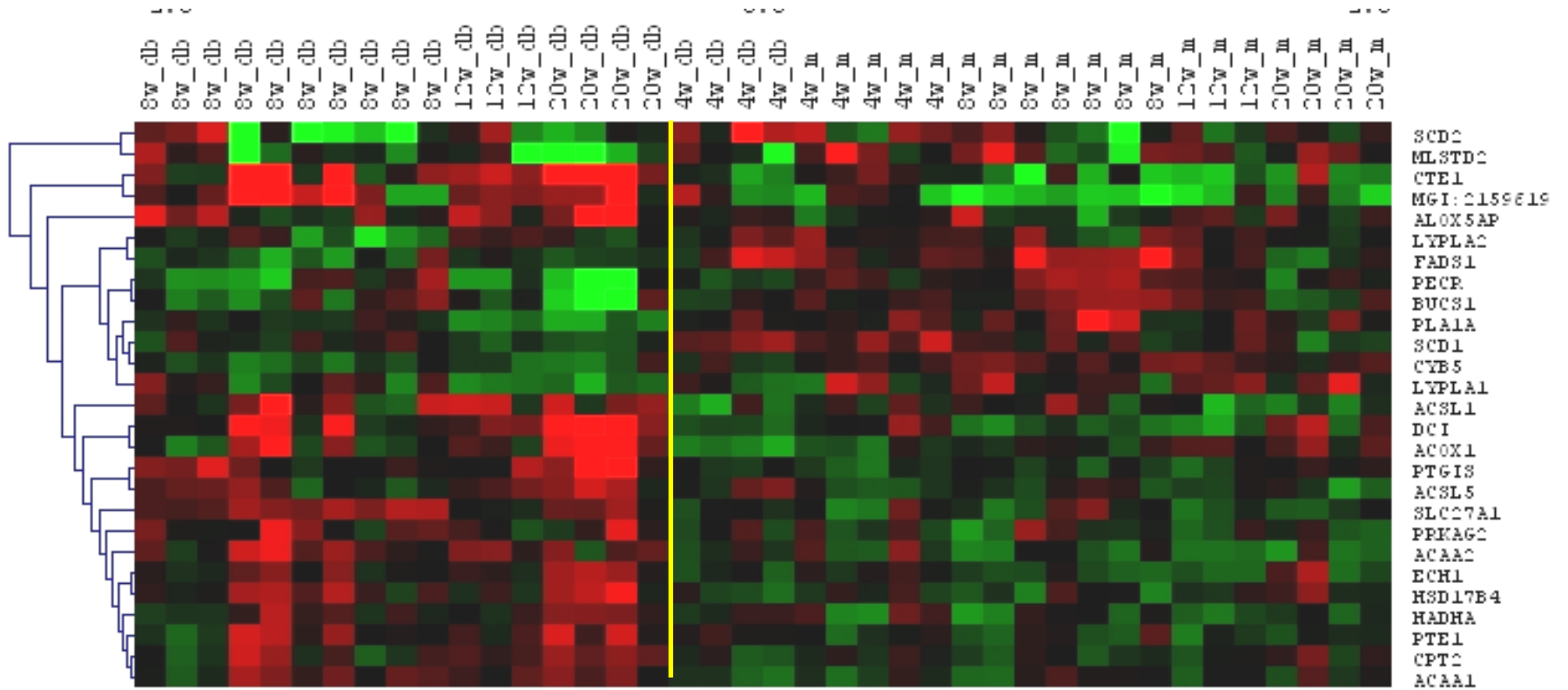
GO:0006790_sulfur_metabolism

Steroid metabolism & biosynthesis

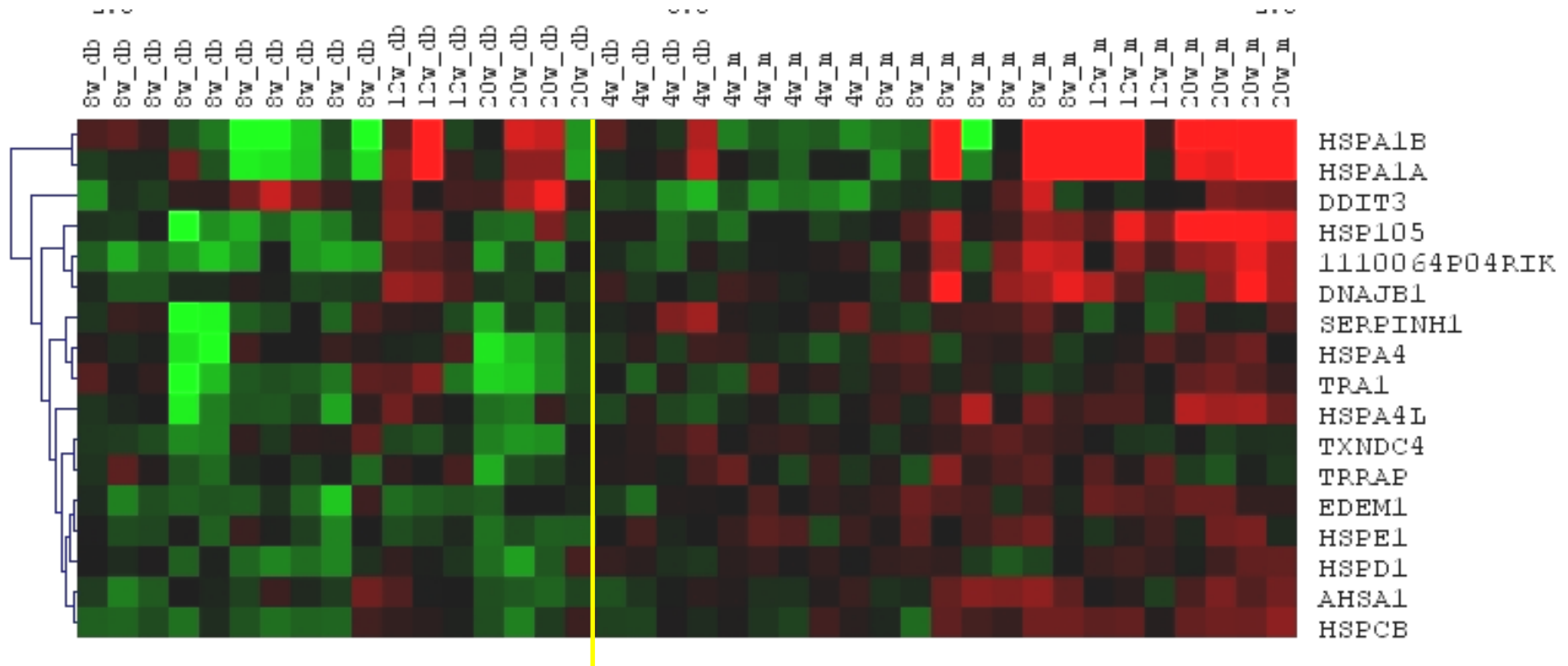
Sterol metabolism & biosynthesis



Fatty acid metabolism



Response to unfold protein



Reduced Podocyte Number in Glomerular Diseases



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- ❑ Type 2 Diabetes Mellitus [Pagtalunan et al., JCI, 1997]
- ❑ Type 1 Diabetes Mellitus [Steffes et al., Kidney Int, 2001]
- ❑ IgA Nephropathy [Lemley et al., Kidney Int, 2002]
- ❑ Focal Segmental Glomerulosclerosis

- ❑ Experimental Models
 - Puromycin aminonucleoside model [Kim et al., JASN 2001]
 - TGF- β 1 transgenic mice [Schiffer et al., JCI 2001]
 - Cd2ap knockout mice [Schiffer et al., JBC 2004]

 - **T1DM (*Ins2^{Akita}*) and T2DM (*Lepr^{db/db}*) mice**
[Susztak et al., Diabetes (In Press)]

Original Article

Glucose-Induced Reactive Oxygen Species Cause Apoptosis of Podocytes and Podocyte Depletion at the Onset of Diabetic Nephropathy

Katalin Susztak,¹ Amanda C. Raff,¹ Mario Schiffer,¹ and Erwin P. Böttinger²

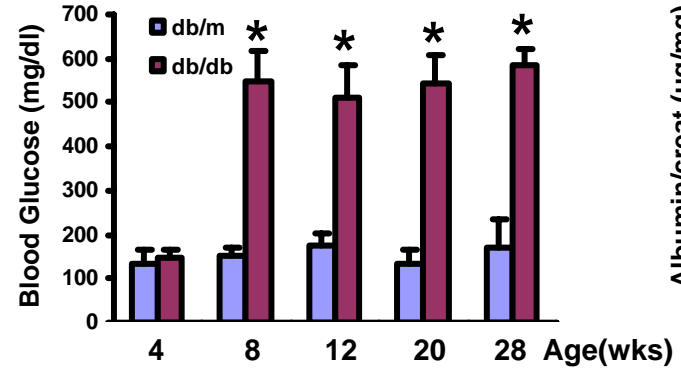
DIABETES,
VOL. 55, January 2006



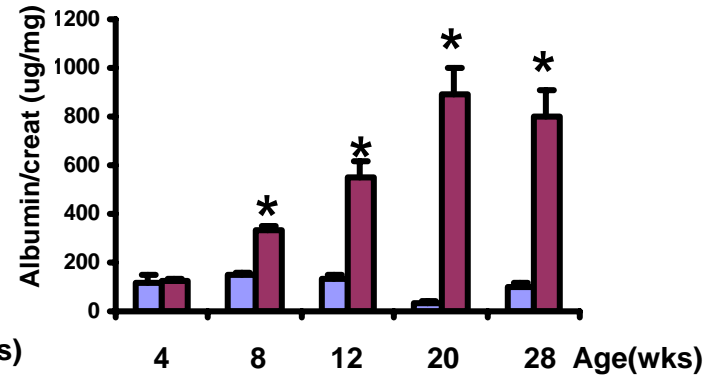
Katalin Susztak

Natural History of Kidney Disease in T2 Diabetic $Lepr^{db/db}$ (db/db) Mice

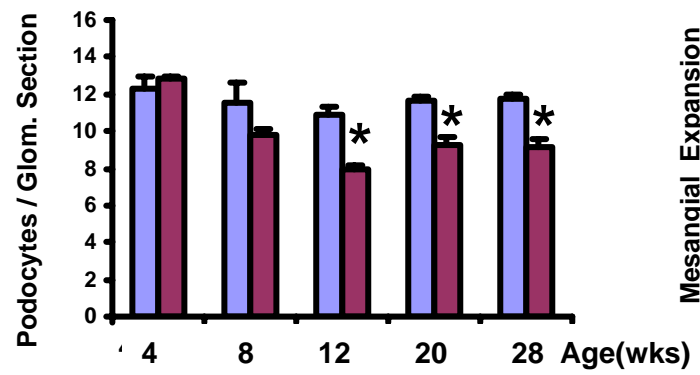
A Blood Glucose



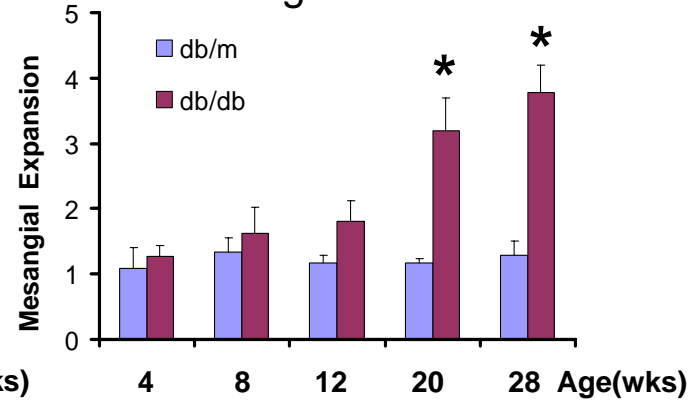
B Urinary Albumin Excretion



C Podocyte Number



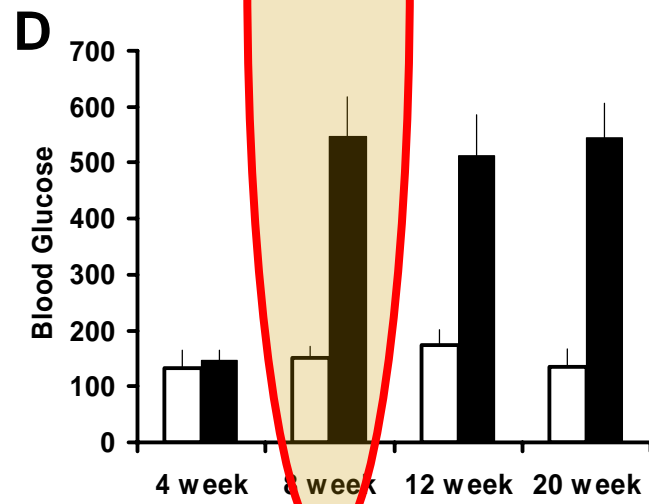
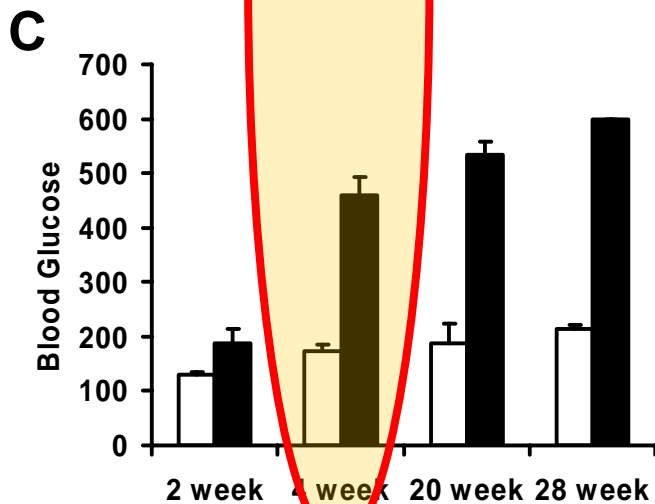
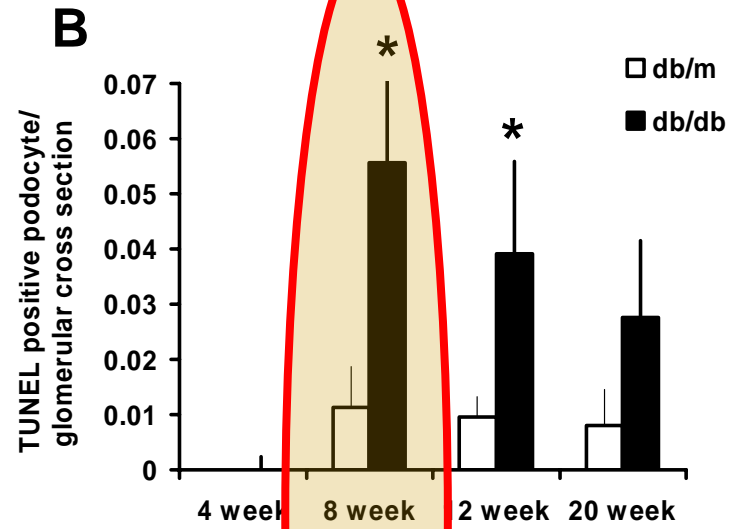
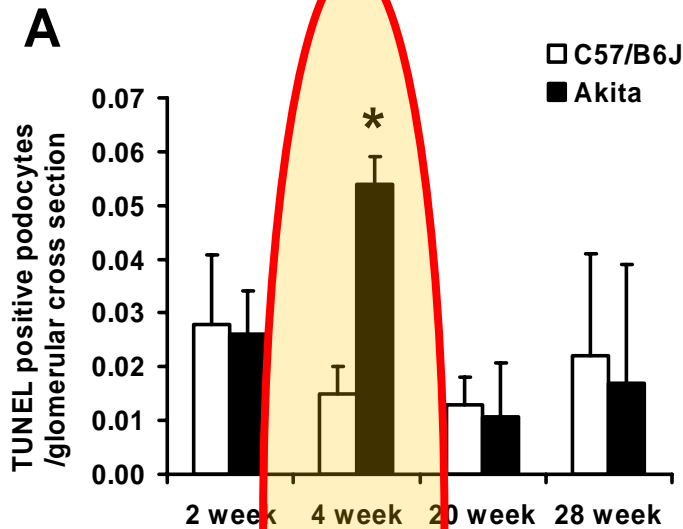
D Mesangial Matrix



Podocyte Apoptosis Coincides With Onset of Hyperglycemia in Murine T1DM and T2DM



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Diabetes, Podocyte Number, and Albuminuria in Murine T1DM and T2DM



BLOOD GLUCOSE

PODOCYTE NUMBER

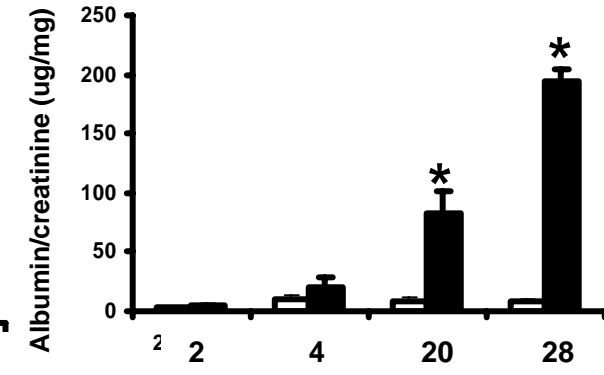
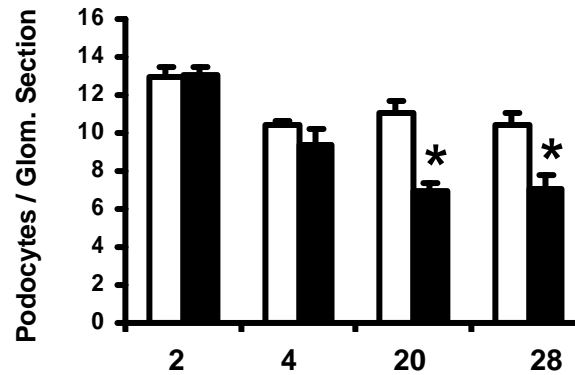
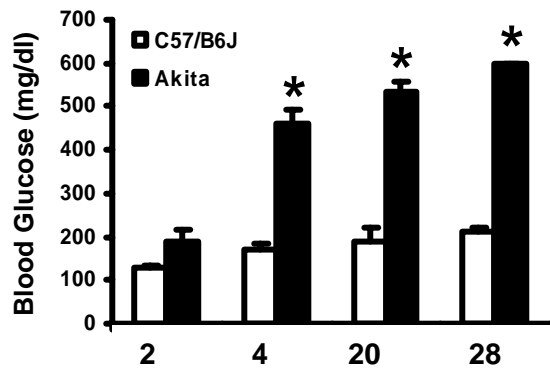
ALBUMINURIA

A

B

C

T1DM Model

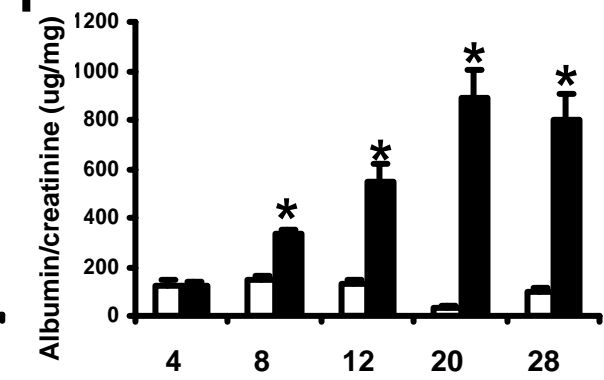
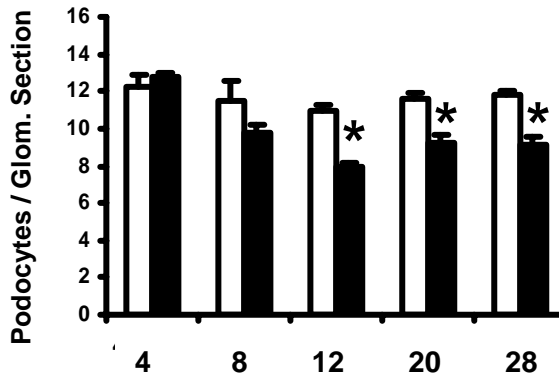
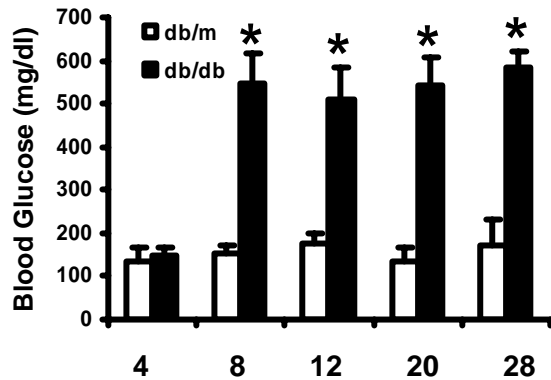


D

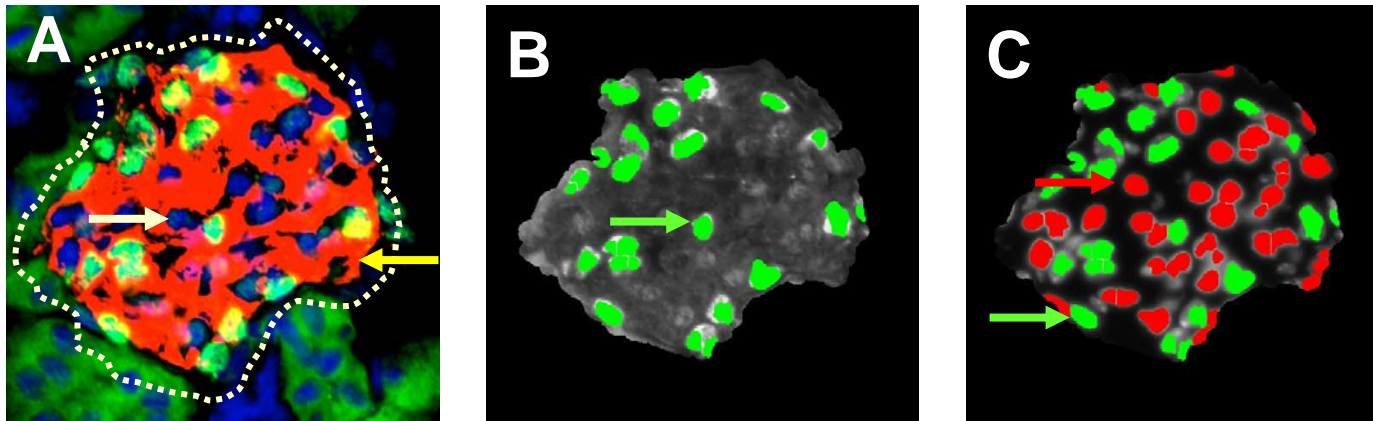
E

F

T2DM Model



Glomerular Cell Count Method using Digital Image Analysis



MetaMorph Digital Image Analysis Software
Nuclei Count Application Module

Thanks to

Advisors

NIH Programs

JDRF

Consortium