

SCHOOL OF MEDICINE Graduate Program in Biomedical Sciences

# **Final Examination**

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# CHARACTERIZING THE EFFECT OF PARENTAL LOW PROTEIN DIET ON OFFSPRING KIDNEY DEVELOPMENT AND FUNCTION

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**Biomedical Sciences Doctor of Philosophy** 

# Abstract

The kidney develops from the intermediate mesoderm from E10 to P4 in mice and weeks 5 to 34 in humans. The development relies on the physical and signaling interactions between the nephron progenitor cells (NPCs), the stroma progenitor cells, and the ureteric branching tip cells (UBTCs). Kidney development relies on signals that vary based on location and temporally with NPC recruitment order determining the part of the nephron they will form. Kidney organogenesis and nephrogenesis relies on signals from BMPs, growth factors, Wnt, cytokines, and autonomous and exogenous cell proliferation and survival signals. These signals lead into or are regulated by cell metabolism, environmental signals, and chromatin modifications. IUGR is an environmental condition known to cause hypertension, chronic kidney disease, and kidney failure. We hypothesized that disruption of metabolic homeostasis in the nephron progenitor cells in the IUGR fetus impairs nephrogenesis and is the direct link between the maternal environment and nephron endowment leading to adult hypertension and chronic kidney disease (CDK). IUGR from low protein diet caused small pups, small kidneys, increased kidney/body weight ratio. The changes begin at E13.5 with a 30% decrease in ureteric tip count, disorganized/smaller cap mesenchyme (CM) (37.5% decrease in Six2+ NPCs), and smaller kidneys. P0 NPCs show dysregulation to growth factors, Wnt, cell metabolism, and autonomous and exogenous cell proliferation and survival signals shown by bulk RNA-seq and immunofluorescence. Changes from LPD IUGR persist with delayed postnatal growth of skin, hair, body, and kidneys. P21 and adult IUGR show damage to kidneys and increased risk of developing hypertension, and CDK. IUGR LPD is the first hit in the multi-hit disease causation of CDK. The P0 NPCs had dysregulated metabolism and chromatin; postnatal development continues to be dysregulated despite removal of LPD environment. The LPD IUGR model produces a new tool for the study of multi-hit kidney disease.

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# **Chapter 1: Introduction**

# **1.1 Kidney Development:**

Mammalian kidney development is novel in organogenesis by forming three successive structures (pronephros, mesonephros, and metanephros) with each successive stage representing a more complex organ over the course of development. The tissue of origin for each of these structures is the intermediate mesoderm (IM), a germ layer between the paraxial and lateral plate mesoderm. The IM will give rise to the entire urogenital system including the kidneys, gonads, their respective duct systems, and the adrenal cortex (Kastu 2012, Barak 2005, Fluming 2013) [Figure 1]. The IM forms from patterning along the anterior-posterior axis of the embryo with





A) Following gastrulation into the germ layers ectoderm, mesoderm, and endoderm there are successive differentiations into increasingly differentiated stem cells and progenitors. The mesoderm will form into the paraxial, intermediate, and lateral mesoderm. B) The intermediate mesoderm forms between the somatic and paraxial mesoderm in early development regulated by patterned signaling of VG1/Nodal into BMPs. (Edgar, R., Mazor, Y., Rinon, A., Blumenthal, J., Golan, Y., Buzhor, E., Livnat, I., Ben-Ari, S., Lieder, I., Shitrit, A., Gilboa, Y., Ben-Yehudah, A., Edri, O., Shraga, N., Bogoch, Y., Leshansky, L., Aharoni, S., West, M. D., Warshawsky, D., & Shtrichman, R., 2013).

distinct mesoderm types from Vg1/Nodal signaling maintaining dorsal/anterior identity and BMPs promoting ventral/posterior identity. The IM is marked first by the presence of Osr1, which is also present in the lateral plate

D

anterior to the IM, and later by Pax2, Pax8, and Lhx1 (Katsu, K., Tokumori, D., Tatsumi, N.,

Suzuki, A., & Yokouchi, Y., 2012, Barak, H., Rosenfelder, L., Schultheiss, T. M., & Reshef, R., 2005, Fleming, B. M., Yelin, R., James, R. G., & Schultheiss, T. M., 2013) [Figure 1]. The IM will be further divided along the dorsal-ventral axis before kidney development begins. The

dorsal IM experiences increasing restriction in differential potential and forms the nephric duct while the ventral IM remains as undifferentiated mesenchyme of the nephric duct cord. A rostral to caudal wave of signal derived from the nephric duct induces the primitive renal tubules which will later form the pronephros and mesonephros. This represents a loss of differentiation potential in the rostral IM. [Figure 2] At the same time the caudal nephric duct cord forms a bean shaped and undifferentiated IM (Kopan, Chen, & Little 2014, Takasute, M., Little, M.H. 2015). [Figure 2 & Figure 3B]

In amphibian and zebrafish, the functional pronephros forms one single nephron that will filter and drain into the cloaca. The pronephros is not functional in mammals. In vertebrates the nonfunctional pronephros atrophies during development after the mesonephros has formed (Figure 2A & B).

The mesonephros forms on embryonic day 9.0 in mice and week 4 in humans. It branches from the nephric duct into a series of tubules that are induced by the lengthening of the nephric duct towards the tail. The nephric duct, formed from the intermediate mesoderm, connects the pronephros, the mesonephros, and the metanephros kidney to the cloaca. The formation of tubules involves the epithelization of the intermediate mesenchyme (Vize, Seufert, Carroll, Wallingford, 1997, Obara-Ishihara, Kuhlman, Niswander, & Herzlinger, 1999, Vainio, Lehtonen, Jalkanen, Bernfield, & Saxen, 1989, Kispert, Vainio, & McMahon, 1989). The mesonephros functions as a filter during early development. It contains structures similar to the nephrons of the metanephric kidney in the series of tubules off the nephric duct. A glomerulus forms with a bowman's capsule around capillaries off the aorta which is attached to the mesonephric duct that leads back to the posterior cardinal vein and drains into the nephric duct and then to the cloaca

(Zhou, Boucher, Bollig, Englert, & Hildebrandt, 2010, Vainio, Lehtonen, Jalkanen, Bernfield, & Saxen, 1989, Ganesh 2017) (Figure 2A & B).

The metanephros will form the adult mammalian kidney. The mammalian kidney is formed from 3 progenitor cell lineages: the ureteric branching cells of intermediate mesenchyme







A) Figure from Banks 1955 showing the development of the nephric system in vertebrate organogenesis. PR: pronephric duct., ND: nephric duct, NGC: nephrogenic cord, G: gonad, MES: mesonephric units, MET: metanephros, UR: ureter, CL: cloaca. B) The ureteric bud grows from the nephritic duct, both shown in yellow, into the metanephric mesenchyme cells, shown in light blue, at embryonic day 10. The UB cells signal the condensing of metanephric mesenchyme into the cap mesenchymes of nephron progenitor cells, shown in dark blue. At e11.5 two cap mesenchymes will be present at the end of the ureteric branches with two caps at the end of a t-shaped UB. Adapted from Banks 1955, Li 2014, and Dressler 2009.

bud (UB) into the metanephric mesenchyme on embryonic day 10 of the mouse and in week 5 of human development. Kidney development ends in week 34 of human gestation and postnatal day 3 or 4 in the mouse. Thus, human kidney development is fully completed during gestation while mouse kidney development continues postnatally.

The metanephros begins to form at e10 in mice, week 5 in human gestation, with the secretion of GDNF and FGF10 from the MM towards the nephric duct activating receptor tyrosine kinases (RTKs). RTK activation in the nephric duct creates a single UB that migrates

and invades the bean shaped MM. The MM at this point already contains the progenitor cell populations that form all epithelial and stroma tissues and some of the vascular components of



# **Figure 3: Sequential Ureteric Branching**

A) The UB branches sequentially spliting the cap mesenchymes and growing the embryonic kidney. At e11.5 there is a single T shaped UB with two cap mesenchymes. As development progresses the UB branches further forming more cap mesenchymes made up of nephron progenitor cells and expanding the embryonic kidney. B) Crosstalk between the ureteric bud, the cap mesenchyme, and the stroma. The ureteric bud signals for cap maintenance and differentiation. From Short, K. M., & Smyth, I. M. (2016). C) Cross talk and staining of the cap mesenchyme (Sall1), UB (Ecad), CSB (Sall1), SSB (Sall1), differentiating structures. C) Crosstalk maintains the cap mesenchyme, UBTCs, and supports/signals differentiation of the pre-tubular aggregare (PA), the renal vesicly, the comma shaped body (CS), and the S-shaped body (SSB). Marked by NCAM, Sall1 (CM, CS, RV, SSB).

the developed kidney (Kopan, Chen, & Little 2014). Angioblasts form from the mesoderm germ layer and migrate based on angiogenic signals for proliferation, differentiate into endothelial cells, and develop into blood vessels (Gomez, Norwood, Tufro-McReddie, 1997). Angioblasts are endothelial precursors and guided by angiogenic signals. The angiogenic signals for angioblasts are growth factors and cytokines including VEGF, TNF- $\alpha$ , FGF, TGF- $\beta$ , FGF-2, and PDGF. Angiogenesis is directed by intrinsic and extrinsic factors of the vascular precursor cells and the tissue progenitor cells the vascularization is occurring in. The tissue specific factors include the extra-cellular matrix and its

receptors (Ucuzian, A.A., Gassma, A.A., East, A.T., Greisler, H.P. 2010). The UB will give rise

to the collecting ducts of the developed kidneys. MM cells condense to form cap mesenchymes

(CMs) of NPCs with the interstitial stroma cells above and beside CMs. The CMs surround the UB whose branches are led by UB tip cells.

The UB outgrowth from the nephric duct at e10.5, invades the adjacent MM (Figure 2B). Reciprocal induction is the two-way signaling between neighboring cell types. The epithelialmesenchymal interaction during kidney development is a form of reciprocal induction between tissue types. The UB is an epithelial sheet of polarized cells which will interact with the nonpolarized MM that formed from the nephric cord. The loss of the MM will stop UB branching in an embryonic kidney and UB mutants for induction signals will have arrested differentiation of the MM into epithelial and not form functional structures. The two tissues rely on signals from each other to continue development (Berk, Zipursky, et. al. 2000). Reiterative branching of the UB with differentiation of NPCs expands the kidney and forms the major and minor calves in the UB through e13.5. After this the ureteric branches elongate and form collecting ducts. The elongated ureteric branches produce the medulla at the core of the kidney with the cortex at the periphery filled with the nephrogenic zone made up of UB tips, CM, and the differentiating nascent nephrons, and comma-shaped and s-shaped bodies (CSB and SSB). The normal mouse UB will go through 11 cycles of branching and elongations with branching ending between birth and postnatal day 3 or 4 (Kopan & Costantini 2010, Hartman, Lai, & Patterson 2007) [Figure 3A &B]. Defects in branching can cause fewer cap mesenchymes and smaller kidneys (Carroll & Das 2013, Dressler 2009, Kopan & Costantini 2010).

Lindström et. al. 2018 demonstrated the temporal role in Six2<sup>+</sup> NPCs as they are recruited into epithelializing in the renal vesicle (RV). Three-dimensional imaging of NPCs in the human CM showed gradients to the expression of NPC markers decreasing along the proximal to distal axis. NPC markers decrease and do not switch off with differentiation. NPCs initiating pre

tubular aggregate formation were directly adjacent to the UB and under the branch tip. NPCs are recruited after a PTA or RV has been established by the first recruits and incorporated into the proximal end of the PTA or RV. Single-cell transcriptome analysis combined with prediction modeling and immunostaining showed that the NPCs that are at the top of the CM are progenitors renewing the NPC pool. A distinct population will be primed to differentiate while remaining mesenchymal. Further along the proximal to distal axis will be the induced cells. The induced cells have been epigenetically reprogrammed and await recruitment into the PTA or RV by those first NPCs. Lindström et. al. adds that the timing of this recruitment determines final cell fate. The final nephron will have 14 distinct cell types and the epithelialized PTA, RV, and SSB already show distinct cell populations with differing cell fates. The first NPC recruits will form the distal precursors and are positive for low Jag1 and low Sox9. These first recruits will connect to the UB and split further into the distal tubule precursors and loop of Henle precursors. The second NPC recruits will be proximal precursors and will not be anchored to the UB instead connecting to the proximal precursors and show no Sox9 expression with high Jag1. The third recruits will be added to the RV and become precursors for the Renal Corpuscle. A proposed source of the expression pattern along the RV and SSB is localized Wnt9b secreted from the UB (Lindström, O., Brandine, G.D., Tran, T., Ransick, A., Suh, G., Guo, J., Kim, A.D., Parvez, R. K., Ruffins, S.W., Rutledge, E. A., Thornton, M. E., Grubbs, B., McMahon, J.A., Smith, A. D., & McMahon, A.P., 2018) (Figure 3B).

The distal part of the polarized RV grows and attaches to the epithelial UB to form CSBs and SSBs (Figure 3B). The proximal, intermediate, and distal sections compose the segmented SSB. SSBs will continue to differentiate and form nephrons, the adult filtering unit of the kidney which contains the glomerulus, the proximal tubule, the loop of Henle, and the distal tubule

which will connect to the collecting duct formed from the UB. The result is the highly specialized structures of the adult kidney.

The glomerulus is dense in capillaries and filters water and solutes out of the blood. The proximal tubule has high surface area to reabsorb and retain necessary substances such as salt, water, glucose, amino acids, potassium, urea, phosphate, and citrate. The proximal tubule also functions in secreting small molecules/drugs and ammonium. The loop of Henle has tightly controlled variation in osmolality, so the descending loop will secrete water and concentrate urea, while the ascending loop of Henle secretes sodium and chloride. This creates concentrated urea and retains water and electrolytes in the body. The distal tubule contains specialized cells to regulate potassium, sodium, calcium and pH in the body and the secreted urea (Carroll & Das 2013, Dressler 2009, Mugford, Spile, McMahon, & McMahon 2008). The function of the adult kidney relies on the proper formation of all these structures in sufficient numbers to allow efficient secretion of waste and the reabsorption of water and solutes as needed.

In both humans and mice nephron formation relies on controlled, induced differentiation of the NPCs to form RVs repeatedly over nephrogenesis while maintaining the NPCs for the entire length of nephrogenesis. The NPC population is maintained by cell survival and proliferation signals. Autonomous cell survival (BMP7, FGF9 and FGF20) and proliferation (Six2, Sall1, Mdm2) along with maintenance signals from the UB (Wnt9b) and survival signals from the UB (FGF2/9) act to maintain the NPC population that makes up the CM (Carroll & Das 2013). Cultured NPCs show decreasing levels of FGF expression over passages with the highest level in freshly isolated NPCs. Introduction of exogenous FGF supported NPC proliferation and stemness (Brown 2011). Wt1 is a regulator of the maintenance signal FGF, the survival signal BMP, and the BMP and MAPK/ERK related signal p-Smad which all regulate NPCs. Motamedi

2014 showed Wt1 as a regulator of FGF, BMP, and p-Smad in kidney development. Chromatin Immunoprecipitation combined with DNA sequencing (ChipSeq) analysis shows the presence of Wt1 binding sites associated with metanephric mesenchyme and kidney development. The Wt1 mutant had no change in Six2, but BMP, FGF, p-Smad, and Wnt/β-catenin were all dysregulated. Supplementing with BMPs and FGFs rescued the Wt1 mutants. Metanephric mesenchyme survival comes partly from a balance of Wt1, BMP/SMAD, and FGF signaling (Motamedi, F. J., Badro, D. A., Clarkson, M., Rita Lecca, M., Bradford, S. T., Buske, F. A., Saar, K., Hübner, N., Brändli, A. W., & Schedl, A., 2014) [Figure 3B & Figure 4].

# 1.2 Intermediary metabolism and cell fate decisions:

Glucose when metabolized in the cell can be processed by multiple metabolic pathways depending upon conditions and needs of the cell. Glycolysis is the cytosolic conversion of glucose into lactate via phosphorylation and kinase reactions generating metabolites that are participants or substrates of lipid synthesis, amino acid synthesis via serine, and netting 2 pyruvates, 2 NADH, and 2 ATPs. The second stage of glycolysis involving glucose-6-P either continues through glycolysis or into the pentose phosphate pathway and produces instead NADPH, pentose, and 5-Ribose-phosphate. 5-Ribose-phosphate is a precursor for nucleotide synthesis. Or, just before the conversion to lactate the pyruvate from glycolysis can feed into mitochondrial oxidation producing 6 NADH+, 2 FADH<sub>2</sub>, 4CO<sub>2</sub>, and 2 ATP per Acetyl CoAs (Hamanaka & Chandel 2012). Acetyl CoA made from long chain fatty acids produces mitochondrial oxidation producing the same products in addition to triglycerides, phospholipids, hormones, and ketones (Morino, Peterson, & Shulman 2006). These are major energy pathways of the cell. The hexosamine biosynthetic pathway (HBP) accounts for 2-5% of glucose

metabolism. HBP controls posttranslational modifications of proteins by glycosylation. Most of these reactions occur in the golgi apparatus and produce N and O linked glycosylated proteins.

Glycosylation is part of cell packaging to direct activity, stability, and subcellular localization of proteins (Fardini, Dehennaut, Lefebvre, & Issad 2013 & Fantus, Goldberg, Whiteside, &Topic 2006).

The amino sugar  $\alpha$ -linked N-acetylgalactosamine, derived from galactose, is a membrane bound substance along the distal tubules of the kidney. Glycosylation is the enzymatic addition



# Figure 4: Interaction of Glycolysis with NPC Renewal and differentiation Pathways

A) NPC cell responding to exogenous signals with glycolysis as an intermediary between MAPK, PI3K/AKT, cMyc, and mTOR1, and the Self-Renewal of NPCs and the inhibition of differentiation signaling. It is when glycolysis is low that differentiation signals are strengthened, and self-renewal signals weakened. B) Glycolysis is not essential for selfrenewal, but its removal primes NPCs for differentiation rather than self-renewal and maintenance. Liu, J., Edgington-Giordano, F., Dugas, C., Abrams, A., Katakam, P., Satou, R., & Saifudeen, Z. (2017).

of oligosaccharides to proteins forming glycoproteins. A-linked Nacetylgalactosamine is a mucin; a highly glycosylated protein that forms physical barriers in epithelial cells lining tubes or body cavities in animal bodies. Mucins are made of  $\alpha$ -linked N-acetylgalactosamine linked to a serine or threonine residue. The sugars galactose, N-acetylgalactosamine, fucose, or sialic acid extend the mucin chain structures. The enzymes that produce  $\alpha$ -linked Nacetylgalactosamine are involved in mammalian disease, physiology, and development. The hydrophilic O-glycans are usually negatively charged allowing them to bind water and salts. Polysialylation used to

extend the DBA recognized α-linked N-acetylgalactosamine is also present in neural cell adhesion molecule (NCAM) when present in the basolateral membrane bound NCAM in the nascent nephron. Lackie, Zuber, and Roth's 1990 development paper showed differences in NCAM when staining mesenchyme and epithelial structures of the rat kidney. E13 immunostaining showed strong PSA staining of the UB and the condensed MM. E14 showed PSA and NCAM present in both the MM and CSB. The PSA staining was stronger and concentrated at the membrane rather than diffuse through the cell as in the MM at e13 and 14. E18 staining for PSA showed intense PSA staining in multiple CSBs and SSBs except for the lower part of SSBs that give rise to podocytes in the developed kidney. NCAM epithelial staining in the embryonic rat kidney co-stained with polysialic acid in the basolateral membrane. It was noted by Roth e. al. that the PSA staining localized where cell to cell adhesion changed during kidney nephrogenesis. PSA, cell-to-cell adhesion, and NCAM are known to work in concert in neural development (Galuska, Lütteke, & Galuska 2017).

During the roughly twelve embryonic days in mice and 29 weeks in humans of kidney development, the embryonic environment is in constant contact with the maternal environment. Maternal food source determines nutrient availability and thus cell metabolism. This does not just mean caloric restriction as shown by famine studies, but also micronutrients epitomized by the developmental importance of folic acid. Cell fuel sources change cell behavior and character in adult tissue and have staggering impacts on developing tissues. Cancer research shines a light on the likely mechanisms. The Warburg effect theorizes cancer cells not just dependent on ATP production, but also the utilization of all metabolic products. High glycolysis means excess carbon for producing nucleotides, lipids, and proteins to increase biosynthesis, and NADPH as a reducing agent in proliferating cells. Both cancer cells and developing organs exist in a

microenvironment. Tumors find themselves in environments with little oxygen and abundant glucose and must efficiently use the resources they have while competing with other cells (Liberti & Locasale 2017). Metabolism usage changes during development. Zhang et. al. 2014 showed human embryonic stem cells (hESCs) have a unique energy phenotype to adult stem cells. hESCs had higher uncoupled oxygen consumption. hESCs were reliant on glutamine to proliferate in culture, but when partly differentiated the cells lost that reliance and had decreased glutamine metabolism. Chen 2009 showed variation in mitochondria number and function as human mesenchymal stem cells (hMSCs) differentiated. Undifferentiated hMSCs were reliant on glycolytic enzymes and lactate production while the differentiated osteogenic cells had increased mitochondria copy number and increased oxygen consumption showing a shift from glycolysis to oxidative phosphorylation with differentiation.

NPCs rely on glycolysis to renew and maintain the progenitor pool, decreased glycolysis primes NPCs to respond to differentiation signals (Liu, J., Edgington-Giordano, F, Dugas, C., Abrams, A., Katakam, P., Satou, R., & Saifudeen Z., 2017). The balance between maintaining the cap mesenchyme and differentiating into nephrons during development has an internal clock as shown by the Kopan NPC transplant studies (Figure 4). In Chen 2015 a mixture of old (P0/P1) and young (e12.5) NPCs transplanted into young e12.5 niches and cultured for 4 days exited the young CM at different rates. The majority of old NPCs injected exited the young niche while less than 30% of the injected young NPCs exited. This shows that there are intrinsic differences between young and old NPCs that direct cells to self-renewal or differentiation despite new environmental signals. But the extrinsic signals of a young niche did change old cells as shown by the persistence of some old NPCs in young niches. P0/P1 cells following only their internal clock would mass differentiate after a few days at their P3. The presence of old NPCs after their

clock would have run out suggests microenvironment plays a role in NPC fate and can overcome intrinsic cell programing. Old NPCs were more likely to remain in the young niche when associated with young NPCs and had differences in cell-to-cell adhesion. FGF20 co-injection increased the old NPCs that engrafted and remained in the young niche. The signals of the young niche are not a fountain of youth as Kopan showed using single cell RNA-seq that the transcription profiles of NPCs change over development and old Cited1+ NPCs are intrinsically closer to differentiate than young NPCs.

The NPCs have a histone landscape unique from differentiated nascent nephron and further unique histone modification in the epithelial tubules. McLaughlin 2014 showed changes to the histone landscape with differentiation from the CM. Proper histone modification is essential for nephrogenesis as deletion of HDAC 1 and 2 in the NPC population arrests nephrogenesis. HDAC 1 and 2 interact with the NPC regulators Six2, Osr1, and Sall1. HDAC1 and 2 regulate proliferation, differentiation, and p53. Direct interaction between chromatin remodeling molecules and regulators of NPC differentiation shows an entwined relationship between epigenetics and kidney organogenesis. As cells differentiate, they have increased deactivation of parts of their genome through chromatin remodeling. The less differentiated a cell the more of its genome that remains open, with differentiation there is a loss of possibilities in cell fate and a loss in genes available for transcription via chromatin remodeling. This is not a byproduct of differentiation though, it is a part of differentiation as agents of chromatin remodeling are essential in kidney progenitor cell fate (McLaughlin, N., Wang, F., Saifudeen, Z., & El-Dahr, S.S. 2014, Liu, H., Chen, S., Yao, X., Li, Y., Chen, C., Liu, J., Saifudeen, Z., & El-Dahr, S.S. 2018).

Studies in cancer and development have shown that cell behavior is tied to cellular metabolism and their histone landscape. Liu 2017 and Yu 2018 show that changes to cellular metabolism changes cell behavior in kidney development and cancer, respectively. Yu 2018 showed metabolic plasticity of cancer cells allows them to respond to the changing microenvironment by histone modifications that regulate expression of genes involved in proliferation and survival.

De novo nephrogenesis only occurs in utero in humans and up to post-natal day 4 in mice. This is at week 34 of human gestation and P3/4 in mice. Mice have a nephron endowment between 11,000 to 20,000 while humans are from 200,000 to over 2 million with most people having 1 million nephrons at birth. Diminished nephron endowment can be caused by inability to maintain NPCs, inability to differentiate NPCs, and failure to deplete the pool of NPCs at the end of nephrogenesis. As nephrons cannot be regenerated, nephron endowment is set at birth and will only decrease over an organism's lifespan (Keller, Zimmer, Mall, Ritz, & Amann, 2003, Yuan, Tipping, Li, Long, & Woolf, 2002).

# **1.3 Intrauterine Growth Restriction:**

The World Health Organization (WHO) historically defined fetal Intrauterine Growth Restriction (IUGR) as full-term newborns in the 10<sup>th</sup> percentile of birth weight. WHO abandoned the 10<sup>th</sup> percentile definition for a set weight based on clinical significance as the 10<sup>th</sup> percentile body weight in newborns varies over time and between countries. The CDC reports the current 10<sup>th</sup> percentile body weight of full-term newborns in the United States as 6 lbs., 2 oz. for boys and 6 lbs., 1.2 oz for girls with 8.07% rate of IUGR for all full-term newborns (CDC National Center for Health Statistics and WHO Growth Standards). Worldwide WHO reports IUGR at a rate of 14.6% but that ranges from 2.4% IUGR in Sweden to 27.8% in Bangladesh (UNICEF, Low Birthweight).

The risk factors for IUGR include external environmental conditions (elevation and water quality), placental insufficiency (decreased nutrient absorption by the placenta), maternal health (diabetes, eclampsia, drug addiction), multiple pregnancies (twins etc.), maternal infections (CMV, rubella), and maternal diet including micro and macro-malnutrition (UNICEF, Low Birthweight, CDC, National Center for Health Statistics Statistics). The variety and increasing rate of risk factors for IUGR is a serious public health concern in both the developing and developed world with the same adult health outcomes regardless of gestational cause. Adult

Control Diet		6% Protein Diet			
Ingredient	(g/Kg)		Ingredient	(g/Kg)	
Casein	230	)	Casein	69	
DL-Methionine	3	3	DL-Methionine	0.9	
Sucrose	431.7	,	Sucrose	571.8	3
Corn Starch	200	)	Corn Starch	200	)
Corn Oil	52.3	3	Corn Oil	53.9	
Cellulose	37.86	5	Cellulose	57.82	
Vitamine Mix, Teklad 40060	10	)	Vitamine Mix, Teklad 40060	10	)
Ethoxyquin, antioxidant	0.01	L	Ethoxyquin, antioxidant	0.01	L
Mineral Mix	13.37	7	Mineral Mix	13.37	,
Calcium Phosphate dibasic	16.66	5	Calcium Phosphate dibasic	21.6	5
Calcium Carbonate	5.1	L	Calcium Carbonate	1.6	5
	% by Weight	% kCal From		% by Weight	% kCal From
Protein	20.3	21.6	Protein	6.1	6.5
Carbohydrate	61.6	65.4	Carbohydrate	75.6	80.4
Fat	5.5	13	Fat	5.5	13.1
Kcal/g	3.8	3	Kcal/g	3.8	3

# Figure 5: Diet Comparison for inducing IUGR:

Ingredients for control and 6% protein diet from Envigo diets. Envigo control diet with 20% protein by weight is Envigo 91352 and Envigo with 6% protein by weight is Envigo 90016. Bolded shows the differences between control and experimental diets. Casein is the protein source, sucrose and cellulose are carbohydrate sources used to maintain equal kilocalories per gram of food, calcium phosphate dibasic and calcium carbonate have changed to account for casein changes. The result is a isocaloric diet that has lower protein by weight and kilocalorie, more carbohydrates, and equal fat content.

health outcomes of IUGR offspring include increased rates of obesity, insulin resistance, hypertension, and chronic kidney disease. IUGR models have been done in sheep, pig, guinea pig, monkey, rat, and mouse using multiple methods including maternal diabetes, glucocorticoid

treatments, hypoxia via a chamber or surgery, umbilical artery ligation, uteroplacental

embolization, caruncletomy, bilateral uterine ligation, and macro or micro nutrient deficiency

related to iron, protein, or caloric intake. An iso-caloric low protein maternal diet is an

established model for IUGR in research animals including mice (Sharma, Shastri, Sharma, 2016, Alexandra-Gouabau, Courant, Le Gall, Moyon, Darmaur, Parnet, Coupé, Antignac, 2013).

Previous studies have linked maternal diet and IUGR through amino acid deficiency. Bhasin 2009 used protein restriction to 9% and hypercholesterolemia maternal diets to produce IUGR and found altered maternal plasma amino acid levels. Maternal plasma had reduced levels of phenylalanine, leucine, isoleucine, and valine and increased maternal lysine in the reduced protein model. Jansson 1998 found reduced transport of leucine and lysine across the placenta in human cases of IUGR by studying donated placentas. Intervention studies for IUGR include amino acid supplementation (Jansson, T., Scholtbach, V., & Powell, T.L. 1998, Brown, L. D., Green, A.S., Limesant, S.W., & Rozance, P.J., 2011, Bhasin, K.K.S., Nas, A.V., Martin, L.J., Davis, R.C., Devaskar, S.U., & Lusis, A.J. 2009). The studies took place in human trials before properly characterizing the sharing of nutrients with the developing fetus. Amino acids are actively transported across the placenta from circulation in the maternal plasma. Transport of amino acids relied on relative concentration in maternal plasma and fetus and in the presence and operation of transporters that are specialized based on amino acid structure. The fetus then uses amino acid shuttles reliant on serine and glutamine to retrieve and release the amino acids into circulation. The complex pathways and relationships that result in net transfer of amino acids into the fetus make the pure supplementation with protein an ineffective intervention in IUGR. The result from protein supplementation in pregnancies at high risk for IUGR were then high risk with variable results (Brown, L. D., Green, A.S., Limesant, S.W., & Rozance, P.J., 2011). Amino acids are the building block of proteins and regulate several cell functions including cell signaling, RNA and DNA synthesis, metabolism, stress response, growth, and development. Leucine specifically activates the mTOR pathway known to be related to kidney development,

via regulation of metabolism, proliferation, and growth, and adult kidney injury. Cerqueira et. al. (2019) showed in utero exposure to maternal diabetes impairs nephron progenitor differentiation. Maternal diabetes is a known risk factor for IUGR and nephron deficit in humans. The wildtype offspring of diabetic mice from the  $Ins2^{+/C96Y}$  mice had no decrease in birth weight but did have impaired kidney development, with a 20% decrease in nephron formation and increased expression of NPC markers Six2 and Cited1 at P2. The inefficient formation of structurally normal glomeruli occurred with decreased Notch and decreased phosphorylated- $\beta$ -catenin. Notch and Wnt/ $\beta$ -catenin signaling pathways are integral to the differentiation of NPCs. The Wnt differentiation signals from the UB changes stroma, MM, and UB as cross talk between these tissues act to maintain and differentiate these cells during development. Wnt and Notch signals prime NPCs for differentiation by decreasing Six2 expression. A loss of Wnt and Notch would leave Six2 unrepressed and maintain NPC Six2 levels and stemness, stopping differentiation and glomeruli formation. This study further supports the importance of studying maternal environment in kidney development.

# **1.4 Significance:**

Dr. David Barker's hypothesis on the developmental origins of health and disease links low-birth weight directly with adult chronic health conditions connecting nutrition during development with adult health including hypertension and chronic kidney disease (Hales, C.N., Barker, D.J., 1992). The CDC reports that 1 in 3 Americans have hypertension and over 1,100 die each day from complications of hypertension such as heart disease and stroke. Impaired filtration from damage or injury over a period of time results in Chronic kidney disease (CKD), affecting approximately 12-14% of the United States. Treatments for CKD include lifestyle changes and pharmaceuticals to prevent further damage, and for severe cases dialysis and kidney

replacement. The projected number of patients receiving dialysis and kidney transplants are expected to double from 2010 to 2030 (American Kidney Fund, 2019, Calkins, Devasker 2011, "The Impact of Kidney Development on the Life Course: A Consensus Document for Action," 2017).

The Dutch famine cohort follows adults that were gestated during WWII where urban daily rations at times fell below 1000 calories. The cohort consists of adults that gestated on low calories at the beginning, middle, end, or for the entirety of pregnancy. This adult population has increased rates of obesity and coronary heart disease when compared to adults born just before or after the famine. The famine cohort had similar life experiences to the control cohort showing a link between caloric intake during gestation and adult health, specifically related to the kidney. Systolic blood pressure was found to increase with the lower birth weight in the famine cohort (Painter, Roseboom, Bleker 2005, Stein, Zybert, Van der Pal-de Bruin, Lumey, 2006).

Moreover, epidemiological studies in humans and ablation of nephron progenitor cells in mice have shown that kidneys of equal size but lower nephron endowment result in hypertensive organisms and chronic kidney disease in adulthood (Cebrian, C., Asai, N., D'Agati, V., & Costantini, F., 2014). Low nephron endowment at the end of kidney development causes hypertension and chronic kidney disease in adults and the maternal and gestational environments drive nephron endowment. The direct link between gestational conditions, nephron endowment, and adult health shows the importance of studying the kidney in IUGR (Cebrian, Asai, D'Agati, Costantini 2014, Wood-Bradley, Barrand, Giot, Armitage 2015). We hypothesized that disruption of metabolic homeostasis in the nephron progenitor cells in the IUGR fetus impairs nephrogenesis and is the direct link between the maternal environment and nephron endowment leading to adult hypertension and Chronic Kidney Disease.

# **Chapter 2 Materials and Methods**

# 2.1 Mouse Model and Breeding:

Iso-caloric protein restriction to induce intrauterine growth restriction. The protein restricted experimental diet was the Envigo TD 90016 diet that is as percent of weight 6.1% protein, 75.6% carbohydrate, 5.5% fat and 3.8 Kcal/g. The control diet is Envigo TD 91352 that is as percent of weight 20.3% protein, 61.6% carbohydrate, 5.5% fat and 3.8 Kcal/g. The only differences between the two diets are the amount of protein, and the 6% protein diet having more sucrose and cellulose to maintain an iso-caloric formula (Figure 5).

CD1 female mice and SixCreGFP wildtype male mice from a mixed CD1 and C57BL/6J background were used. Male and female mice were put on diet for 3 weeks starting at 6 weeks of age before pairing and diets were continued during all pairing and pregnancy. Timed pregnancies are defined as female mice being paired with male mice overnight where the next day is counted as E0.5. Postnatal day zero (P0) is the day mice are born. Time points after P0 must account for litter size and breastmilk quality. Female mice have 10 nipples for feeding so all growing litters were 10 pups or smaller, in cases of larger litters pups were sacrificed at P0. This controls for postnatal food access. Protein restriction had a noticeable effect on maternal weight gain with the mice remaining slimmer, showing that maternal growth was changed and thus breastmilk quality could be impacted. To account for this, pups from 6% maternal diet grown past P0 were fostered with a CD1 female mouse that had given birth the same day from either the 20% diet population or from normal vivarium diet of 21% protein. Both IUGR and control would have equal access to milk and similar milk quality postnatally.

Six2Cre GFP males are heterozygous for Cre and the Six2+ NPCs have green fluorescent protein. The NPCs have no developmental changes with the presence of GFP. GFP cells can be sorted for using Fluorescence-Activated Cell Sorting (FACS).

The historical definition of IUGR in humans was term infants at the 10<sup>th</sup> percentile of body weight. Based on this inclusion/exclusion criteria were developed. A 6% maternal diet does not consistently create IUGR mice and IUGR by definition can occur with a normal maternal diet. All mouse pups were weighed at birth and the 10<sup>th</sup> percentile for control mice was calculated to be 1.42g. This became the threshold for inclusion and exclusion of samples. Control mice below 1.42g were not considered control and to be considered IUGR pups from the 6% maternal protein diet had to be below 1.42g.

# 2.2 IUGR Characterization:

All mouse pups were weighed at birth for inclusion/exclusion. Kidney weight from harvested P0 kidneys was measured after removal of ureter and capsule for combined kidney weight. Growth curves for P21 samples were done by daily measurement of body weight until sacrificing. Blood sugar from mice was measured using a Freestyle blood sugar meter and Freestyle test strips. P0 blood came from post decapitation pool and P21 blood sugars came from tail snips. At P21 mice were weighed and kidneys harvested with capsule and ureter removed for combined kidney weight at P21. Animals kept for blood pressure measurements were weighed daily from P0 to P30 with weekly measurements after P30.

# 2.3 Immunohistochemistry:

Paraffin embedded kidneys were sectioned at 5  $\mu$ M. Paraffin was removed with xylene and sections were rehydrated using alcohol. Antigen Unmasking with acidic sodium citrate followed by quenching in H<sub>2</sub>O<sub>2</sub> (10% solution in TBS). Blocking Buffer for 1 hour at Room Temperature with environmental moisture (TNB (0.5% blocking reagent in TBS) + 10% Normal Donkey Serum + 15µl/ml donkey anti Rabbit Fab anti Mouse Fab).

Primary Antibody mixture is made in Antibody Buffer (TNB (0.5% Blocking Reagent in TBS) + 2% Normal Donkey Serum). Incubated on sections for 1 hour at room temperature or overnight at 4C.

Secondary Antibody at 1:400 with Hoechst nuclear stain at 1:800 in antibody buffer. Lectins are added with secondary antibodies. They are incubated at Room Temperature for 90 minutes.

Samples are then washed and mounted. TBS Washes are used between steps and before mounting. Six2(R) 11562-1-AP 1:200. Mesi1/2 (R) 12744S 1:200+TSA 2 minutes. Mesi1/2/3 (m) MBS605057 1:200+TSA 2 minutes. Sox9 (R) 82630 1:200. Aquaporin 1 (R) 243-261 1:200. Pancytokeratin (m) 1:400. Lhx1 (m) 4F2 1:100. Cleaved PARP (R) 1:200 +TSA 3 minutes. BrdU (m) sc-32323 1:200. E-cadherin (R) ab40772. Sall1 (R) MBS9203689 1:200. P-ATF2 (R) 24329S 1:200. LTA FL-1321 1:400. DBA B-1035 1:400. NCAM (m) C9672 1:400. Calbindin (R) ab108404 1:400. WT1 (R) 1:400.

# 2.4 Count Data for BrdU Proliferation and PARP Apoptosis:

BrdU is suspended in PBS at a concentration of 10 mg/mL and injected at a dose of 100 mg/kg based on pup weight. Each pup was weighed, injected, and incubated for 3 hours before being sacrificed. The kidneys were fixed with 10% formalin, embedded, and then sectioned at 5 µM for immunohistochemistry. The BrdU mouse antibody thermoFischer B35128 was used at 1:100 with markers for tissues of interest. The immunostaining was imaged at 40X with equal exposure times. All tissue sections were sagittal plane and deep within the kidney showing cortex and ureteric branching to control for part of the CMs and UB tips being counted. CMs and UB tips counted contained a ureteric branch that showed NPCs forming CM on both branches. The staining for Six2, Sall1, and Calbindin was done in consecutive sections Counting was done in NIS Elements 4.5.0. Regions of Interest (ROIs) were selected based on the co-staining and then overlaid on the BrdU channel. The BrdU is then counted by MCH thresholding to create and object count and object catalog. The object catalog is images of each BrdU positive stain. The object catalog was used to check that positive stains have not merged with multiple cells being counted as a single object. The final count for BrdU includes objects manually counted from the object catalog.

PARP counts used the same method with NIS elements. The PARP positive cells were a rare event and object catalog did have merged cells decreasing the count by NIS Elements.

# 2.5 Magnetic Activated Cell Sorting:

Mice are dissected, and kidneys are isolated with capsule and ureter removed then washed in HBSS. Damaged kidneys are not used. Kidneys are incubated in digestion mixture (Accutase or PBS + Collagenase and Pancreatin) rotating in an incubator at 37C. Digestion is stopped using fetal bovine serum and DNase mixture then incubated for 5 minutes rotating at 37C. Cell suspension is removed and washed using isolation buffer of PBS and bovine serum albumin. Cell suspension is filtered through a Miltinenyl Biotec 30 µM filter. Cells are incubated with PE conjugated primary antibodies: CD105 for endothelial cells, CD140 Foxd1+ stroma cells, CD119 for RBCs and erythroblasts, and CD326 for epithelialized/differentiated cells for 13 minutes on ice. After washing the cells with isolation buffer, the cell suspension is incubated for 18 minutes on ice with Anti-PE beads. After further washing the cell suspension is run through a Miltinenyl Biotec LD column that will collect all cell populations bound to the Anti-PE beads leaving the unbound nephron progenitor cells to flow through the column and isolating them via negative selection. The NPCs are Cited1/Six2 dual positive.

# 2.6 Fluorescence-Activated Cell Sorting:

Cell suspension is isolated and digested as described in MACS. After filtration, the cell suspension is sorted for GFP+ using a Beckton Dickerson FACS Aria Fusion and the FACS DiVa software v8.02. The isolated population will be Six2+ NPCs.

# 2.7 RNA-Seq:

NPCs of mouse pups from three independent litters of 6% and 20% maternal diet were isolated as described using MACS. The unexpanded isolated NPCs created 3 biological replicates for experimental and control. Total RNA was isolated using Qiagen RNeasy Mini-kit

(74104) with on column DNase digestion. Samples were sent to Genewiz and passed quality control by them. RNA sequencing was non-strand specific and run-on Illumina-HiSeq 2x150bp per lane. The RNA library was prepared with poly-A tail selection.

Before starting alignment and differential expression FASTQ files are checked for quality control using FASTQC. Alignment of the reads was done using STAR to the mm9 and mm10 genomes, not to provide read counts but to provide the best alignment. This produces wiggle files for visualizing tracts. Wig coverage files can be viewed using UCSC web-based viewer, IGV, or IGB. Junction files show isoforms of RNA reads. RSEM provides read counts and normalizes those counts to create a relative molar concentration for the reads from the FASTQ files. While some programs provide only unique reads, RSEM will look at multiple map locations for reads. Reads in RSEM are normalized based on reads and the exon lengths. RSEM results go into the EBSeq R program to produce what are empirical basian genes showing differential expression data. It uses raw counts, not the normalized ones, to compare groups and show statistically significant differences in expression levels between groups. With a p < 0.05there were 6,036 differentially expressed genes, of those 1,694 had a fold change of +1.5 or greater, 2,114 had a fold change of -1.5 of greater, and 2,228 had a fold change between +1.5 and -1.5. Those up or down regulated by 1.5 were put into Ingenuity Pathway Analysis (IPA). iPathway analysis uses a p < 0.05 and a fold change expression absolute value of at least 0.6.

# 2.8 Kidney Function:

Blood pressure measurements are from tail-cuff using the Visitech BP-2000 Blood Pressure Analysis System. It takes noninvasive measurements of conscious mice using transmission photoplethysmography to measure light transmission through the tail to measure blood pressure and heart rate. The heartbeat of the mouse pushes out through the vascular system

and the dilation of the blood vessels in the tail correspond to systolic while the end of that pressure wave corresponds to diastolic. Mice where acclimated to the machine with at least 3 trial runs before measurements were taken.

Plasma creatinine is a measure of kidney filtration. Creatinine is a waste product filtered by the kidneys and leaves the body in urine. High serum creatinine shows decreased kidney filtration (CDC: NCCDPHP, 2020). The animal was sacrificed, and blood was collected using heart puncture. At least 500 µL of blood was put into plasma collection tubes which were inverted 10 times to prevent coagulation. Plasma was then spun down and stored at -80 until shipped to the UAB-UCSD O'Brien Center for Acute Kidney Injury to measure creatinine, a marker for filtration, or Blood Urea Nitrogen, another marker for kidney filtration. Urine was also collected from the animals to test for kidney damage by testing for urine albumin.

# **2.9 Glomerular Count:**

Hematoxylin and Eosin stained kidney sections show the glomeruli. A large image grab creates a complete image of the kidney section and NIS elements can count and measure the size of selected structures. Based on the fractionator method described in Aresenault et. al. 2014 glomerular are around 15  $\mu$ M thick. When sections are 15  $\mu$ M or more apart the glomerular present would be new structures and not a recounting of the same glomerular. Counting 3 or more mid-sagittal sections that are 15  $\mu$ M or more apart would represent 3 independent samplings from that kidney and averaging those counts would produce an average count per section for that kidney. Animals were counted at 4 months of age except for 1 IUGR male that was excluded from glomerular count due to poor integrity of sections.

# 2.10 Six2+ Percent by GFP:

P0 and e13.5 are both counted by kidney pair. Kidney is digested as described in MACS then mechanically broken up by pipetting. Cell suspension is spun down at 350 rpm at 4C to

wash twice in PBS. Then the percent fluorescence is measured using Beckman Colter Gallios Flow Cytometer.

# 2.11 Extracellular Flux Measurements of MACs P0 NPCs:

NPCs isolated by MACs are not expanded and directly plated on Seahorse Extracellular flux plates. The cellular metabolism is measured in live cultured cells on the XF<sup>e</sup>24 Extracellular Flux Analyzer (Agilent Seahorse Technologies). Extracellular cell acidification rate (ECAR) measuring glycolysis, and oxygen consumption rate (OCR) measuring oxidative phosphorylation.

# 2.12 Statistics:

Body weight, kidney weight, and glomerular counts were compared using a student's ttest. Blood sugar was compared using Mann-Whitney U test. Two-way ANOVA analysis with replication was used for testing the interaction of sex and control versus IUGR in adult samples. A p value cut-off of 0.05 was used for all statistics. Excel and Prism 8 were used for statistical analysis and graph building. Error bars on graphs represent standard error measurements.

# **Chapter 3: Results**

# **3.1a.** Physiology and Vital Statistics of newborn pups from dams on a 20% vs 6% protein diet:

We used a 6% protein maternal diet compared to a 20% protein control diet to produce low birth weight offspring. Figure 5 shows a comparison of the components of the two diets. Casein is the protein used in the diet and is, as expected, lower in the experimental 6% protein diet. DL-Methionine is an essential amino acid found in protein sources; its decrease is part of the restriction of protein. Sucrose and cellulose are both increased to compensate for the loss of kilocalories with decreased protein. The calcium phosphate is increased due to the decreased protein. The casein protein contains phosphorous, with decreased casein the phosphorous levels have decreased, so calcium phosphate is increased in the 6% diet. Calcium carbonate is then decreased to maintain equal amounts of calcium in the isocaloric diets. The result is isocaloric diets that vary in protein and protein related nutrients and increased carbohydrates (Figure 5). There was no variation in blood sugar between the CD1 mothers on control or experimental diet.

# 3.1b. Morphology and Morphometrics:

Low protein parental diet (LPD, 6% protein) produced full-term mouse pups with decreased

body weight at day of birth Postnatal day zero (P0). The average body weight of P0 pups from





A) PO IUGR have a lower body weight than control p<.0001. B) IUGR mice have decreased kidney weight. p<.0001. C) Kidney weight as percent of body weight is higher in IUGR than control P<.01. D) Kidney and Body weight XY plot. Red line at 1.42 grams is the 10th percentile of control weights at P0. This is the cut off for accepting or rejecting control and IUGR. IUGR n=22, control n=42. These weights were tracked across 5 litters for control and IUGR with control n=26 IUGR n=24.

parents on 20% (control) protein diet was 1.61g, while pups from 6% parental diet weighed at an average 0.869g, a statistically significant decrease of 54% (p<0.0001). Pups from 6% parental diet have significantly smaller kidneys than the control, with an average combined kidney weight of 0.0082g versus 0.0129g, a statistically significant decrease of 37% (p<0.0001). Interestingly, the kidney weight/body weight has increased with 6% parental diet (Figure 6 A-C). Whereas

control kidneys were 0.8% of body weight, 6% LPD (IUGR) pup kidneys were significantly

higher (P<0.01) at 0.95% of body weight. Thus, although IUGR pups have lower body and kidney weight their kidney/body weight ratios are higher than of control pups. These data were



# Figure 7: Low Protein Impacts Pup Size, Litter Size, and Growth into adolescence:

A) XY plot of pup weight by litter size of that pup. Graph on the left is only control with the graph on the right only parental protein restricted. Control pup weight at PO decreases with litter size with larger litters trending towards more pups of lower weight. IUGR weights do not change with litter size. The 1.42 gram cut off for inclusion or exclusion as IUGR and control. Note that there are control mice that have IUGR pups. PO pups weighing less than 1 gram is only present in 6% protein litters. Control n= 125 from 10 litters. Low Protein n=72 from 7 litters. B) Growth curves for IUGR and control from postnatal day zero and postnatal day 21. IUGR pups are significantly decreased from PO to P21. All pups tracked were selected using the inclusion/exclusion cut-off of 1.42 grams. These weights were tracked across 5 litters for control and IUGR with control n=26 IUGR n=24. collected from 42 pups from 8 control litters and 24 pups from 5 LPD litters.

Due to the variable penetrance of IUGR by LPD and occurrence of IUGR independent of maternal diet criterion for accepting and rejecting P0 samples was established. IUGR in humans was defined as newborns that were full term and-in the bottom-10<sup>th</sup> percentile by body weight. Extending these to mouse studies, 10<sup>th</sup> percentile for 42 control pups across eight litters was determined to be 1.42g. Thus, this weight was used as the

threshold for defining IUGR versus normal birth weight and denoted by the redline in figure 6 D. P0 control pups weighing less than 1.42g were considered as IUGR and not used. Pups from LPD with a less than 1.42g are considered as IUGR were used. This criterion was used for P0 immunostaining, cap size measurements at P0, metabolic profile (Seahorse) at P0, and for pups used for P21 and 4-month analysis. The 1.42g criterion was not used for the P0 bulk RNA-seq



# Figure 8: Differences in P21 Body Weight and Kidney Weight

A-C) At postnatal day 21 adolescent IUGR weigh less than control overall, as do male IUGR, female IUGR do not weigh less. D-F) Kidney weight is lower in the IUGR mice overall and in female mice, but not in male mice at the day of weaning postnatal day 21. G-I) Kidney weight as percent of body weight is lower overall and in female IUGR, but not in male IUGR. Showing Male mice are small, with proportionally smaller kidneys at this stage while female mice have caught in body weight with control but have smaller kidneys. At P21 all control n=17, male n=9, female n=8 all IUGR n=10, male n=4, female n=6. samples. The embryonic samples from LPD dams showed no change in weight so there was no sample exclusion for this age groups. The significant decrease in P0 body weight and increase in kidney/body weight found in LPD pups represented all samples not just samples accepted or rejected based on the 1.42g cut-off of IUGR.

Low protein parental diet impacts the growth of the mouse pups and impacts litter size. Control diet produces a large range of litter size from eight to seventeen pups, while low protein diet produces litters with two to twelve pups. Control diet litters also show a relationship between litter size

and pup weight with increasing litter size having lower pup weights. Interestingly, the low protein litters are dissociated from the litter size and pup weight relationship and are small regardless of litter size. This is shown across seven low protein litters and ten control litters,

control n =125 and low protein n=72. This comparison included control pups of low weight and low protein pups of higher weight disregarding inclusion/exclusion criterion at this stage (Figure 7A).

The low birth weight from protein restriction persists to day of weaning (P21), despite controlling for postnatal factors such as milk quality and access. IUGR mice for longitudinal study were fostered by CD1 female mice on normal or control diet that had given birth within a day of IUGR birth. Both IUGR and control litters used for longitudinal study were controlled for size of litter. All longitudinal litters were limited to ten pups to control for access to food as mice possess only ten nipples. This would control for both milk quality and access to milk so that the postnatal environment of IUGR and control pups were similar. Thus, phenotypic differences would be a result of differences in gestational conditions and not postnatal factors. Pups were weighed daily from P0 until postnatal day 21 (P21). The IUGR mice continued to be low weight through P21, at which time they were weaned from their foster mother (Figure 8B). The P0-P21 measurements included IUGR n=24 and control n=26 from five separate litters.

IUGR mice also exhibit differences in postnatal growth and development. At birth IUGR mice were thin with bright red skin and delicate skin. Although the IUGR pups lose the bright red coloring at P2 or P3, they remained more reddish in appearance than the control pups which transitioned from red to pink then a pale white color. The thinness of IUGR pups remained until P9 when some IUGR pups, despite average weight being less than control, looked stouter. Control pups grew a thin but consistent hair cover over their body similar to peach fuzz by P6 with full hair at P9-10. The IUGR pups, however, showed 2-3 days delay in acquiring the peach fuzz at P8-9. Occasionally, the smallest IUGR pups that look like runts until P30 developed the peach fuzz at P10. These pseudo runt mice have shorter bodies and tails with leaner builds. Controls can be

sexed at P8 with prominent nipples on female mice and genital dimorphism being apparent, while IUGR cannot be consistently sexed until P11-12. IUGR mice also showed delayed movement and activity. Whereas at P5 the control mice were active crawlers IUGR pups showed some movement and shift but did not cover great distances until P8 or P9. Therefore, the delayed growth patterns observed in IUGR pups were morphometric and anatomical as well in body weight.

IUGR pups' body weights remained significantly low in males at P21, but not in IUGR



# Figure 9: IUGR Adult Body Weight and Kidney Weight Changes

A-C) Adult mice at 3-4 months of age show no difference in body weight overall or for male or female alone. D-F) Shows all IUGR groups have smaller kidneys with sex interaction by ANOVA. G-I) All have a lower kidney weight as percent of body weight. At P21 all control n=17, all IUGR n=10. Control male n=9, IUGR male n=4. Control female n=8, IUGR female n=9. Adult control all n=12 IUGR n=11. Male control n=7 IUGR n=5, female control n=5 IUGR n=6.

females. Averaged combined males plus female body weight at P21 in control pups was 16.23g and 14.49g in IUGR pups. Average weight of control male was 16.66g versus 14.73 in IUGR males. The lowest weight recorded was in one pseudo runt IUGR male that weighed 13.2g. Female offspring did not demonstrate significant weight disparity at P21 (average weight control 15.75g versus IUGR 13.89g) despite the inclusion of two female pseudo runts weighing 10.8g and 11.6g (Figure 8 A-C). Average P21 IUGR kidney weights were lower than control P21 kidney weights particularly in female
offspring. Kidneys from male IUGR offspring did not show significant weight differences from the control. The difference in kidney weight was much smaller than at P0 (Figure 8 D-F). This could come from the mouse kidney continuing through organogenesis postnatally. Mouse kidney development occurs from embryonic day 10 to postnatal day 4 for a total of 16 days with roughly one quarter occurring after birth and removal from the embryonic condition of LPD. But these 4 days of postnatal kidney development were not fully normal despite control and IUGR being under the same conditions postnatally. The lower kidney/body weight ratio persists at P21 in IUGR pups even with female IUGR that have caught up in body weight with control, indicating the lower kidney weight is likely maintained. Furthermore, the kidney/body weight ratio showed differences in kidney development postnatally. The IUGR P0 kidney/body weight ratio was 0.0095 significantly higher than 0.008 in control. At P21 control increased by 75% to 0.0140 while IUGR only increased by 31% to 0.0125. Then at 4 months neither ratio had increased from the P21 ratio (Figure 7C, 8G, 9G). IUGR mice begin with a higher kidney/body weight ratio then by adolescence have a significantly lower kidney/body weight ratio which persists into adulthood. The lower kidney/body weight ratio was present in significantly smaller mice as well (Figure 8 & 9). But the change was from P0 to P21 when control increased their kidney/body ratio while IUGR mice did not. Both had a similar lack of change P21 to 4 months. It was during the 4 days of postnatal kidney development and full 21 days of growth, when control and IUGR were under the same conditions, that IUGR experienced altered kidney development to impact adult kidney/body weight ratio. Thus, despite nearly identical postnatal environment conditions, the IUGR mice maintain morphometric and developmental differences into adolescence. IUGR kidneys retain memory of LPD conditions postnatally and that memory impacts development and growth of the kidney as shown by the changes and sometimes lack of changes from P0 to P21.

At 4 months of age adult IUGR mice (n=11, male n=5 and female n=6), showed no significant difference in body weight from control mice (n=12, male n=7 and female n=5).



#### Figure 10: Blood Pressure at 4 months and P21 Blood Sugar Are Unchanged

A-C) No change in blood pressure either over all or in a sex specific analysis. A 6% IUGR male has the highest measured blood pressure of 178.06 mmHg. The average blood pressure for control is 128.4 mmHg and the average for IUGR is 134.7 mmHg. D-F) At postnatal day 21 there is no change in blood sugar overall or in the male or female specific adolescent mice. At P21 all control n=17, all IUGR n=10. Control male n=9, IUGR male n=4. Control female n=8, IUGR female n=9. Adult control all n=12 IUGR n=11. Male control n=7 IUGR n=5, female control n=5 IUGR n=6.

Although male IUGR mice trended lower in body weight than the control, the female IUGR mice showed an opposite trend with higher body weights than the control (Figure 9 A-C). Control males weigh more than control females by about 10g while male and female IUGR adults have no difference in body weight. Female IUGR had caught up at P21 and may be headed towards the higher rate of obesity found in IUGR adult humans. Kidney weights, however, remain lower in the 4-month-old IUGR mice.

The IUGR kidneys weigh less when looked at as a group or separated by sex despite male at P21

trending lower in weight with no significance (Figure 9 D-F). Male P21 kidneys not weighing

significantly less may be due to small sample size at P21.

Kidney as percent of body weight in 4-month IUGR mice remains lower when comparing

both male and female mice, and when comparing male mice alone. The adult IUGR had smaller

kidneys in bodies trending towards higher body weight.

#### 3.1b. Blood pressure and kidney function measurements:

Plasma creatinine, urine albumin, and blood urea nitrogen were measured in adult IUGR and control mice as a measure of kidney function. Tail blood was used to measure blood sugar at P21 using a blood sugar meter. These physiological measures are not significantly changed but are of interest. Blood pressure was measured by the tail-cuff method. No significant change in blood pressure was observed in IUGR vs. control mice (Figure 10 A-C). An average blood pressure reading of 128.4 mmHg was recorded in control offspring, with an average reading of 134.7 mmHg in IUGR offspring. The highest blood pressure recorded was 178.06 mmHg from one IUGR male (6.23M1), which contributed to the higher blood pressure trend in IUGR males compared to control males.

Blood sugars were measured at P21 by one-time stick testing on a blood sugar meter. Measurements were done under non-fasting conditions. No changes in levels were observed between control and IUGR mice (Figure 10 D-F).

Plasma creatinine measures kidney function by measuring the waste product of creatine not removed by the kidney. Higher creatinine levels are indicative of decreasing kidney function. Although creatinine levels from adult IUGR mice were not significantly different from control. A strong trend towards increased creatinine was observed, especially when considering values from male mice (figure 11 A-C). The highest plasma creatinine levels were recorded from the adult male 6.23M1 with plasma creatinine of 0.14 mg/dL which is almost 3 times the average creatinine levels of either all controls or control males. The second highest plasma creatinine level of 0.12 mg/dL (Table 9).

Blood urea nitrogen (BUN) test measures the urea nitrogen in the blood. Urea is produced by the liver when digesting protein. The kidney filters urea as a waste product out of



Figure 11: Little Changed in Kidney Function Measures at 4 Months

A-C) Plasma Creatinine is unchanged when comparing all animals and when comparing female, plasma creatinine is higher in male IUGR with the same male with the highest blood pressure having the highest plasma creatinine of 0.14 mg/dL. Control n=12, Control male n=7, female n=5. IUGR n=11, male n=5, female n=6 G-I) Urine albumin is not changed at 4 months, but the male with high blood pressure, and the highest plasma creatinine has the highest urine albumin. An IUGR female with unchanged blood pressure has the second highest urine albumin and the second highest plasma creatinine. This IUGR female and male have high urine albumin of 0.352 g/dL and 0.477 g/dL respectively. Control urine albumin has a mean 0.0744 g/dL. BUN sample sizes are the same, Urine Albumin Control n=10, control male n=5.

renal health. High BUN in humans can be caused by a high protein diet, decreased glomerular filtration (GFR), heart failure, hypovolemia, and increased catabolism. Although, there is no significant change in BUN in IUGR adults at 4 months, there is a trend towards increased BUN in IUGR mice. One male control, 20.23M4, had the highest BUN of 49.27 mg/dL. This mouse was otherwise normal. One IUGR female (6.23F3) with second highest BUN of 42.61 mg/dL also has the second highest plasma creatinine. Excluding the control male 20.23M4, the male with the highest BUN is the previously noted 6.23M1 with a BUN of 40.56 mg/dLalong with his elevated plasma creatinine levels (Anderson, L., Otto, G., Pritchett-

the blood. High urea is a sign of poor

Corning, K., & Whary, M., 2015) (Table 9).

Albumin is a protein found normally in the blood at  $36.7 \pm 5.2$  g/L in males and  $46.4 \pm$ 

7.0 g/L in females (Anderson, L., Otto, G., Pritchett-Corning, K., & Whary, M. 2015).

Functional kidneys prevent the movement of albumin from blood to urine. Albumin is filtered by the glomerulus of the kidney and reabsorbed by the proximal convoluted tubules, the loop of



#### Figure 12: Glomeruli Count and Morphology:

A-C) Glomeruli area measured on H&E staining using NIS elements. No change in glomeruli area, but there is a trend of larger glomeruli in male mice. The Eqi diameter is the longest diameter through the glomeruli measured. This is larger overall and in female. G-H) Glomeruli counts from 3 h&e tissue sections 20 uM distance from each other. Glomeruli number is decreased in IUGR. The lowest glomeruli number is from male with cysts visible in histology and the highest blood pressure, plasma creatinine and urine albumin. This data is supported by glomeruli counting from three 10X images per animal and counted independently. Adult control all n=12 IUGR n=10. Male control n=7 IUGR n=4, female control n=5 IUGR n=6.

Henle and distal tubules, and the collecting ducts. Elevated urine albumin is a marker of kidney damage and decreased function. IUGR adult mice do not have significantly increased levels of urine albumin, but there is a definite trend to increased albumin driven mainly by three IUGR animals. The highest urine albumin level was 0.477 g/dL found in 6.23M1 showing one animal with the highest plasma creatinine levels, highest urine albumin and elevated BUN. The second highest urine albumin is 0.352 g/dL from 6.23F3 which had the second highest BUN and second highest plasma creatinine levels. Their IUGR male litter mate 6.23M2 has the third highest urine albumin at 0.26 g/dL. For comparison

only four of the 11-control measured had urine albumin over 0.1 g/dL and none of these animals were over 0.14 g/dL. The mean for all control urine albumin was 0.0744 g/dL compared to male IUGR at 0.352 g/dL and 0.477 g/dL for female IUGR (Figure 11 G-I and Table 9).

These physiological measures are not significantly changed but suggest impaired kidney function in offspring from LPD parents. One important consideration here is the genetic background of the mice used – this point is discussed further in the discussion.

There are sex differences in the impact of IUGR. This was first apparent in growth from P0 to P21. ANOVA two-way analysis showed changes to physiology at P21 and adulthood (4 months). There are significant changes in adulthood kidney weight with interaction between sex, IUGR, and kidney weight with IUGR having smaller kidneys than control, IUGR males and females both having smaller kidneys, and IUGR females having the smallest kidneys (p<0.05). Control male n=7, total control n=10 with control female n=5. IUGR total n=11, IUGR male n=5, and IUGR female n=6. The adult measurements for body weight, systolic blood pressure, glomeruli count, plasma creatinine, urine albumin, and plasma BUN all showed no interaction. P21

## **3.1c.** Adult Kidney Histology, Glomerular counts, and Immunofluorescence staining of molecular markers:

All control and IUGR adult kidneys were fixed and sectioned for immunostaining. Tissue sections were stained for hematoxylin and eosin. Hematoxylin stains the cell nuclei blue by marking the basic and cationic parts of the tissue. Eosin stains the acidic and anionic parts red

## Table 1: Structural Changes in IUGR Relative to Control viaImmunostaining

Ker NC-1	Six2	Meik1/2/3	i Uhati	Sell	1	DBA	NCA	M	Wei		So	a sti	Calbindin	E-Cadherin	LTAATL		AQ91		AQP2	Pan Cytokeratin
Char +:U -:Do	cap Cap Mesenchyme	Stroma	Nascent Nephron	Cap Mesenchyme	Nascent Nephron	Collecting Duct	Cap Mesenchyme	Nascent Nephron, CSB, SSB	Cap Mesenchyme	Podocyte	UB Tip Cells	S- Shaped Body	Uneteric Branching	Distal Tubule. Collecting Duct	Proximal Tubule	Proximal Tubuk	Descending Loop of Henle	Descending Vasa Recta	Principal Cells Collecting Duct	Collecting Duct
E13	5	NC	-			NC														NC
P13	NC	NC	-	-	NC	-	-	NC	-	-	*	+	NC	NC	-				NC	NC
4 Mo	dh					NC							NC	NC	NC	NC	NC	NC	mislocalized	*

showing the extracellular matrix and cytoplasm. The stains also overlap creating different combinations.

IUGR kidneys showed stronger eosin staining and presence of cysts (Figure 13 and 14 A) which were absent in control. Enlarged glomeruli are a sign of kidney disease as the kidney struggles to filter waste. Glomeruli were counted and size estimated on the H&E stained sections. Ten glomeruli were measured per animal from all control and adult IUGR from random fields of stained kidneys. The glomerular area showed no significant difference between control and IUGR kidneys (Figure 12 A-C). Male kidney glomeruli trend towards larger but the difference is not significant (Figure 12 A-C). The EqiDiameter, the longest point across an area, was also measured on the same glomeruli. A significant increase in the EqiDiameter of glomeruli from the female IUGR mice was recorded, with glomeruli from male mice trending towards an increase (Figure 12 D-F). While glomeruli at 4 months were not significantly larger in IUGR kidneys, the shape of glomeruli had changed.

In a young adult glomerular counts reflect glomerular endowment at birth. Glomerular counts showed decreased glomerular number in IUGR kidneys versus control (Figure 12 G). Kidneys from both male and female mice showed a trend towards decreasing glomerular number. The adult glomerular count is the average total count from 3 sections 20 µM apart per animal. This distance provides counts of unique glomeruli based on the established fractionator method (Buzello, 2000, Weibel, E.R., & Gomez, D.M., 1962). Tissue sections were deep showing the cortex, medulla, and ureter. The counts were confirmed by independent counting of glomeruli from three 10X images from the same sections. Both counting methods show IUGR with a significant decrease in glomeruli number (Table 9 and Figure 12). The IUGR male mouse

6.23M1 kidneys had the lowest glomeruli count. This IUGR male also has elevated plasma creatinine, urine albumin, and plasma BUN, and presence of renal cysts by H&E staining.

Consecutive adult kidney sections were stained with antibodies against E-cadherin (Cdh1), lotus tetragonolobus lectin (LTL), aquaporin 1 (Aqp1), pan cytokeratin 8 (CK8), dolichos biflorus agglutinin (DBA), and aquaporin 2 (Aqp2) (Table 9). E-cadherin is a calcium dependent cell adhesion protein that spans the cellular membrane in epithelial cells (Lee, S.-Y., Han, S. M., Kim, J.-E., Chung, K.-Y., & Han, K.-H., 2013). LTL marks the proximal tubules of the kidney by binding to the α-linked L-fucose containing oligosaccharides (Yallowitz, A. R., Hrycaj, S. M., Short, K. M., Smyth, I. M., & Wellik, D. M., 2011). Aquaporin 1 (AQP1) that stains the basolateral and apical plasma membranes of the proximal tubules, the descending loop of Henle, and the descending portion of the vasa recta. AQP1 is a water channel present in cell membranes (Monzani, E., Bazzotti, R., Prego, C., Laporta, C.A.U., 2009) [Brown, D. (2017)].



#### Figure 13 Adult Female Histology:

A) Hematoxylin and eosin staining of tissue sections from a control female and all IUGR females. This shows the presence of cysts including fluid filled cysts in 6.23 F3 and F4. B) Low and high magnification of immunofluorescence. E-cadherin stains the distal tubule and collecting ducts of the kidney. LTA lectin stains the proximal tubules. Aquaporin 1 marks the basolateral and apical plasma membrane in the proximal tubules and the descending loop of Henle. The fluid filled cysts that are pink in H&E are positive for E-cadherin. C) Low and high magnification of pan cytokeratin marking distal tubule, DBA lectin marks the distal tubules, and aquaporin2 marks the apical membrane of the collecting ducts. Staining done on Control females n=5, IUGR females n=6.

Figures 13 and 14 B shows at high and low magnification that IUGR adults have normal

distal tubules, collecting ducts, proximal tubules, and loop of Henle. The cells of these structures

are present and normally organized. LTL marking of the proximal tubules was decreased in adult

IUGR kidneys compared to control.

Separate consecutive sections in all adult control and IUGR were stained with Pan

cytokeratin (CK8) marking the collecting ducts. Cytokeratins are proteins found in the

cytoskeleton of epithelial cells, specifically the intermediate filaments. There are 29 types of



#### Figure 14 Adult Male Histology:

A) Hematoxylin and eosin staining of tissue sections from a control male and all IUGR males. This shows the presence of cysts including fluid filled cysts in 6.23 F3 and F4. B) Low and high magnification of immunofluorescence. E-cadherin stains the distal tubule and collecting ducts of the kidney. LTA lectin stains the proximal tubules. Aquaporin 1 marks the basolateral and apical plasma membrane in the proximal tubules and the descending loop of Henle. The fluid filled cysts that are pink in H&E are positive for E-cadherin. C) Low and high magnification of pan cytokeratin marking distal tubule, DBA lectin marks the distal tubules, and aquaporin2 marks the apical membrane of the collecting ducts. The fluid filled cysts are visibly stained with E-cadherin and pan cytokeratin. Staining done on Control males n=7, IUGR males n=5.

cytokeratins, the antibody used has nonspecific affinity for cytokeratins (Bates, C., Kharzai, S., Erwin, T., Rossant, J., & Parada, L., 2000). DBA marks the collecting ducts by binding the carbohydrate α-linked N-acetylgalactosamine (Holthöfer, H., Schulte, B. A., & Spicer, S. S., 1987). Aquaporin 2 (AQP2) marks the apical membrane of the collecting ducts. AQP2 is a second water transporter essential for water balance maintained by the kidney (Monzani et. al. 2009) [Brown, D. (2017)]. Figures 13 and 14 C confirms the normal formation of distal tubules and the collecting ducts. There was no loss of DBA in adult IUGR.

The 4-month-old IUGR mice had fluid filled cysts visible with H&E staining (13A and 14A). Epithelial cell staining by E-cadherin of the distal tubule and collecting ducts marked the fluid filled cysts in 6.23M1, 6.23F3, and 6.23F4 (Figure 13B & 14B). The cysts were also positive for the collecting duct marker pan cytokeratin (Figure 13C & 14C). DBA, another collecting duct marker, does not stain the cysts and was not changed between control and IUGR. Aqp2 marks the apical membrane of the principal cells of the collecting ducts. IUGR kidneys had more disperse Aqp2 staining not specific to the apical membrane irrespective of sex and presence of cysts.

IUGR adult kidneys were damaged with 6.23M1 showing the worst histology. 6.23M1 had the most and largest cysts and the brightest staining for E-cadherin and pan cytokeratin in the cysts. This damage coincides with markers of kidney function like blood pressure, plasma creatinine, urine albumin, and blood urea nitrogen (Table 9).

#### 3.2 Embryonic Kidney Development in IUGR vs. Control Mice:

E13.5 and P0 kidneys were collected for molecular marker analysis. P0 pups were weighed and exclusion criteria were applied to ensure pups from LPD mothers reflected IUGR by body weight. Embryonic mice were not weighed so there was no cut-off for inclusion of exclusion of the e13.5 samples. These results are summarized in table 1. by body weight. Embryonic mice were not weighed so there was no cut-off for inclusion of the e13.5 samples. These results are summarized in table 1.

**3.2a Embryonic IUGR Kidneys have decreased Cap Mesenchyme and Ureteric Branching:** Size of CM was explored by FACS, kidney section staining, and whole organ

immunostaining. Six2CreGFP+ kidneys were fully digested and then counted for percent GFP+



# **Figure 15: Cap Mesenchyme Markers at P0** A) There is no consistent change in CM size by Six2 staining at P0. The CMs of the smaller IUGR kidneys are diffuse in the cortex with more space between CMs. B) Sall1 staining of the CM is dimmer and smaller in IUGR with no change to Sall1 staining of nascent nephrons. C) NCAM staining of the CM is drastically decreased despite the presence of CM, this loss is often but not always accompanied by a loss of DBA staining in the ureteric branching. D) Wt1 staining in the CM is decreased along with a decrease in NCAM. The loss

of Wt1 and NCAM occurs with or without the loss of DBA.

by FACS count to determine the size of the Six2+ CMs. Ureteric branching was determined by kidney section staining, and whole organ immunostaining. Immunostaining of E13.5 organs and sections at the beginning of kidney development shows inconclusive results for cap size. The Six2+ staining in

whole organ appears larger at times in the 10 IUGR and 8 control kidneys stained and imaged. Although the IUGR kidneys are smaller with less UB branching from pan cytokeratin staining (Figure 16 A and B). Sectioned e13.5 kidneys appear to have fewer Six2+ cells that are more dispersed, giving the appearance of more diffuse caps around the ureteric tips, and NPCs that are

not closely aligned with UB tips (Figure 16 B). The lhx1 staining at e13.5 showed no change to nascent nephrons in size, number, or molecular character in section staining (Figure 16 B) [Cirio et. al. 2011].

Unnormalized percent GFP+ of digested kidneys shows the significant decrease in Six2+ NPC at e13.5 in LPD embryos. To quantify Six2+ NPC in IUGR kidneys, Six2+/GFP+ NPC were counted per kidney pair by flow cytometry at P0 (control n=3;IUGR n=5) and e13.5 (control n=3; IUGR n=4). E13.5 IUGR kidneys have 40% less GFP+ Six2 cells compared to control E13.5 kidneys. Over development, a 37.5% decrease in Six2+/GFP+ NPC was observed. This significant decline in Six2+/GFP+ NPC number from e13.5 to P0 in control is expected as the NPC population differentiates during development. An age-related decline in Six2+ NPC was not observed in IUGR kidneys (Figure 16 C).

Ureteric branching of pan cytokeratin positive structures plays a role in organ size, structure, and the maintenance and differentiation of NPCs (Costantini, F., & Kopan, R., 2010). Whole organ staining of 16 kidneys from 10 control embryos and 10 kidneys from 8 IUGR animals for pan cytokeratin showed changes in the branching at e13.5. DBA co-stained with pan cytokeratin was unchanged at e13.5 (Figure 16 A). Counting the UB tips in the organs shows a significant decrease in branching in IUGR embryonic kidneys. There was nearly a 30% decrease in average UB tips in IUGR kidneys at e13.5 (Figure 16 E). At e13.5 overall NPC quantity and UB tip number were decreased showing early development of the kidney had changed with LPD.



#### 3.2b Impact of IUGR on NPC and Nephrogenesis:

Six2 is a transcription factor that regulates the self-renewal and maintenance of the multipotent NPCs that will differentiate into the nephron. Six2 inhibits the Wnt/β-catenin differentiation signal while activating CM maintenance signals including Osr1, Pax2, and Six2 while signaling the branching of the UB (Katsu et. al. 2012, Barak et. al. 2005, Fleming et. al. 2013). Individual CMs were not changed in IUGR at P0 based on Six2 staining. Six2 did show changes to the overall kidney structure at P0. The smaller IUGR kidneys at low magnification have CMs that are more diffuse along the cortex of the kidney with space between CMs (Figure 15 A). The diffuse caps along the cortex could be evidence of changes to branching in the IUGR kidney.

Sall1 is expressed in the NPC and the differentiated structures of the CM including the pre-tubular aggregate, (RV), CSB, and SSB. Sall1 is activated by Wt1 and is active in the initial UB growth into the metanephric mesenchyme and the successive branching of the UB (Kanda, S., Tanigawa, S., Ohmori, T., Taguchi, A., Kudo, K., Suzuki, Y., Sato, Y., Hino, S., Sander, M., Perantoni, A. O., Sugano, S., Nakao, M., & Nishinakamura, R., 2014). Sall1 expression domain appears smaller, and the staining less intense in IUGR kidney sections (Figure 15 B). The Sall1 transcription factor is required for CM maintenance, UB branching, but not for differentiation Nishinakamura, R., & Takasato, M., 2005).

Neural cell adhesion molecule (NCAM) stains similar cell populations of the kidney as Sall1 marking the CMs and remaining during the mesenchymal to epithelial transition as NPCs differentiate. NCAM is a glycoprotein present on the surface of cells acting as a cell-to-cell adhesion molecule. It is present in development playing a role in cell movement and arrangement during morphogenesis and development (Lackie, Zuber, & Roth, 1990). NCAM staining in the CM was consistently decreased in IUGR kidneys despite the obvious presence of the CM based

on structure and staining of the animals. The loss of NCAM occurred with or without the loss of staining by the lectin DBA which marks the distal tubule by binding the glycosylated protein  $\alpha$ -linked N-acetyl galactosamine (Figure 15 C). The tumor suppressor gene and transcription factor Wilm's Tumor 1 (Wt1) is active in the metanephric mesenchyme during the invasion of the UB at the start of kidney development. It activates NPC maintenance signals of Sall1, Pax2, and Bmp7 and the proliferation pathway MAPK/PI3K through FGF16/20. Wt1 is active during differentiation and will regulate differentiation pathways. Wt1 staining at P0 will mark the CM and the differentiated podocyte in mature nephrons (Motamedi et. al. 2014, Nishinakamura, R., & Takasato, M., 2005). The IUGR CM shows decreased Wt1 staining despite the clear presence of defined CMs by the also decreased NCAM co-stain. The low Wt1 is present with IUGR kidneys that show a loss of DBA in the distal tubules (Figure 17 D). The lectin DBA which marks the distal tubule by binding the glycosylated protein  $\alpha$ -linked N-acetyl galactosamine (Lackie et. al. 1990).

#### 3.2c Changes in Differentiation Markers Result in Altered Physiology at P0:

Lotus tetragonolobus lectin (ltl) marks the proximal tubules of the kidney by binding  $\alpha$ linked L-fucose containing oligosaccharides. It then marks differentiated and formed structures of the adult kidney (Yallowitz et. al. 2011). IUGR had decreased ltl staining showing fewer



### Figure 17: Markers of differentiation and mature glomerular structures at P0:

A) The diffuse cap mesenchymes (CM) are shown by Six2 and NCAM staining with less proximal tubules in IUGR. Control n=10, IUGR n=11. B) The LTL staining for proximal tubules is low in multiple animals along with decreased Wt1 staining for the precursors for the proximal tubules renal vesicle (RV) and comma shaped body (CSB). Control n=8, IUGR n=11. C) Lhx1 marks the nascent nephrons. IUGR has fewer Lhx1+ nascent nephrons that are smaller, and less organized. Control n=6, IUGR n=6. D) Sox9 stains the ureteric tip cells and the interstitial cells of the s-shaped body (SSB). NCAM stains the CM, the RV, and the SSB. DBA stains the ureteric branches (UB). The ureter remains with loss of DBA staining as shown by Sox9 in the tip cells. Sox9 shows more intense staining in the UB tip cells and disorganization of the SSB. Control n=6, IUGR n=6.

proximal tubules (Figure 18 A-B). Proximal tubules form from the epithelialized NPCs. Figure 18B shows low NCAM and Wt1 in the CM with decreased Wt1 positive podocytes and weakly stained and fewer proximal tubules. IUGR nascent nephrons are decreased in number and size by Lhx1 staining (Figure 17 C). **IUGR** produces disorganized nascent nephrons. The Lhx1 transcription factor is required for the formation of nephrons during

development and is under the regulation of Wnt9b from the UB (Cirio e.t al. 2011). IUGR shows

changes to the CM and differentiating structures from the CM at P0 that can lead to changes in

the adult kidney in the form of structural deficiencies.

Unlike the CM where markers are altered but the CM is unchanged in presence or organization the differentiating structures showed molecular, organizational, and physiological changes. Early markers of differentiation show nascent nephrons, RVs, CSBs, and SSBs are disorganized, smaller, and fewer. This led to a deficit in differentiated structures as shown by decreased in proximal tubules.

#### 3.2d Expression of Ureteric Markers in P0 IUGR Kidneys:

Overall IUGR P0 kidneys have all the structures of ureteric branching with no clear change in the amount and structure of collecting ducts. AQP2 is a water transporter on the surface of principal cells of the collecting duct. Low and high magnification images showed no changes to the presence of AQP2 within the collecting ducts or the amount of collecting duct of the IUGR P0 kidneys (Figure 18 A, C, D). However, AQP2 localizes to the apical membrane and in IUGR it was instead diffuse within the cell (Monzani et. al. 2009) [Brown, D. (2017)]. Diffuse CMs along the cortex shown by Six2 staining is often due to decreased branching of the UB. The diffuse Six2 CMs along the cortex of the kidney with normal AQP2 structures show that while the organization of the CMs at the UB tips has been changed the formation of collecting ducts had not been (Figure 18 A).

E-cadherin is a calcium dependent adhesion molecule present in the distal tubules (Lee et. al. 2013). Figure 18B shows loss of DBA staining with E-cadherin staining present showing a loss of DBA while distal tubule structures are maintained. Figure 18 C confirms normal distal tubule and collecting duct development in IUGR by E-cadherin and AQP2 staining. Pan cytokeratin also marks the collecting ducts of the kidney. Figure 18 D shows no change to the



collecting ducts in overall structure or in the presence of principal cells of the collecting duct. At P0 the ureteric branching of the kidney is not changed in the smaller IUGR kidneys. The branching and structures of

the collecting duct

are not changed in

#### Figure 18: Normal Ureteric Tree Branching:

A) Shows the normal pattern of collecting duct forming in the smaller IUGR kidney by AQP2 staining of the principal cells of the collecting duct. Control n=5, IUGR n=5. B-C) E-cadherin and DBA mark the distal tubules. Even with loss of DBA E-cadherin and distal tubule staining is unchanged in IUGR. Control n=12, IUGR n=16. D) Pan Cytokeratin marks the collecting ducts of the kidney, AQP2 marks the principal cells of the collecting ducts Control n=12, IUGR n=12. Both are unchanged in IUGR. The collecting ducts show normal cell patterns.

IUGR kidneys at P0, but the UB tip cells are changed. Sox9 is a transcription factor present in the UB tip cells and the intermediate and distal domains of the SSB (Reginensi, A., Clarkson, M., Neirijnck, Y., Lu, B., Ohyama, T., Groves, A. K., Sock, E., Wegner, M., Costantini, F., Chaboissier, M.-C., & Schedl, A., 2011). As shown in Figures 18 A-D Sox9 staining appears qualitatively higher in IUGR P0 kidneys at the UB tips and in the SSB (N control=2; N IUGR=3). IUGR UB tip cells were changed in immunostained e13.5 sections and whole mount, combined with at e13.5. The overall UB tree at e13.5 stained by pan cytokeratin did not show

macroscopic changes to the UB branching, but the UB tip number is significantly decreased (Figure 16 A & E). The IUGR e13.5 kidney also had prominent ampullae formed (Figure 16 B). UB tip development cycles through a t-tip then either into two ampullae or a tri-tip. These have implications for the UB tree formation and for the appearance and organization of the CM. A ttip has two UB tip ends surrounded by a cloud of continuous NPCs from 1 CM, while the two ampullae have two UB tip ends extending with their own distinct CMs surrounding them. The e13.5 characterized by Short et. al. 2014 showed almost half the number of ampullae as T-tip and Tri-tip with the number and proportion of ampullae increasing over development (Short, K.M., Combes, A. N., Lefevre, J., Ju, A.L., Georgas, K.M., Lamberton, T., Cairncross, O., Rumballe,. B.A., McMahon, A.P., Hamilton, N.A., Smyth, I.M., Little, M.H., 2014). The sectioned IUGR e13.5 staining showed more ampullae than control. The increased ampullae could be impacting the elongation step of UB development and be the reason for the significantly less UB tips counted in whole mount e13.5 IUGR kidneys (Figure 16 E). The IUGR UB having elongation rather than branching changes would explain the normal levels of pan cytokeratin, Aqp2, Ecadherin, and calbindin at e13.5 and P0 with smaller kidneys (Figures 16B, 18A-D, & 19D). Further evidence for the changes in UB tips and elongation are the smaller IUGR kidneys at e13.5 and P0, and the higher staining for UB tip cell marker Sox9 (Figure 17D & 18 A-D).

#### **3.2e Expression of Stromal Markers:**

The renal stroma cells are a heterogenous cell population present in the cortex surrounding the CMs and through the medulla. Meis1/2/3 marks the stroma cells that provide

structure to the kidney while crosstalk signals with the NPCs of the CM maintain NPC stemness. Stroma cells of the kidney are derived from the same metanephric mesenchyme that gives rise to the NPCs. Stroma cells will give rise to glomerular mesangial cells, pericytes, and vascular smooth muscle cells and vasculature in the adult kidney (Chang-Panesso, M., Kadyrov, F. F.,

Machado, F. G., Kumar,

A
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6% Protein -2

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**Figure 19: Ureteric Branching Tip Cells:** A-B) Consistent high Sox9 staining in the UB tip cells of IUGR kidneys at P0. Control n=6, IUGR n=6 C) Loss of DBA has no impact on intensity of Sox9 staining.

A., & Humphreys, B. D., 2018). Stroma in the IUGR P0 kidney was unchanged from control with similar thickness of the stroma around the CM (Figure 20).



**Figure 20: No Change in Cortical Stroma thickness:** Meis1/2/3 staining for the stroma cells of the kidney shows no change in stroma around the cap mesenchyme (CM). There is no thinning or decrease in stroma cells around the CMs.

#### 3.2f Proliferation and Apoptosis in P0 IUGR Kidneys:

Bromodeoxyuridine (BrdU) is an analog for of the nucleotide thymidine. Tissue or cells

will take up BrdU and integrate it into the DNA of replicating cells. BrdU can then be

immunostained in fixed tissue to identify replicating cells (Muskhelishvili, L., Latendresse, J. R.,

Kodell, R. L., & Henderson, E. B., 2003).

By co-staining with markers of regions of interest proliferation rates can be found for cell types (Muskhelishvili et. al. 2003). Four control and three IUGR mice were stained and only CMs and nascent nephrons from above a branched UB were counted. The UB tips counted were also always branched. At least 10 unique regions of the sectioned kidneys were counted per animal. Six2, Sall1, and Calbindin was stained in consecutive sections of the kidney. Proliferation in Six2+ stained CM is decreased in IUGR at P0 when looking per CM across animals or per animal. The average number of proliferating cells is decreased by a third in IUGR Six2+ CMs. This is shown when looking per CM measured and when averaged by animal. The



#### Figure 21: Decreased proliferation in IUGR Six2+ Cap Mesenchyme

A) Decreased replication in the cap mesenchyme by BrdU positive cells in Six2 staining. Co-staining of BrdU for proliferating cells, Six2 for the cap mesenchyme, and DBA for the ureteric branching. B) No change in cap mesenchyme based on Sall1 marked cap mesenchyme. Staining shows BrdU marking proliferating cells, Sall1 marking the cap mesenchyme and the nascent nephrons, and DBA marking the ureteric branching. C) Sall1 marked nascent nephrons has no change in replication. D) Calbindin marked UB tips has no change in replication. Calbindin marks the ureteric branching, DBA marks the ureteric branching, and BrdU marks the proliferating cells. E) PARP marker for apoptosis shows no change in NCAM marked cap mesenchyme or nascent nephrons. BrdU control n=4, IUGR n=3. PARP n=2 for control and IUGR.

IUGR animals used all showed a loss of DBA staining (Figure 21 A). Sall1+ CMs show a trend towards a decrease in proliferation, but it is not significant when looking per CM or per animal. The Sall1 staining for RVs was selected separately and showed no change in proliferation with no trend when looking per nephron. There was a slight trend in decreased proliferation when looking at average per animal per nephron (Figure 21 B-C). The Sall1 RV showed a greater range in proliferation rates compared to the CM. Calbindin marks the ureteric branching of the kidney. The tips of the UB were selected for counting and showed no significant change in proliferation, but there was a trend towards less proliferation in IUGR P0 UB tips (Figure 21 D).

Poly (ADP-ribose) polymerase (PARP) is related to DNA repair, genomic stability, and apoptosis. Here it was used as a marker for apoptosis in the CM and the nascent nephron based on co-staining with NCAM (Muskhelishvili et. al. 2003). IUGR kidneys had no significant change in PARP in the CM or nascent nephron. PARP remains a rare event as shown by the number of control and IUGR kidney fields that had no PARP present in the counted area. There is a trend towards increased apoptosis in the CM and a decrease in the nascent nephrons. The lack of significance might be due to the small sample size of only two control and two IUGR (Figure 21 E).

In summary, NPC, different structures of the nascent nephron, stromal and ureteric components are present in IUGR kidneys. However, decrease in NPC number and fewer nascent nephrons may explain the nephron deficit observed at birth. Maintenance, proliferation, differentiation, and morphogenesis signals have been downregulated.

#### 3.3 RNA-Seq Results:

Three independent P0 control and IUGR RNA samples from MACS isolated NPCs were sequenced on Illumina-HiSeq 2500 platform. Despite low RNA concentrations for 1 control and

1 IUGR sample all were useable for sequencing (Figure 22 A-B). Figure 18C shows samples had between 57 and 67 million with read lengths of 302 base pairs, with the mouse genome being 2.5 x 10<sup>9</sup> bp the samples have a read depth of 8-10X for the 3 control and 3 IUGR RNA samples. Figure 22 D is the Principal Component Analysis (PCA) on the RNA-seq samples. PCA simplifies large data sets into smaller components that retains the components of the full data sets. First the data was standardized so that high value items do not dominate the analysis. For RNA-seq this would be a handful of genes with fold changes in the hundreds being given more weight than hundreds of genes with fold changes below 20. Then the covariance matrix was calculated to determine how variables of the data sets are related to each other, principal components are then calculated to determine the similarity and difference of data sets. The data sets were aligned to mouse genome mm10 and analyzed twice for differential expression.

The first analysis was done by STAR aligner and produced 6,036 differentially expressed genes all with a p<0.05. It has 1,694 genes increased by 1.5 or more-fold in IUGR NPCs, 2,114 with a fold change increased or decreased by less than 1.5 but more than 1.005, and 2,228 decreased by more than 1.5-fold in the IUGR NPCs (Figure 22). The genes that are increased or decreased by 1.5-fold or more were then run through Ingenuity Pathway Analysis (IPA) (Supplemental Table 1). IPA by QIAGEN bioinformatics analyzes omics data to arrange it into



#### Figure 22 RNA-Seq Differential Expression STAR Aligner:

With a p<.05 there were 6,036 differentially expressed sequences with statistical significance. Of those 1,694 had a fold change of +1.5 or greater show as green dots, 2,114 had a fold change of -1.5 of greater shown as red dots, and 2,228 had a fold change between +1.5 and 1.0001 and -1.5 and - 1.0001, shown as yellow dots. All are significant changes. Those up or down regulated by 1.5-fold or more were put into Ingenuity Pathway Analysis (IPA). A) Shows all 6,036 points, B) Y-axis decreased cutting off the 11 points with the largest change. C) Accounting for all points. 28% Upregulated  $\geq$  1.5, 36.9% are downregulated  $\geq$ 1.5, 35% are > -1.5 and <1.5, but all 6,036 points are statistically significant.

biological pathways and predict upstream regulators, and downstream outputs including diseases based on published data and biological relationships. IPA related the 3,992 genes up or down regulated by 1.5-fold as related to diseases and biological functions, regions of the cell, top canonical pathways, predicted causal networks, and predicted upstream regulators based on IPA curated

databases and published data. IPA analysis shows development has been altered in the IUGR P0 NPCs. Figure 23 A shows the top diseases and biological functions changed. Diseases and biological functions come from categories of molecular functions from the differentially expressed RNA-seq IPA analysis. Disease and abnormalities at 34% were the most common category with cancer and inflammation the most common subcategories of diseases and

abnormalities. Cell survival was next at 25% of categories including markers of necrosis, cell

survival, and apoptosis. Necrosis and apoptosis categories were both up and down regulated in

#### A Disease & Biological Functions



#### Figure 23 RNA-Seq Differential Expression IPA:

A) The 3,992 genes that are up or downregulated by 1.5-fold or more are associated with cell survival, development and morphology, adhesion and morphology. Adhesion and Migration is of note due to the migration and condensing of epithelizing NPCs when they differentiate. Disease and abnormalities are mostly cancers meaning pathways are developmentally related as well. The dependence of NPCs on glycolysis and shift to oxidative phosphorylation as they age shows that all parts are related to development. B) Parts of the cell with significantly changed RNA expression. The changes are from throughout the cell.

IUGR P0 NPCs. Development and morphology were 19% of categories including proliferation, tissue organization, translation, transcription, and posttranslational modification. Cell adhesion and migration represented 14% of categories coming from cell to cell contact and signaling, cell migration, and cell movement of endothelial, epithelial, and mesenchymal cells. Cell adhesion and

migration categories decreased in IUGR. Adhesion and migration are related to NPC

differentiation as NPCs induced into differentiation migrate out of the CM and condense as they

## Table 2: Predicted Top CanonicalPathways differentially expressedRNA-seq NPCs by IPA

Table 3: Predicted Top Causal Networksfrom differential expression in NPCs by IPA

Top Canonical Pathways	P-Value			
		Causal	Distant Date	Predicted
EIF2 Signaling	5.95E-19	Networks	Biological Role	Activation
mTOR Signaling	1.27E-08	MYCN	Proto-oncogene/Development. Transcription dysregulation	Activated
		NUPR1	Transcription dysregulation	Activated
Regulation of eIF4 and		SERPINH1	Heat Shock protein 47, Cell Proliferation	Inhibited
p70S6K Signaling	4.13E-06	Alpha Catenin	Cytoskeleton and Cell polarity	Activated
TNFR1 Signaling	8.19E-05	AMBRA1	Cell senescence and mitophagy	Inhibited
Glycolysis I	9.01E-05			

## Table 4: Predicted Top Upstream Regulators from RNA-seqdifferential expression in NPCS by IPA

Top Upstream Regulators	Biological Role	Predicted Activation
	Proto-oncogene/Development	
MYCN	Transcription dysregulation	Activated
POLG	Mitochondrial Polymerase	
NUPR1	Transcription Regulator	Activated
Alpha Catenin	Cytoskeleton and Cell polarity	Activated
RRP1B	Ribosomal RNA processing, Serine/Threonine associated	

epithelize and differentiation. Metabolism contains 8% of categories including carbohydrate metabolism, post-translation related biochemistry, and amino acid metabolism. All categories related to nephron development. Figure 23 B shows changes to molecules located throughout the cell meaning the cytoplasm, nuclease, mitochondria, and organelles.

Top canonical pathways by IPA are predicted to be changed based on the significantly changed RNAs in the RNA-seq differential expression analysis. Table 3 shows the top 5 predicted pathways. Eukaryotic initiation factor 2 or EIF2 signaling regulates the inflammatory

and cytokine response of cells. The 88 molecules changed in the EIF2 signaling pathway includes kinases, transcription and translation regulators, and several ribosomal proteins. mTOR signaling is a central regulator of metabolism, growth, proliferation, and survival. The pathway is A

Symbol	Entrez Gene Name	Expression Fold Change	Location	Type(s)
ENO1	enolase 1	2.119	Cytoplasm	enzyme
ENO2	enolase 2	3.084	Cytoplasm	enzyme
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	2.577	Cytoplasm	enzyme
GPI	glucose-6-phosphate isomerase	1.844	Extracellular Space	enzyme
PFKL	phosphofructokinase, liver type	2.153	Cytoplasm	kinase
РҒКР	phosphofructokinase, platelet	1.706	Cytoplasm	kinase
PGAM1	phosphoglycerate mutase 1	1.672	Cytoplasm	phosphatase
PGK1	phosphoglycerate kinase 1	2.152	Cytoplasm	kinase
РКМ	pyruvate kinase, muscle	2.234	Cytoplasm	kinase
TPI1	triosephosphate isomerase 1	2.064	Cytoplasm	enzyme



Figure 24 Glycolysis Increased in IUGR P0 Nephron Progenitor Cells:

A) Top molecules changed glycolysis by RNA-seq analysis of MACSs isolated P0 nephron progenitor cells (N{PC). Multiple glycolytic enzymes have increased expression in IUGR NPCs leading to glycolysis being a top pathway changed as predicted by IPA and iPathway. B) Seahorse extracellular Flux measurement shows increased glycolysis in MACs isolated NPCs. By ECAR or extracellular acidification rate. C) Seahorse measurement of OCR showing no change in oxidative phosphorylation. N=2 litters for Seahorse.

targeted in cancer treatment and is associated with diabetes. The 63 molecules changed identified by IPA as associated with mTOR are ribosomal proteins, AKT3, DNA damage response, translation factors, and vascular endothelial growth factors C & D. Regulation of eIF4 &

p70S6 kinase is part of the control of translation. It responds to stress, energy balance, hypoxia,

hormones, and growth factors. It is regulated by signals from mTORC1, Wnt, and PI3K/AKT.

There are 47 molecules identified by IPA as associated with regulation of eIF4 & p70S6 kinase.

Among the 47 molecules are several ribosomal proteins, AKT3, a number of translation

initiation factors, and insulin receptor substrates. Tumor necrosis factor 1 or TNFR1 signaling

affects inflammatory response impacting lipid metabolism, coagulation, insulin resistance, and endothelial function. TNFR1 signaling can be for both cell survival and cell death. There were 19 molecules changed in TNFR1 signaling with several apoptosis factors heavily downregulated, and Jun proto-oncogene AP-1 is upregulated. Glycolysis I is a top canonical pathway and has multiple kinases upregulated. The increase in glycolysis is confirmed by measurement of extracellular acidification rate (ECAR) using the Seahorse XF analyzer (Figure 25 A and B). NPCs were isolated using MACs and passage 0 cells were cultured and the Seahorse XF analyzer measured the acidification of seahorse culture media. It showed a significant increase in glycolysis in IUGR NPCs at P0. Oxidative phosphorylation, measured by oxygen consumption rate or OCR, is unchanged in the same IUGR NPCs (Figure 25 C).

IPA predicts the top causal networks from the differentially expressed genes (Table 4). MYCN functions in development and transcription dysregulation and is a proto-oncogene. NUPR1 is a second network activated associated with transcription dysregulation. SERPINH1 is also knows as heat shock protein 47 and is active in cell proliferation and collagen biosynthesis. Alpha catenin is a linker protein that functions in the cytoskeleton and cell polarity. AMBRA1 is inhibited in IUGR NPCs and is active in cell senescence, mitophagy, and autophagy by regulating protein turn over. AMBRA1 relates to cell senescence and mitophagy and is involved in neural development.

Table 4 shows the IPA predicted top upstream regulators based on the pathways IPA predicts to be changed based on the differentially expressed RNAs. MYCN was again present as activated, as was NUPR1 and Alpha Catenin. Polymerase G or POLG is the polymerase active in

A		
RNA	-Seq Differential Expression Upregulated ≥1.5	RNA-Seq Differential Expression
p53	Signaling Pathway	Downregulated ≥1.5
mTC	R Signaling Pathway	TNFR1 Signaling Pathway
Soni	c Hedgehog Pathway	Mitochondria Apoptotic Signaling
Oxid	ative Stress Induced Gene Expression Via Nrf2	WNt/LrP6 Signaling
Glyc	olysis/Glucogenesis	Regulation of Pluripotency of Stem Cells
FOX	O Signaling Pathway	P53 Signaling Pathway
В	Control	IUGR
20X Phosho-ATF-2/Cyto		

### Figure 25 RNA-Seq Differential Expression Up and down regulated ≥1.5:

A) The 1,694 upregulated genes previously used in IPA were uploaded into The **D**atabase for **A**nnotation, **V**isualization and Integrated **D**iscovery (**DAVID 6.8**) resulting in 1,354 DAVID IDs. The pathways found were P53 Signaling pathway, mTOR signaling pathway, Glycolysis/Glucogenesis, FOXO Signaling Pathway, Sonic Hedgehog Pathway, Oxidative Stress Induced Gene Expression Via Nrf2. B) Phospho-ATF2: stress marker upregulated by immunostaining of P0 tissue at 40X. N=3 for staining. mitochondria during mitochondrial replication. POLG is known to interact with TP53-inducible glycolysis and apoptosis regulator (TIGAR) and superoxide dismutase 2 (SOD2). TIGAR is a regulator of glycolysis, DNA repair, and cellular degradation of organelles. SOD2 clears reactive oxygen species form mitochondria and is active in

oxidative stress and apoptosis. RRP1B is a serine/threonine associated with ribosomal

biogenesis. RRP1B is also a transcription factor cofactor for apoptotic signals in response to

DNA damage.

There were no molecules that are present in all five top canonical pathways from IPA analysis and none of the predicted upstream regulators are present in all five top canonical pathways. Glycolysis I contained the most unique molecules altered with no shared molecules present in the other 4 top canonical pathways. It does contain the upstream regulators of GPI and PKM. EIF2 signaling, mTOR pathway, and regulation of eIF4 & p70S6 kinase pathway had the most similarity with over 40 identical molecules changed in all three pathways, most of which are ribosomal proteins. All three also contain the IPA predicted upstream regulators of EIF3E, IRS1, PIK3CG, and PIK3R1. The only duplicated molecule between the TNFR pathway and EIF2 is the upstream regulator XIAP. TNFR also contains the upstream regulators of FADD, JUN, MAP2K4, and MAP3K1. This shows that the top canonical pathways were not driven by the same molecular changes.

The Database for Annotation, Visualization, and Integrated Discovery (DAVID 6.8) is an analysis tool for functional annotation of large biological data sets. It provides functional interpretation based on large data sets. The uploading tool for DAVID allows only for gene lists, not expression level data unlike IPA analysis. DAVID analysis was done by splitting the significant data by up or down regulation (Figure 26 A). The previously identified 1,694 genes upregulated by RNA-seq were analyzed by DAVID (Supplemental Table 1, Figure 25).

There were six pathways identified from upregulated RNA genes shown in Figure 18A. P53 signaling pathway is a tumor suppressor that controls cell cycle progression and apoptosis. It has previously been described as a control mechanism for cell proliferation in first cancer and then development. Normal p53 function is required for normal embryonic development and balancing NPC differentiation and self-renewal with links to cellular metabolism. P53 was found by DAVID analysis of both down and up regulated genes. mTOR signaling is present again. Sonic hedgehog pathway was not in the IPA analysis but present from DAVID. Sonic hedgehog pathway is a developmental pathway that regulates tissue patterning during multicellular organisms, the formation of complex organs including the kidney, and cell polarity. Oxidative Stress Induced Gene Expression Via Nrf2 is a stress response pathway. Nrf2 signaling is related

#### A Wnt Differentiation Signal Decreased D Histone Modification

		6% NPCs		20% NPCs			
Gene Name	TPM	TPM	TPM	TPM	TPM	TPM	
Wnt9a	0.48	1.07	0.84	1.63	1.95	1.35	
Wntll	5.49	27.2	9.25	9.4	17.07	7.96	
Wnt5a	0.66	0.86	1.82	2.96	4.32	4.05	
Wnt16	0.73	0.77	2.33	2.55	2.78	1.98	
Wnt5b	7.01	5.3	10.61	19.18	16.46	15.79	
Wnt4	89.11	125.36	100.15	131.24	144.18	110.95	
WintSh	018	012	0.36	3 30	3 7 7	3.44	

#### B BMP Proliferation Decreased

		6% NPCs		20% N PCs			
Gene Name	TPM	TPM	TPM	TPM	TPM	TPM	
Bmp7	43.55	49.92	56.66	82.63	90.23	64.77	
Bmp4	13.11	13.87	23.81	37.6	43.53	43.07	
Bmp1	109	142.65	92.17	134.55	162.01	141.28	
Bmp 2	9.8	9.03	8.73	17.48	18.13	17.93	
Bmp3	0.62	0.51	1.6	2.91	4.96	2.62	
Bmp2k	11.68	10.09	10.61	7.6	8.04	7.98	
Bmp5	4.92	4.89	7.25	7.29	6.77	7.44	

#### C Fgf Signal: NPC Maintenance Downward Trend

		6% NPCs		20% N PCs			
Gene Name	TPM	TPM	TPM	TPM	TPM	TPM	
Fgf10	6.22	10.65	9.54	13.2	12.74	10.33	
Fgf9	2.57	0.53	4.68	6.87	4.34	5.61	
Fgf8	29.42	11.31	39.32	48.49	41.58	50.69	
Fgf20	0.69	4.22	2.05	6.96	11.84	5.47	
Fgfl	22.99	24.2	35.57	39.87	56.66	30.17	
Fgf2	0.42	1.81	1.92	3.37	4.32	2.34	
Fgf11	3,43	2.66	5.02	2.95	3.49	3.45	

			6% NPCs		20% NPCs			
I.	Gene Name	TPM	TPM	TPM	TPM	TPM	TPM	
35	Ezhl	24.65	23.36	42.01	29.46	39.85	35.54	
96	EzhZ	54.06	39.96	94	118.27	112.65	118.65	
.05	Hdac5	115.94	128.91	114.97	48.25	54.55	58.74	
98	Hdac2	113.91	114.19	132.85	181.5	171.05	158.5	
79	Hdac7	62.92	69.93	48.83	52.67	55.17	54.39	
95	Hdac3	62.19	65.72	65.96	81.55	79.24	78.33	
44	Hdac4	11.97	12.31	10.86	11.52	11.67	11	
	Hdacl	111.5	116.27	113.39	123.87	129.57	99.13	
	Hdac6	27.68	39.02	31.97	37.68	48.54	35.39	
	Hdacll	16.61	17.33	17.58	17.44	19.94	19.62	
	Hdac10	9.95	8.44	11.64	11.03	11.83	11.04	
	Hdac8	5.48	5.88	7.05	6.84	8.63	8.05	
_	Hdac4	12.51	13.57	9.51	11.11	12.21	9.91	
	Dnmtl	58.35	54.72	81.54	122.25	107.52	107.72	
	Dnmt3a	34.7	40.71	56.01	73.36	74.85	75.83	
77	Dnmt3b	5.22	4.58	6.56	9.65	10.52	9.87	
07	Sirt2	43.49	46.84	48.74	45.76	48.11	50.77	
28	Sirt1	31.27	32.92	28.73	22.57	25.07	26.5	
93	Sirt7	14.25	15.18	13.86	23.74	28.45	23.55	
62	Sirt3	18.57	19.21	19.83	17.9	18.33	18.83	
98	Sirt4	18.72	22.33	20.21	24.23	30.01	29.29	
44	Sirt6	25.21	36.54	34.52	35.94	45.35	44.83	
	Sirt5	1.58	1.82	1.98	3.46	4.74	4.57	
	Trp53	79.24	71.06	133.47	180.9	195.87	193.6	
	SinBa	33.88	26.79	47.5	53.59	53.67	65.67	
	Sin 3b	101.65	102.06	109.91	115.4	125.14	1 10.34	
	Sap130	15.22	16.01	27.28	37.26	38.11	37.35	
	ingl	41.5	53.8	55.43	55.39	56.74	59.8	
	Ing2	36.28	33.36	32.7	23.47	24.93	28.21	
	Mtal	151.35	146.62	161.21	157.88	158.3	155	
22	Mta2	108.77	118.29	111.54	117.91	127.11	120.69	
51	Mta3	34.61	40.91	42.59	41.39	38.53	41.53	
60	Mbdl	26.69	31.42	27.97	31.51	34.55	37.2	
47	MbdZ	48.08	50.73	57.32	75.06	75.35	78	
17	Mbd3	173.22	169.04	174.68	238.85	2 33.94	2 23.55	
2.0	Mbd4	4.33	5.69	7.17	10.34	11.55	11.63	
34	Mbd5	22.57	26.95	17.14	17.68	21.05	19.75	
45	Mbd6	100.75	98.62	61.87	65.93	88.72	76.92	

#### Figure 26 RNA-seq TPM Trends:

Transcripts Per Kilobase Million (TPM) is normalized RNA read number. Highlighted yellow are significantly changed in differential expression analysis. Shows average for NPCs from the three control and IUGR litters used for RNA-seq analysis.

A) The Wnt differential signal is decreased. B) BMP proliferation signal is decreased. C) Downward trend in Fgf maintenance signal. D) Histone modification signals are changed. HDACs associated with NPC maturation are decreased and HDACs that are associated with NPC differentiation are decreased. Factors changed are related to acetylation, methylation, glycosylation, and chromatin remodeling. Many are significantly changed while others are trends in TPM levels.

to environmental and metabolic stress. Glycolysis is the enzymatic breakdown of glucose producing energy and pyruvic acid while glucogenesis is the formation of glucose from glycolysis products. FOXO signaling pathway regulates apoptosis, cell cycle, glucose metabolism, and oxidative stress resistance. A major down regulator of FOXO signaling is the activation of Akt/PI3K pathways via insulin or growth factor signaling. FOXO is activated by JNK and AMPK, which respond to energy availability and nutrient stress. The activity of these pathways is related to phosphorylation, acetylation, methylation, and ubiquitylation as posttranslational modifications (Figure 25 A).

The 1,354 downregulated genes DAVID analyzed provided five pathways. TNFR1 signaling pathway was also present in the IPA results, confirming changes related to cell death and survival signaling, further confirmed by mitochondria apoptotic signaling. LrP6 is from the Wnt canonical pathway. Wnt canonical pathway feeds into β-catenin, a necessary part of NPC differentiation. Finally, the ability to maintain stemness is changed in the regulation of pluripotency of stem cells. The changes to cell stress are shown by staining of P0 tissue sections. There is an increase in Phospho-ATF2 throughout the kidney, but especially in the cap mesenchyme above the pan cytokeratin staining ureteric branching (Figure 25 B).

The sequencing data before differential expression analysis is shown as Transcripts Per Kilobase Million or TPM. TPM is calculated by read counts divided by the length of each gene in kilobases producing the RPK. The RPK values in a sample are counted up and divided by  $1 \times 10^{6}$  and then divide by a scaling factor to produce a TPM per gene for each sample. This provides a read number that is normalized by gene length. Looking at groups of genes related to development showed significantly changed genes and trends. Figure 26 A shows the differential signal Wnt trends down with three significantly decreased (Wnt5a, Wnt5b, and Wnt8b). The

NPC proliferation signal BMP has multiple molecules significantly down with more trending down without significance (Figure 26B). A second NPC maintenance signal Fgf trends down but with no molecules significantly changed (Figure 26C).

Previous work has shown that NPC differentiation and maintenance is regulated by the histone modification pathways HDAC and their co-factors. HDACs 1-4, 7, and 9 decrease with embryonic maturation. HDAC5, 6, and 8 are constitutively expressed, while HDAC1, 2, and 3 decrease with differentiation in NPCs and HDAC3 is high in podocytes. Histone modifications are known to respond to environmental factors. Figure 26D shows histone associated molecules. Ezh2 is significantly decreased along with Dmnt3a, and Dmnt3b. Ezh2 actively represses differentiation pathways. Hdacs 4, 5, and 7 were all significantly increased in IUGR P0 NPCs. HDACs act with transcription complexes Sin3, Mi-2/NuRD, Co-REST, and SMRT/N-CoR. HDAC/Sin3 complexes regulate cell proliferation, apoptosis, and cell cycle. Mi-2/NuRD is an ATP dependent complex that regulates chromatin remodeling. The Co-REST or RCOR1 complex is downregulated at birth and inhibits neural cell differentiation. SMRT/N-CoR complex is a repressor of cell checkpoint AP-1. The complexes share more components than just HDACs.

Sin3 histone deacetylase complex associated with HDAC 1 and 2, RBBP7 and 4, and SDS3. Sin3a was down regulated 1.27-fold and Sin3b was unchanged. The Sin3 associated growth inhibitor Ing2 is upregulated 1.63-fold. The Mi-2/NuRD complex includes Mta1 and 2 which were both significantly upregulated (1.29 and 1.2). The glycosylation associated Mbd4 was down regulated 1.49-fold with other Mbds trending down. Mbd3 was trending down in IUGR NPCs which inhibits induction of IPSCs. Multiple sirtuins were significantly changed

with IUGR. Sirt1 and 2 were both upregulated (1.62 and 1.27-fold), while Sirt7 is downregulated 1.30-fold while Sirt4-6 have no significant change are all trending down (Figure 26D).

The tumor suppressor gene Trp53 had a fold change of -1.59. Trp53, as previously described, is a link between embryonic development regulating NPC self-renewal and differentiation and metabolism. IUGR P0 NPCs also had significantly decreased Ezh2, Dnmt3a, and Dnmt3b and trending down with no significance were Ezh1 and Dnmt1 (Figure 26D). Ezh2 expression is associated with proliferation in the undifferentiated cells of the embryonic kidney. NPC maintenance and proliferation signals are significantly changed are known intermediaries between environmental signals and transcriptome regulation. This is evidence of changes t histone remodeling, glycosylation, metabolism, and NPC maintenance and differentiation in IUGR P0 NPCs.

The second analysis was by iPathway Guide Analysis. The alignment and differential expression analysis show 3791 differentially expressed genes all with p<0.05. There were 282 upregulated over 1.5-fold, 491 downregulated by 1.5-fold, and 3,018 genes statistically significant between -1.5 and +1.5-fold change (Figure 27). All significant genes were analyzed using the Kyoto Encyclopedia of Genes and Genomes (KEGG), Gene Ontology Consortium Database (GO), miRNA analysis from miRibase, and TARGETSCAN databases.

Gene Ontology or GO Analysis with highest FDR selected are in table 5. GO Biological process and molecular function analysis confirmed changes to metabolism and the ribosomal changes found in the IPA RNA-seq analysis. Cellular Macromolecule Metabolic Process are the chemical reactions that process macromolecules. Macromolecules are high molecular mass including proteins, glycoproteins, carbohydrates, polysaccharides, nucleic acids, and lipids. The processing includes metabolic, macromolecule biosynthesis, and methylation. Cellular metabolic


## Figure 27 RNA-Seq Differential Expression iPathway Guide:

With a p<.05 there were 3791 differentially expressed sequences with statistical significance. Of 23358 genes measured with expression. These genes were analyzed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database, Gene Ontology Consortium database, miRNAs from the miRbase, and TARGETSCAN databases. A total of 90 pathways were found to be significantly impacted with 2182 Gene Ontology (GO) terms, 41 miRNAs, and 46 diseases found to be significantly enriched. A) Shows the differentially expressed genes found by this analysis with 282 upregulated at or above 1.5-fold, 491 genes downregulated at or above 1.5 fold, and 3,018 between +1.5 and +0.6 and -0.6 and -1.5. All points are statistically significant.

# Table 5: Top GO Biological Processes RNA-Seq Differential Expression IUGRNPCs by iPathway Analysis

GO Biological Process Pathways	Differentially Expressed Genes	Total Genes	FDR
Cellular Macromolecule Metabolic Process	1707	7423	1.00E-24
Cellular Metabolic Process	2020	9195	1.00E-24
Primary Metabolic Process	1995	9174	1.00E-24
Nitrogen Compound Metabolic Process	1899	8628	1.00E-24
Metabolic Process	2154	10148	1.00E-24
Macromolecule Metabolic Process	1807	8173	1.00E-24
Organic Substance Metabolic Process	2059	9657	1.00E-24
Cellular Nitrogen Compound Metabolic			
Process	1336	5691	1.00E-24
Biosynthetic Process	1257	5324	1.00E-24
Organic Substance Biosynthetic Process	1241	5248	1.00E-24

processes are the reactions and pathways that transform molecules into energy for the cell. Primary metabolic process includes lipid metabolism, carbohydrate metabolism, protein metabolism, cellular amino acid derivative metabolic processes, and the metabolism of nucleobase, nucleoside, nucleotide, and nucleic acids. This includes catabolic, maturation, biosynthesis, metabolic, and regulation of these processes. The rest of the Go biological process pathways are subcategories of the previous processes and are nitrogen compound metabolic process, metabolic process, macromolecule metabolic process, organic substance metabolic process, biosynthetic process, and organic substance biosynthetic process.

The top GO molecular function found by iPathway analysis found a series of compound binding pathways (Table 6). The bonds are related to structures of macromolecules (heterocyclic compounds, nucleic acid, organic cyclic, ribosome, protein, and DNA), and cell activity (transcription regulation, transferase). Transferase activity relates to the movement of functional groups between molecules. Functional groups include methyl, alcohol, and others that change the activity and localization of the molecules being modified. The functions found in P0 IUGR relate to transcription activity, protein binding, and protein synthesis changes.

The top altered pathways were ribosome which process messenger and transfer RNA and synthesize polypeptides and proteins (Table 7). The AGE-RAGE signaling pathway in diabetic complications relates to glycation, MAPKs, NF-κB, Il-1, Il-6, TNF-alpha, JAK-STAT, and PI3K-AKT and signals into proliferation and apoptosis. MAPK signaling pathway is a signaling cascade that responds to environmental signals into the cell. MAPK signals relate to cell proliferation, differentiation, and migration.

Glycosphingolipid biosynthesis- globo and ispglobo series is a metabolic and biosynthesis pathway. The globo and isoglobo series specifically process GalNAca1 into

# Table 6: Top GO Molecular Function RNA-Seq Differential ExpressionIUGR NPCs By iPathway Analysis

	Differentially Expressed		
GO Molecular Function Analysis	Genes	Total Genes	FDR
heterocyclic compound binding	1179	5169	1.00E-24
nucleic acid binding	834	3414	1.00E-24
organic cyclic compound binding	1190	5258	1.00E-24
binding	2491	12604	1.00E-24
structural constituent of ribosome	80	147	1.69E-21
DNA binding transcription factor activity	305	1105	2.73E-15
transcription regulator activity	375	1434	4.26E-15
transferase activity	534	2241	1.43E-13
protein binding	1697	8514	2.07E-12
DNA binding	475	1996	8.45E-12

# Table 7: Top Altered Pathways RNA-Seq DE Show Energy Sensing and StressResponse

Pathway Name	Pathway ID	P-Value	P- Value(FDR)	P-Value (Bonferroni)
Ribosome*	3010	1.00E-24	1.00E-24	1.00E-24
AGE-RAGE Signaling pathway in diabetic complications	4933	1.34E-05	0.02	0.004
MAPK Signaling Pathway	4010	2.90E-05	0.003	0.009
Glycosphingolipid biosynthesis- globo and ispglobo series*	603	3.88E-05	0.003	0.012
AMPK Pathway	4152	6.85E-05	0.004	0.021

Pro	uning Type	: None		Pruning Type: Elim		Pruning Type: Weight	
GO Term	P-value	P-Value (FDR)	P-Value (Bonferroni)	GO Term	P-value	GO Term	P-value
Intracellular	1.00E-24	1.00E-24	1.00E-24	Cytosolic large Ribosomal Subunit	1.00E-24	Organelle	1.00E-24
Intracellular Part	1.00E-24	1.00E-24	1.00E-24	Cytosolic small Ribosomal Subunit	1.40E-18	Cytosolic Ribosome	1.00E-24
Intracellular Organelle	1.00E-24	1.00E-24	1.00E-24	Nucleus	6.10E-12	Intracellular	3.40E-24
Organelle	1.00E-24	1.00E-24	1.00E-24	Cytosol	6.50E-07	Nuclear Lumen	7.40E-10
Membrane-bounded Organelle	1.00E-24	1.00E-24	1.00E-24	Nucleolus	6.90E-07	Focal Adhesion	1.30E-06

## Table 8: Differential Expression Shows Changes throughout the Cell



## Figure 28 RNA-Seq Differential Expression Gene Track

Gene sequence tracks showing from GENCODE M14. Reference sequence is for mus musculus. The RNA isolated is from Cited1/Sx2 dual positive NPCs. A-B) NPC Renewal markers Six2 and Sall1. IUGR NPCs have no change in Six2 expression. Sall11 is lower in the IUGR NPCs by track and in both analyses. RNA-seq differential expression analysis has -2.246 fold change in IUGR NPCs. C-D) Jagged1 and Wnt4 are differential genes for NPCs. Jagged1 has much smaller peaks and has a fold change of -2.35. The Wnt4 peaks look a bit smaller but differential expression has no significant fold change. Average of 3 litters.

ceramide. AMPK pathway is a sensor of cellular energy status. It activates when the AMP:ATP

ratio increases from metabolic stress interfering with ATP production or an increase in ATP use.

Top cellular components show not just changes throughout the cell as shown by IPA

analysis but also changes to intracellular components of tissue (Table 8).

NPC renewal genes Six2 and Sall1 tracks show no change to Six2 while Sall1 is

decreased a change confirmed by a significant fold change of -2.25 (Figures 28, 15A & 15B).

The lack of change in Six2 and decrease in Sall1 is confirmed in staining data previous staining

data.

									Plasma Cre	atinine		Plasr	na BUN
Animal	Weight (g)	Kidney Weight (g)	Systolic (mmHg)	Pulse (bpm)	Diastolic (mmHg)	Mean Arterial Pressure (mmHg)	Glomerular Count Average Entire Sections	Glomerular Counts Average 10X Fields	μg/ml	mg/dL (x0.10)	Urine Albumin (g/dL)	Mean urea Conc. (mg/dL)	Mean BUN conc. (mg/dL)
20.7.M.1	48.9	0.99	128.08	711.01	65.8	87.81	183.33	6.67	0.5	0.05		39.66	18.53
20.7.M.2	49.4	0.798	123.43	703.02	67.99	85.89	144.67	6.33	0.8	0.08	0.056	67.15	31.38
20.7.M.3	49.8	0.656	149.07	706.90	83.55	105.12	91.33	6.00	0.8	0.08	0.139	79.30	37.06
20.23.M.1	45.7	0.705	122.33	695.11	72.09	90.75	145.67	6.67	0.4	0.04	0.078	64.24	30.02
20.23.M.2	51.8	0.756	120.83	695.21	68.54	86.17	136.67	5.67	0.3	0.03	0.095	71.18	33.26
20.23.M.3	54.1	0.852	124.46	713.44	67.85	86.66	152.33	7.33	0.6	0.06		52.62	24.59
20.23.M.4	50.3	0.801	130.45	698.29	72.75	92.97	148.33		0.6	0.06	0.12	105.45	49.27
20.7.F.1	43.6	0.456	123.96	561.28	74.01	96.26	115.00	6.67	0.7	0.07	0.034	69.36	32.41
20.7.F.2	43.7	0.475	105.40	546.11	64.79	79.61	125.33	5.33	1.0	0.10	0.059	83.96	39.24
20.7.F.3	40.2	0.545	133.75	658.70	86.54	102.53	122.33	9.00	0.6	0.06	0.05	56.58	26.44
20.23.F.1	34.3	0.4231	121.86	568.15	72.54	92.25	162.00	9.00	0.7	0.07	0.038	78.19	36.54
20.23.F.2	33.4	0.4743	143.88	712.12	85.98	105.33	149.67	6.75	0.7	0.07	0.075	65.31	30.52
6.7.M.1	49.1	0.555	115.65	645.55	59.90	79.45		3.67	0.6	0.06	0.112	70.07	32.74
6.7.M.2	50.1	0.573	127.99	657.41	76.33	94.85	135.00	5.00	0.7	0.07	0.114	60.09	28.08
6.7.M.3	36.9	0.409	131.00	603.15	80.55	98.46	90.00	5.67	0.8	0.08	0.059	81.66	38.16
6.23.M.1	39.5	0.544	178.06	559.92	116.48	137.84	43.33	3.75	1.4	0.14	0.477	86.79	40.56
6.23.M.2	48.5	0.698	120.89	651.66	66.25	86.07	135.67	4.00	0.6	0.06	0.26	65.26	30.49
6.7.F.1	34.9	0.39	119.28	698.58	65.01	84.09	123.67	5.67	0.8	0.08	0.038	73.17	34.19
6.7.F.2	32.7	0.431	130.44	672.87	75.90	95.19	130.33	5.00	0.7	0.07	0.041	65.11	30.43
6.23.F.1	45.8	0.376	130.44	672.87	75.90	95.19	131.33	5.67	0.7	0.07	0.139	83.72	39.12
6.23.F.2	46.6	0.385	119.95	656.74	62.63	79.80	102.67	5.00	0.8	0.08	0.057	70.54	32.96
6.23.F.3	49.7	0.428	112.80	745.05	65.41	83.24	103.67	6.33	1.2	0.12	0.352	91.18	42.61
6.23.F.4	42.9	0.4093	120.37	728.69	71.11	87.21	135.00	5.33	0.6	0.06	0.054	62.04	28.99

## Table 9: Adult Summary

Green background are control males, blue are control females, yellow are IUGR males, and orange are IUGR females. Animals come from 4 litters born on 1/7/2019 or 1/23/2019 and are either 20% or 6% parental diet. Systolic pressure has no significance, but IUGR male 6.23.M.1 has the highest systolic and diastolic blood pressure with the highest plasma creatinine and urine albumin levels. The IUGR female 6.23 F.3 has no change to blood pressure but has the second highest Plasma creatinine and urine albumin.

Despite large differences in the number of genes found to be significantly changed by the

two analyses the pathways implicated were very similar. Both show changes throughout the cell

and related to ribosomes, developmental pathways, metabolism, differentiation, proliferation,

and stress responses. The sequencing data itself supports the environmental signals altering

pathways that change cell character and activity.

## **Chapter 4 Discussion:**

IUGR mice from LPD are not just small mice at P0, but mice that continue to have developmental differences from control postnatally and into adulthood (table 10). The kidney is physically smaller before changes in size are apparent in with LPD. The severity of changes to kidney size persists even in adult animals that have caught up in weight with adult male 6.7.M.2 and adult females 6.23.f 1 and 2 (table 9). Kidney size is not just decreased in adulthood, but also shows a sex influenced change with IUGR showing female mice with the smallest kidneys in

adulthood. Sex differences are not found at P21 and could not be looked at earlier time points at sex was not recorded for earlier samples. This would be an important future direction when

<b>Table 10: Summary</b>	and	Timeline	of
Physical Changes			

NC: No					
Change					Kidney/
+:UP	Body	Body	Kidney	Kidney	Body
-: Down	Weight	Size	Weight	Size	Weight
E13.5		NC		-	
PO	-	-	-	-	+
P21	-	-	-	-	-
4 Month	NC	-	-	-	-

looking at kidneys at P0 and even embryonically as epigenetic regulation, which was greatly altered by the LPD, is known to vary with hormones.

Changes to the skin and hair of IUGR

mice postnatally are evidence of changes to cell cycle in stem cells with IUGR. Embryonically the skin begins as a single layer of epidermal stem cells (formed from the ectoderm) which rests on dermis from the paraxial mesoderm (Figure 1). The dermis will form hair follicles, sweat and oil glands, blood capillaries, nerve endings, and lymph vessels. Hair follicles form during embryogenesis from dermal papilla (specialized mesenchymal cells) which experience rapid proliferation postnatally. Hair growth comes from stem cells progressing through cycles of quiescence and activation which lead into proliferation, cell fate choice, differentiation, and apoptosis. This process will continue throughout the life of the organism as hair is lost and regrown. The process is regulated by growth factors, neutrophils, p53, TGF $\beta$ , and BMPRIa (a repressor of Wnt). This process relies on a stem cell compartment, cell to cell interaction, and interaction/availability of ECM. It is proposed as a model of stem cell quiescence and activation (Blanpain, C., Horsley, V., & Fuchs, E., 2008, Schmidt-Ulrich, R., & Paus, R., 2005, Alonso, L., & Fuchs, E., 2006). The morphological and morphometric changes in IUGR mice are evidence to changes to mesenchymal derived stem cells. The postnatal delayed skin and hair development supports changes to mesenchymal stem cells in IUGR pups from LPD. The germ layer is the same as the kidney and many signaling pathways for maintenance, proliferation, and

differentiation of the stem cells are the same between the kidney and skin development. The changes in IUGR pups come from changes to stem cell cycling and activation which leads to changes in differentiation and development. Unlike with kidney development, delayed skin and hair development has time to occur on a delayed schedule. Delayed kidney development will run into the wall of mass differentiation of NPCs at P4. Skin and hair development do not have that same end point with skin and hair growth continuing throughout adulthood. Changes in skin and hair development were present in all IUGR mice. Changes that persisted after removal from LPD conditions. As IUGR mice mature they lose the differences from control in appearance, but histology of the skin is a future direction for IUGR research.

IUGR embryonic kidneys have a deficit in Six2+ cells that are in poorly organized CMs as shown by FACS counting and immunostaining of whole organ and tissue section. The IUGR Six2+ population at P0 did not change in quantity from control as shown by count and staining (Figure 16 C, D, F). The deficit in embryonic IUGR kidneys has implications for proliferation and expansion of NPC populations. The lack of change in percent Six2+ population size in IUGR during development has implications for differentiation of NPCs and the intermediate and fully differentiated structures that form from the Six2+ NPCs. These changes are the core of why adult IUGR kidneys show damage and why there is a trend towards diminished kidney function. The changes to CM organization, Six2+ quantity, and Six+ as percent of total embryonic IUGR kidney from LPD are significant statistically and developmentally.

NPC balance between expansion/maintenance and differentiation is regulated by multiple pathways and mechanisms. This balance is essential for successful kidney development. The decreased quantity of Six2+ CM at e13.5 without changes to nascent nephron size or number at e13.5 shows changes to expansion and maintenance of the CMs. Changes to the balance of NPC

maintenance and expansion in the CM versus exiting the CM and differentiating would explain the deficit in differentiated structures in the kidney. This has been seen in previous work altering kidney development. IUGR has the addition of not just tipping the balance away from differentiation, but also decreasing expansion of the NPCs in the CM resulting in the smaller cap early in development and a smaller pool of NPCs for differentiation (Figure 29). The result is not just disordered differentiation, but NPCs that have shifted to survival and maintenance of stemness without expanding the CM they are within. The NPCs are then unable to respond to signals to differentiate at the appropriate time resulting in fewer NPCs to create differentiated structures, NPCs fighting the signal to differentiate through the pathways activated to fight apoptosis and differentiating NPCs that are poorly organized as they continue to signal to



### Figure 29: Epigenetic Reprograming Results in Changes to NPC Cell Fate

A) Environmental stress, in this case IUGR from low protein diet changes the epigenetics of parents and alters the maternal environment resulting in changes to the embryonic environment during the pregnancy. The changes to inherited epigenetics from both parents exposed to environmental stresses and changes to the embryonic environment will change the embryonic epigenetic programing from the beginning of embryogenesis.

B) Normal nephrogenesis by nephron progenitor cell (NPC) development requires a balance of Self-Renewal/Expansion in the cap mesenchyme (CM) and differentiation. Environmental stress, low protein diet in this case, changes this balance by decreasing the NPCs differentiating and increasing the Self-Renewal and maintenance of stemness in the CM. But the NPCs are not expanding the NPC population in the CM as shown by the smaller NPC pool at E13.5 and the lack of change in NPC pool over the course of development.

maintain stemness when development tries to progress. This is supported by the RNA-seq analysis and the molecular changes found in the IUGR kidneys.

The changes to the NPCs in the CM are at the start of kidney development. The changes in molecular composition to NPCs at P0 are a result of changes during all of kidney organogenesis (Table 1). Wt1 regulates Sall1, both decreased, and the regulators of NPC maintenance and proliferation BMP, FGF, MAP/ERK, and P-SMAD. All shown changed in RNA-seq at P0. Wt1 can be regulated by hypoxia-inducible factor  $1\alpha$  (Hif1 $\alpha$ ). Hif1 $\alpha$  is regulated in response to environmental signals by phosphorylation of the protein. Hifla did not change in the RNA-seq, which is expected when regulated on the protein level. Hypoxia-inducible factor 1alpha inhibitor (Hif1na) is also activated by environmental stress signals to the cells, it is upregulated by 2.72-fold in the RNA-seq. The upregulation of Hif1na and pathways downstream of Hifla is evidence of its upregulation. Hifla is an upstream regulator of glucose metabolism, apoptosis, proteolysis, angiogenesis, erythropoiesis, cell proliferation and survival, and pH regulation (Masoud, G. N., & Li, W. 2015). Hifla regulates p38-MAPK, ARK1/2, VEGF, p53, Myc, and metabolism pathways. This makes Hifl $\alpha$  a strong possibility for the upstream regulator that connects environmental signals of LPD to molecular and physical changes in the developing kidney. This would also explain why so many hypoxia related causes of IUGR exist in epidemiology and in IUGR animal models (glucocorticoid treatments, hypoxia via a chamber or surgery, umbilical artery ligation, uteroplacental embolization). Of further note is the expression of Hifl $\alpha$  in the epithelial cells of the ampullae in the collecting ducts of the kidney which are present in e13.5 IUGR kidneys at an unusually high rate. Hif1a is present in the CSB and SSB during glomerular development, but not in the mature glomerular in rats (Bernhardt, W. M., Schmitt, R., Rosenberger, C., Münchenhagen, P. M., Gröne, H. J., Frei, U., Warnecke, C.,

Bachmann, S., Wiesener, M. S., Willam, C., & Eckardt, K. U., 2006). Making it a candidate for changes in the development of first the UB and then collecting duct of the kidney. Hif $2\alpha$  is also present in the developing kidney and any future work exploring hypoxia inducible signals would need to consider both molecules as candidates for regulators in response to changes in maternal environment.

The pathways changed in the RNA-seq and confirmed in extracellular flux measurements and immunofluorescent staining is likely from epigenetic modifications. Histone modification is a known regulator of NPC maintenance and differentiation. NPCs, nascent nephrons, and epithelial tubules all have unique histone modifications (McLaughlin, et. al. 2014). Old vs. young NPCs show different chromatin landscapes with old NPCs poised for differentiation. The transcription factors Bach2 and AP1 were proposed as a link between renewal signaled by MAPK/AP1 and the Six $2/\beta$ -catenin regulators of NPC differentiation. In ATAC-seq previous work on the binding motifs of Bach2, AP1, and BATF all showed changes in enrichment of binding sites with NPC age. Bach2 is also an active transcription factor in the distal RV. (Hilliard, S., Song, R., Liu, H., Chen, C, Li, Y., Baddoo, M., Flemington, E., Wanek, A., Kolls, J., Saifudeen, Z., & El-Dahr, S.S., 2019). These histone modifications are essential for the formation of mature glomeruli by testing knockouts of HDAC 1 and 2 (Liu, H., Hilliard, S., Chen, S., Yao, C., Li, Y., Chen, C., Liu, J., Saifudeen, Z., & El-Dahr, S.S., 2018). Multiple HDACs associated with differentiation of the NPCs are decreased while HDACs that decreased with NPC maturation are increased in the IUGR NPCs. The massive dysregulation of epigenetic components like HDAC, Ezh, and Dnmt are a potential source of the large changes found in the RNA-seq. The chromatin regulators associated with differentiation are decreased in IUGR NPCs while maintaining high levels of regulators involved in maintaining stemness. Changes to the

histone landscape of NPCs would come from regulation of these factors and the components used in histone modification. The changes to cellular metabolism found in RNA-seq and cellular flux relate to the histone landscape as products from metabolism are essential for histone modifications. Metabolism products such as nicotinamide adenine dinucleotide (NAD), Acetyl-CoA, SAM,  $\alpha$ -keotgluterate, and flavin adenine dinucleotide (FAD) are cofactors for methylation, acetylation, and thus the epigenetic landscape (Berger & Sassone-Corsi 2016). The RNA-seq shows changes to the expression level of many enzymes used in metabolism pathways, and the increased glycolysis measured by extracellular flux confirms changes to pathway activity levels. The difference in kidney growth from P0-P21, outside of LPD conditions and in the same environmental conditions of control pups, is strong evidence that these changes are persistent and alter development and growth of IUGR pups even after progenitor cells have differentiated. The physiological changes are not just to the embryonic or P0 CM.

P0 IUGR pups were smaller than control with smaller kidneys (Table 10). These smaller kidneys had changes to structure and differentiation that began early in development. There are significant changes in branch tip number at e13.5 showing early changes to the developing collecting duct from LPD. At P0 the markers for the collecting duct structures and patterns are unchanged, but the gaps between Six2+ caps along the cortex are evidence of changes in the ureteric tree. Kidney size is driven by ureteric development with decreased branching and elongation leading to smaller kidneys (Short & Smyth, 2016). At the advancing end of ureteric branching in the cortex of the kidney there are the P63+ ureteric bud tip cells (UBTC). The proliferating UBTC are the progenitors of all cells in the collecting duct and will lengthen the ureteric branches, expand the kidney, split the CMs, and through crosstalk signal the maintenance, expansion, and differentiation of the NPCs of the CMs. UBTC maintenance and

proliferation are not perfectly characterized, but Wnt/ $\beta$ -Catenin signaling is known to play a role in the UBTCs that are P63 and Sox9 positive (El-Dahr, et. al. 2017). IUGR at P0 showed increased Sox9 staining at the P63+ UBTCs (Figure 18). P63 is of interest in cancer research where it is known to regulate cell adhesion, movement, and cellular metabolism. P63 maintains proliferative potential of epithelial cells and it activates the transcription of hexokinase 2, the first step in glucose utilization and part of mitochondria function regulating the ADP/ATP ratio. Loss of P63 in transgenic mice causes defects in fatty acid oxidation and obesity (Candi, E., Smirnov, A., Panatta, E., Lena, A. M., Novelli, F., Mancini, M., Viticchiè, G., Piro, M. C., Di Daniele, N., Annicchiarico-Petruzzelli, M., & Melino, G., 2017). P63 in the ureteric branches is temporally and spatially regulated, first being detected in the UBTCs at e15.5 and being lost at P5 (El-Dahr, S. S., Li, Y., Liu, J., Gutierrez, E., Hering-Smith, K. S., Signoretti, S., Pignon, J.-C., Sinha, S., & Saifudeen, Z., 2017). The embryonic branching in IUGR pups and the cells directing that branching were not isolated as the NPCs of the CM were, but they are in a similar microenvironment as the NPCs. The environmental stress signals apparent in the RNA-seq of P0 NPCs will also be interacting with the UBTCs. If P63 regulating metabolism is directing UBTC activity as it does in cancer, then the changes to metabolism found in NPCs is a future direction of study for ureteric branching in normal and IUGR kidneys. Isolating P63+ UBTCs would provide RNA-seq and protein data to show metabolism activity. The branching issues in IUGR could be from increased glycolysis as found in IUGR NPCs as decreasing P63 leads to decreasing glucose metabolism in cancer cells. P63 decreases as UBTCs differentiate to form the ureteric branches behind the UBTCs as the UBs elongate and branch to form first the ureteric tree and then collecting ducts of the kidney. If glycolysis is artificially high the UBTCs would be maintaining a progenitor state and not form the non-progenitor cells that make up the elongating

ureteric branches. Cell adhesion and migration were highly dysregulated in the IUGR P0 NPCs and their products of differentiation. If the stress response pathways are also impacting cell adhesion and migration in the UBTCs, they could be unable to organize and move as needed to elongate the ureteric tree and grow the kidney.

The changes in development across the IUGR mice, the RNA-seq of the P0 NPCs, and the persistence of those changes after exposure to the LPD shows IUGR NPCs and kidneys have changes to the histone landscape. The histone landscape is known to not only change during development of the kidney but to direct and be essential for it. The NPC chromatin landscape changes between young (E13, E16) and old (P0, P2) NPCs via ATAC-seq analysis in Hillard et. al. 2019. The chromatin landscape also varies between high and low GFP NPCs at P0 with GFP varying with level of Six2 as the mice are a Six2CreGFP mouse. The high GFP/Six2 cells are the renewing NPC population while low GFP/Six2 are primed for or beginning the process of differentiation. ATAC-seq analysis of old versus young NPCs showed distinct changes to the chromatin landscape with development. Both NPC populations are Six2+ and yet old NPCs are primed for differentiation and young NPCs are a self-renewing population. There are distinct changes in chromatin accessibility and predicted gene activity with a high presence of stem cell maintenance genes and pathways in young NPCs and high differentiation genes and pathways in old NPCs. Specifically, there is a 2.4-fold increase of Six2 in young versus old NPCs, and a 16fold change in Old NPCs compared to young for Wnt4. Among the changes from young to old NPCs is the increased accessibility of Bach2/AP1 transcription factors. Overall young NPCs have more cell growth and cell cycle while the old NPCs tend towards differentiation functions like cell-to-cell junction and inactivation of the MAPK pathway (Hilliard, S., Song, R., Liu, H., Chen, C., Li, Y., Baddoo, M., Flemington, E., Wanek, A., Kolls, J., Saifudeen, Z., & El-Dahr,

S.S. 2019). Hillard et. al. 2019 shows that the chromatin landscape changes over development and that the regulation of pathways created NPCs poised for the epithelization which occurs with nephrogenesis. These changes are present in old versus young NPCs and the high versus low GFP/Six2 NPCs sourced from the same P0 kidneys. The changes to the character of the CM niche are intrinsic changes to the cells and not environmental signals from the niche. Hillard et. a. 2019 hypothesizes the chromatin remodeling is mediated by epigenetic machinery like NuRD/HDAC, ATP-dependent chromatin remodelers, and DNA methylation. These are found dysregulated in the IUGR P0 NPC RNA-seq. IUGR does not have the same penetrance and severity as the genetic models of chromatin dysregulation, but the chromatin landscape is clearly changed by LPD and chromatin landscape changes direct NPC renewal and differentiation and has caused fatal mouse phenotypes in knockout models who fail to develop functional renal systems.

H3K27me3 is an epigenetic modification associated with downregulation of nearby genes. The presence of the tri methylated H3K27me3 forms heterochromatic regions that are tightly packed making those regions of the DNA inaccessible to translation machinery. It is enriched in NPCs relative to the rest of the nephrogenic zone. Loss of Ezh1, a component of the complex that mediated methylation of H3K27, does not change the relative prevalence of H3Kme27 in the developing kidney. However, loss of Ezh2 resulted in the loss of H3K27me3 in NPCs and their derivates while its presence in the stroma, UB, and CD is normal. Ezh2 knockout causes a decrease in NPC proliferation, a thinner CM, downregulated Cited1, and fewer nascent nephrons with less Lhx1, Pax8, and Wnt4. There is a 30% decrease in GFP+ NPCs with the Ezh2 knockout. Cell cycle is altered along with an increase in apoptosis. Dual inactivation of Ezh1 and 2 caused early activation of Wnt4, and a decrease in Six2 the net result being early

differentiation of the CM but fewer differentiated structures in the final kidneys along with cysts and poorly developed kidneys. The loss of Ezh1 and 2 in NPCs resulted in premature differentiation as they failed to maintain stemness (Liu, H., Hillard, S., Kelly, E., Chen, C., Saifudeen, Z., & El-Dahr, S.S., 2020). Kidney development requires careful balance that utilizes epigenetic regulation to progress properly. Epigenetic changes are susceptible to environmental signals and result in lifelong changes to organisms.

The IUGR adult mice are not significantly changed in measurements of kidney function. Physiological changes are present in adult IUGR mice. The IUGR adult mice have significantly decreased glomeruli and many of the IUGR adults have damaged kidneys. The lack of disease state from just IUGR is explainable from the multi-hit theory of disease in humans. The multi-hit hypothesis is supported in disease progression of nonalcoholic fatty liver disease (NAFLD) and nonalcoholic steatohepatitis (NASH). NAFLD is the accumulation of triglycerides in the liver without excessive alcohol consumption. NAFLD occurs in approximately 30 to 40 percent of adults in the United States, of those 20 percent have NASH with the rest of NAFLD patients having fatty liver disease. NASH occurs in NAFLD patients where the fat build-up leads to inflammation and scarring, fatty liver patients do not have inflammation (CDC: NCCDPHP, 2020). NAFLD patients with fatty liver disease typically do not have further symptoms, while NASH patients can develop cirrhosis and liver failure requiring a liver transplant. The development of NASH and NAFLD is believed to be caused by a multi-hit system where patient's dietary habits, environment, and genetic predispositions, also causing a high comorbidity with insulin resistance, and obesity, lead to the formation and build up triglycerides in the liver. The build-up of fat in the liver is not itself enough to damage the liver. Triglycerides and inflammation from ER stress and ROS cause inflammation, apoptosis, and fibrosis lead to

the more serious NASH. The ER stress and ROS can be caused by a variety of factors from the environment or genetics with many related to metabolic pathways (Buzzetti, E., Pinzani, M., & Tsochatzis, E. A., 2016). There is also a two-hit hypothesis for Alzheimer's disease with oxidative stress and aberrant mitotic signaling both capable of initiating, but Alzheimer's developing only when both occur (Zhu, X., Lee, H. G., Perry, G., & Smith, M. A., 2007). Alzeheimer's, NAFLD, and NASH are linked to a multi-hit model of disease with both neurological and liver diseases associated with metabolic and inflammatory changes. Metabolic and inflammatory changes are found in the IUGR kidney.

The multi-hit hypothesis is key in the current study and understanding of kidney disease. IgA neuropathy (IgAN) is the most common glomerulonephritis worldwide. It is the inflammation of the filtering glomerulus. The majority of IgAN occurs sporadically while 5-10% occur in families, but both familiar and sporadic IgAN are linked to genetic factors. IgAN is an autoimmune disease with pathology caused by a multi-hit system. Unknown upstream factors lead to the formation of galactose deficient IgA1, which is recognized by an autoantigen, this can then lead to inflammation of the kidney in response to antigen complexes, these immune cells form deposits in the kidney and activate the mesangial cells. Mesangial cell activation causes protein build up and lesions in the glomerulus. It is believed that the multiple steps of this process are regulated by environmental and genetic factors. The galactose deficiency comes from improper O-glycan processing in B cells. IgAN patients show deficiencies in glycosyltransferases and an increase in sialyltransferases. These enzymes are under the regulation of interleukins which respond to cell or organism stress. Mesangial activation by inflammatory signals varies based on receptor activity and sensitivity. The IgAN multi-hit hypothesis of disease comes from layers of environmental and genetic factors coming together

rather than single events of causation (Lai, Tang, Schena, Novak, Tomino, Fogo, Glassock 2016). IUGR kidneys also showed evidence of dysregulation of sialylation and glycosyltransferases. The complete loss of DBA staining in five IUGR mice at P0 is of interest as the DBA lectin binds α-linked N-acetylgalactosamine. As co-staining shows the distal tubules are present it is the specific glycosylated amino sugar that is lost. This is supported by expression changes in glycosylation related genes in the RNA-seq of NPCs. All animals that lack DBA staining have decreased NCAM staining in the CSB and SSB with clear NCAM staining in the mesenchymal CMs. The NCAM loss in differentiating structures is also present in animals that have DBA staining. NCAM is a cell adhesion molecule and as NPCs condense and epithelialize during differentiation NCAM localization changes. It has been shown that NCAM staining is colocalized with staining for polysialic acid along the basolateral membrane of the epithelial structure of the differentiating kidney. This co-localization is not present in the mesenchymal staining by NCAM. NCAM is polysialylated during late embryonic development. Polysialylation is a signal for localization within the cell. NCAM can be at the basolateral membrane in CSB and SSB without polysialylation, but it was suspected that it will not be concentrated there without polysialylation (Lackie, Zuber, & Roth, 1990). The dependence of NCAM localization and binding function is supported by its role in neural development where polysiallylation is required for NCAM to NCAM binding during development (Rutishauser, 1988 & Galuska et. al. 2017). IUGR has alterations of molecular modifications that are already known to lead to kidney damage in a multi-hit system.

The separate and combined roles of genetics and environment on nephron endowment and kidney function is supported by research into hypertension. There are genetic components like Pax2 mutations and chromosomal disorders causing oligomeganephronia, or the smaller

kidneys with decreased nephron endowment in p53 mutants and environmental factors, like IUGR and maternal smoking, causing decreased nephron endowment. Extremely low nephron endowment is sufficient to cause hypertension, but this is less common than the wearing down of kidneys born with low endowment. Humans are born with between 250,000 and over 2 million nephrons, with most having 1 million nephrons. Those at the lowest end of the range would have immediate complications when fully one third of the cardiac output is pumped into kidneys with so few structures to process it. But what of those with lower, but more normal nephron endowments? Human nephron endowment is inversely linked to age with an estimated 4500 glomeruli lost per kidney per year through all of adulthood. A person could then expect to lose 450K glomeruli between two kidneys over 5 decades of life. The person starting with 1 million glomeruli and ending with 550K is in much better shape than a person starting with 700K glomeruli and ending with 250K. This level of glomeruli loss comes from the 2010 study Effects of aging on glomerular function and number in living kidney donors by Tan, Busque, Workeneh, Ho, Derby, Blouch, Sommer, Edwars, & Myers. Donors older than 55 compared to those younger than 45 showed the lowest quartile of estimated glomeruli per kidney. Older subjects had nearly a quarter of the median estimated glomeruli per kidney then in the younger group with comparative decrease in kidney function as measured by glomerular filtration rate and increased rates of sclerosis in older subjects.

The multi-hit theory for CDK from IUGR is further supported by a 2011 twin study by Rajan, Barbour, White, and Levin. Where monozygotic twins that are identical in genetics and maternal environment have different kidney disease states as adults with Alport syndrome. The case study traced the more rapid progression of kidney failure to the twin being born with IUGR and decreased nephron endowment at birth. Twin A was 5 lbs. 9.5 ounces at birth and Twin B

was 4 lbs. 9.8 ounces. Twin A just misses the cut off for IUGR in humans, 5 lbs. 8 ounces, while Twin B is clearly IUGR. Both twins have kidney issues as adults, but Twin B has severe problems with kidney function. Both are medicated, but Twin B has had high urine albumin and low estimated glomeruli filtration rate his entire adult life and Twin A has been able to keep urine albumin low and maintained glomeruli filtration into late adulthood. Kidney function is not just genetics or maternal environment as both create a range of outcomes in adulthood. The impact of later challenges to kidney function cannot be ignored in studying kidney disease.

IUGR from LPD alone is not causing hypertension or CDK in adult mice. But given the complexity of disease causation in mice and humans it should not be expected to. IUGR is impacting the developing tissues of the kidney and changing the organ that is formed, but it is not sufficient to cause adult diseases at 4 months. The animals produced would be at high risk if faced with another hit. The next step in IUGR study would be to look at the IUGR model with multiple hits. There are several established genetic models for kidney disease that would serve as a model for populations with genetic predispositions for hypertension combined with an environment of deprivation. This would be of interest for hypertension in African American populations as they have an increased rate of hypertension, CDK, and kidney failure. There are known genetic predispositions in the African American population and the socioeconomic issues faced by the population could easily mimic a genetic predisposition combined with micro or macro malnutrition during development. There are also models for challenging kidney function in adult mice including diet changes, injury, or stress. This would model situations where an adult was gestated during a time of deprivation and faced a challenge to their renal system as an adult by either injury or poor diet. IUGR by parental protein restriction is a sledgehammer to the developing mouse impacting multiple pathways throughout the cell and organism. These

pathways are associated with development and adult renal diseases. For all the changes that occur from IUGR, they are not targeted like genetic models or models of injury in adult mice. The more general harm from these varied changes is of use in further study of ways humans develop hypertension and CDK over a lifetime.

The complexity and severity of the changes in IUGR kidneys means intervention to prevent IUGR can be tested at multiple points and with environmental, drug, and genetic interventions. The first changes with LPD are to the epigenetic programing of the adult mice that will be used for breeding, so changes will be present before fertilization. But a good starting point would be the mesoderm which forms at E6.5 from the primitive streak and further differentiate into many critical organs of the body including the entire urogenital system via the intermediate mesoderm (Figure 1 and 30). The intermediate mesoderm will be marked first by Osr1, then later by Pax2, Pax8, and Lhx1. This offers options for genetic intervention during the development of IUGR mice. Cre-Lox mice can be used to create a knock-in or knock-out genetic model specific to the intermediate mesoderm to rescue partially or completely the pathways impacted by the IUGR signals of stress that re-programmed the developing mouse and its kidneys. Based on the RNA-seq published research into kidney development genetic options include p53, mTOR, one of the changed genes in Glycolysis or a known regulator of Glycolysis. The goal would be to inhibit the stress response of the cells to undo or prevent the epigenetic reprograming caused by IUGR. Intervention at E6 or E6.5 is possible, but difficult and would not model many realities of IUGR. This intervention could work for planned pregnancies for humans with chronic medical conditions, or at high altitude, but would not be useful for humans with other causes of IUGR. Early restriction of calories or micronutrients that was stopped, as in some of the subjects from the Dutch Famine cohort, would the reason for the next potential

intervention point for IUGR. The nephric duct and metanephric mesenchyme have both formed by E10. The development of the metanephros will begin at E10.5 with the growth of the UB out of the nephric duct into the neighboring metanephric mesenchyme and the formation of the cap mesenchyme (Figure 2 and 30). This represents all cells needed to form the adult kidney being in one place for the first time. Embryonic kidneys can be harvested at this time for organ culture providing not just genetic manipulation, but also efficient uptake of drugs as previously used by our lab to change kidney development. Partial glycolysis inhibition, proven to prime NPCs for differentiation under normal conditions, can be done by YN1 and may normalize the IUGR NPCs to create normal differentiation rather than the decreased development found in IUGR. For environmental intervention the maternal diet could be changed to normal at this or other set times, this is unlikely to result in large changes in IUGR as shown by studies like the Dutch Famine cohort and what is known of the long-term changes form epigenetic programing during development. The NPCs at E11.0 are Cited1/Six2 dual positive making genetic models possible either through constitutively active or inducible Cre-Lox systems. These could target known regulators of cellular stress or kidney development. The goal would be to inhibit stress response pathways, and activate cell replication pathways, developmental pathways for the kidney, and to possibly inhibit the stem cell maintenance pathways as maintaining the NPC population is already being done by the IUGR embryos. The smaller pool of NPCs at E13.5 and lack of change in NPC pool over the course of development (Figure 16), shows that stemness is maintained probably to the detriment of the developing kidney and adult structures. Instead Wnt and FGF maintenance signals from the UB and BMP and FGF signals from NPCs should be inhibited so NPCs can be primed for differentiation. Previous work by our lab showed that

partial inhibition of glycolysis will accomplish this priming and it can be done genetically in the Six2 population or by use of many anti-cancer drugs.

Moving into later kidney development an important shift is at E15.5 when NPCs normally change from "young" to "old." At this time their cell metabolism changes from glycolysis dependent to oxidative phosphorylation, epigenetic changes occur showing the NPCs are unique from earlier NPC pools and shifting increasingly into a state primed for differentiation rather than maintenance and expansion of the CM (Liu, 2017). These cells remain Cited1/Six2 dual positive meaning an inducible genetic change is possible at this time. Decreasing glycolysis in the progenitor population, inhibiting p53, or mTOR at this time has the potential to partially rescue the IUGR kidneys as they complete development. A large amount of nephrogenesis occurs at the end of kidney development, with much occurring postnatally in mice. Intervention at this stage is unlikely to fully recue development but would be a realistic model of IUGR in humans when a problem is discovered late in pregnancy. Embryonic organ culture is not an option at this stage, but the isolation of large populations of NPCs either for culturing or analysis is possible. Experiments with NPCs would show a simpler system of the genetic or pharmaceutical changes to developmental pathways and the impact on RNA-seq and the epigenetic landscape from interventions before and at E15.5.

The final time point for intervention is postnatal day zero (P0). There is evidence that subtle intervention at P0 would not improve kidney development as shown by the changes to IUGR in both skin/hair and kidney development despite controlling for breastmilk quality and access in the P21 and adult mouse samples. Despite this it would be easy to access a large number of NPCs for experimentation and easily get drugs or induce genetic mutations at this time point. A large signal to differentiate, either through inhibiting Six2, Sall1, Mdm2,

glycolysis, or the Wnt9b signal from the UB. A combination of these interventions would be possible at P0. This would model late intervention of IUGR in humans which is expected to occur given the lack of access to prenatal care worldwide.

This project focused on the NPCs, CM, and nephrogenesis and did not focus heavily on the UB and the UBTCs. The UBTCs are an important focus in the future of IUGR research not just in relation to the crosstalk with NPCs, but as they are crucial in forming and expanding the kidney. The obviously smaller kidneys with IUGR are strong evidence that UBTCs are changed by IUGR. It is possible to genetically manipulate the UBTCs and any environmental or drug change done in utero would impact the UBTCs. The MACS isolation protocol can be altered to isolate NPCs and UBTCs from the same kidney simultaneously providing an important part of the puzzle. This paper theorized that the changes in the NPCs from environmental stress would be present in the UBTCs as they share a microenvironment and RNA, protein, and epigenetic analysis would easily show not just if the same pathways are changed but provide insight into what those changes have led to in development of the ureteric branching of the IUGR kidney. Any intervention in IUGR must consider the UBTCs neighboring the NPCs explored in this paper.

The interventions also need to consider the appropriate time for determining if the intervention worked. An early indicator are the previously described changes to mouse behavior and delay in growth and development of the skin and hair making the end point around P15. The clearest direction for an end point is having IUGR mice progress to a disease state. Obviously, some IUGR must be grown until they are actually older and not just in the young adult stage of 4 months. IUGR mice grown to 18 - 24 months would provide a model for an elderly IUGR patient and would determine if IUGR alone can cause kidney disease (Hagan, 2017). Models for

the multi-hit theory of disease would likely not need to use mice at that age and would be expected to find disease state much earlier, but still after the 4-month time point used here. The multi-hit model in IUGR could use environmental and genetic as the intervention studies did. High salt and high fat diet have both been used to cause renal injury in mice and could act as a second hit in adult IUGR mice, modeling the poor diet available to many that develop kidney disease. Alternative genetic hits would include the Six2P53 mutants used in the Saifudeen lab, or the combination of diabetic mothers from the *Ins2*<sup>+/C96Y</sup> mice previously shown in Cerqueira et. al. 2019 to have changes to kidney function in their wild type offspring. The contributing factors for the multi-hit models can be other challenges during development either through genetic changes, or further environmental strain. They could also occur postnatally but during childhood; poor diet post birth using LPD females for poor quality breast milk, low quality diet given to a previously well-fed mouse leading into poor diet then for the IUGR offspring as they wean.

Central to the intervention and multi-hit models for IUGR are the cellular pathways LPD changed to create IUGR. IUGR from LPD adds to kidney research that environmental changes are altering the previously identified metabolic, histone, and cell cycle pathways to change kidney development by early re-programing. Future work with IUGR will be in the exploitation of this, or stopping or re-writing this re-programming.



#### Figure 30: Proposed Points of Intervention for IUGR Development

IUGR from Low protein diet results in changes from the beginning of embryonic development. Multiple points of intervention must then be explored from early in embryo development up to the very end of kidney development. Potential interventions are diet to compensate for thrifty developmental signals, to genetic manipulation of the pathways changed by low protein IUGR. A) Rescue of Mesenchyme: Mouse development runs to approximately embryonic days 18 to 21. At the very beginning cleavage and blastulation starts before the embryo has even implanted. These steps already begin differentiating into germ layers. The mesoderm, the source of mesenchyme which give rise to the urogenital system, forms on e6.0 after implantation. The primitive streak and formation of the mesenchyme are on e6.5. Intervention at this point would change the programing signals of the mesenchyme from low protein parental diet. B) The mesenchyme does not begin formation of the metanephric kidney until E10.5. An intervention at E10.0 or E10.5 could either reprogram the forming cap mesenchymes, or prevent their reprograming by low protein diet if earlier exposure to low protein diet had yet to change their character. C) NPCs, formed from the metanephric mesenchyme and maintained by the signals of UB, shift from "young" to "old" at E15.5. At this time the cell metabolism, epigenetic regulation, and maintenance versus differentiation signals change. IUGR has shown differences to kidney development between e13.5 and PO, this would-be late intervention for the NPCs that have spent 2 weeks receiving the signal from low protein environment. D) The latest point of intervention would be PO. After birth increasing the signal to mass differentiate NPCs as control mice do would be expected to have only a small change in kidney development. But presents a model for human disease intervention. Modified and using graphic from Xu, Y.H., Barnes, S., Sun, Y., & Grabowski, G.A.. 2010.

Supplemental Table 1: RNA-Seq Fold Change in LPD NPCs				
Ensembl_id	Gene Name	Fold Change in LPD RNA		
ENSMUSG0000048938	Nr1h5	202.46		
ENSMUSG0000078889	Gm14288	142.55		
ENSMUSG0000081516	Gm12470	90.96		
ENSMUSG0000090381	Gm6158	85.57		
ENSMUSG0000078436	Gm4767	84.42		
ENSMUSG0000078284	Cdc73	82.69		
ENSMUSG0000091084	BC065403	43.21		
ENSMUSG0000070979	Actl7a	36.15		
ENSMUSG0000058922	Gm10052	35.24		
ENSMUSG0000083650	Gm13357	23.13		
ENSMUSG0000037887	Dusp8	21.12		
ENSMUSG0000091106	Gm17625	20.61		
ENSMUSG0000073741	4732440D04Rik	20.20		
ENSMUSG0000048153	Olfr49	17.31		
ENSMUSG0000090516	Gm6202	17.03		
ENSMUSG0000072451	Gm10359	16.79		
ENSMUSG0000083207	Gm14780	16.12		
ENSMUSG0000090992	Gm17588	16.02		
ENSMUSG0000087579	1500017E21Rik	15.96		
ENSMUSG0000082686	Gm12961	15.87		
ENSMUSG0000082374	Gm12741	15.33		
ENSMUSG0000091997	Gm6611	14.65		
ENSMUSG0000090885	Gm3944	14.56		
ENSMUSG0000090980	Gm17274	13.98		
ENSMUSG0000054136	Adm2	13.35		
ENSMUSG0000092509	Gm20394	13.22		
ENSMUSG0000089651	Gm16353	13.17		
ENSMUSG0000044352	Sowaha	13.13		
ENSMUSG0000028553	Angptl3	12.59		
ENSMUSG0000079436	Kcnj13	12.38		
ENSMUSG0000018865	Sult4a1	12.01		
ENSMUSG0000089896	Wnk1	11.80		
ENSMUSG0000082265	Gm15547	11.62		
ENSMUSG0000067189	Gm7335	11.28		
ENSMUSG0000070980	Actl7b	11.09		
ENSMUSG0000093717	RP23-345J21.1	11.06		
ENSMUSG0000090278	D130062J21Rik	11.01		
ENSMUSG0000090604	Gm17378	10.95		
ENSMUSG0000058812	0610039K10Rik	10.71		
ENSMUSG0000079906	Gm15846	10.69		

ENSMUSG0000090070	Gm16577	10.65
ENSMUSG0000041062	MsInI	10.61
ENSMUSG0000085335	Gm13684	10.56
ENSMUSG0000076433	BC100451	10.46
ENSMUSG0000086625	Gm11831	10.38
ENSMUSG0000085185	BC028777	10.22
ENSMUSG0000078249	Hmga1-rs1	10.09
ENSMUSG0000086062	Gm16853	9.84
ENSMUSG0000039384	Dusp10	9.76
ENSMUSG0000004902	Slc25a18	9.75
ENSMUSG0000081989	Gm13300	9.50
ENSMUSG0000090447	Gm17652	9.47
ENSMUSG0000081801	Dnmt3l-ps1	9.40
ENSMUSG0000079138	Gm8818	9.38
ENSMUSG0000083796	Gm13369	9.35
ENSMUSG0000085364	Gm16641	9.34
ENSMUSG0000082829	Gm15780	9.30
ENSMUSG0000078373	2010109K11Rik	9.29
ENSMUSG0000085289	Gm15337	9.26
ENSMUSG0000082984	Gm10599	9.21
ENSMUSG0000081289	Gm14857	9.14
ENSMUSG0000084792	1700056N10Rik	9.09
ENSMUSG0000091105	Gm5633	9.00
ENSMUSG0000086167	Gm13827	8.94
ENSMUSG0000087373	Gm15892	8.78
ENSMUSG0000093392	RP23-71G16.1	8.78
ENSMUSG0000082806	Rpl13-ps1	8.68
ENSMUSG0000080957	Gm15739	8.67
ENSMUSG0000090888	Gm17429	8.54
ENSMUSG0000026073	ll1r2	8.52
ENSMUSG0000086484	A630071L07Rik	8.48
ENSMUSG0000086192	Gm13609	8.37
ENSMUSG0000024215	Spdef	8.29
ENSMUSG0000069712	4930444G20Rik	8.26
ENSMUSG0000074213	Gm10642	8.25
ENSMUSG0000055691	Gja6	8.21
ENSMUSG0000089281	Scarna6	8.15
ENSMUSG0000037161	4930583H14Rik	8.12
ENSMUSG0000071552	Tigit	8.12
ENSMUSG0000028214	Gem	8.11
ENSMUSG0000026628	Atf3	8.09
ENSMUSG0000086400	Gm16789	8.09
ENSMUSG0000032715	Trib3	8.03

ENSMUSG0000083014	Gm11764	7.78
ENSMUSG0000085471	4933423P22Rik	7.66
ENSMUSG0000084781	D930015M05Rik	7.59
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ENSMUSG0000042197	Zfp451	1.85
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### Biography

The author was born June 22, 1990 in Woonsocket, Rhode Island, United States. They attended Montrose Area jr/sr High School in Montrose, PA, United States from 2004 to 2008 before going to Emory University in Atlanta, GA, United States (2008-2012). At Emory they majored in Biology and minored in Global Health, Society, and Culture and studying abroad in London for a summer to explore sociology and compare the clinical and public health systems of the United States and United Kingdom. They worked for three years of undergrad as a lab technician in the Fridovich-Keihl genetics lab. After completing a Bachelor of Science in Biology they attended the Tulane School of Public Health and Tropical Medicine in New Orleans, LA, United States (2012-2014) receiving a Master's in Public Health in Global Environmental Health Sciences specializing in Disaster Management. The author then continued at Tulane in the Tulane School of Medicine doctoral program in Biomedical Sciences starting classes in 2014 and in the Saifudeen lab in 2015. While in the Saifudeen lab the author contributed as second author to one publication, and presented abstracts at the American Society of Nephrology, the Southern Region AFMR/SSCI for Regional Meeting winning a Trainee Travel award and being selected for an oral presentation in 2016, and several abstracts at the Tulane Health Science Research Days poster presentations wining the Michael A. Gerber Prize for Research in Molecular and Cellular Biology award (2017), and winning outstanding morning speaker at the BMS Student Retreat for presentation of their preliminary thesis data. The author has just begun a job as a Regulatory Compliance Specialist at the Tulane HRPO.