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A stylized icon of a microRNA molecule, represented as a blue double-stranded structure with colorful bases.

## MicroRNAs in renal fibrosis and transplantation

- mediators and therapeutic targets.

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Centre for Cardiovascular Science  
University of Edinburgh



Denby Lab @dr\_denby



# Non-coding RNA

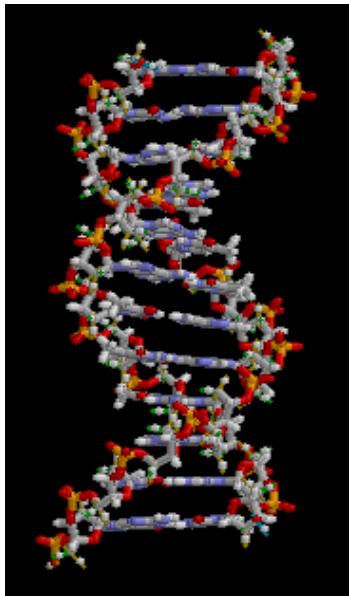


The central tenet of molecular biology :-

RNA functions mainly as an informational intermediate between a DNA sequence i.e. gene and its encoded protein.

## DNA Sequencing revolution - Human Genome Project

- 22 287 known or predicted protein-coding gene loci.
- coding regions occupy 1.2% of the euchromatic genome.
- total fraction of bases occupied by known protein-coding transcripts is only about 2%.
- summation of the sequences covered by known genes, 'mRNAs' and spliced expressed sequence tags (ESTs) indicated that (at least) 60 –70% of the mammalian genome is transcribed on one or both strands.



By brian0918&#153; - Own work, Public Domain, <https://commons.wikimedia.org/w/index.php?curid=404735>



# Non-coding RNA

## Types of non coding RNA

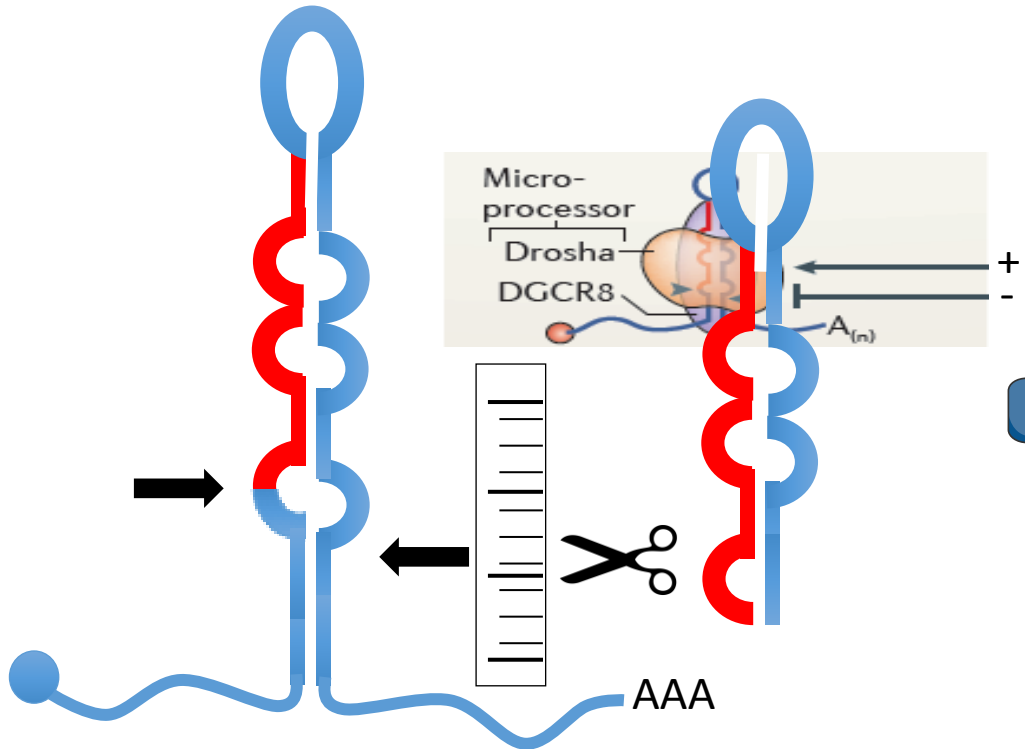
- Ribosomal RNA (rRNA)
- tRNA
- Long non-coding RNA (lncRNA)
- Small non-coding RNA
  - ✓ microRNA (miRNA)
  - ✓ snoRNA
  - ✓ siRNA
  - ✓ piRNA
- Circular RNA

- **miRNAs** are small (<25nt) non-coding RNA molecules.
- 1<sup>st</sup> discovered in 1993 in *C.elegans*.
- 1<sup>st</sup> detected in humans 2000.
- Over a 1000 miRNA in humans.
- At least 60% of protein coding genes coding miRNA complementary sites.
- Canonical and non-canonical biogenesis.



# miRNA Biogenesis

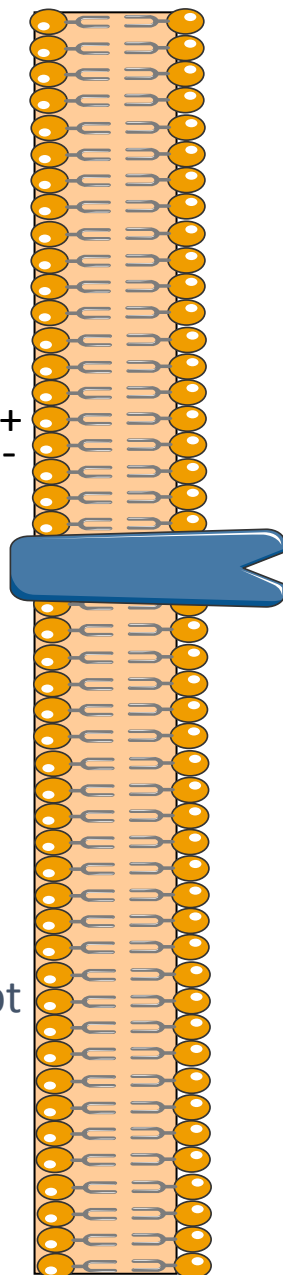
Nucleus



Pri-miRNA transcript      Pre-miRNA transcript

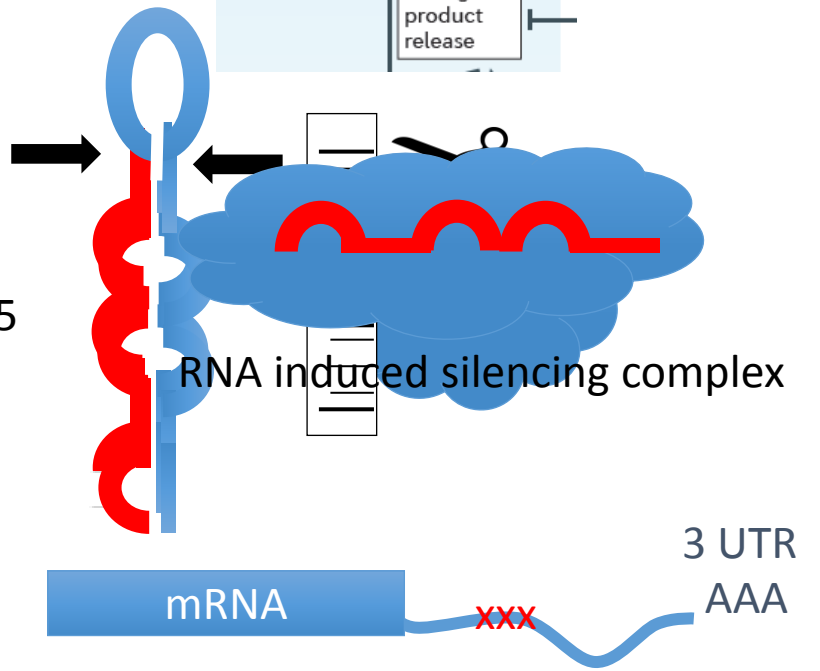
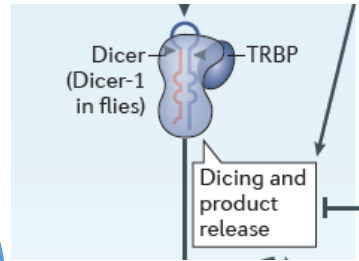
- Transcribed by Pol II
- Contain one or more stem loops

Ha and Kim, Nature Reviews 2014



Exportin 5

Cytoplasm

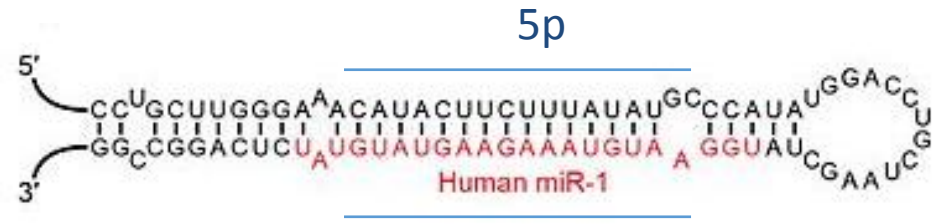


Translational repression / mRNA decay      mRNA cleavage

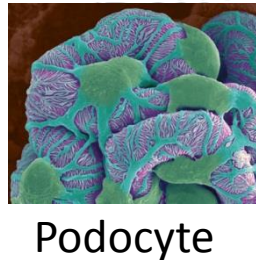
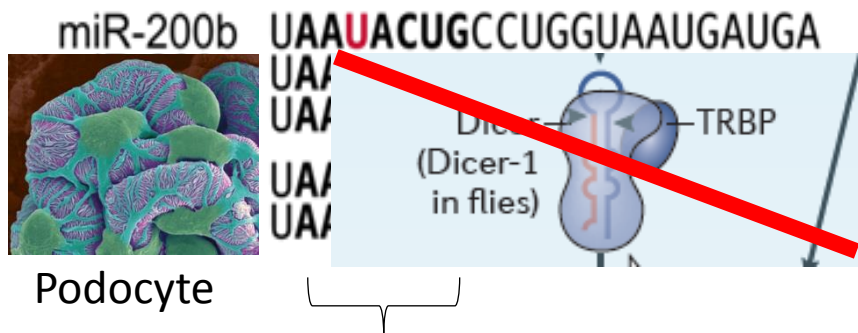


# miRNAs

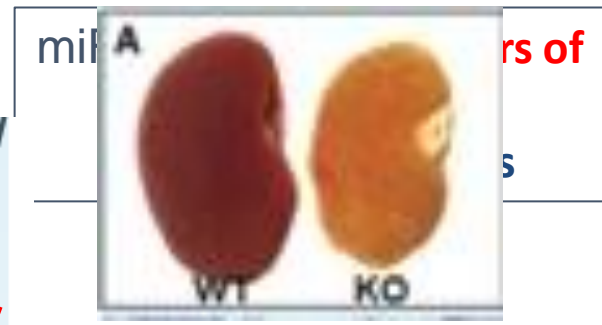
- Each pre-miRNA stem loop encodes 2 miRNA.
- Nomenclature agreement
  - 5p and 3p designation based on position in stem loop.
- miRNA interact with mRNA with specific region called seed region.
- A single miRNA has the ability to hit multiple genes and influence many pathways.
- Frequently miRNA complementary sequences are found in functionally related but distinct mRNAs.
- Essential for normal kidney function.
- Phase I/II clinical trials underway with Anti-miRs for HCV, Alport's Syndrome.



miR-200 family – TGFβ regulated



Podocyte

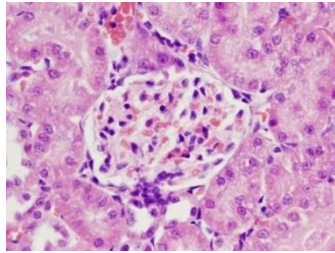


Shi et al, 2008

Seed Region – interacts with 3'UTR (5' UTR and CDS)

# Are miRNAs involved in glomerulonephritis??

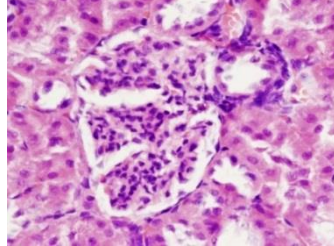
## Anti-Thy1.1 model – rat model of glomerulonephritis



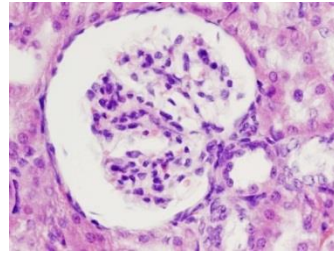
Normal glomeruli



ER-4  
(2mg/kg)



Global  
mesangial proliferation

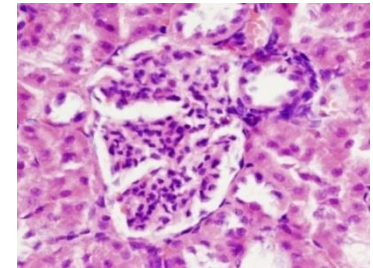


Segmental  
mesangial proliferation

### Histologic Evaluation of Kidney Damage in Anti-Thy1.1 Animals

Group	Glomerular score	Tubular score	Total
Control	0.25	0.25	0.5
1 x ER4, 7 days	1	0.5	1.5
3 x ER4, 7 days	2	2	4
3 x ER4, 14 days	2.1	1.3	3.4

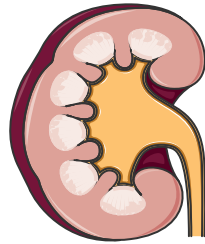
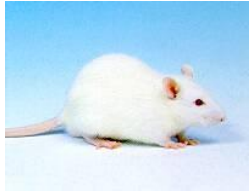
25% of glomeruli had a glomerular lesion. Evidence of tubular damage (5-25%)





# Are miRNAs involved in glomerulonephritis??

ER-4  
(2mg/kg)



RNA

N=3/gp

3 injections

1 week apart

Sacrificed at 7 days post last injection

## MiRNA Microarray

3xGlomerulonephritis (D) vs Control (C) 7days



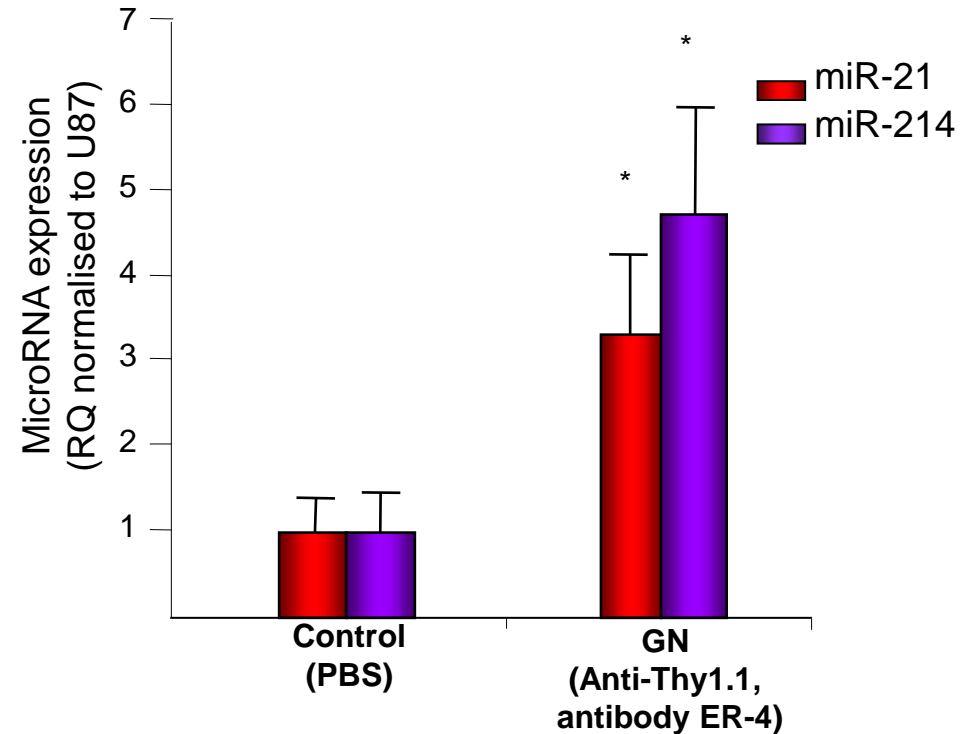
**rno-miR-214**

\*p<0.05

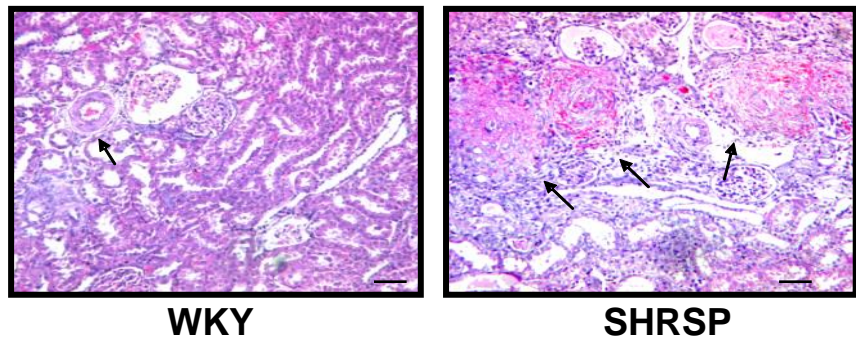


**rno-miR-21**

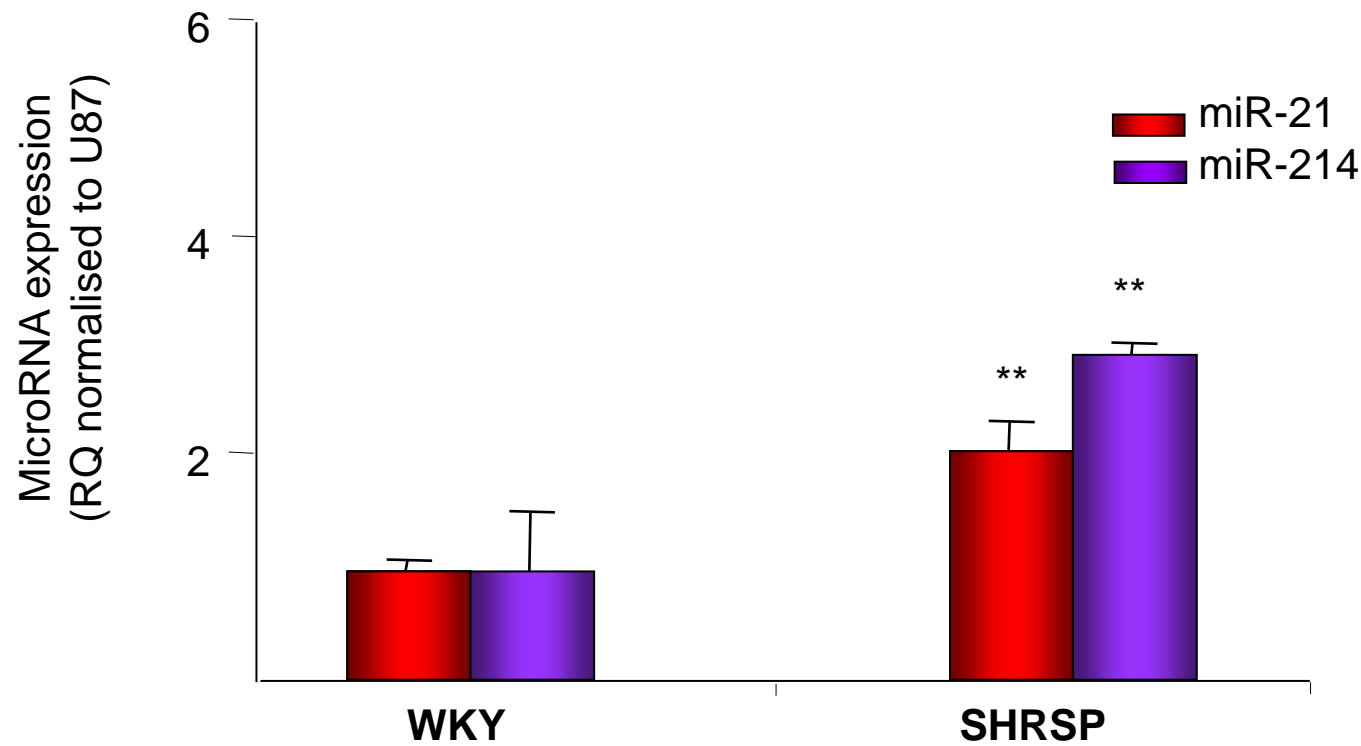
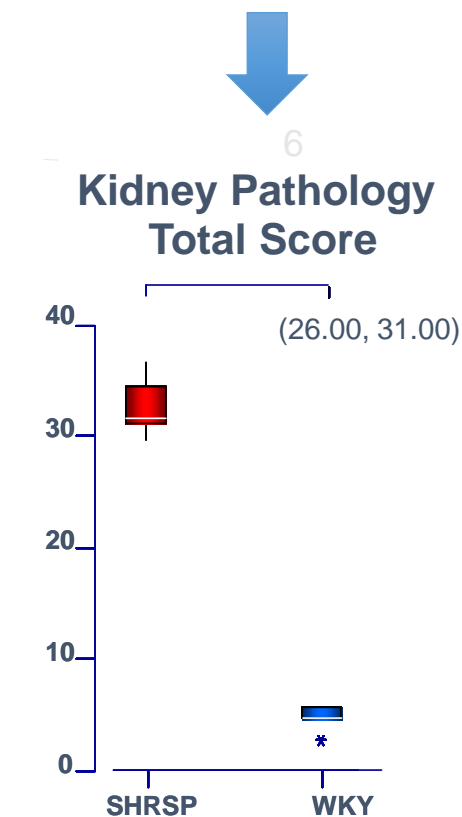
p=0.05



# Hypertension induced nephropathy



Malignant hypertension -  
Gross vascular lesions  
(onion skin pattern)

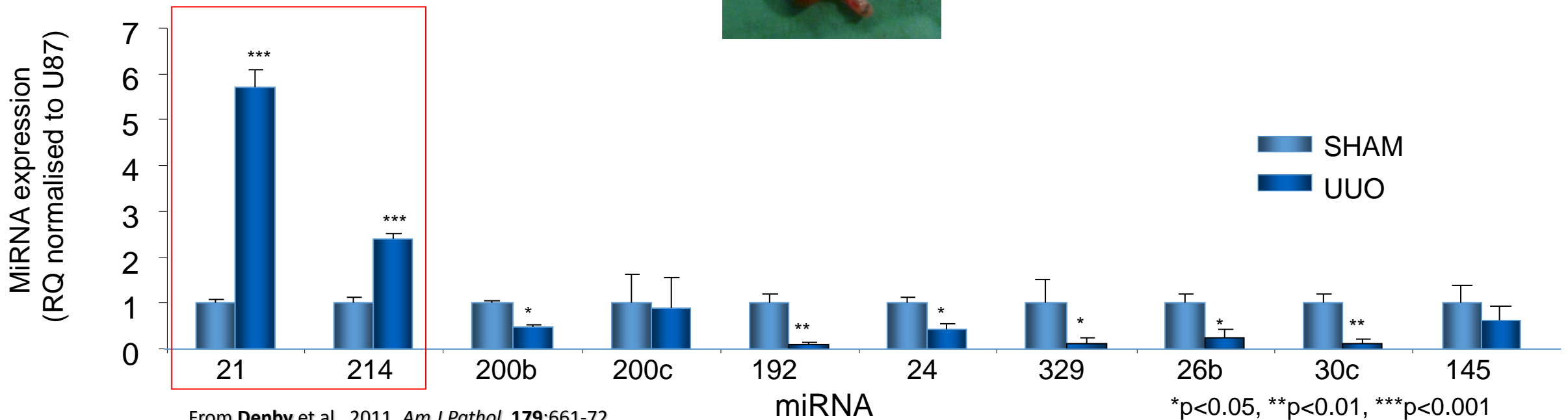




# Renal Fibrosis

- is the final common pathway for most forms of progressive renal disease.
- involves glomerular sclerosis and/or tubulointerstitial fibrosis.
- tubulointerstitial fibrosis is best histological predictor of progression.

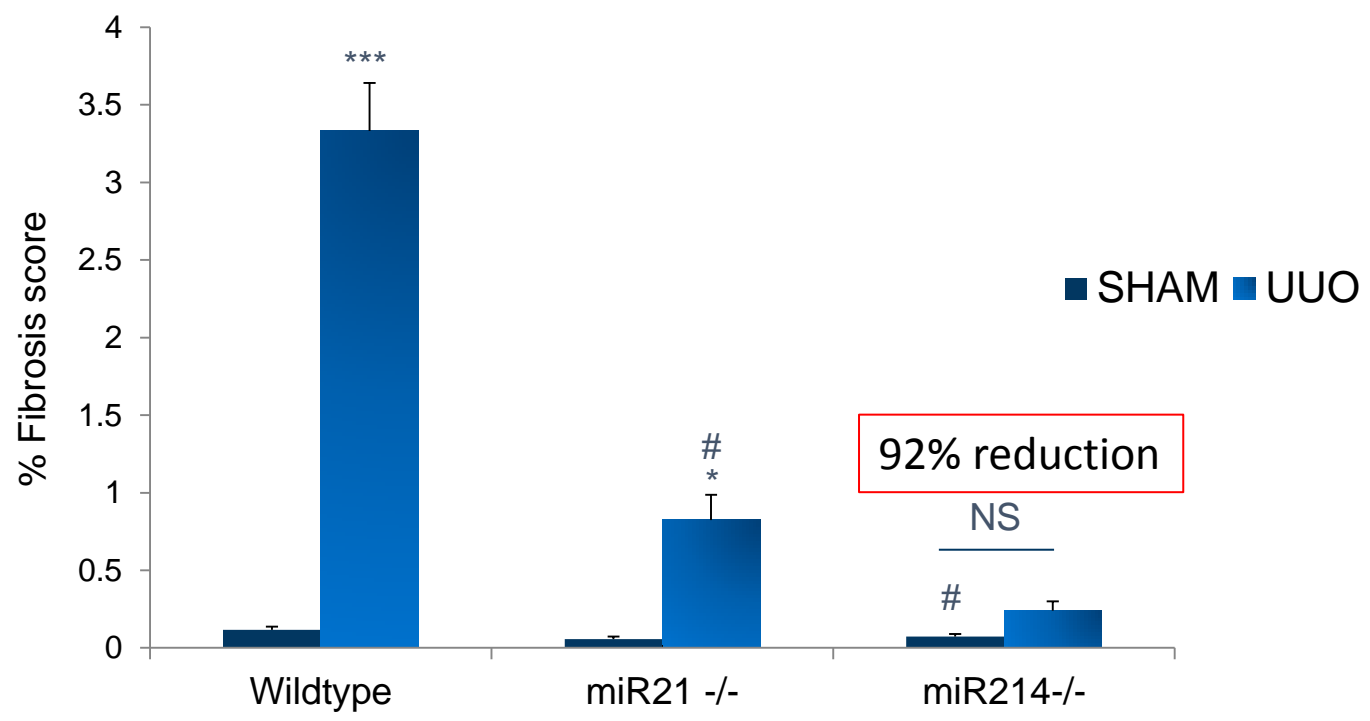
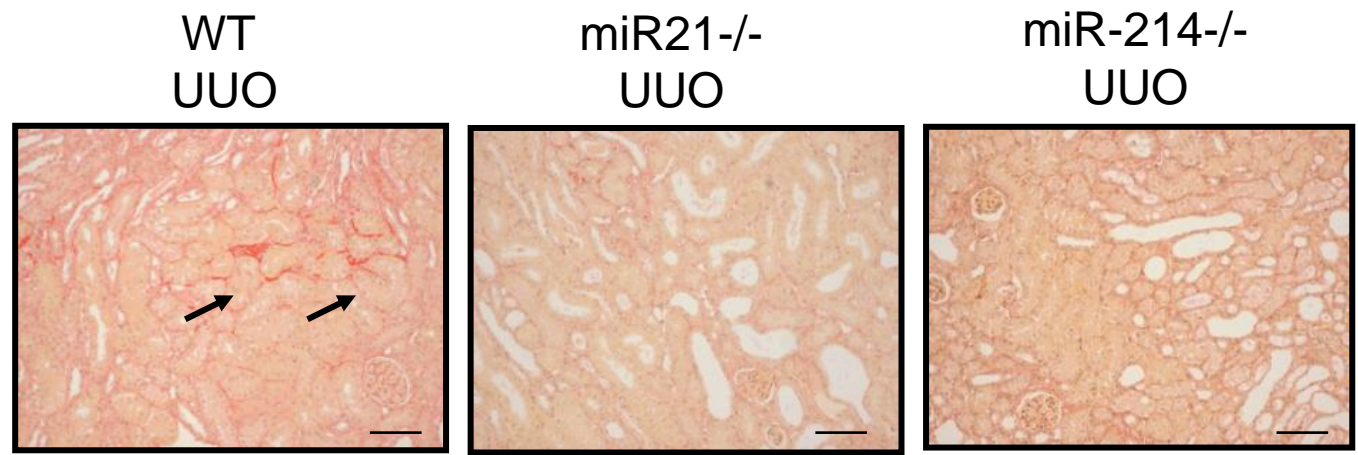
Unilateral ureter obstruction (UUO) model of fibrosis





# miR-21 and miR-214 are mediators of renal fibrosis.

Global  
miR-214 -/-  
miR-21 -/-

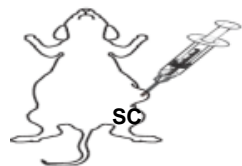


From Denby et al., 2014. *J Am Soc Nephrol.* 25:65-80.

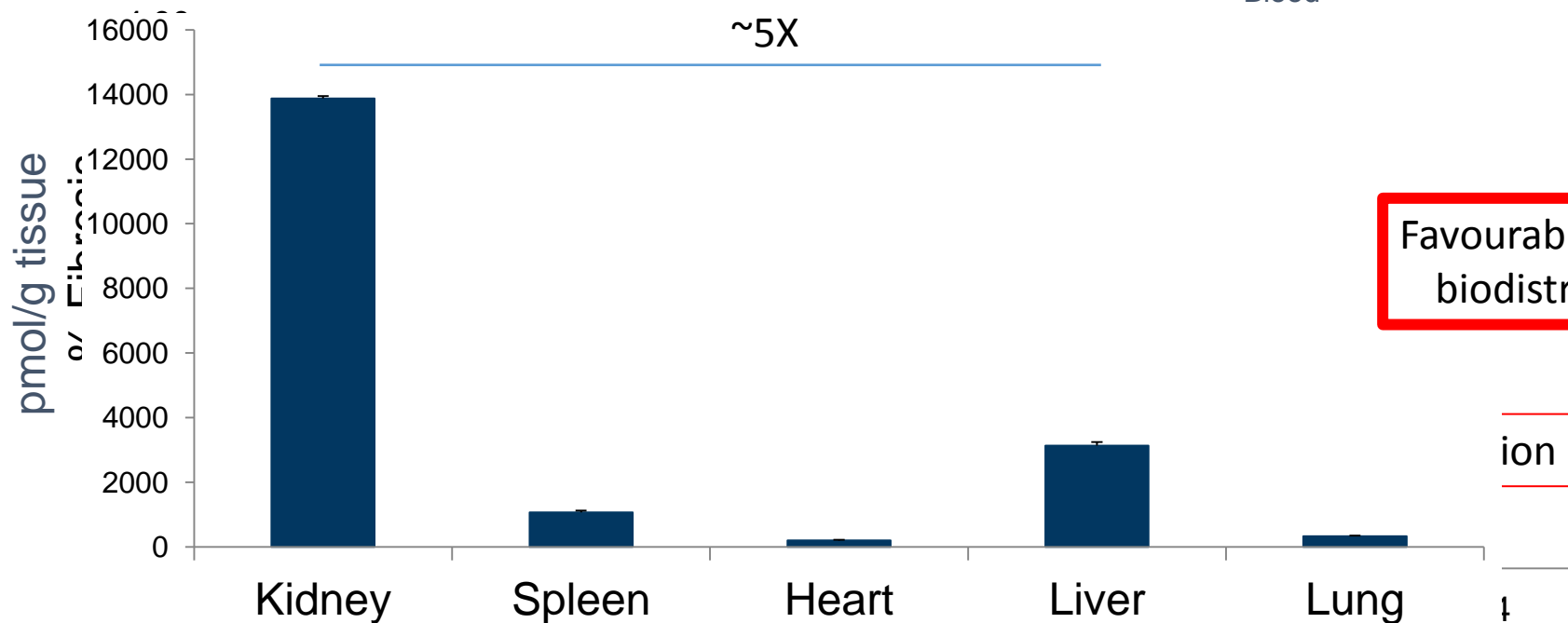
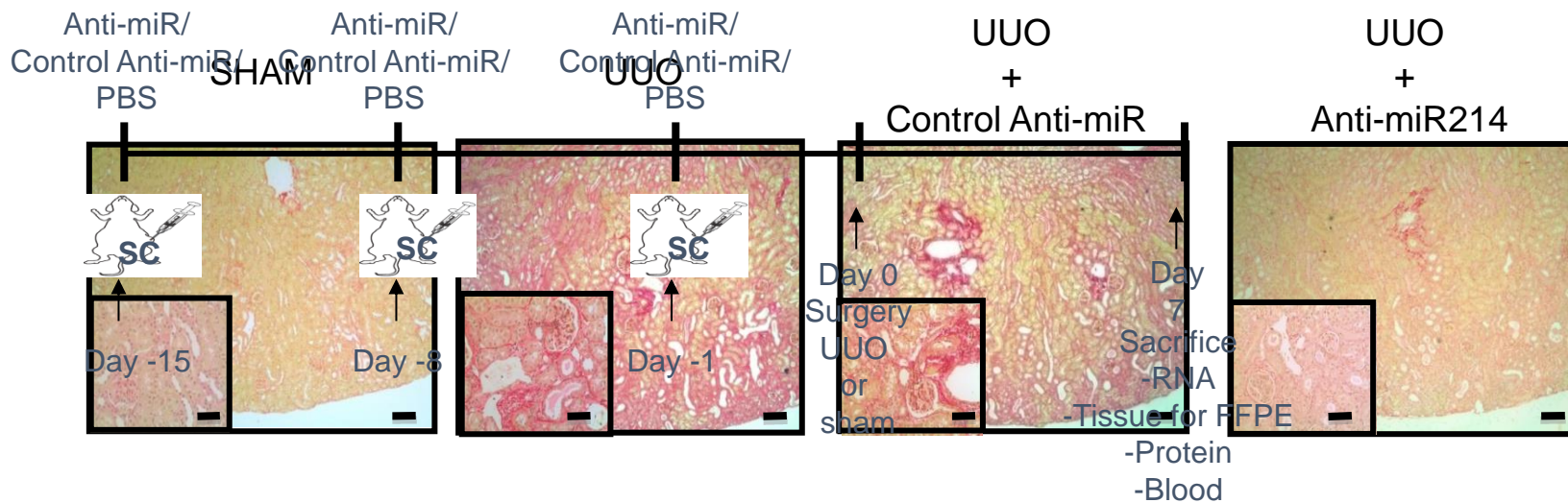
\*p<0.05, p<0.001 vs SHAM; #p<0.001 vs WT UUO



# Anti-miR-214-3p as a potential therapeutic for renal fibrosis.



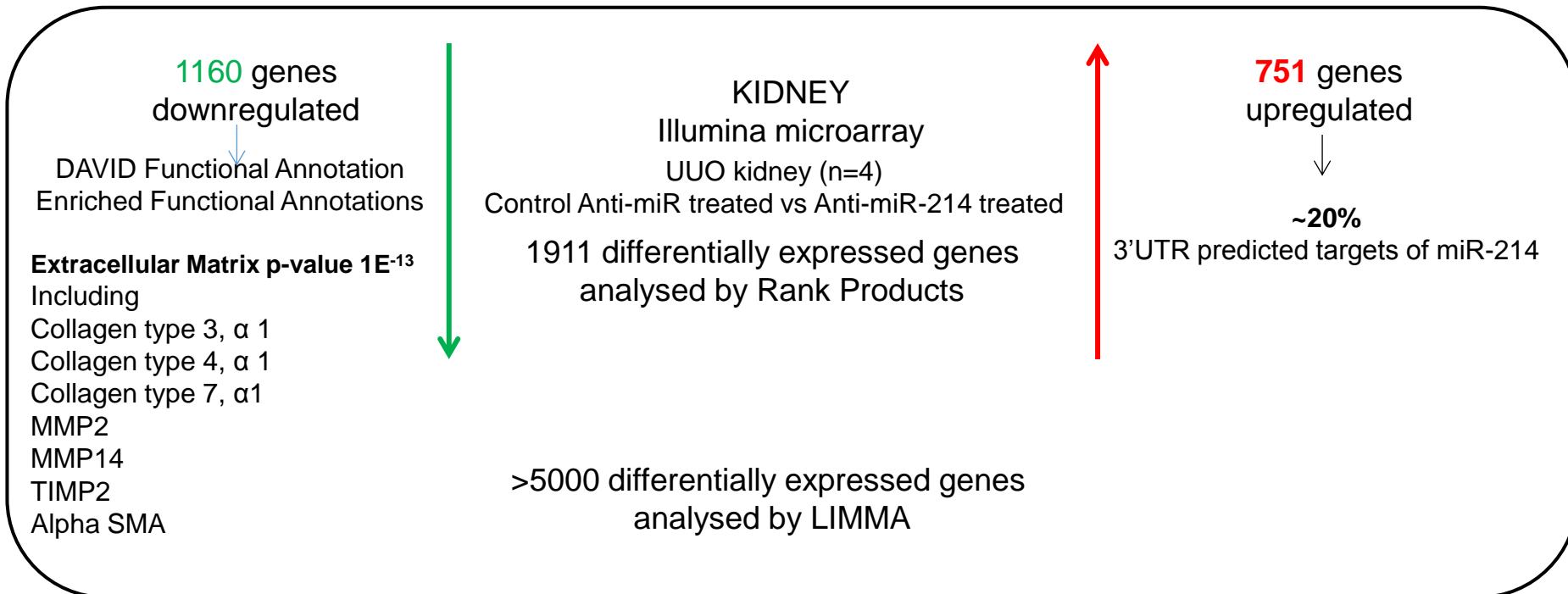
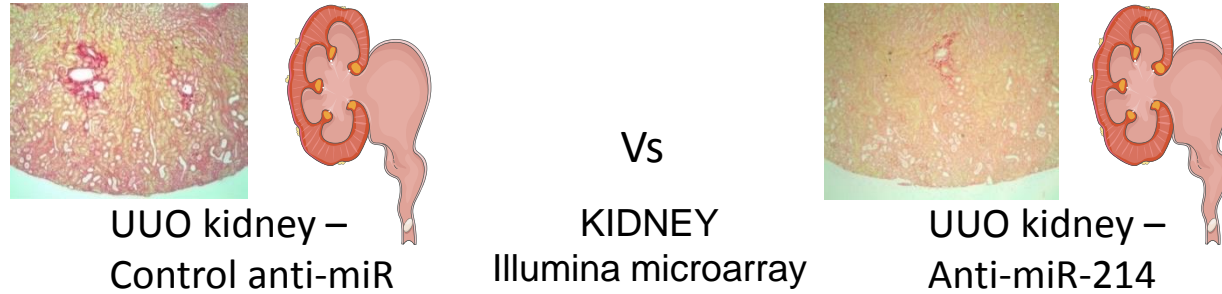
5mg/kg



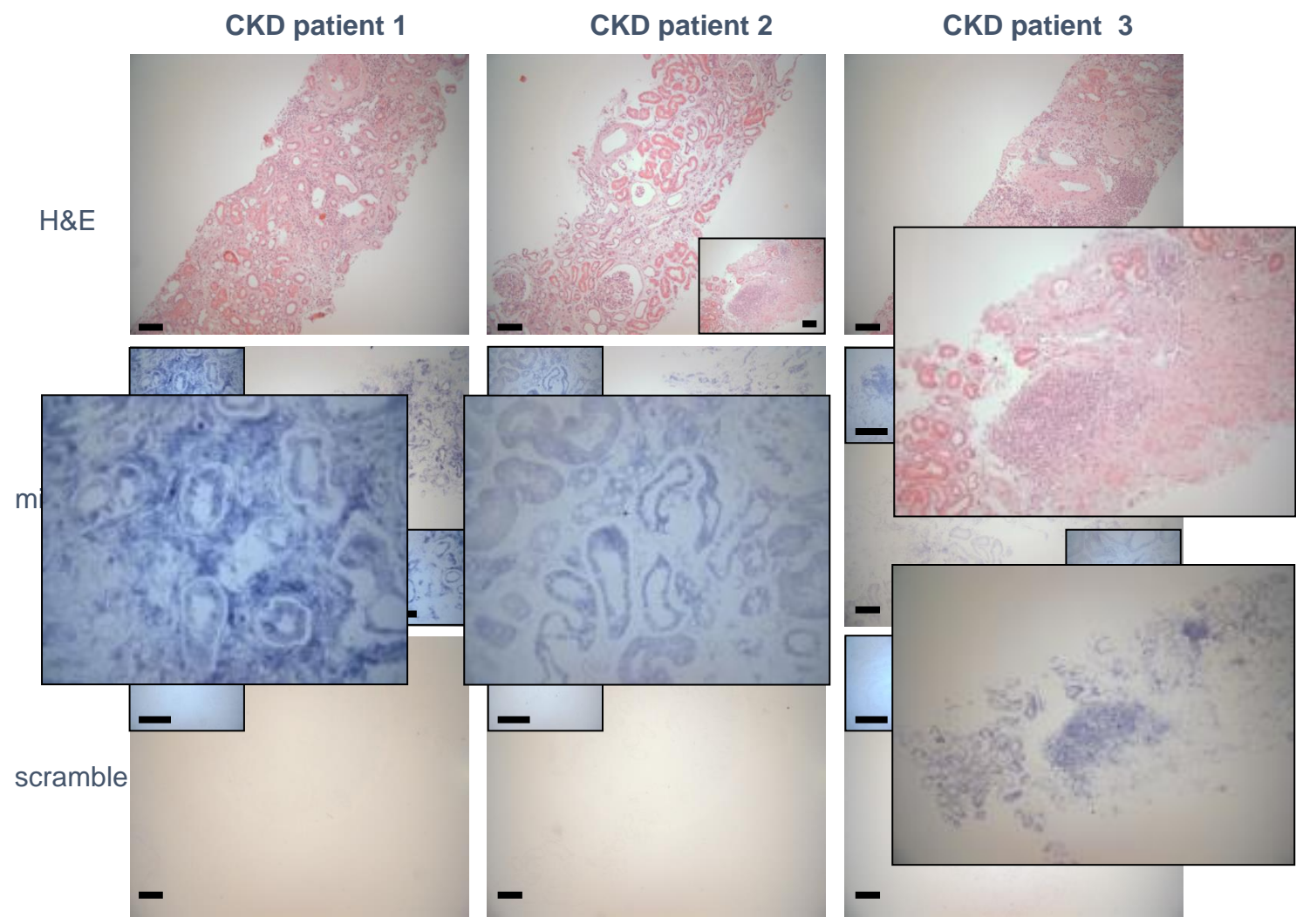
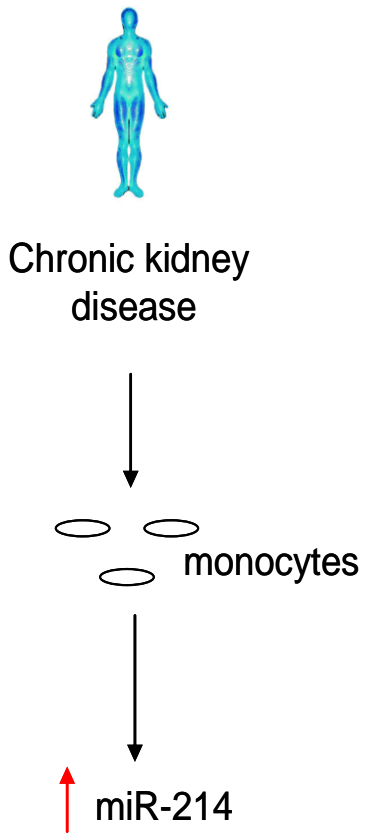


# Mechanism of action of miR-214

- miRNA targets can be organ/cell type/injury specific!
- Algorithms give false positives – regulation of biogenesis and expression exist!

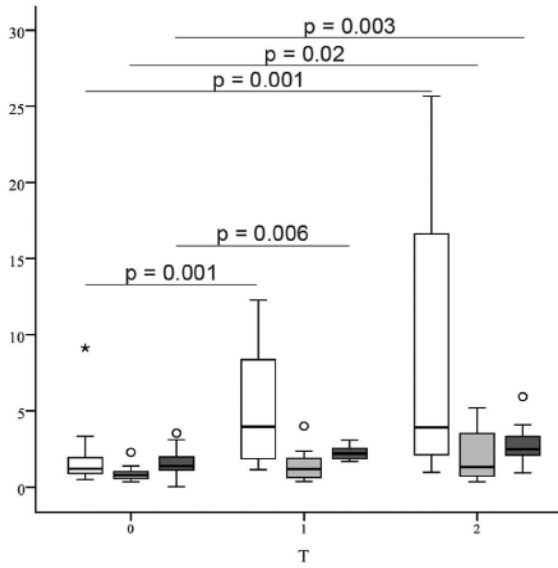
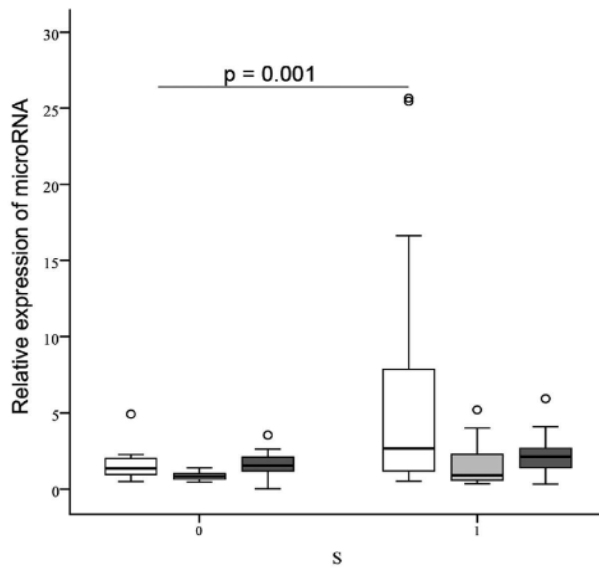
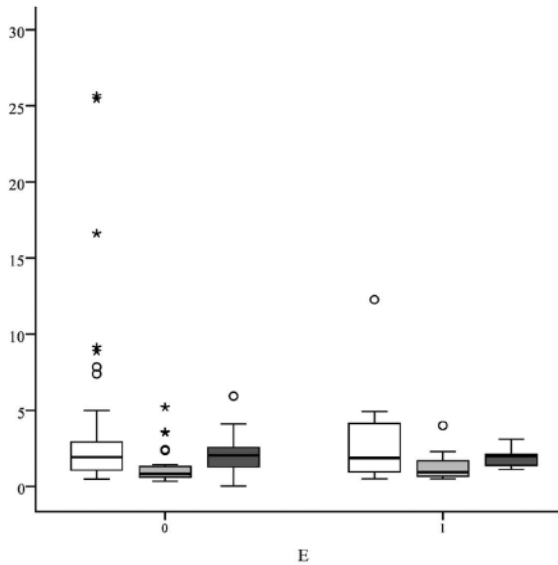
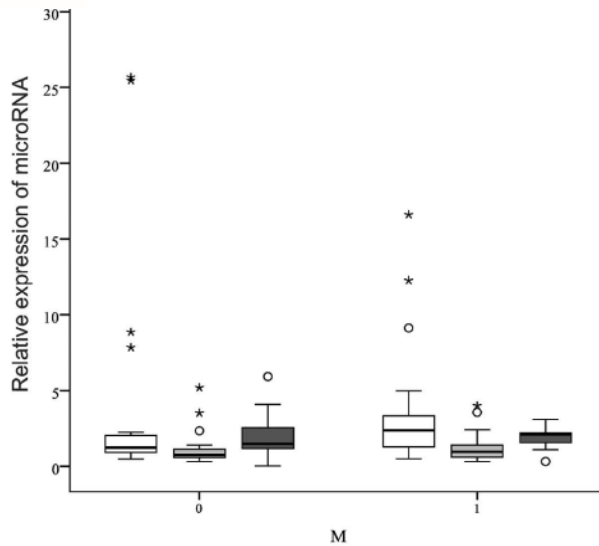


# Is miR-214-3p a translatable target?





# miRNAs in biopsy proven IgAN



miR-21-5p  
  miR-199a-5p  
  miR-214-3p

## miR-214-3p and miR-21-5p

are overexpressed in renal tissue of patients with moderate-severe fibrosis.

For example:

### miR-214-3p

- with moderate fibrosis (T1: median RQ = 2.20 [1.67–3.07])
- with severe fibrosis (T2: median RQ = 2.48 [2.03–5.93])



# miRNAs in transplantation

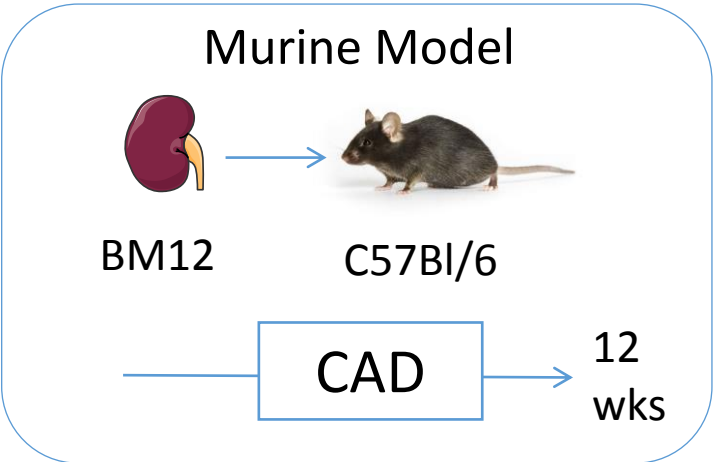


Victoria Banwell

Is there a role of miR-214 in chronic allograft damage (CAD) ?

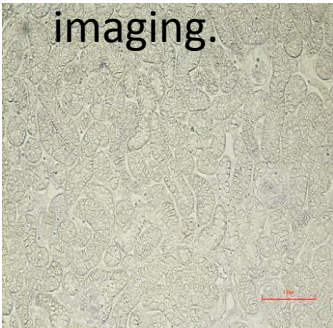
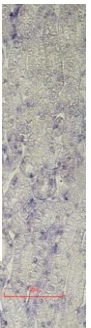
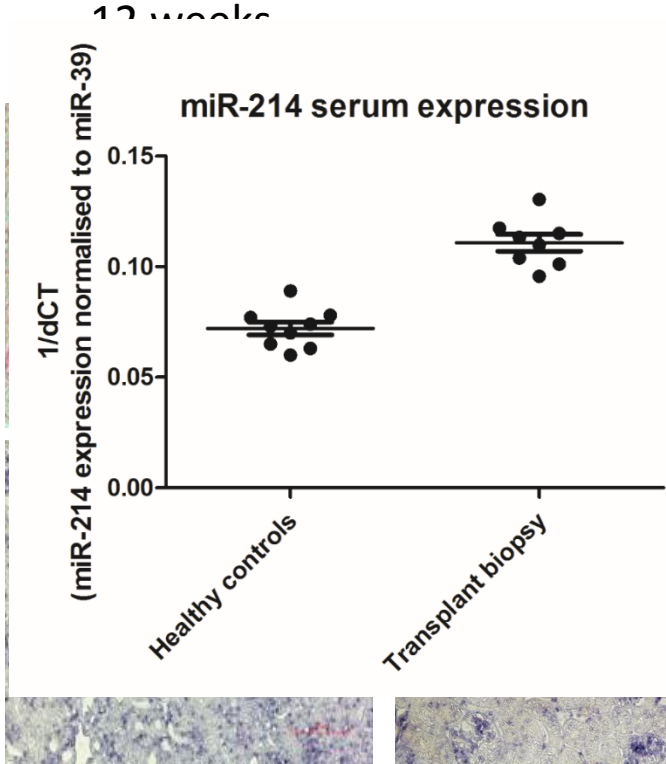
### CAD

- significant cause of graft failure following renal transplantation.
- characterised by **interstitial fibrosis** and **tubular atrophy** (IFTA).
- leads to the failure of up to 5% grafts annually.
- there are no specific therapies available.



PSR

miR-214 expression



??Potential Non-invasive biomarker of CAD in combination with imaging.



# miRNA biomarkers

- Identified a miRNA signature in IgAN patients that correlated with fibrosis on biopsy and eGFR.



seNSOR

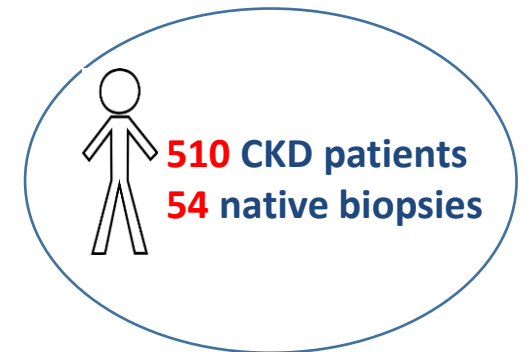
Non-invasive biomarkers of renal disease



## AIM:

- **predicts functional outcome in IgAN patients (including in a validation cohort).**  
n=100 historical with followup; n=400 validation cohort
- **is limited to IgAN or is present in other renal diseases.**  
n=300 generic age, sex and eGFR matched CKD patients with IgAN pts n=200.
- **reflects the severity of renal pathological changes.**  
n=75 newly diagnosed IgAN

? Treatment effect- disease modifiable biomarker would be useful.







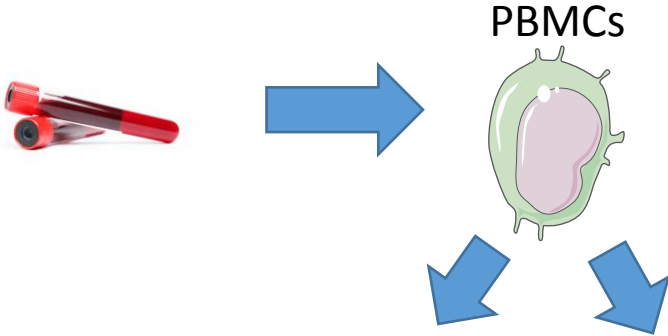
# miRNAs in transplantation



Katie Connor

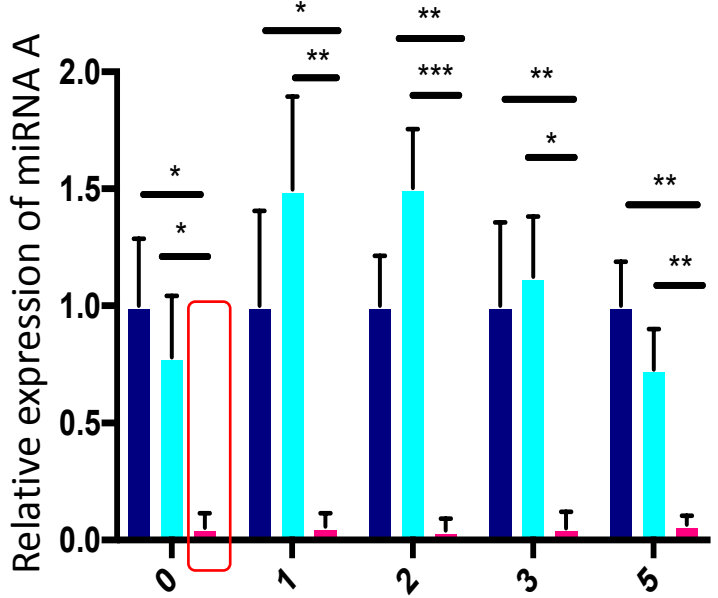
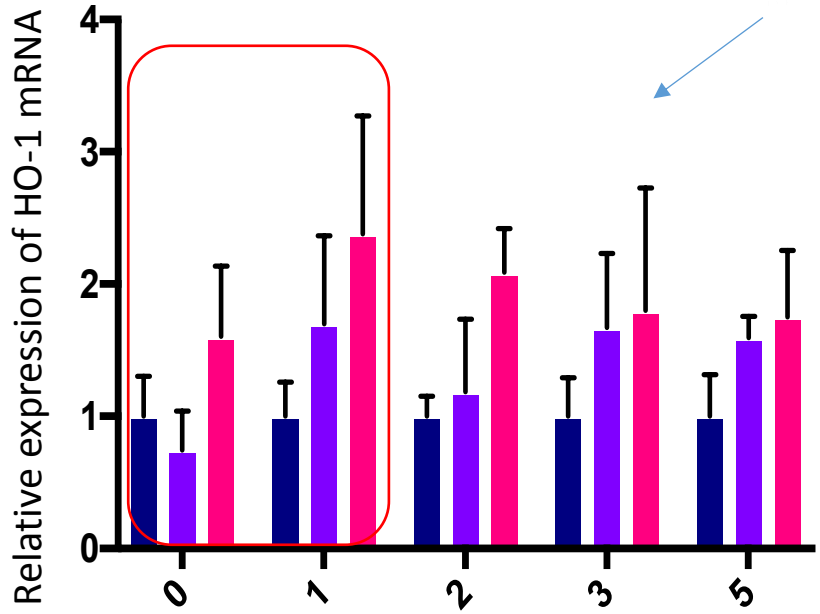
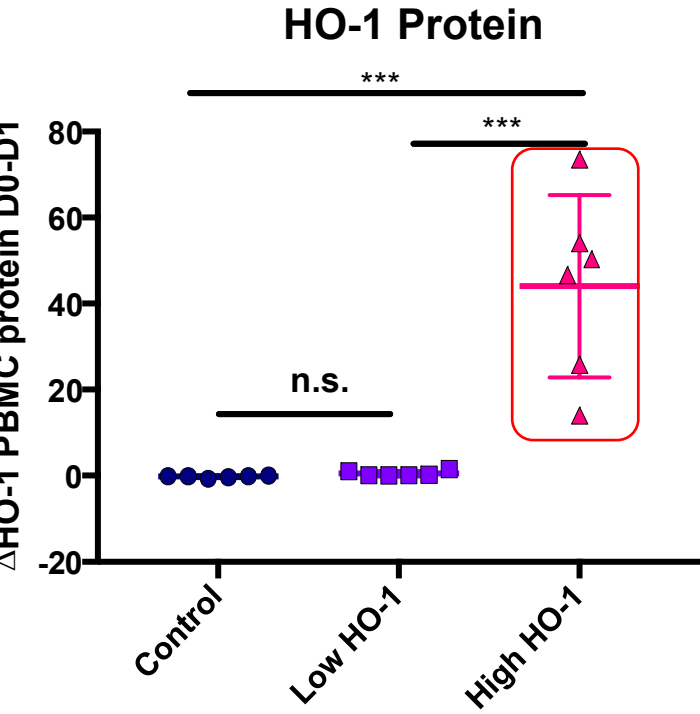
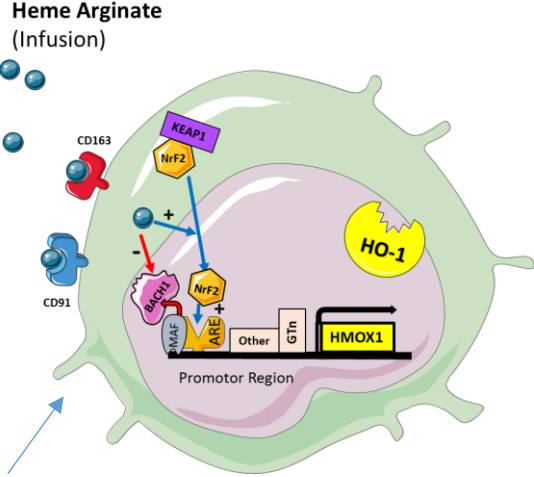
## Hemin Preconditioning Upregulates Heme Oxygenase-1 in Deceased Donor Renal Transplant Recipients: A Randomized, Controlled, Phase IIB Trial

Rachel A. B. Thomas, MBChB,<sup>1</sup> Alicja Czopek, PhD,<sup>1</sup> Christopher O. C. Bellamy, MBChB, PhD,<sup>2</sup> Stephen J. McNally, MBChB, PhD,<sup>1,3</sup> David C. Kluth, MBBS, PhD,<sup>1</sup> and Lorna P. Marson, MBBS, MD<sup>1</sup>



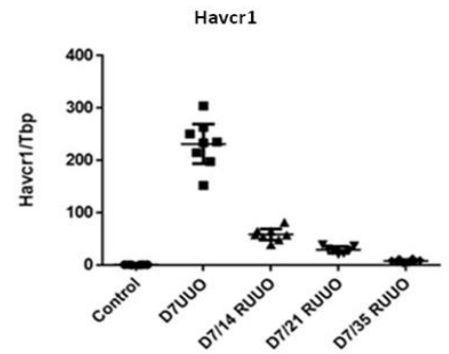
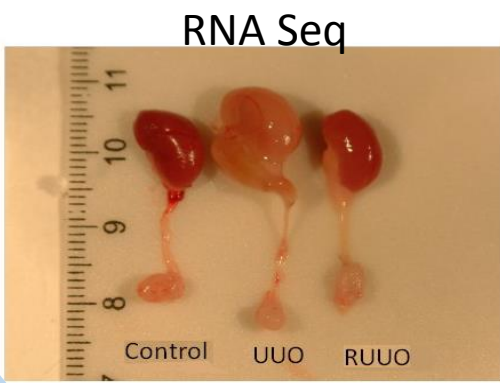
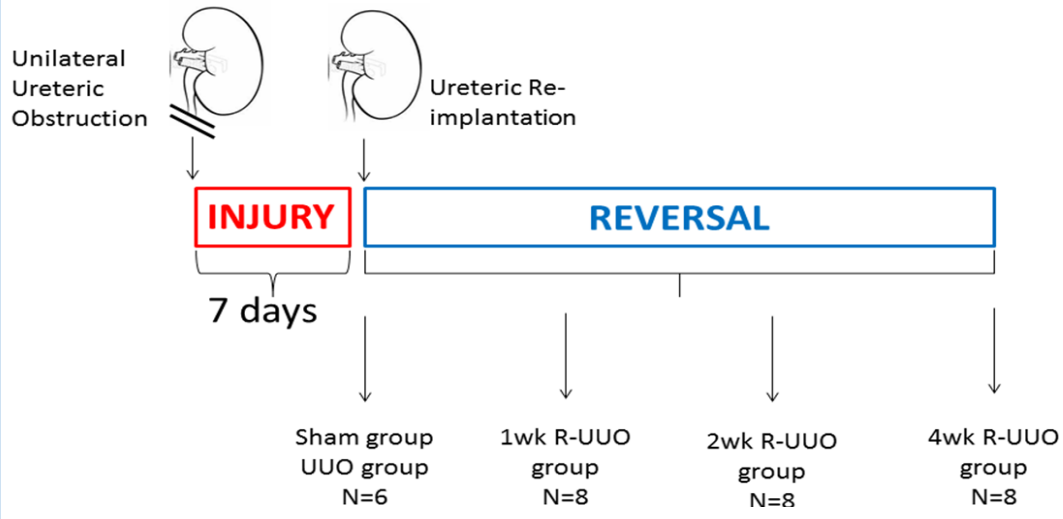
HA + Surgery

HA

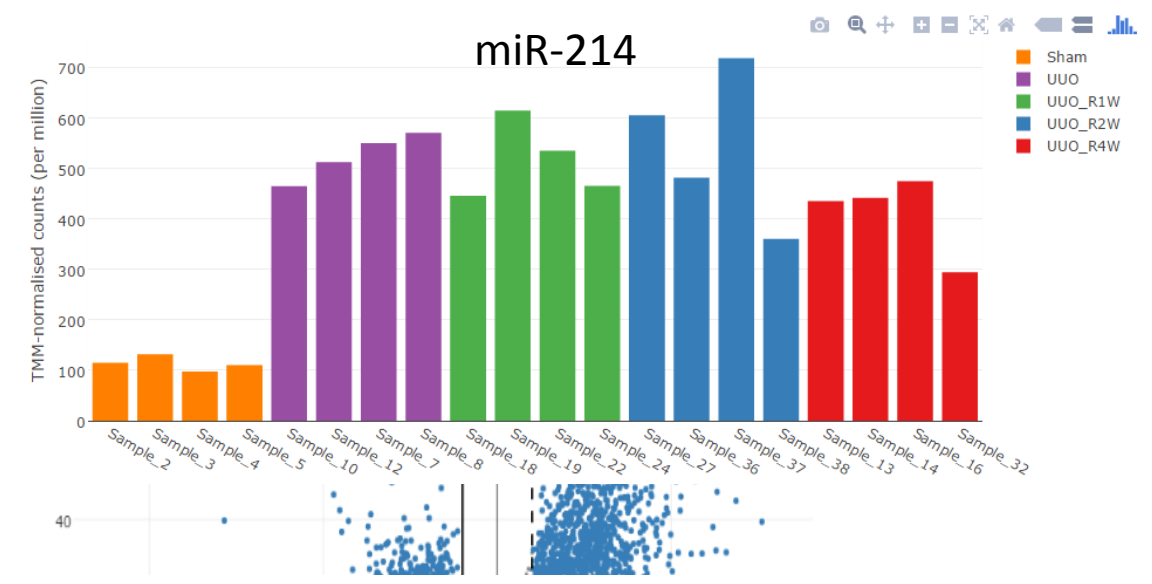


# miRNA as mediators of repair?

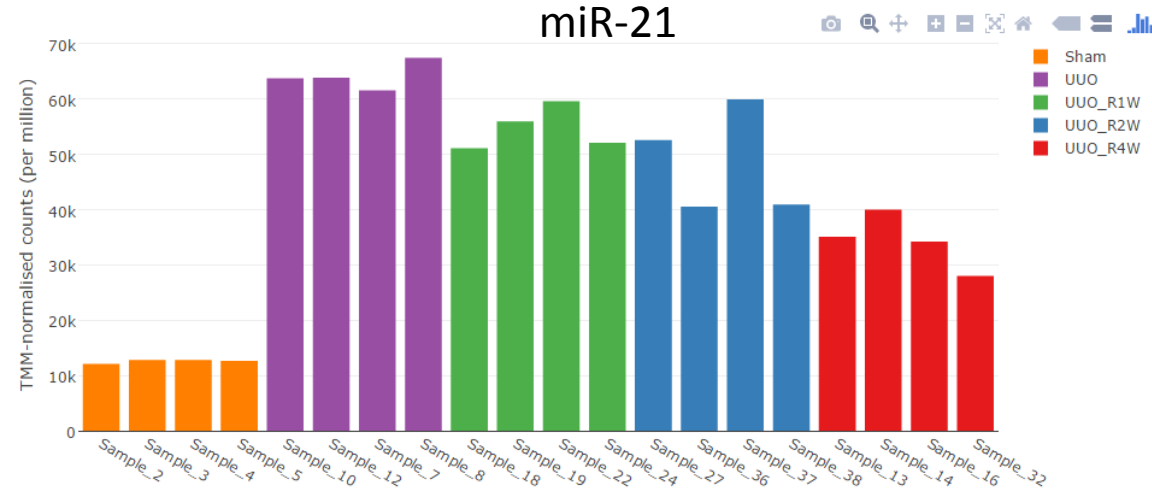
## Reversible Unilateral ureteric obstruction model (rUUO)



Smallrna cluster expression bar plot

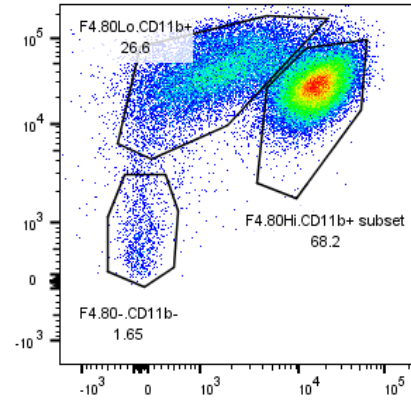
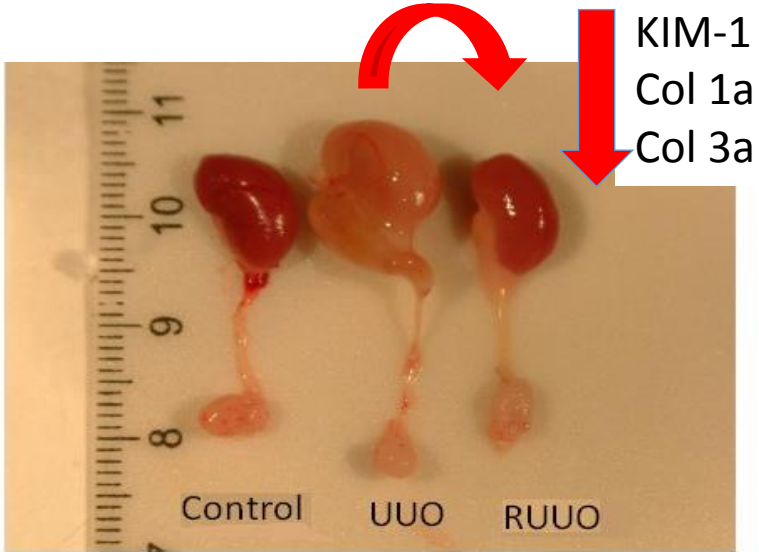


Smallrna cluster expression bar plot



# miRNA as mediators of repair?

Cell type ?

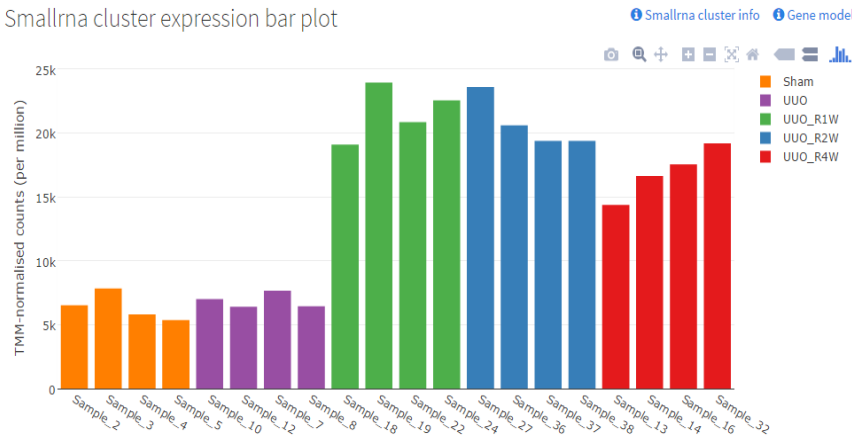


## Kidney FACS

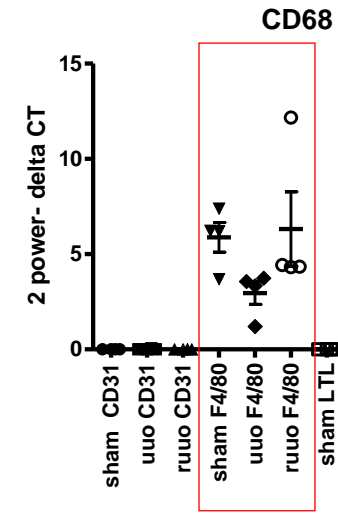
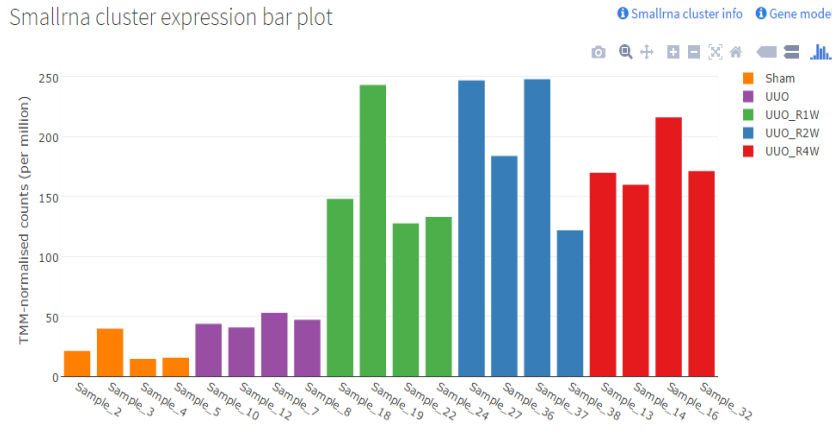
- Endothelial cells
- PDGFBR+
- Proximal Tubules
- Gli +ve
- Myeloid cells e.g. Macrophages



Smallrna cluster expression bar plot



Smallrna cluster expression bar plot

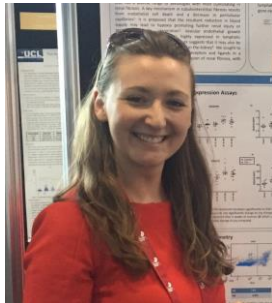
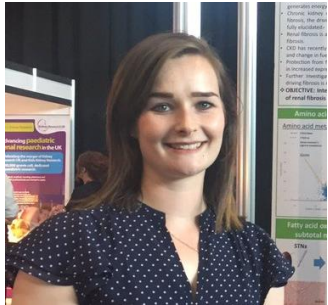


- sham CD31
- uuo CD31
- ▲ ruuo CD31
- ▼ sham F4/80
- ◆ uuo F4/80
- ruuo F4/80
- sham LTL
- △ uuo LTL
- ▽ ruuo LTL
- ◇ sham PDGFRb
- ✱ uuo PDGFRb
- ★ ruuo PDGFRb



# Acknowledgements

## Team Denby



**Renal and Transplant Patients of Glasgow and Edinburgh.**

**Liz, Hayley, Deborah, Rowan – Clinical Research Nurses**

**Vasudev Menon**

**Lorna Marson**

**Prof S Wigmore**

**Bryan Conway**

**Carolynn Cairns**

**Prof Jeremy Hughes**

**David Ferenbach**

**Jon Manning**

**Patrick Mark**

**Prof E van Rooji**

**Prof E Olson**

**Emily McQuarrie**

**Prof Jon Barratt**

**Kate Stevens**

**Alison Taylor**

**Prof Alan Jardine**

**Prof Andy Baker**

