

Identification of new therapy for kidney disease by systems approach



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Treatment of Kidney Disease

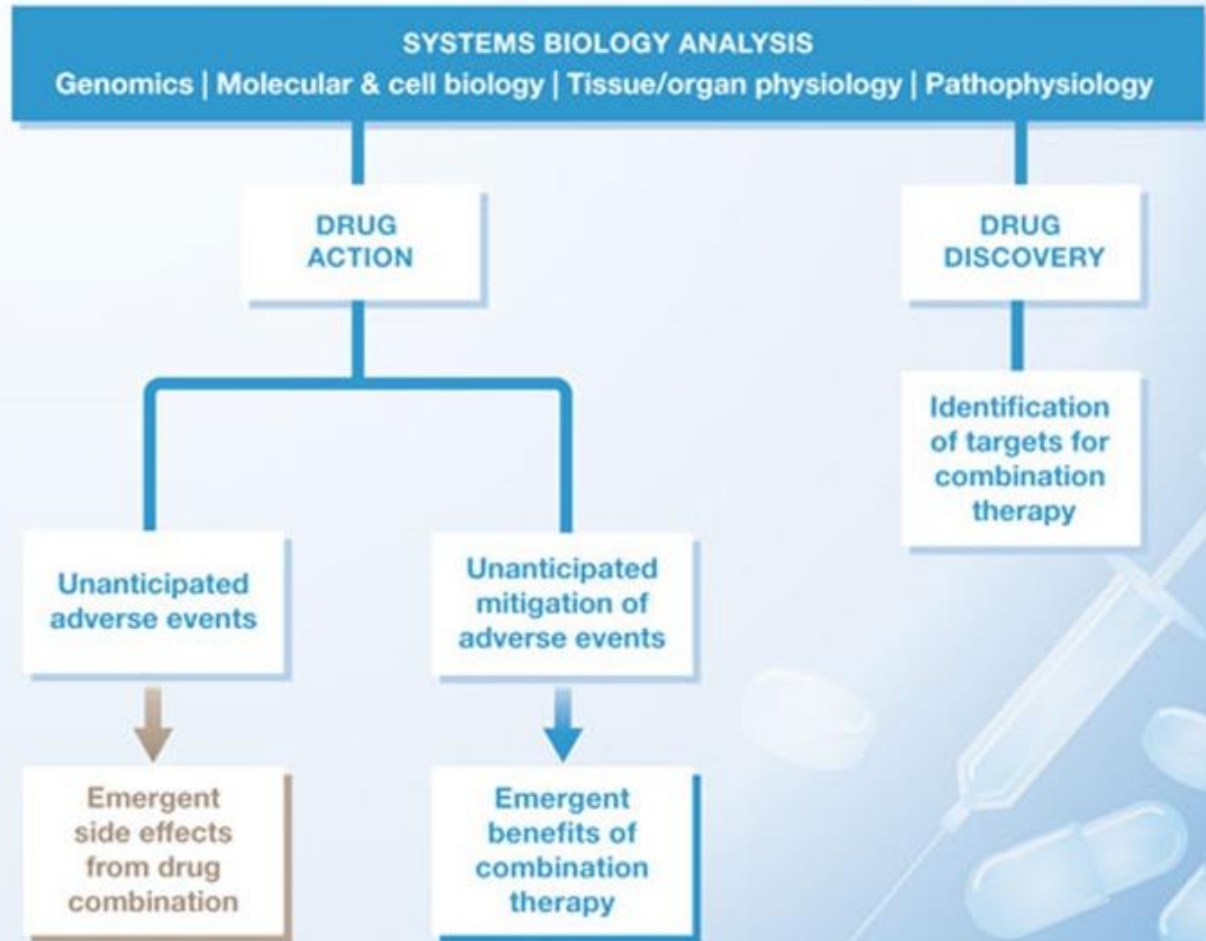
- Steroids and Immunosuppressive therapies:
 - Significant side effects
 - Resistant and recurrent
- ACEI/ARBs:
 - Only classes of medications have renal protection.
 - Partial effect
 - Slow progression rate but not for the cure of disease
- New therapies:
 - Good data from Phase II clinical trials
 - Phase III clinical trials failed.



Complex diseases require complex therapies

Ravi Iyengar

Author Affiliations





Systems Pharmacology

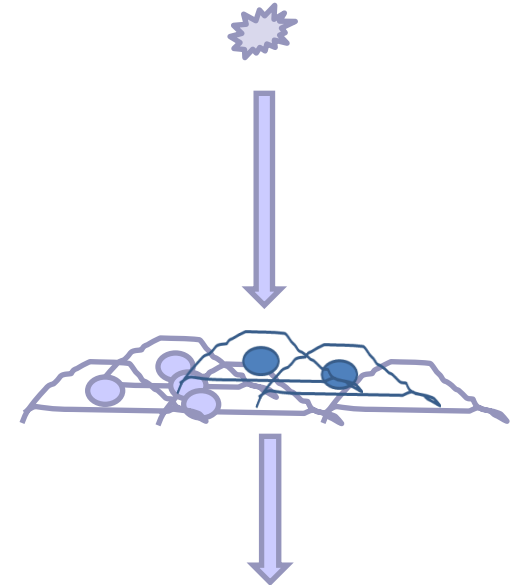
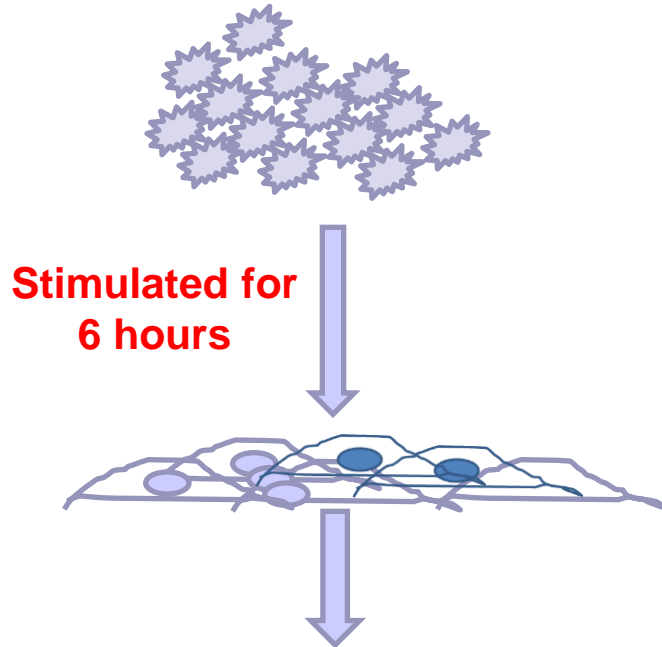
Systems approach to identify combinational drug therapy and drug repurposing for kidney disease

- Combination therapy is likely more effective than monotherapy for complex disease such as HTN and kidney disease.
- However, combination therapy targeting the renin-angiotensin system (RAS) fails to provide additional benefits.
- We developed here a new approach by applying CMAP to deduce the best drug combination therapy for kidney disease based on gene expression profile (Zhong et al JASN 2013).

Connectivity Map (CMAP)

1300 drugs

Each drug

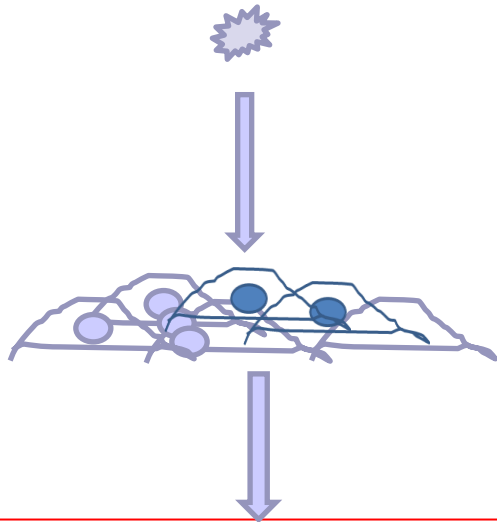


The idea behind the CMAP study is to promote **signature based drug profiling**, instead of **specific drug targets**.

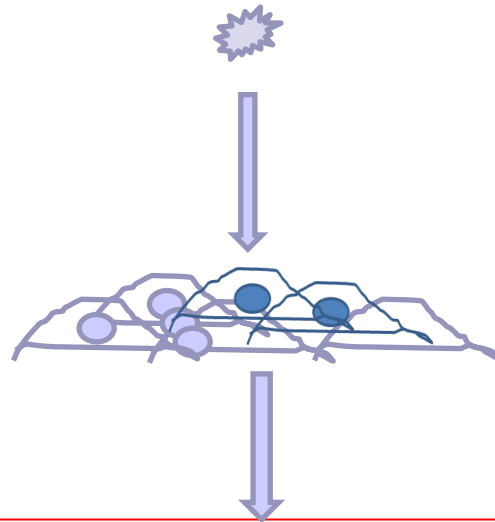
Identification of pairs of drugs

Drug A

Drug B



+



=

500 up-regulated genes and 500 down-regulated genes by each drug

500 up-regulated genes and 500 down-regulated genes by each drug

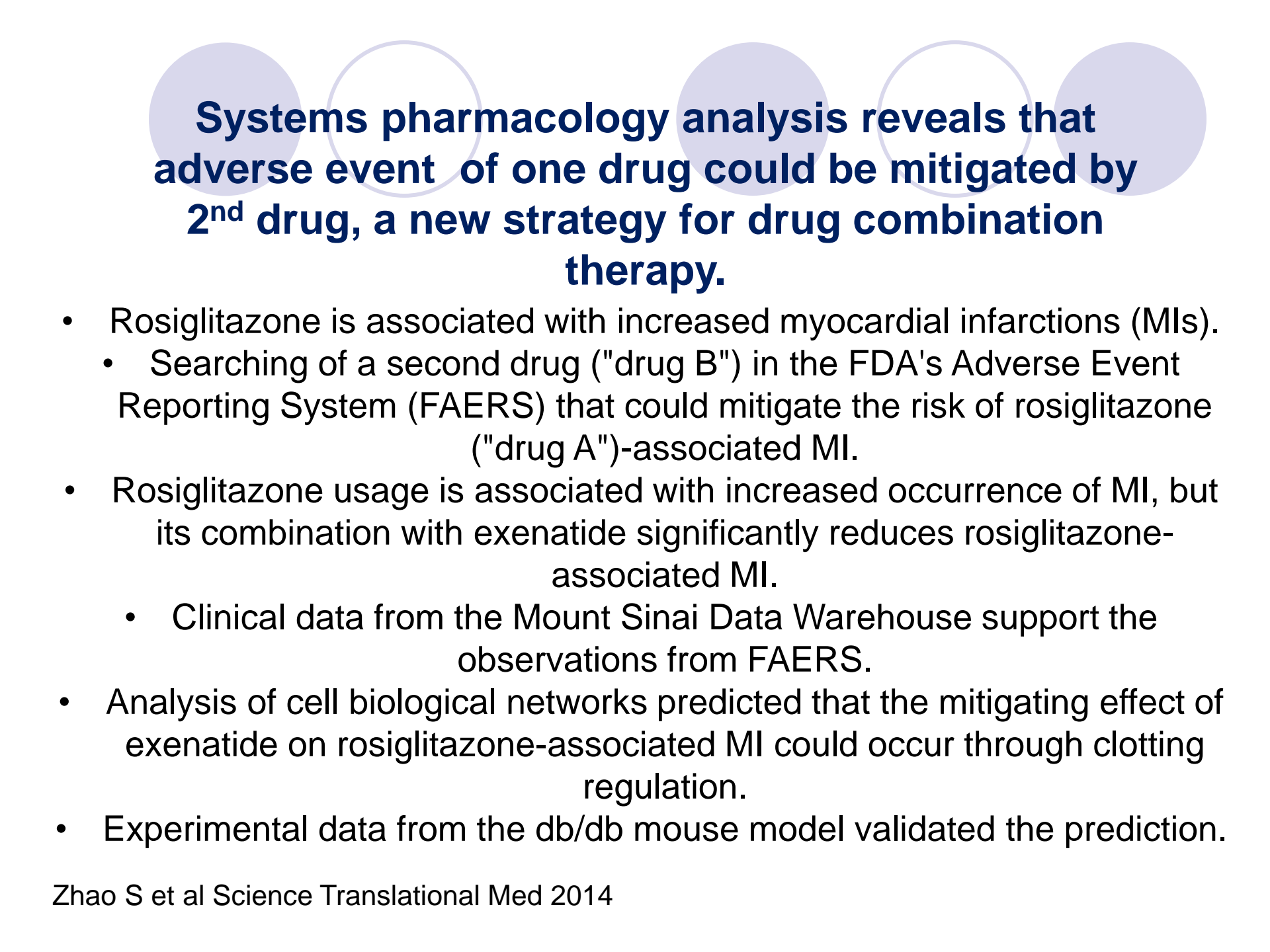
Compare with the genes altered in the disease kidney

A pair of drugs that reverse the maximal number of the genes that altered in the disease kidney while aggravating the minimal number of the genes.

The best combination is ACEI and HDACi

Total coverage Trichostatin A and Captopril	Coverage by Trichostatin A	Coverage by Captopril	Total Conflicts Trichostatin A and Captopril	Conflict by Trichostatin A	Conflict by Captopril
119 genes	70 genes	51 genes	51 genes	22 genes	31 genes

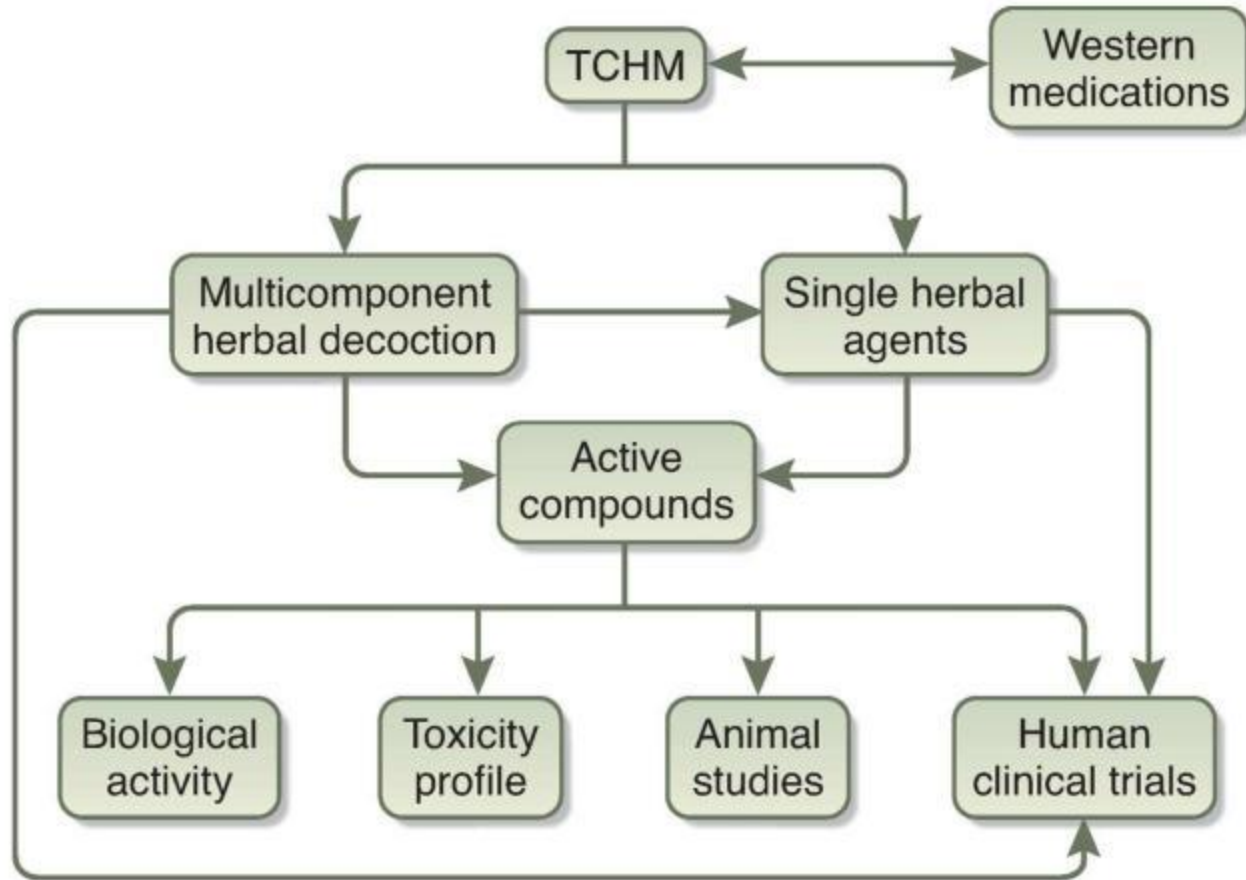
This is obtained by analyzing potential combination of any two drugs among 1200 FDA-approved drugs in a unbiased manner.



Systems pharmacology analysis reveals that adverse event of one drug could be mitigated by 2nd drug, a new strategy for drug combination therapy.

- Rosiglitazone is associated with increased myocardial infarctions (MIs).
- Searching of a second drug ("drug B") in the FDA's Adverse Event Reporting System (FAERS) that could mitigate the risk of rosiglitazone ("drug A")-associated MI.
- Rosiglitazone usage is associated with increased occurrence of MI, but its combination with exenatide significantly reduces rosiglitazone-associated MI.
 - Clinical data from the Mount Sinai Data Warehouse support the observations from FAERS.
- Analysis of cell biological networks predicted that the mitigating effect of exenatide on rosiglitazone-associated MI could occur through clotting regulation.
- Experimental data from the db/db mouse model validated the prediction.

Role of Chinese Medicine in the treatment of kidney disease



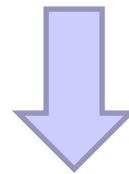
Systems Biology Approach to Identify New Drug Targets

Systems Biology Approach identifies JAK-STAT pathway in Diabetic Nephropathy

[Diabetes](#). 2009 Feb;58(2):469-77. doi: 10.2337/db08-1328. Epub 2008 Nov 18.

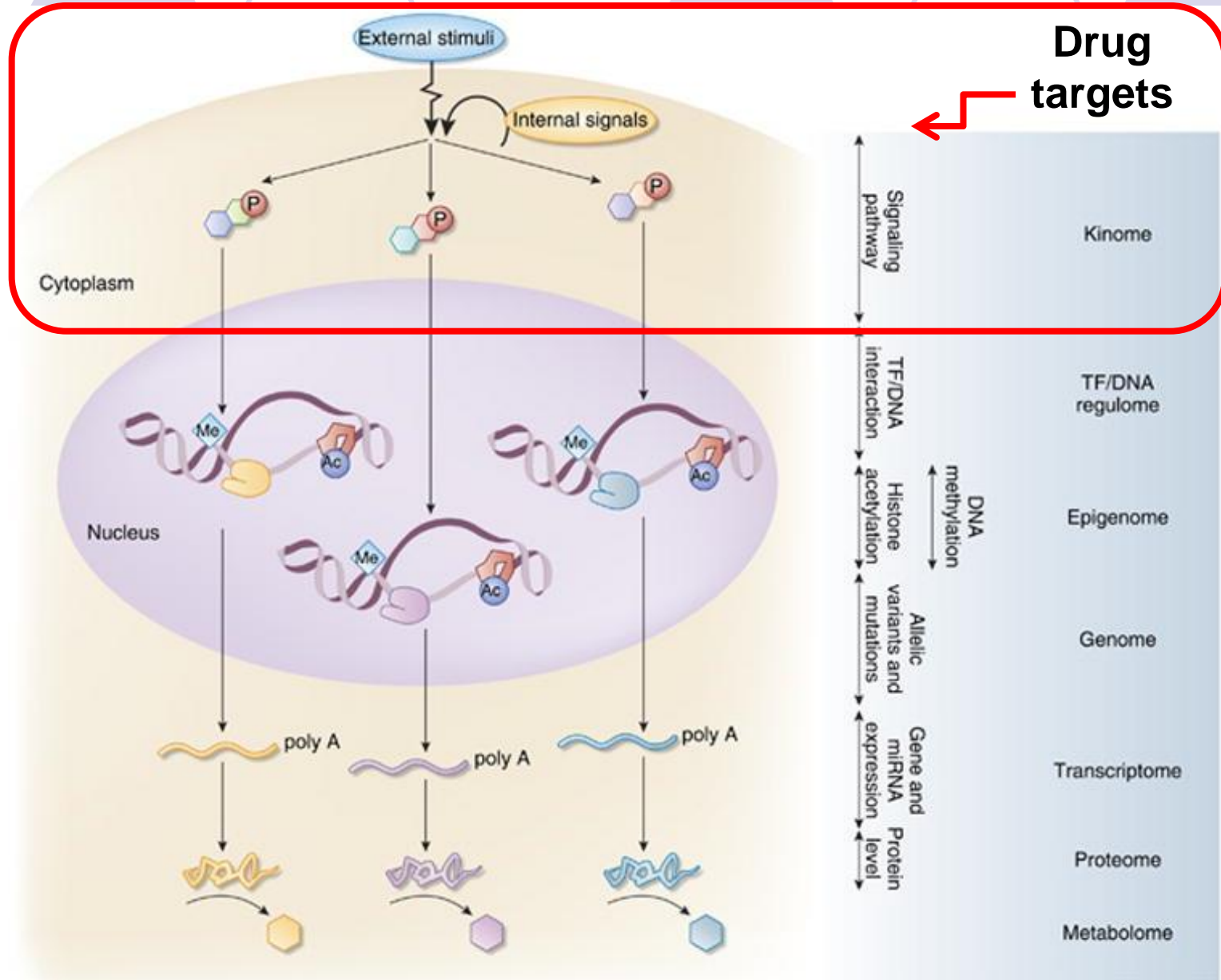
Enhanced expression of Janus kinase-signal transducer and activator of transcription pathway members in human diabetic nephropathy.

[Berthier CC](#)¹, [Zhang H](#), [Schin M](#), [Henger A](#), [Nelson RG](#), [Yee B](#), [Boucherot A](#), [Neusser MA](#), [Cohen CD](#), [Carter-Su C](#), [Argetsinger LS](#), [Rastaldi MP](#), [Brosius FC](#), [Kretzler M](#).



A phase 2 clinical trial will determine whether a JAK1/JAK2 inhibitor (Baricitinib from Eli Lilly) will be effective in patients with progressive diabetic nephropathy (ClinicalTrials.gov identifier: NCT01683409).

Systems Biology Analysis of Drug Targets



Analysis of cellular network

Signaling network

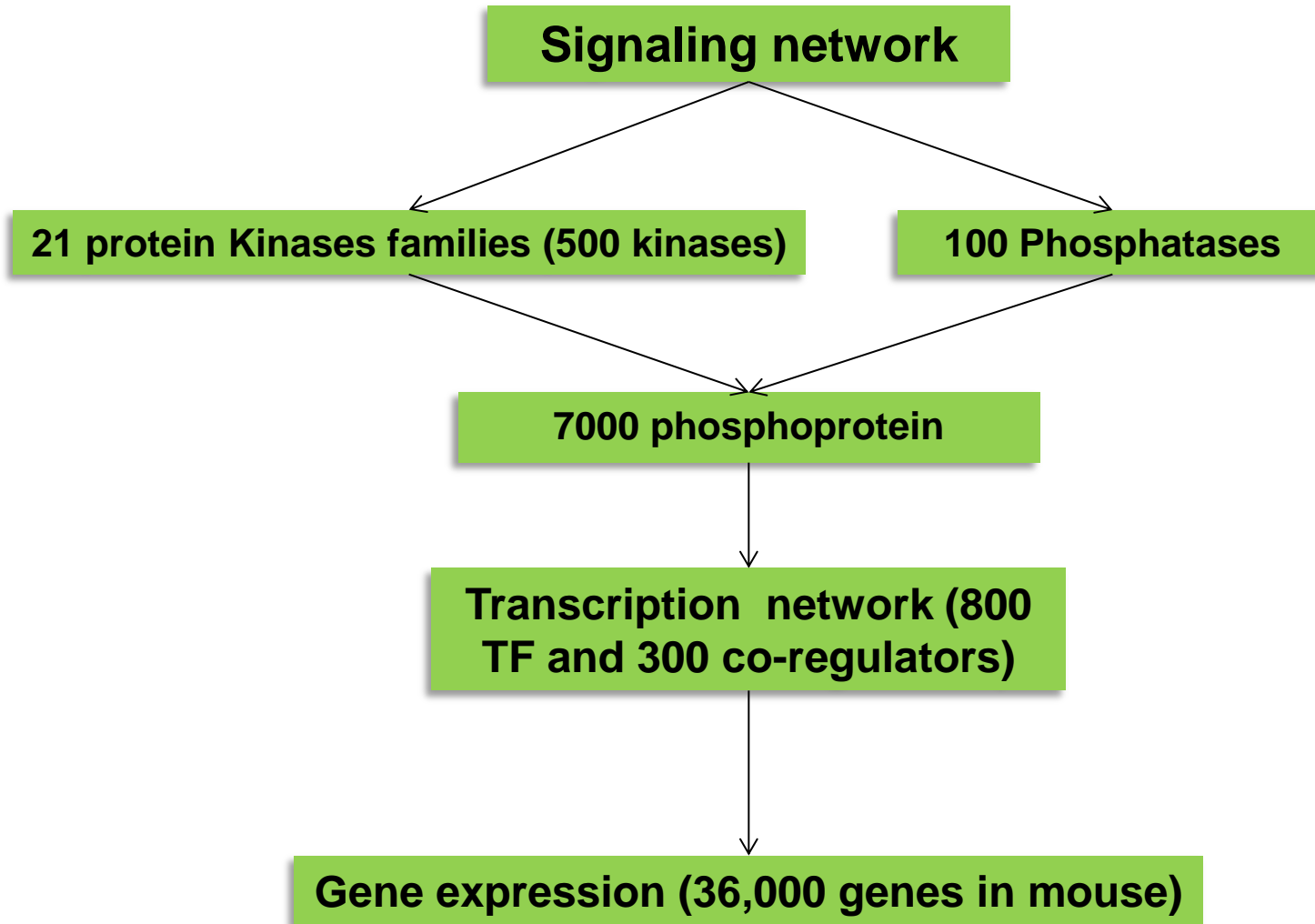
21 protein Kinases families (500 kinases)

100 Phosphatases

7000 phosphoprotein

**Transcription network (800
TF and 300 co-regulators)**

Gene expression (36,000 genes in mouse)

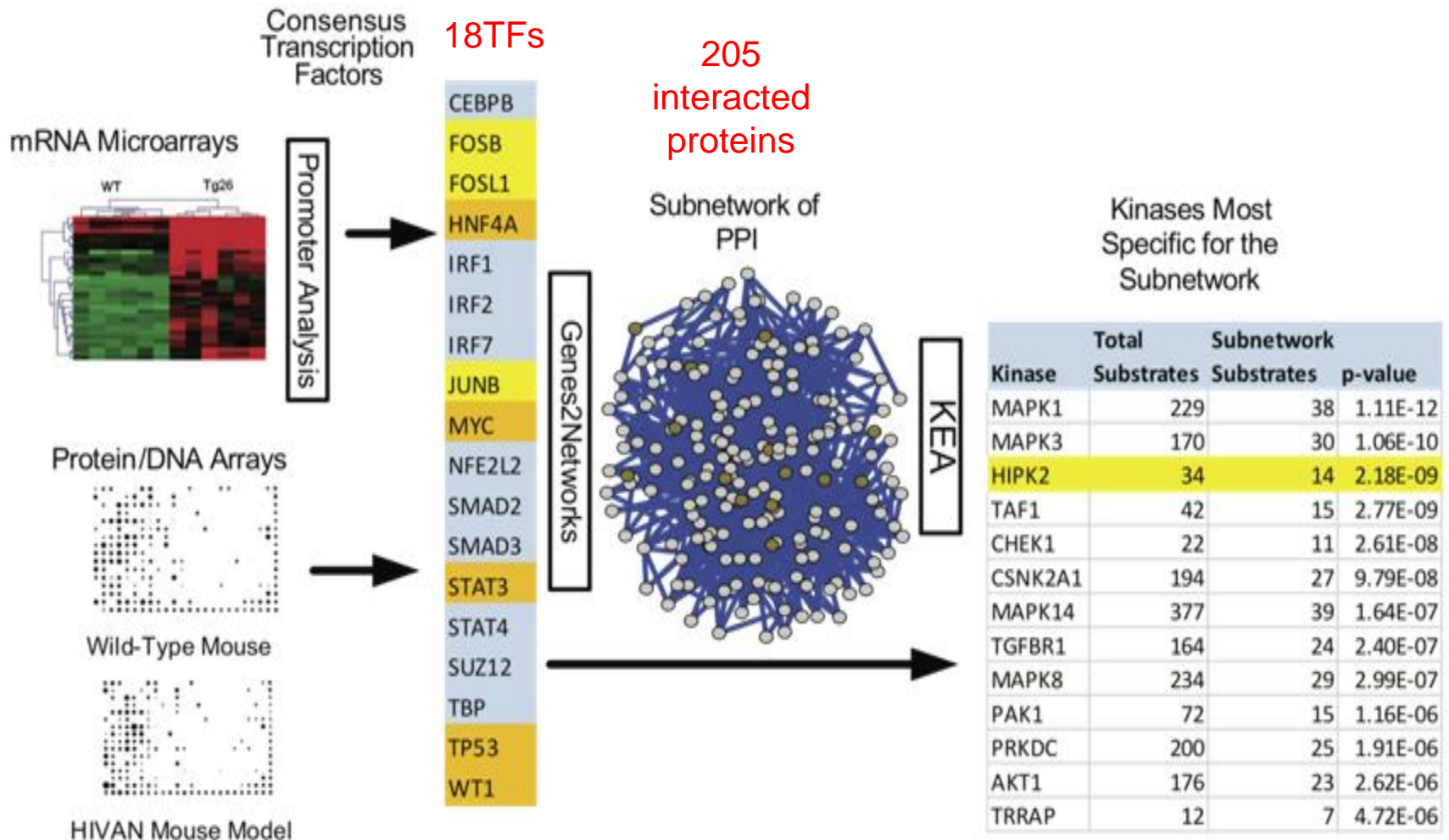




Study of Signaling Network

- Signaling pathway activation usually occurs at the post-translational level such as protein phosphorylation. Therefore, it is difficult to deduce simply from gene expression datasets.
- It is technically challenged to screen protein kinase activity and protein phosphorylation profile using proteomic approach.
- **We developed a combined computational and experimental approach to deduce upstream signaling pathways from gene expression datasets.**

Identification of HIPK2 as a key regulator of gene network in kidney disease





HIPK2

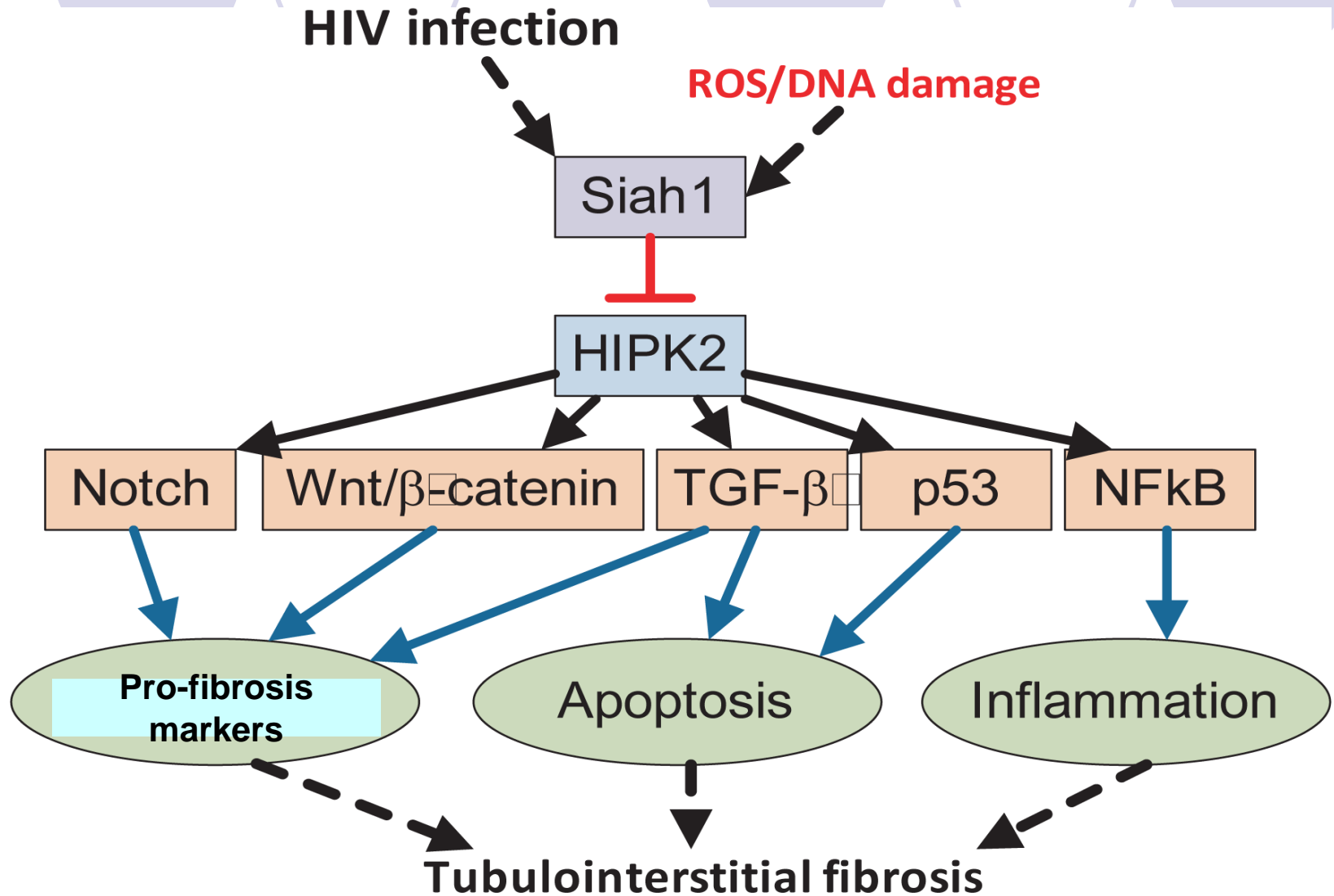
A nuclear serine-threonine protein kinase acting as a transcription regulatory factor.

It mediates apoptosis by interacting with p53 pathway.

It mediates TGF-beta signaling pathway.

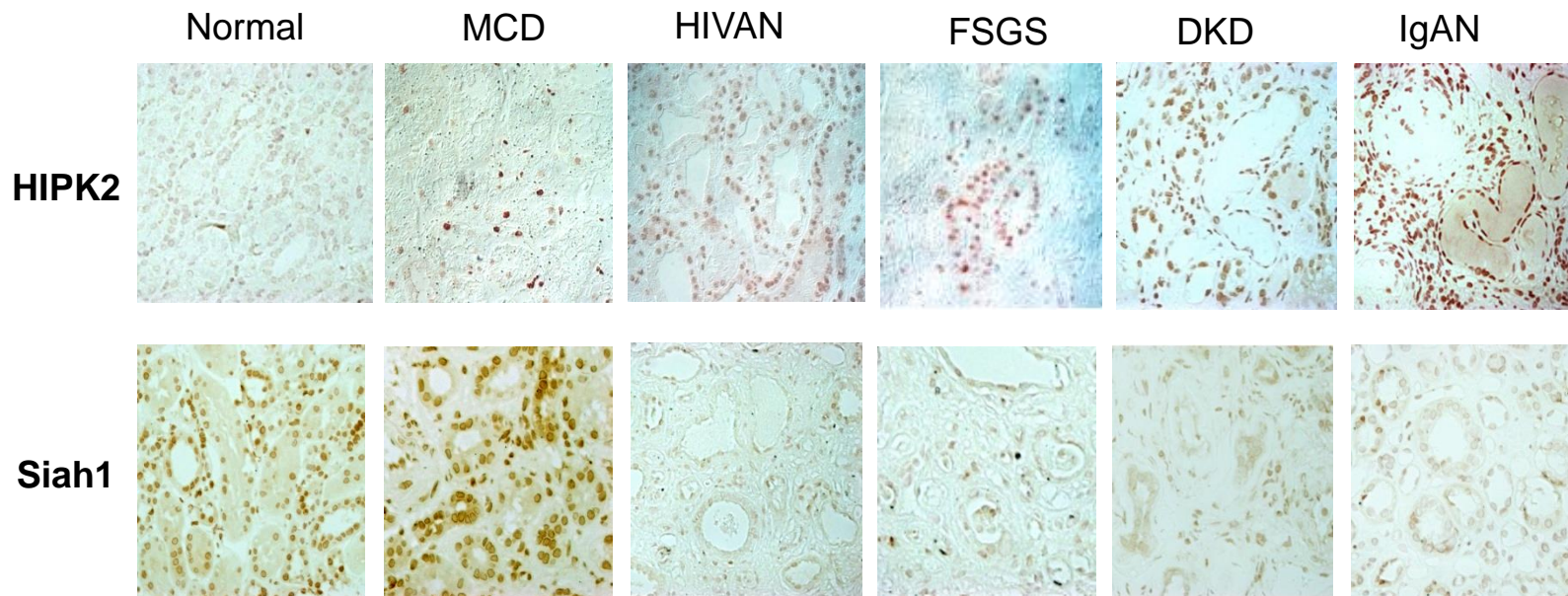
It interacts with Notch and Wnt/ β -catenin signaling pathway.

Summary of HIPK2 pathway in kidney cells



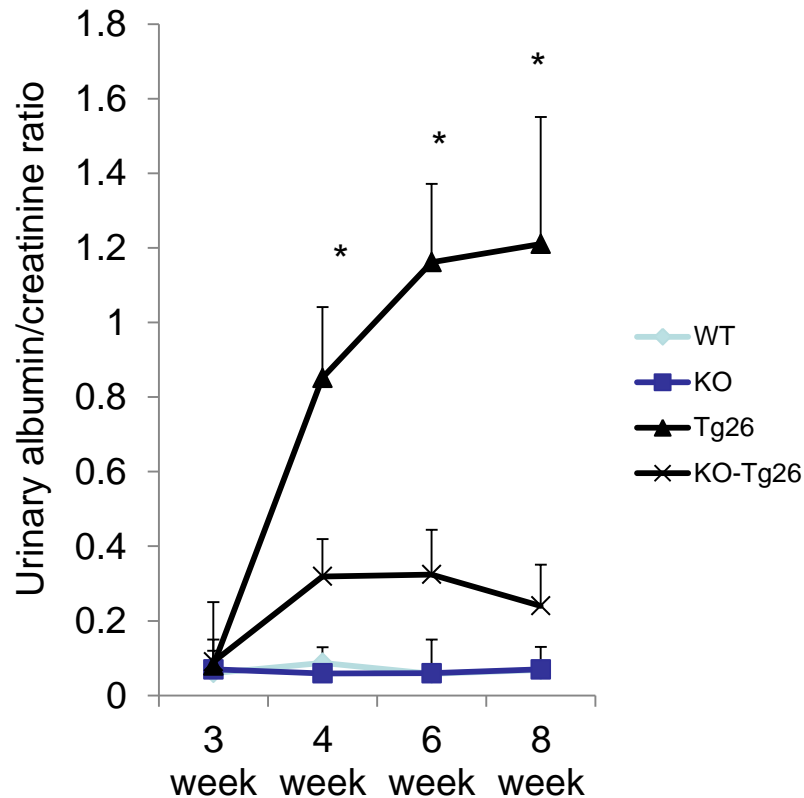


There is an inverse relationship between HIPK2 and Siah1 expression in disease kidneys

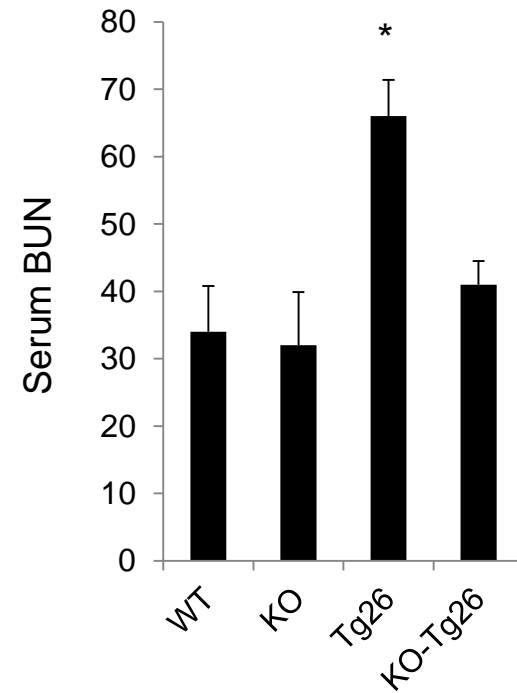


Knockout of HIPK2 improves proteinuria and renal function in Tg26 mice

A.



B.



Knockout of HIPK2 attenuates renal fibrosis in Tg26

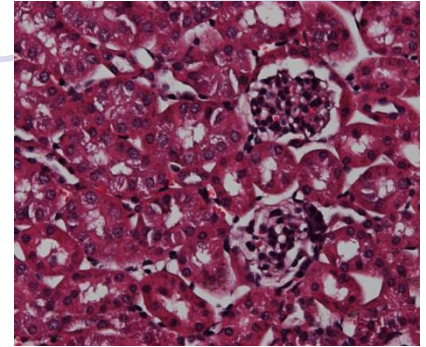
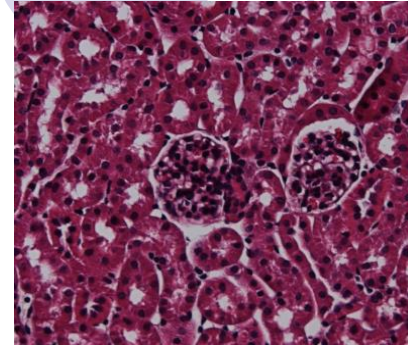
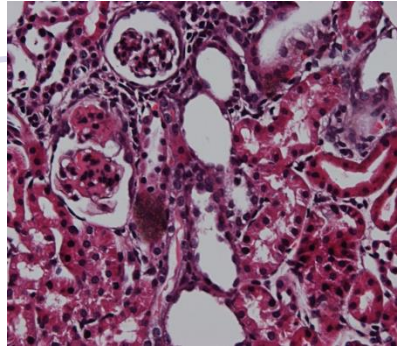
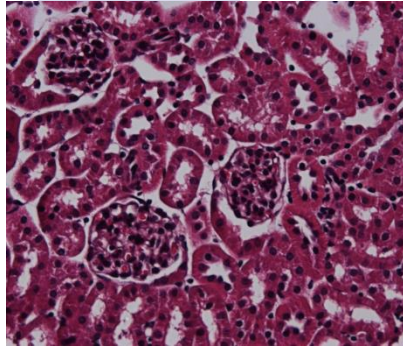
WT

Tg26

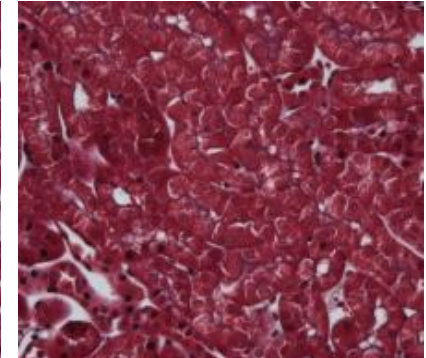
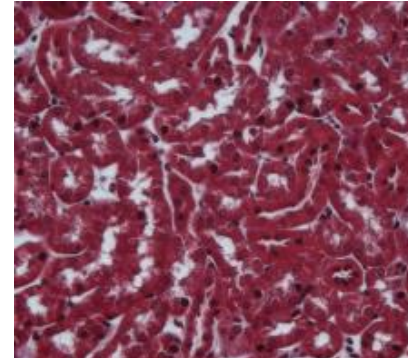
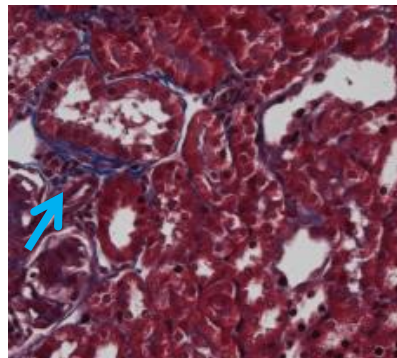
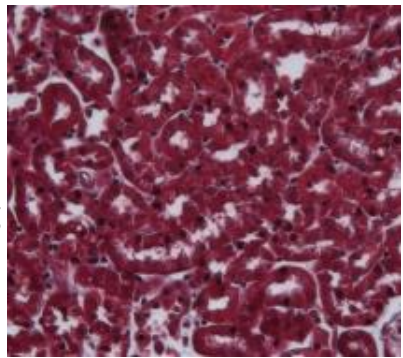
KO

KO-Tg26

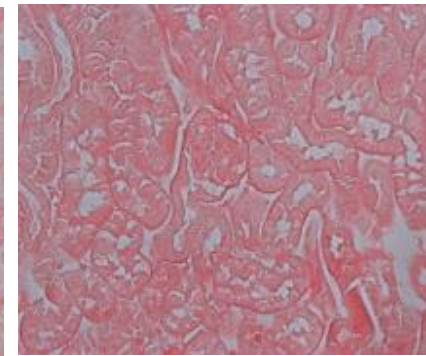
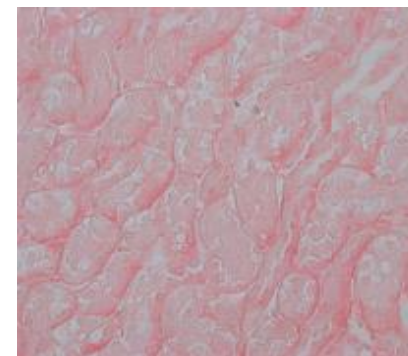
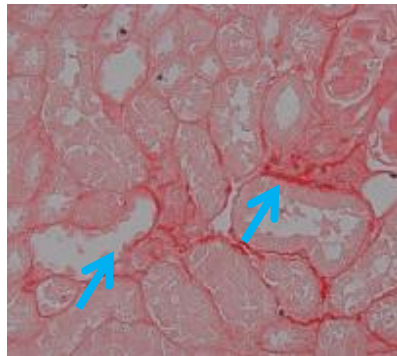
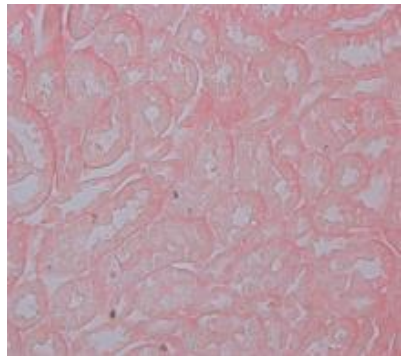
H&E
staining



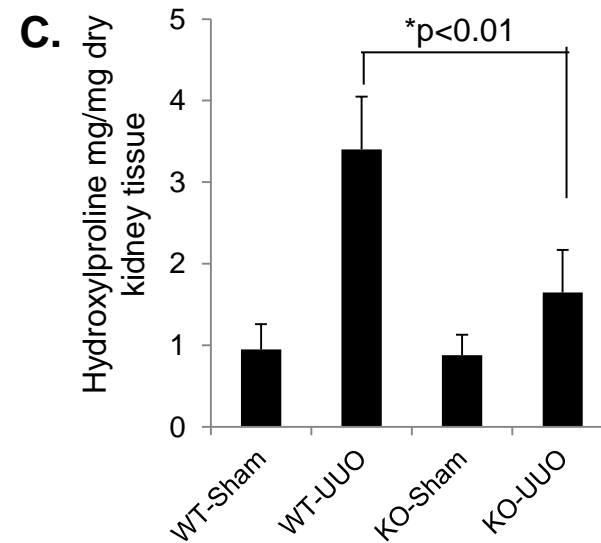
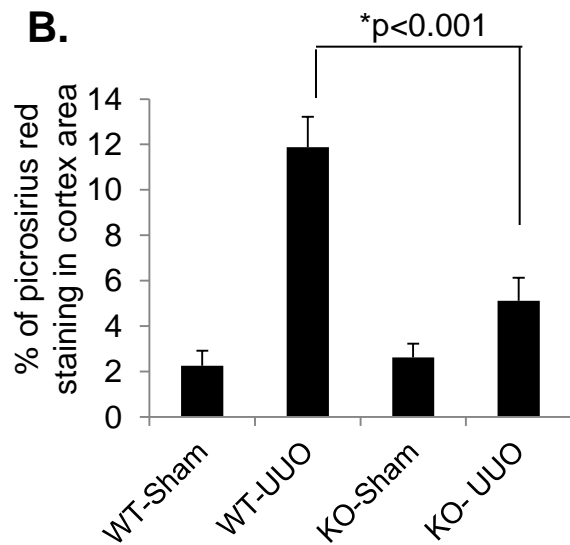
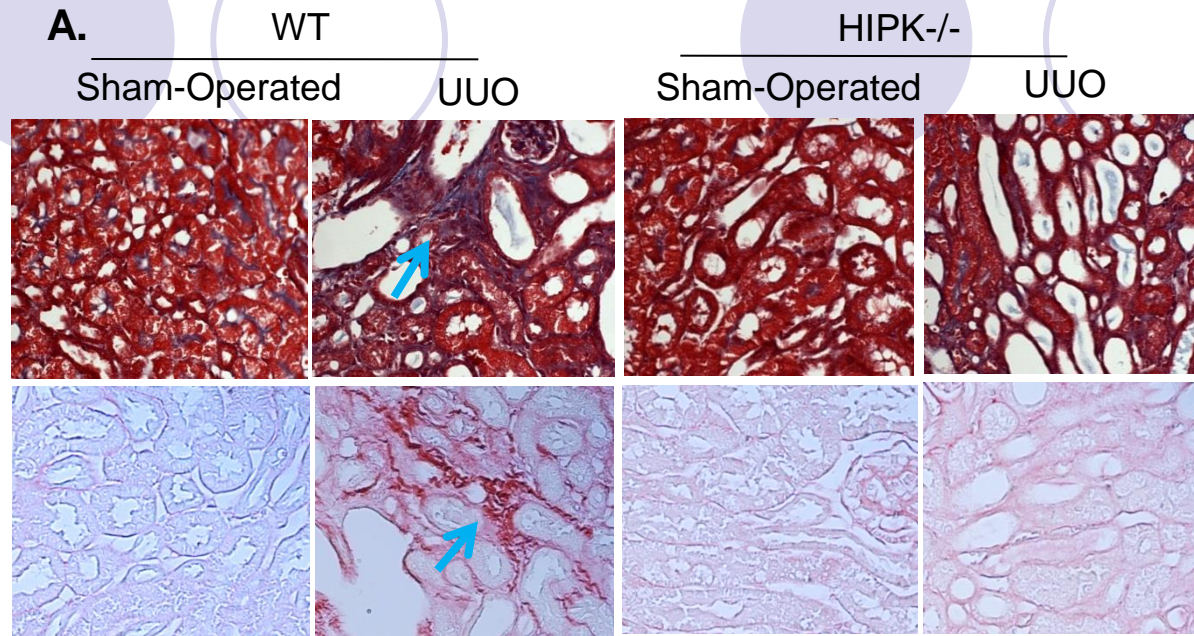
Masson
staining



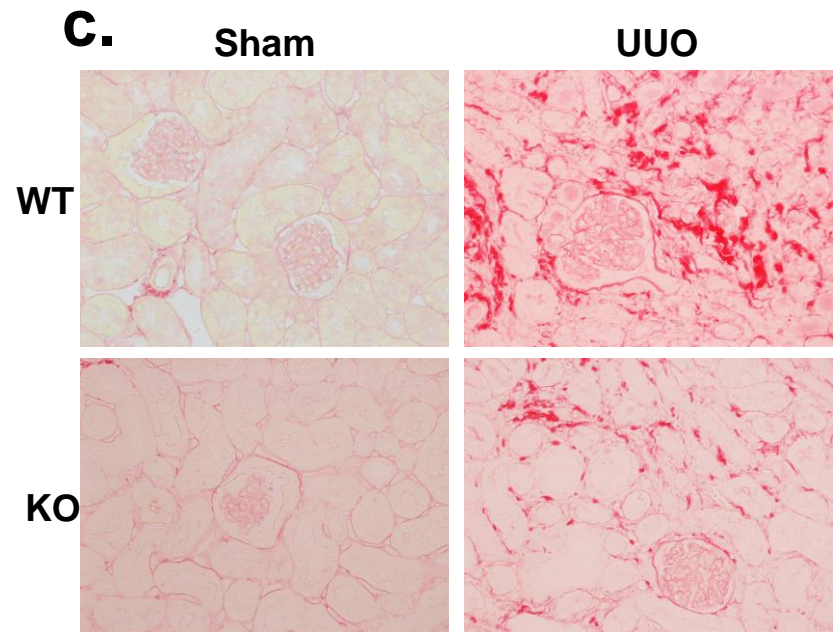
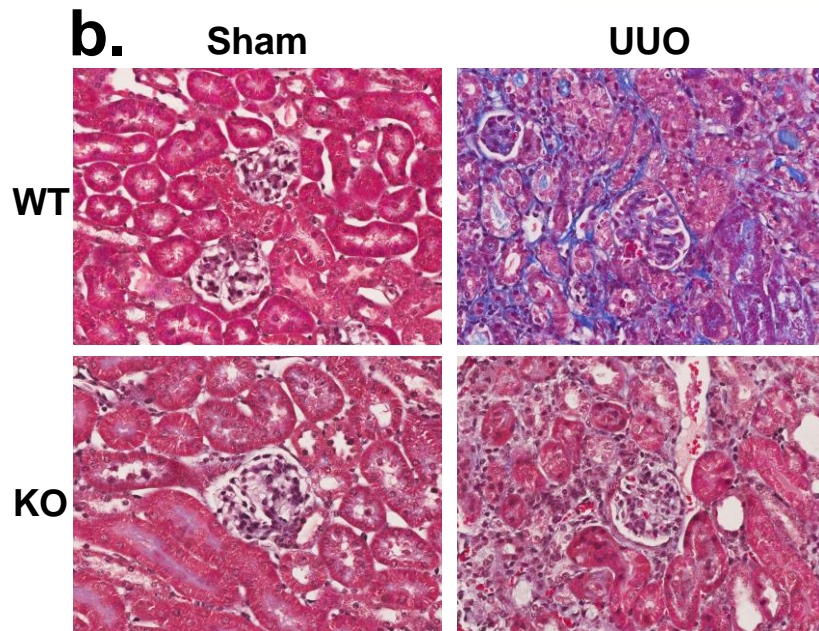
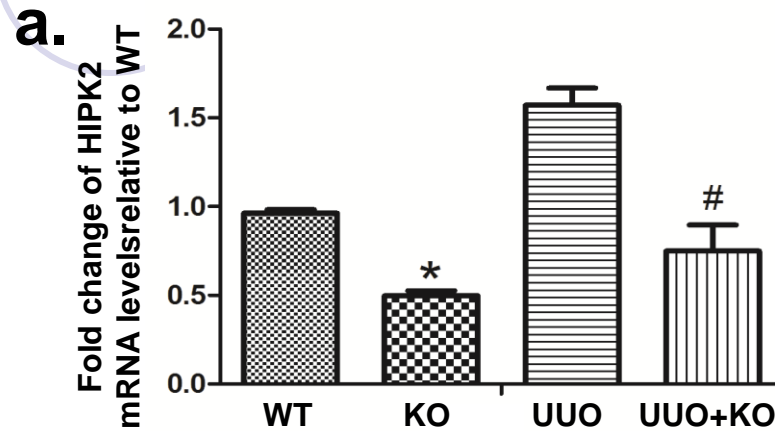
Picrosirius
red
staining



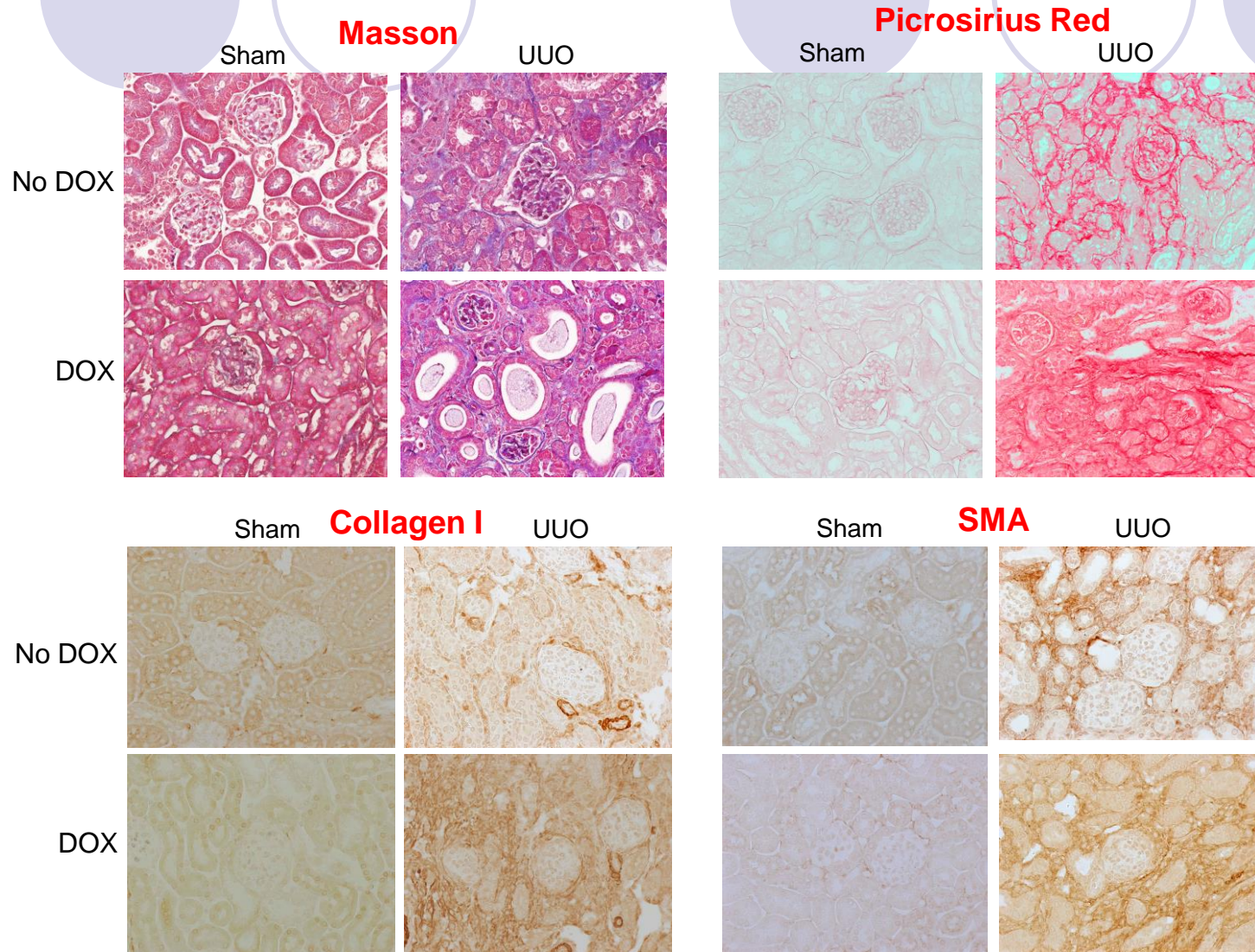
Knockout of HIPK2 attenuates renal fibrosis in UUO mice



Knockout of Hipk2 expression in proximal tubular cells attenuates renal fibrosis in the UUO model



Induction of HIPK2 expression in renal tubular epithelial cells aggravates renal fibrosis in the UOU mice



HIPK2 as a potential drug target for anti-fibrosis therapy: Pros and Cons

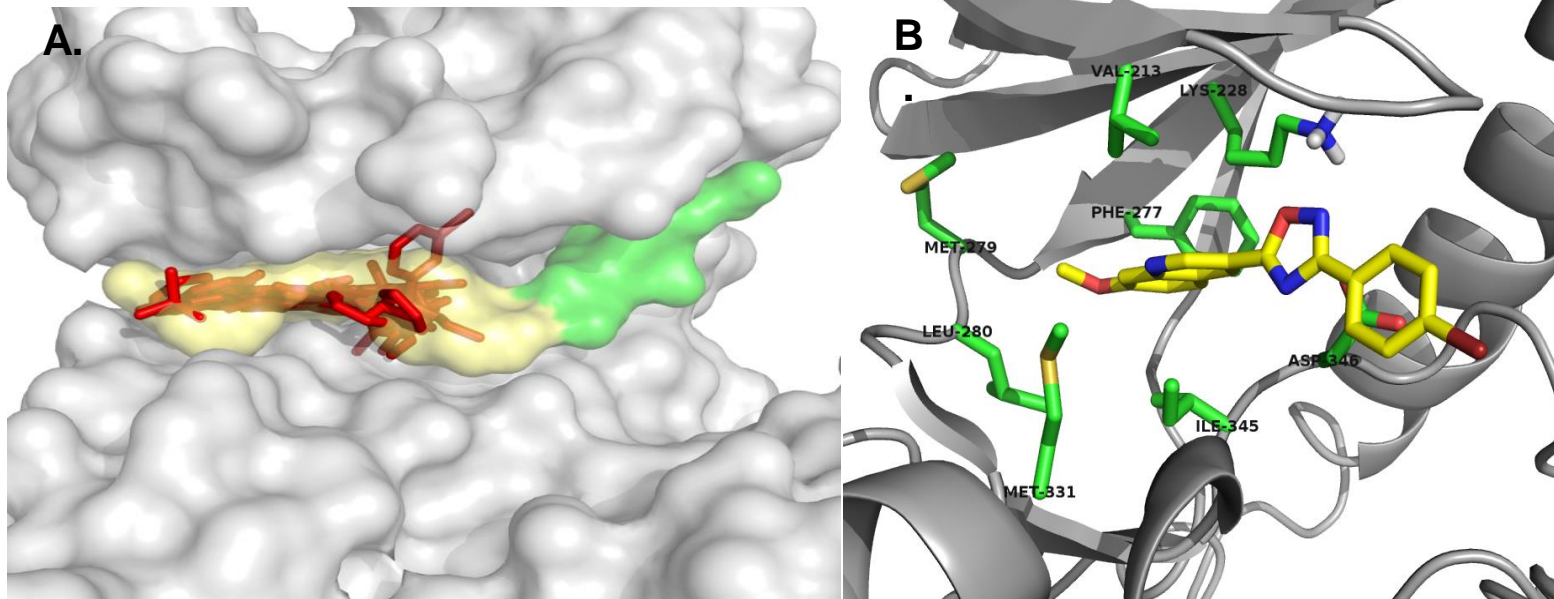
● Pros:

1. Protein kinase is considered as good drug targets.
2. HIPK2 knockout mice do not have obvious phenotype, suggesting that HIPK2 inhibitors should have low toxicity profile.
3. HIPK2 affects multiple pro-fibrosis pathways and may have potent anti-fibrosis effects as compared to the drug targeting the individual pathway.

● Cons:

- Most protein kinase inhibitors have off target effects.
- HIPK2 and HIPK1 double knockout mice embryonic lethal.
- Some previous studies suggest that inhibition of HIPK2 may have oncogenic effect through inhibition of p53.

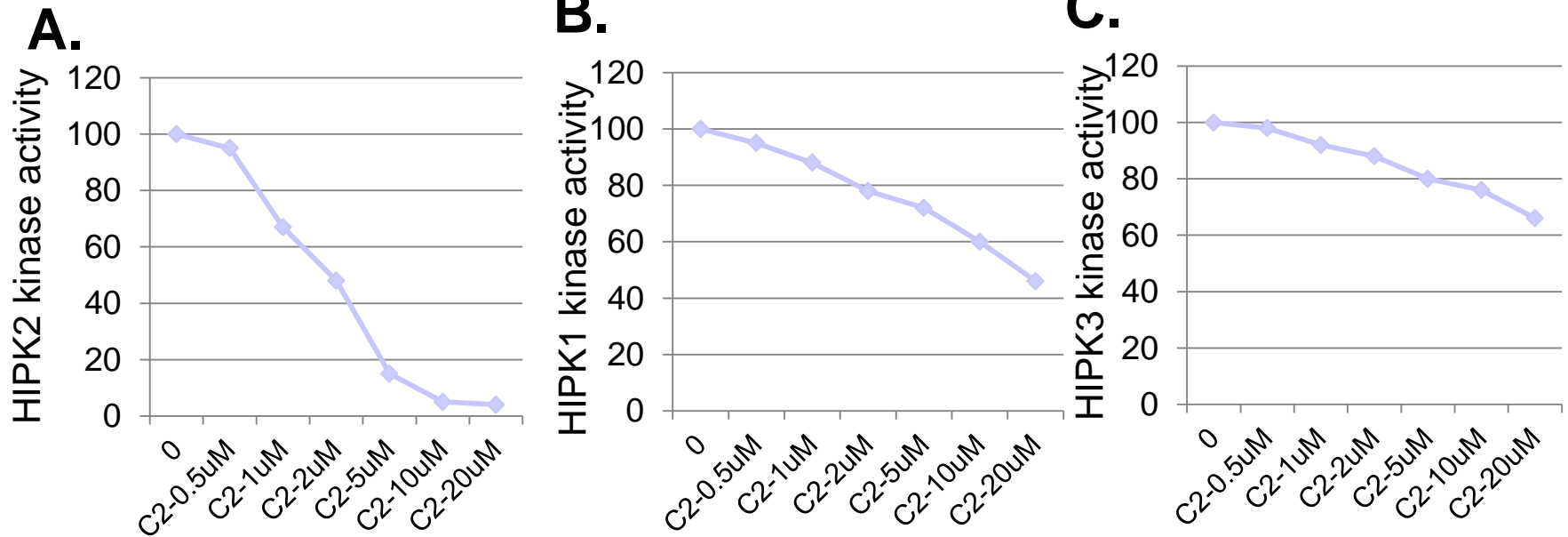
Modeling of HIPK2



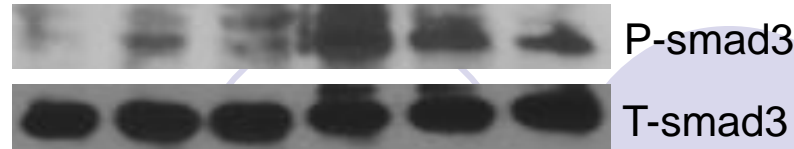
Modelling of HIPK2. A. Comparative model of HIPK2 (gray surface) is shown with the ATP-binding site highlighted in yellow and the structures of inhibitors of homologous kinases (DYRK1A, DYRK2, CLK1, CLK2, CLK3) shown in red. A region that can be exploited for enhancing the selectivity of HIPK2 inhibitors is highlighted in green. B. Stick model of HIPK2



C2 has selective inhibition on HIPK2 kinase activity

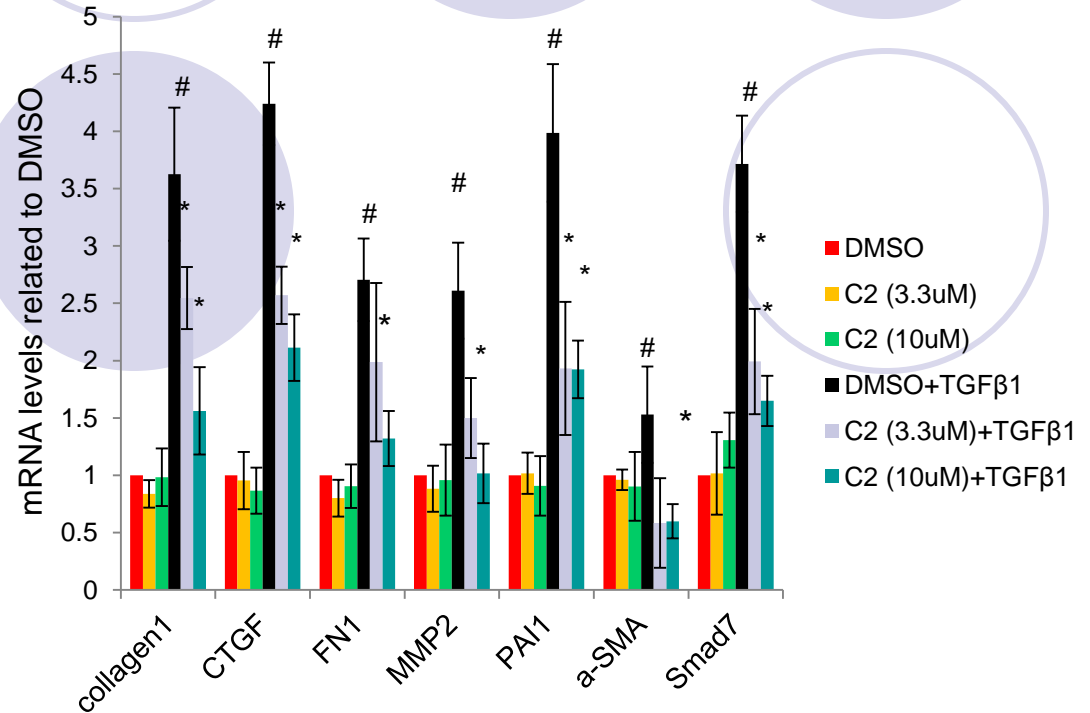
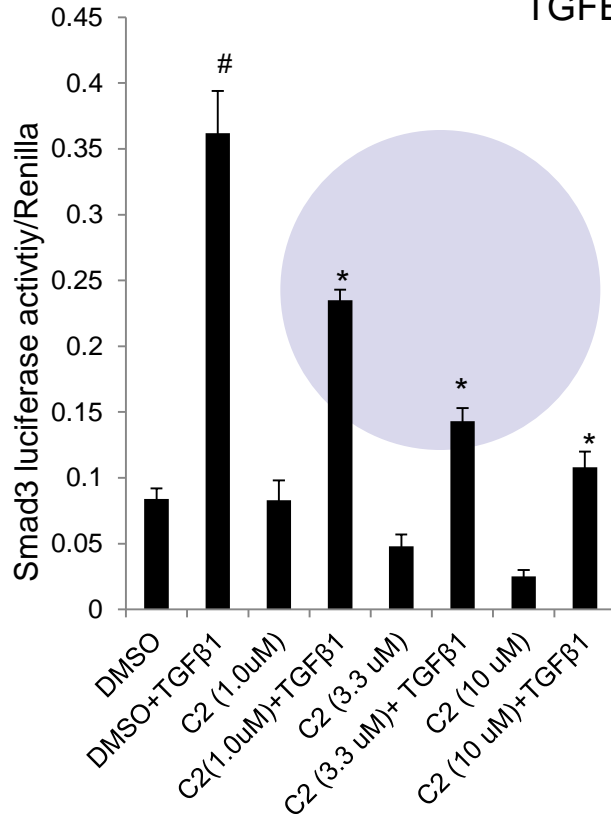


Inhibitory effects of compound #2 on TGF- β -induced Smad3 activation

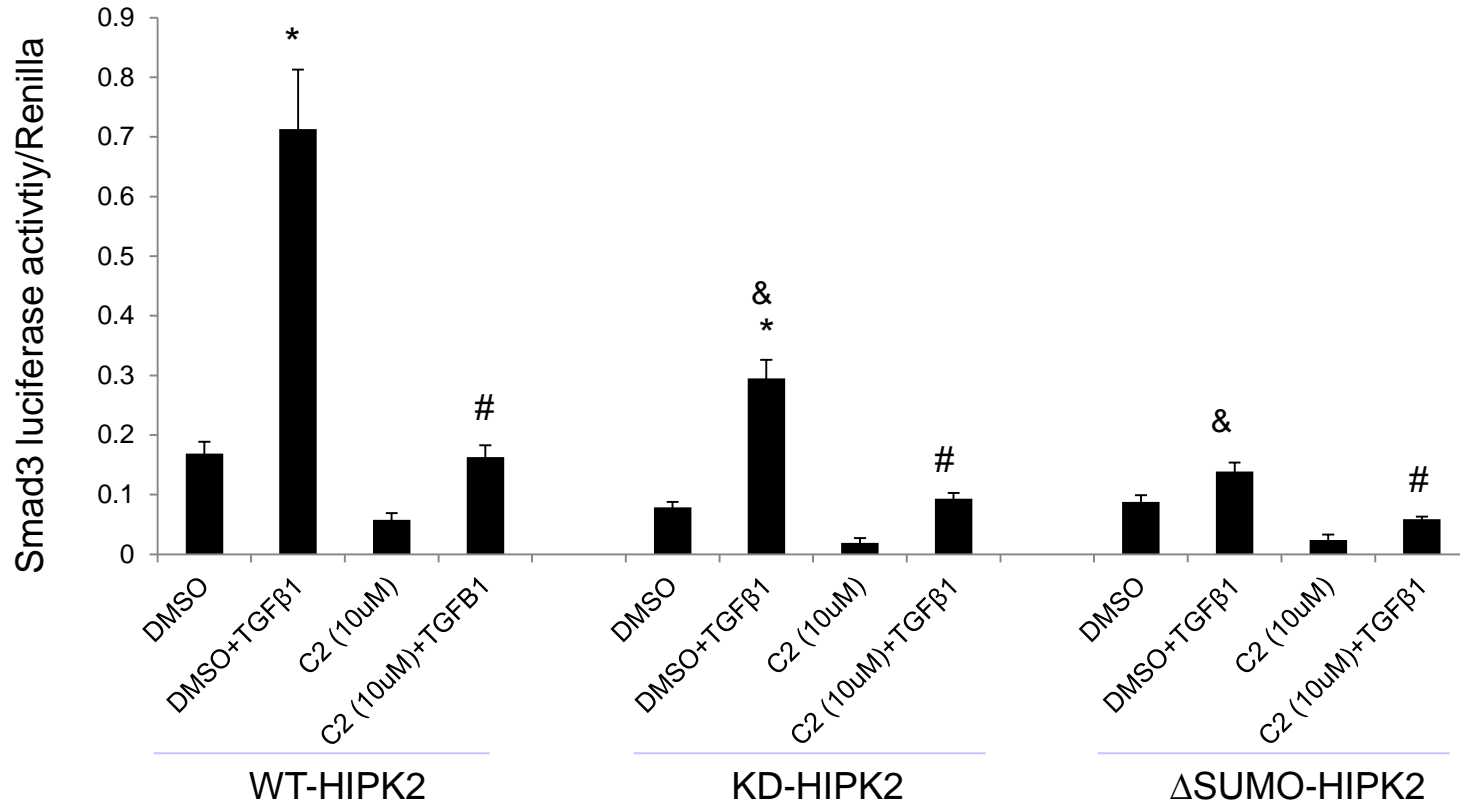


C2 (μ M): 0 3.3 10 0 3.3 10

TGFB1- TGFB1+



HIPK2 inhibitor (C2) suppressed TGF- β -induced Smad3 activation.

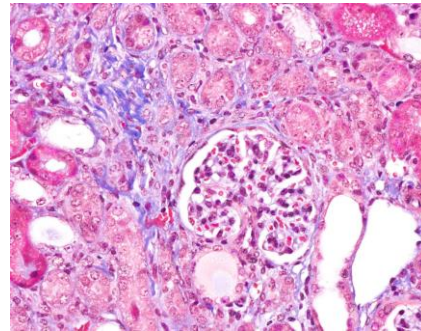
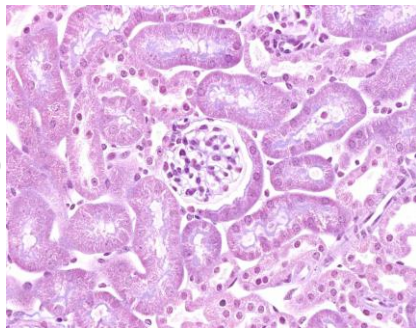


Treatment with HIPK2 inhibitor (C2) reduces renal fibrosis in the UUO mice.

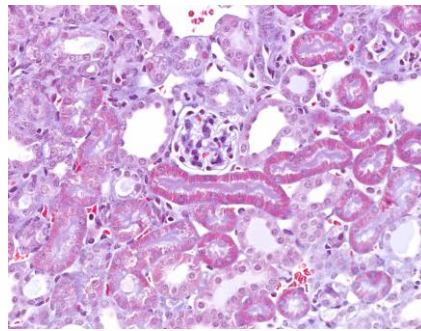
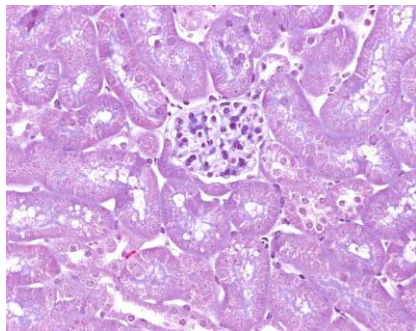
Masson Trichrome

Picrosirius Red

DMSO



C2

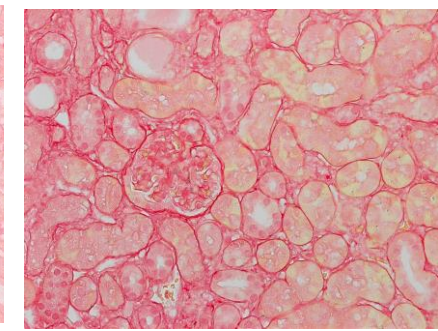
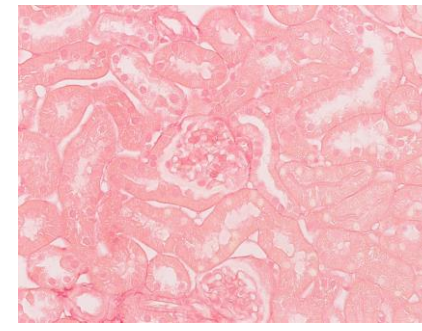
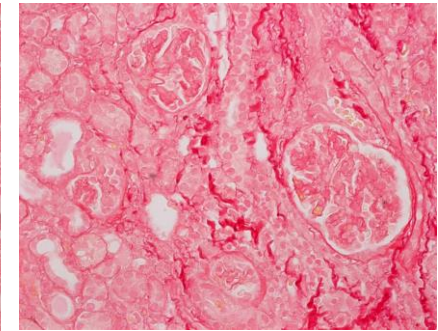
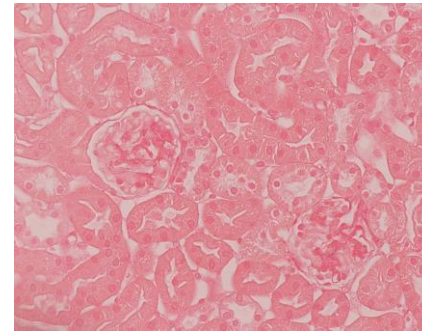


Sham

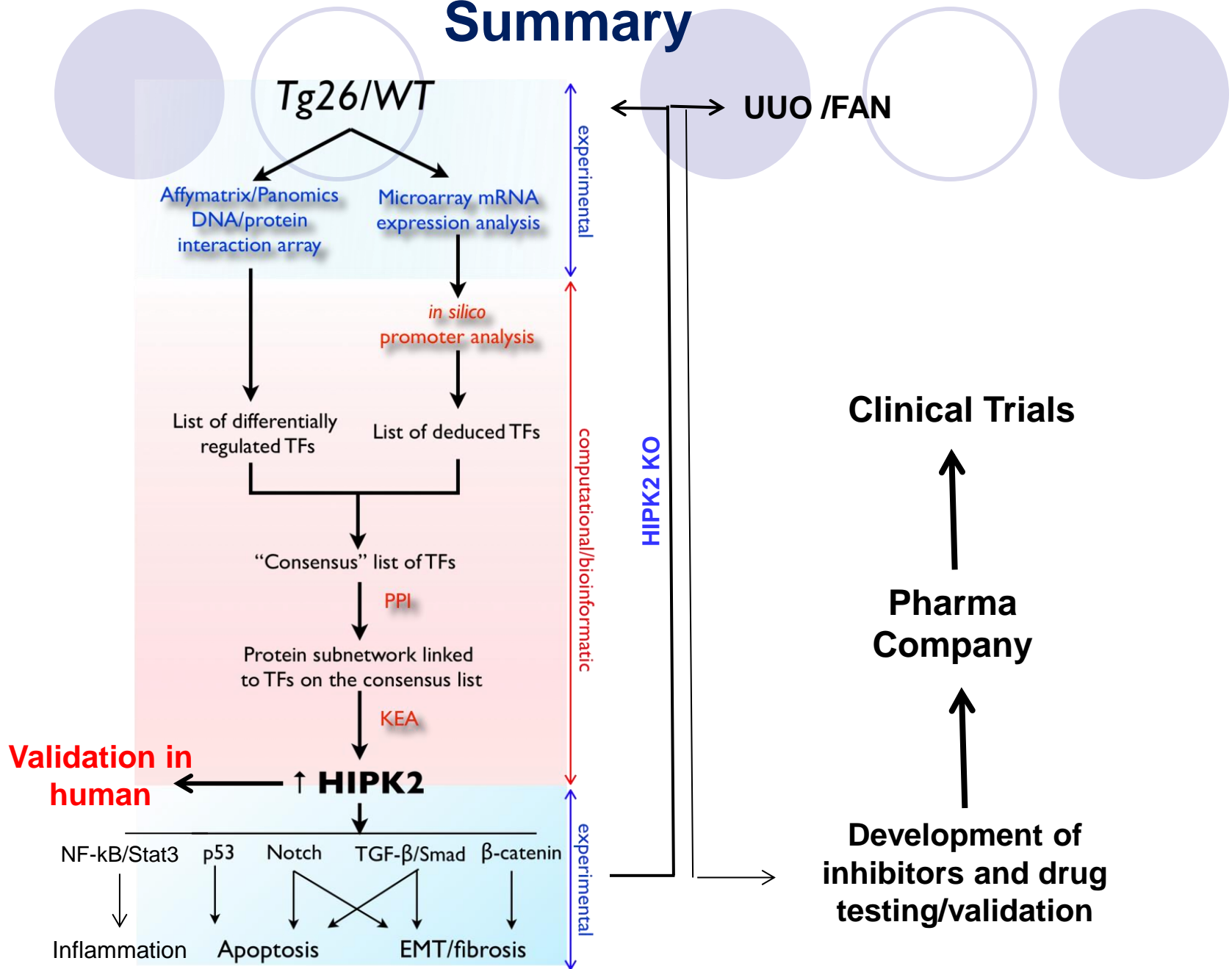
UUO

Sham

UUO



Summary



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