单细胞联合空间转录组学揭示黄蜀葵花（*Abelmoschus manihot* (L.) Medic）治疗糖尿病肾病的潜在分子机制

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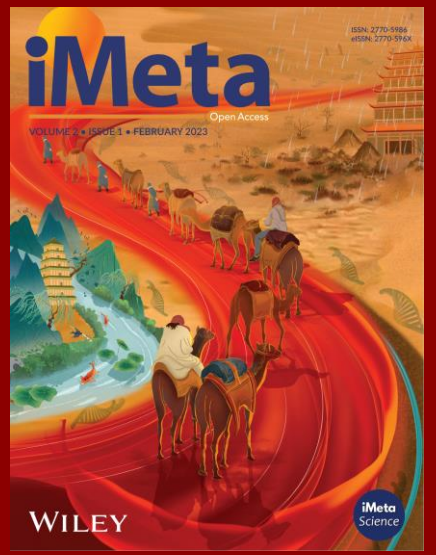
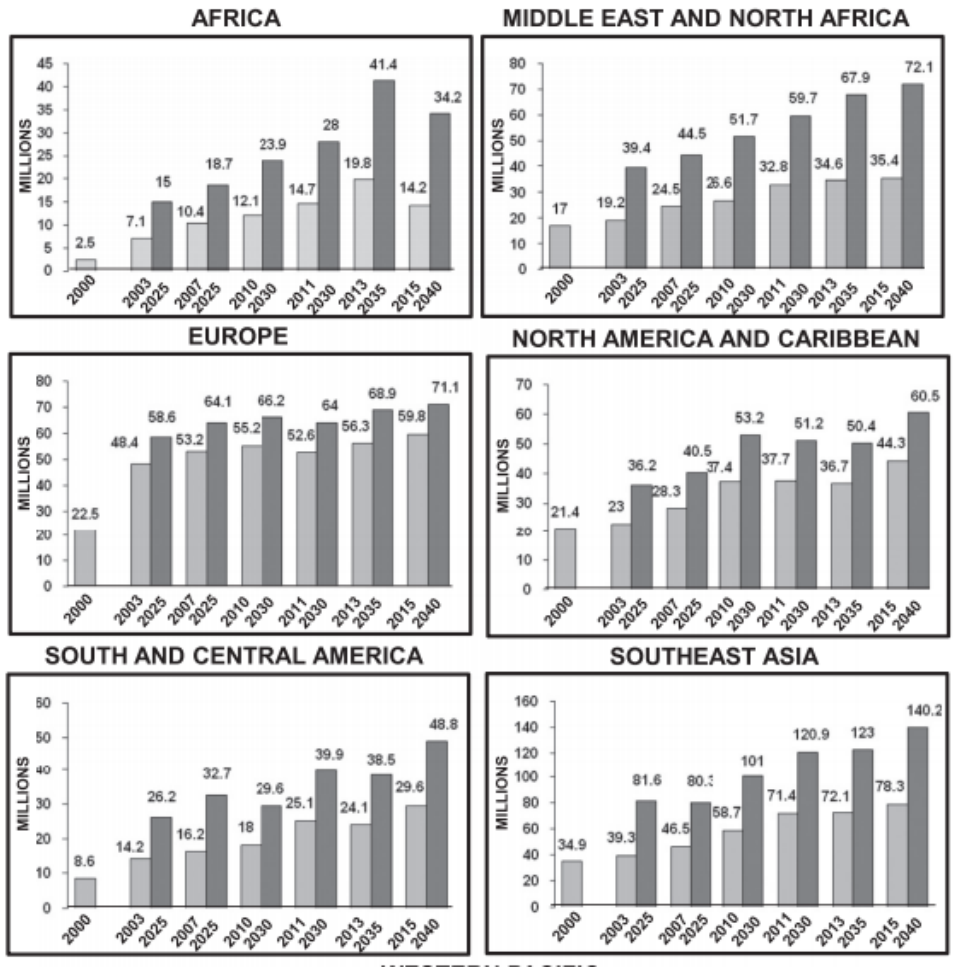
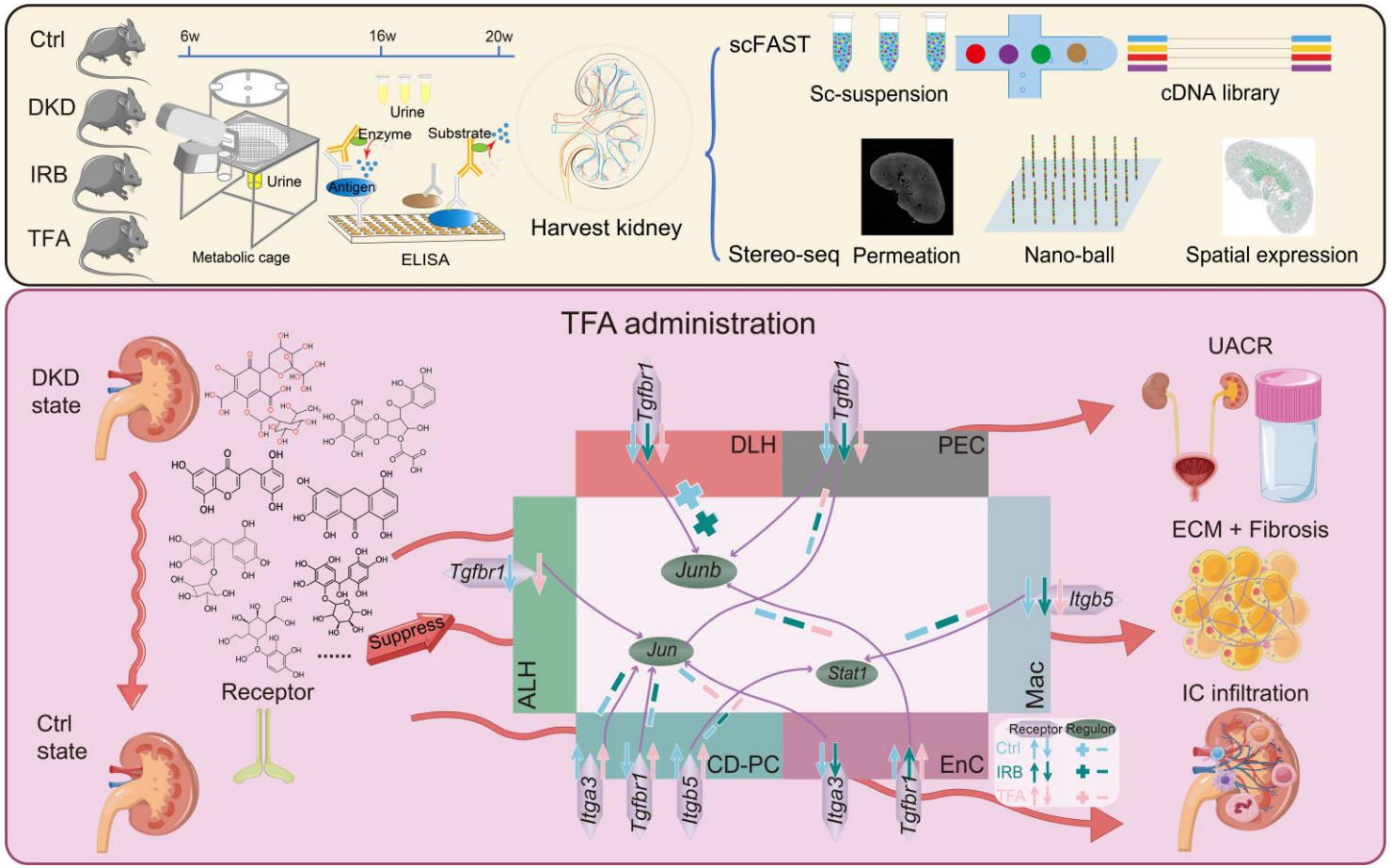


Chenhua Wu, Haitao Tang, Yihong Yu, Yuhui Song, Haitao Ge, Yiming Shen, Jie Wu, et al. 2025. Single-cell and spatial transcriptomics reveals potential molecular mechanisms of Abelmoschus manihot (L.) Medic in treating diabetic kidney disease. ***iMeta*** 4: e70099. https://doi.org/10.1002/imt2.70099

简介

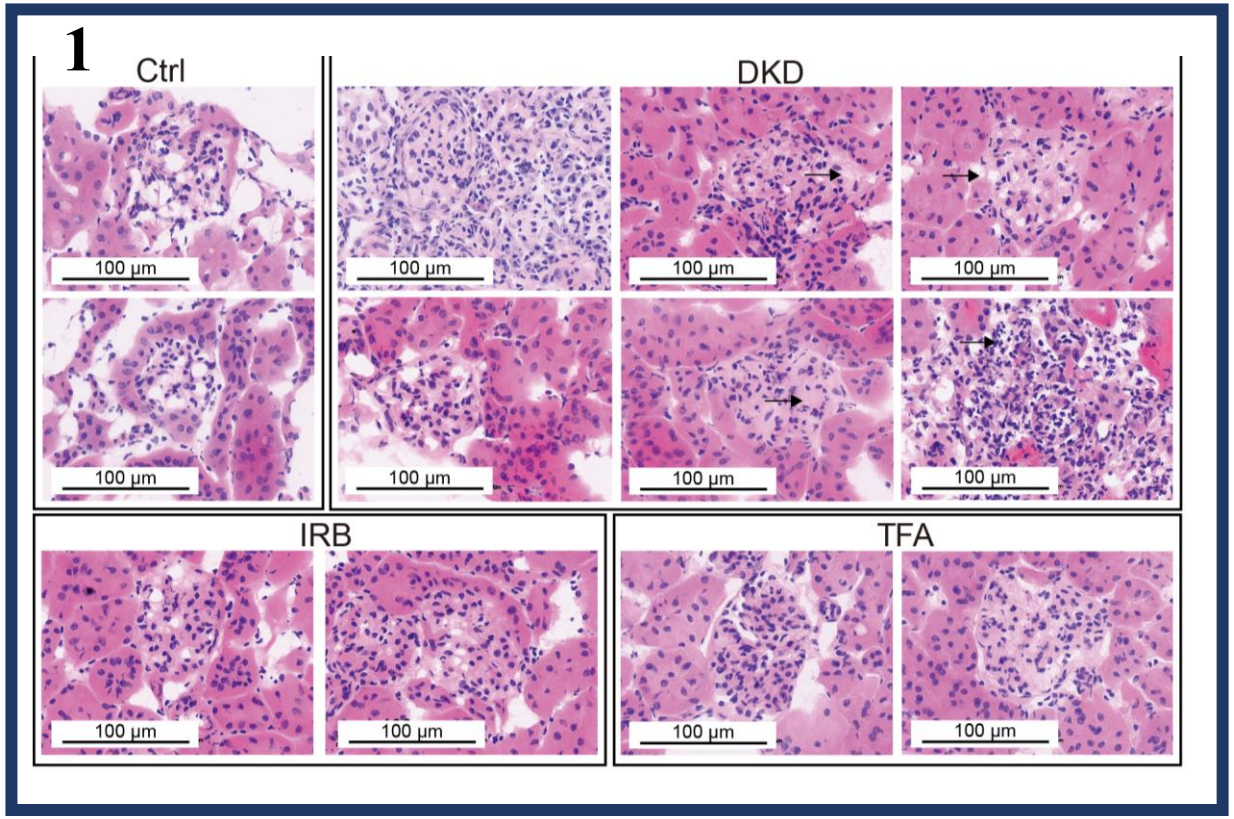


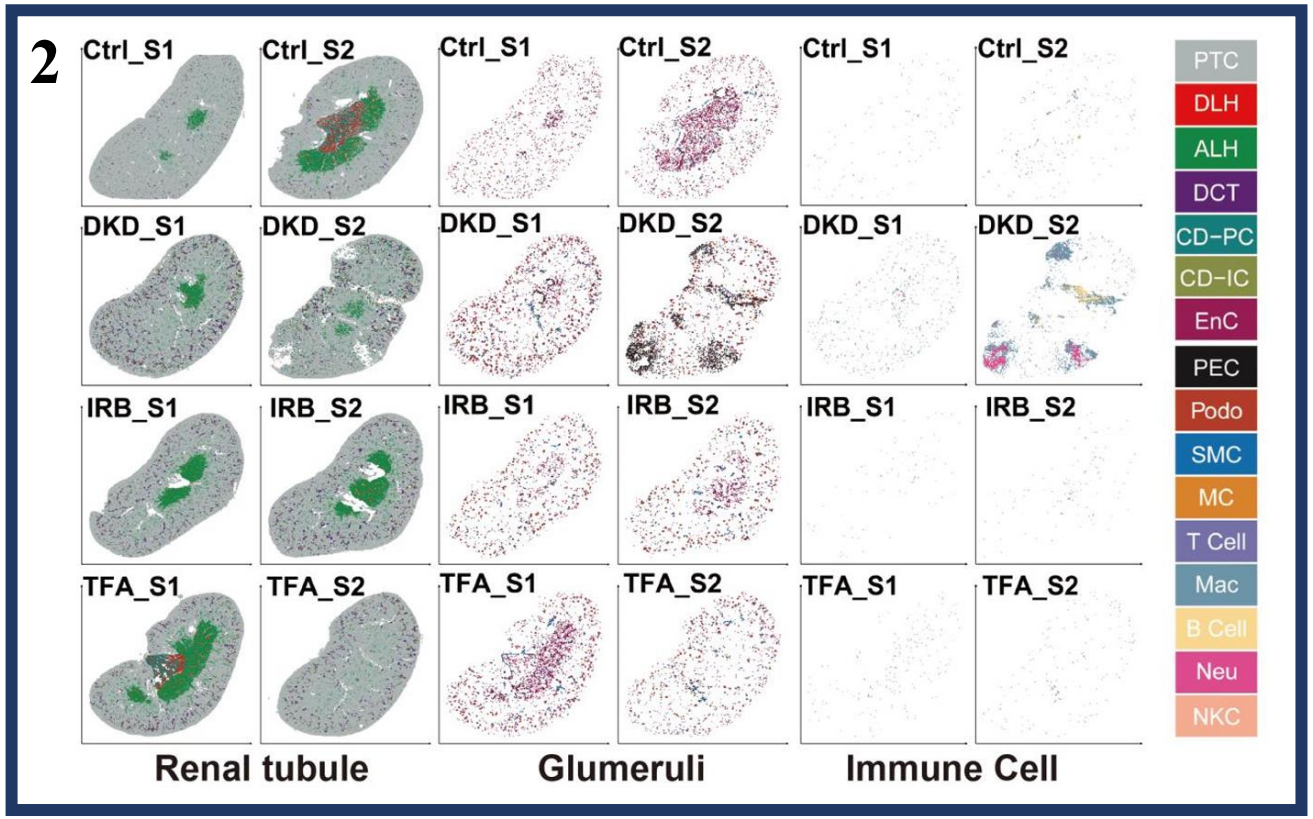


二型糖尿病与糖尿病肾病的全球患病人数不断攀升，为患者带来巨大的健康及财产损失。DKD的发病及治疗机理有待进一步阐明。

通过《Nature Methods》2020年年度技术——空间转录组联合scRNA-seq解析糖尿病肾病中的线粒体稳态、免疫浸润与厄贝沙坦和黄葵总黄酮对其治疗机制

主要结果-空转图谱

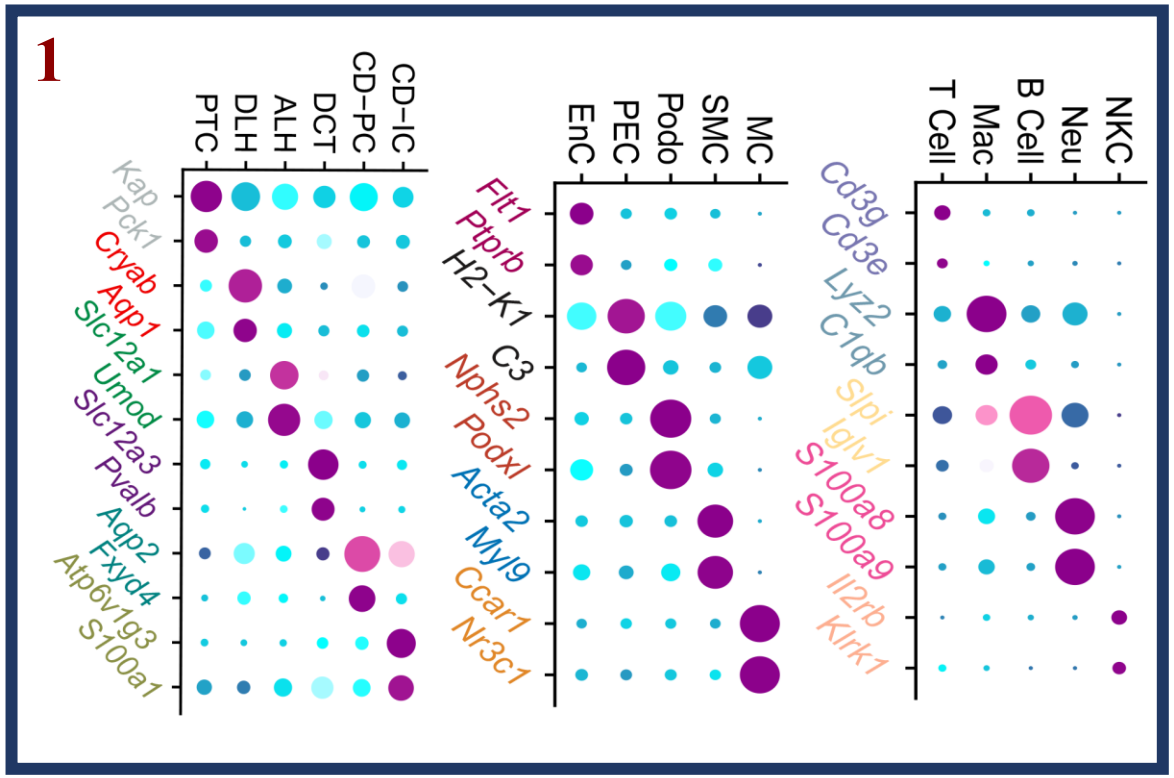


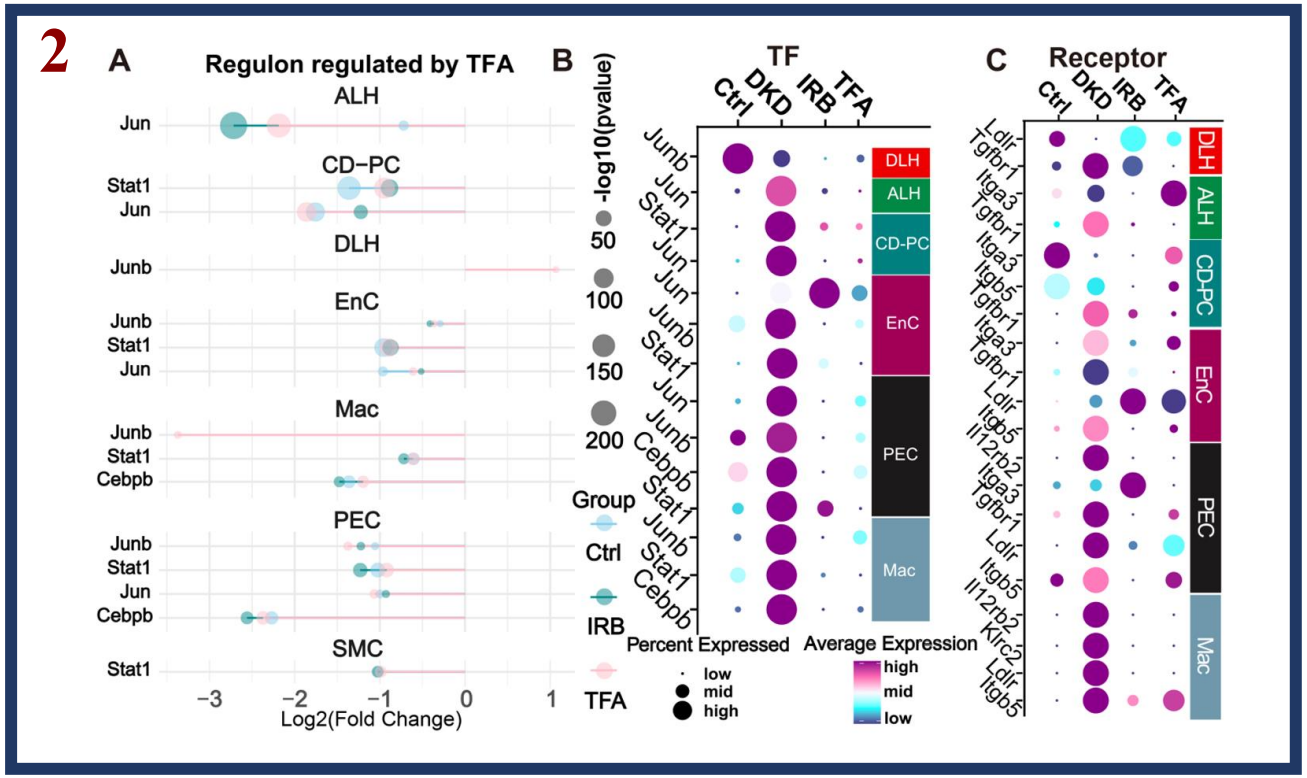


1. 评估了黄葵总黄酮能够缓解肾小球硬化、系膜基质扩张、胶原沉积、KW结节、GBM增厚、过度炎性细胞浸等糖尿病肾病经典病理特征

2. 初步获取包含肾小管、肾小球、免疫细胞三类组织共16种细胞类型的空间转录组

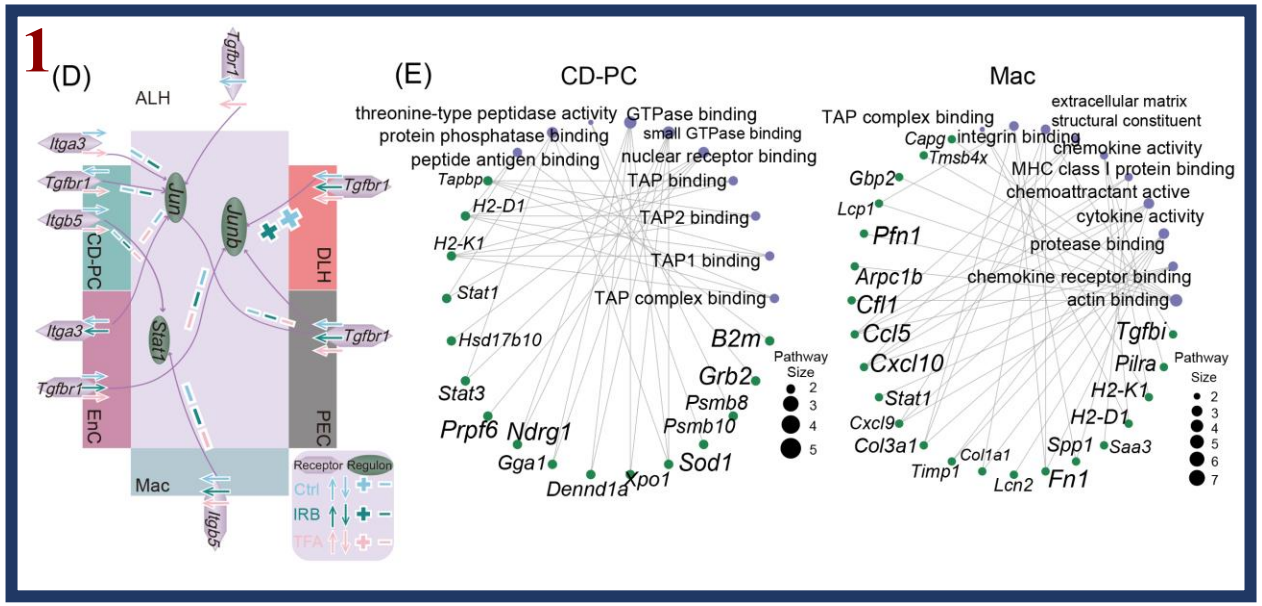
主要结果-黄蜀葵花治疗机制

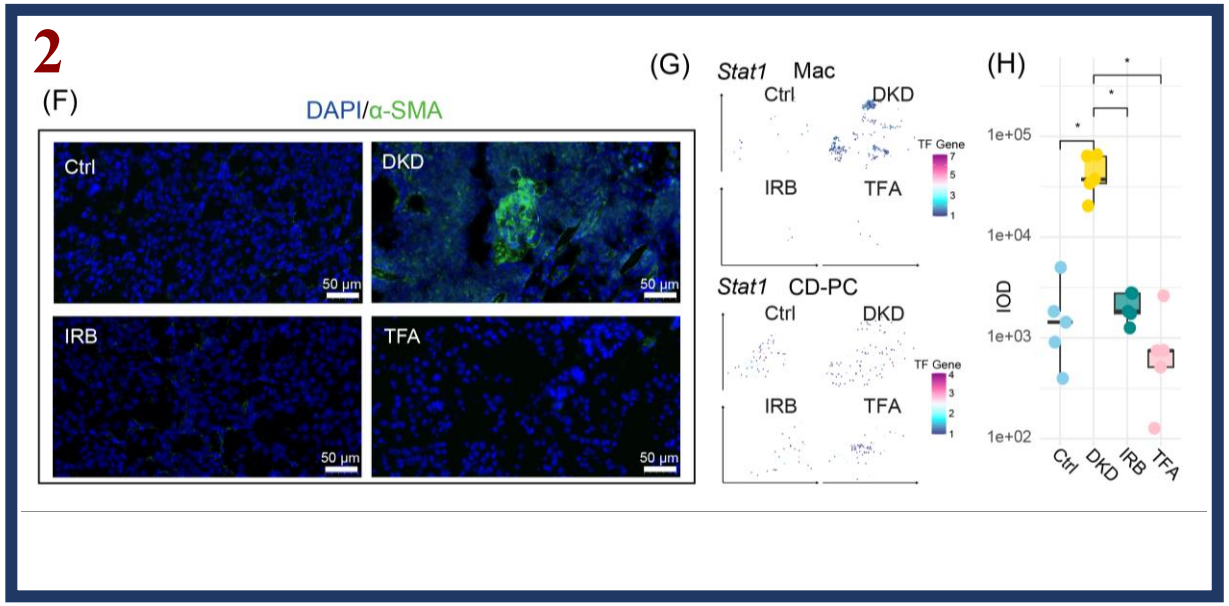




空间转录组数据中重现了我们此前发表于《Phytomedicine》中构建的黄葵胶囊治疗糖尿病肾病的配体→受体→转录因子→靶基因调控网络。黄葵总黄酮与黄葵胶囊一样能够通过调控Tgfbr1、Itgb5、Itga3受体作用与Junb、Jun、Stat1并影响免疫浸润、纤维化等通路，从而缓解糖尿病肾病。

主要结果-黄蜀葵花治疗机制





在CD-PC、EnC、Mac、PEC及SMC中，Stat1调控子与其基因表达均受到IRB与TFA的负向调控。空间分析结果显示，转录因子Stat1在DKD样本的CD-PC中特异性呈现出密集的高强度表达模式且与免疫细胞共定位，而其它组则表达强度较低。Stat1 regulon中共表达最强的50个靶基因富集结果显示：CD-PC 中Stat1调控子的靶基因主要富集于肽抗原结合、TAP结合及TAP复合物结合通路，而Mac中该调控子的靶基因则富集于整合素结合、趋化因子活性、细胞因子活性通路。免疫荧光染色趋势与基因表达一致。

交互式网页发布

Spatial Transcriptomics - DKD

Introduction | Spatial Plot | DotPlot | Pathway DotPlot | Sample Metadata

Welcome to explore!

This site provides an interactive spatial transcriptomics dataset related to DKD, enabling visualization of spatial distribution of cell types, gene expression levels, pathway activity scores, and metadata queries.

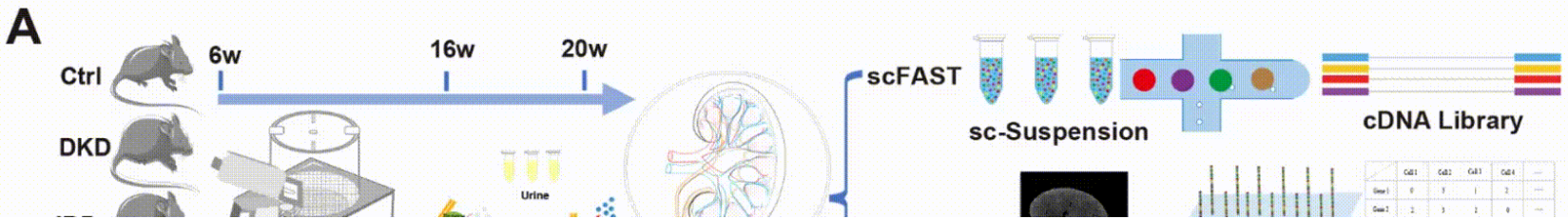
Study Description

In the current study, we administered 75.5 mg/kg body weight of TFA (TFA Group), 20.0 mg/kg body weight of IRB (IRB Group), or an equivalent volume of water (DKD Group) via gavage to BKS.Cg-Dock7m +/+ Leprdb/J (db/db) mice for a period of four weeks, with db/m mice serving as healthy controls. The progression of diabetic kidney disease (DKD) and the therapeutic effects of the treatment groups on renal function were assessed by collecting urine samples using metabolic cages and measuring the urinary albumin-to-creatinine ratio (UACR) via ELISA.

Summary

Utilizing a combination of single-cell full-length RNA sequencing (scFAST) and subcellular-resolution SpaTial Enhanced REsolution Omics-sequencing (stereo-seq) (A), we obtained a comprehensive dataset encompassing 16 distinct cell types, including proximal tubule cells (PTC), descending loop of Henle (DLH), ascending loop of Henle (ALH), distal convoluted tubule (DCT), connecting tubule principal cells (CD-PC), collecting duct intercalated cells (CD-IC), endothelial cells (EnC), parietal epithelial cells (PEC), podocytes (Podo), smooth muscle cells (SMC), mesangial cells (MC), T cells, macrophages (Mac), B cells, Neutrophil (Neu), and natural killer cells (NKC) (B).We have confirmed the biological identity of these cells through the canonical cell marker. RT included PTC (Kap, Pck1, 1,020,959), DLH (Cryab, Aqp1, 7,394), ALH (Slc12a1, Umod, 101,460), DCT (Slc12a3, Pvalb, 38,735), CD-PC (Aqp2, Fxyd4, 19,925), and CD-IC (Atp6v1g3, S100a1, 18,749). Glomerular cells included EnC (Flt1, Ptprb, 13,359), PEC (H2-K1, C3, 4,971), Podo (Nphs2, Pdoxl, 12,676), SMC (Acta2, Myl9, 6,172) and MC (Ccar1, Nr3c1, 9). IC include T Cell (Cd3g, Cd3e, 129), Mac (Lyz2, C1qb, 6,804), B Cell (Slpi, Iglv1, 1,409), Neu (S100a8, S100a9, 1,569), and NKC (Il2rb, Klrk1, 43). (C)

Graphic Summary



http://biomamba.com:34038/DKD_ST_dataset/

总结

1、TFA具有与IRB相当的DKD病理进程治疗作用

2、TFA与IRB可有效降低DKD小鼠的免疫细胞浸润水平

3、TFA中的七种主要黄酮类成分可抑制*Tgfbr1*通路、*Itgb5-Stat1*通路治疗DKD

4、欢迎大家通过我们的在线网站查阅感兴趣的DKD相关通路

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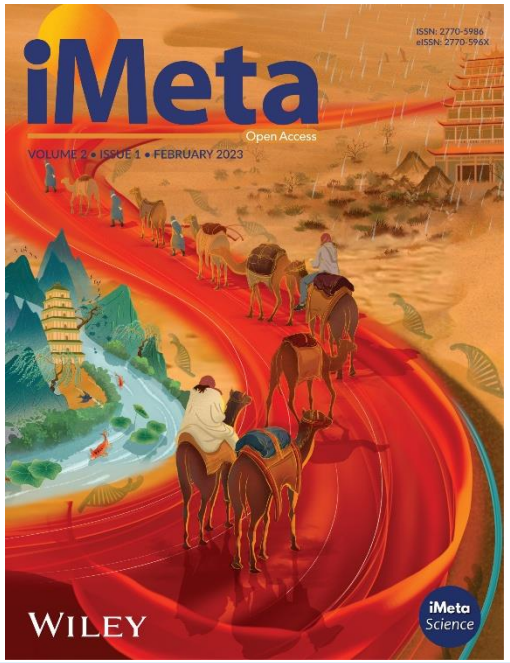

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