

# Unlocking the complexities of human kidney and heart disease

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## Valorisation

The studies “Spatial multi-omic map of human myocardial infarction” and “Decoding myofibroblast origins in human kidney fibrosis” have significant potential for drug discovery and therapeutic development. The use of cutting-edge single-cell sequencing and spatial sequencing techniques, as well as the integration of multiple omics data, allows for a more comprehensive and detailed understanding of the underlying molecular mechanisms of these human diseases for the first time.

One key aspect of the myocardial infarction study is the identification of disease specific cardiac cell states, which can be targeted for therapeutic intervention. For example, it has been recently demonstrated that engineered CAR-T cells directed against the antigen FAP (fibroblast activating protein) on fibroblasts can be used therapeutically to treat heart fibrosis (Ruel et al. Science). Additionally, the study provides an integrative molecular map of human myocardial infarction, which can serve as a valuable reference for the field and pave the way for advanced mechanistic and therapeutic studies of cardiac disease.

The kidney fibrosis study also contributes to the understanding of the underlying molecular mechanisms of disease, specifically in the identification of specific cell populations that drive fibrosis. By pinpointing these myofibroblast origins, new targets for therapeutics can be identified and developed. NKD2, a WNT-regulator, has already been identified and using in-vitro organoid models showed involvement in regulating fibrosis pathways. Furthermore, the study highlights the potential of using organoids as a model for disease, which can aid in drug discovery and development.

The “Adult human kidney organoids originate from CD24+ cells and represent an advanced model for adult polycystic kidney disease” and COSMOS paper also provide insights into the use of organoids in disease modeling, specifically in the case of polycystic kidney disease. This can provide a valuable tool for drug discovery and understanding disease progression.

Additionally, the “Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses” demonstrates the importance of integrating multiple omics data with prior knowledge to generate more accurate mechanistic hypotheses, which can aid in the identification of new drug targets. Using such models based on spatially resolved multi-omics data will be an important step forward towards reaching personalized medicine not only in the field of cancer but also other fields like nephrology and cardiology.

Overall, these studies demonstrate the power of cutting-edge technologies and multiomics data integration in advancing our understanding of human diseases, leading to new opportunities for drug discovery and therapeutic development.

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