CASE STUDY:
GENOMICS

Research Question

Can we establish the transcriptomic profile of renal epithelial cells exposed to the profibrotic cytokine transforming growth factor beta (TGFB1) as an in vitro model of renal fibrosis?

Our Approach

Human kidney epithelial cells (HK-2) were stimulated with TGF-β1 and three independent experiments gave rise to six samples for RNA-Seq analysis. We identified 2027 differentially expressed genes using RNA-Seq and then validated the responses of several genes in our *in vitro* model using TaqMan Real-Time PCR. Subsequent promoter analysis of transcription factor binding sites in the TGF-β1 responsive gene set allowed us to predict the activation of multiple transcriptional networks, including NFκB.

'The use of the Genomics Core is an invaluable service for our research into the mechanisms underlying renal fibrosis. In particular, as part of our RNA-seq experiment, we received considerable advice from staff on the design and execution of these experiments.'

Professor Catherine Godson, *UCD*

Dr Eoin Brennan, *postdoctoral fellow*