

Supplementary Figures

Supplementary Figure 1. Validation of genes correlating with CKD traits

(A) Correlation plots of the top 5 eGFR-correlated genes (LPA, PLG, XPNPEP2, ALB, UMOD) and the top 5 fibrosis-correlated genes (LPA, IGHG1, PLG, XPNPEP2, TRBC1) identified in the primary dataset drawn using the validation dataset. (B) The number of genes correlating with eGFR or fibrosis in the primary and validation dataset, in the unadjusted and adjusted model. The absolute probe number is presented on the left side, while the percentages on the right. (C) Pathway analysis using Gene Ontology of total CKD associated genes (left panel) and of genes with direct (middle panel) or inverse (right panel) correlation with CKD.

Supplementary Figure 2. Validation of known biomarkers correlation

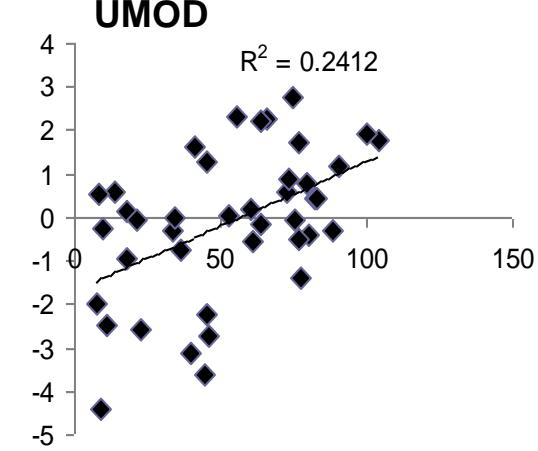
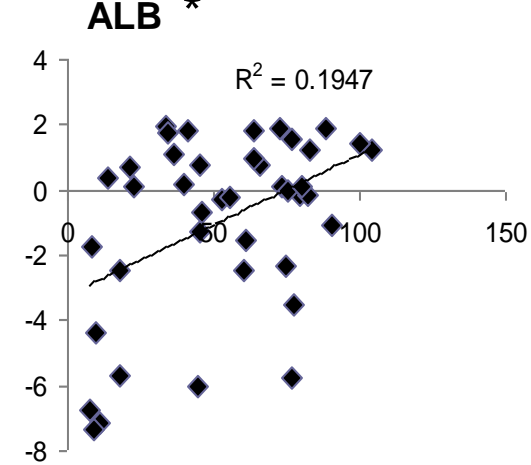
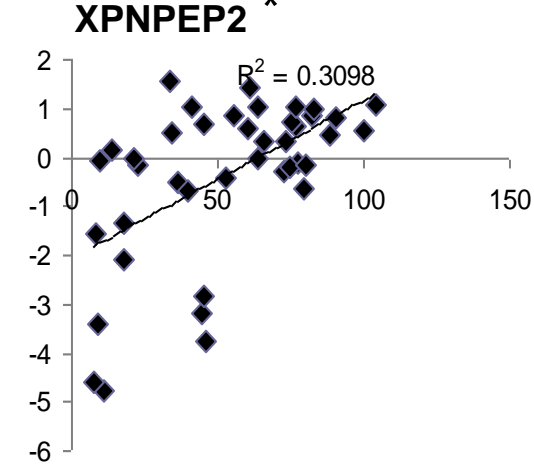
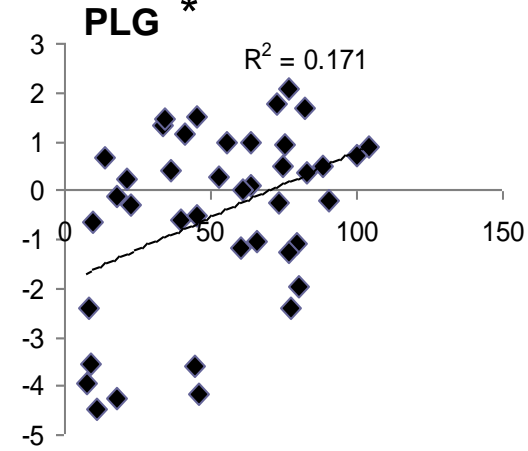
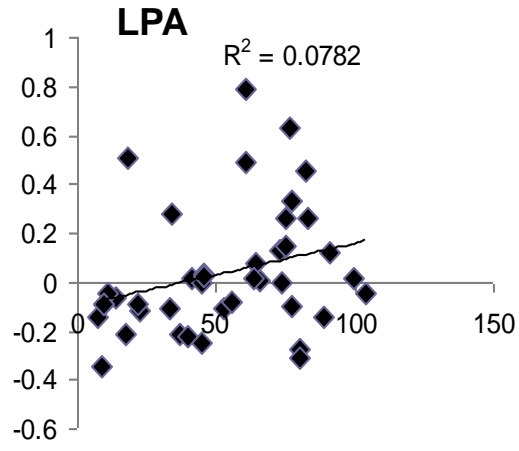
Expression levels of the following biomarkers (y-axis): FABP1, NGAL, KIM1, IGFBP1, IL18 and EGF and eGFR (x-axis) and interstitial fibrosis (x-axis) using the validation dataset. The R^2 value was examined for linear correlation. * p value<0.05.

Supplementary Figure 3. Principal component analysis plot

Principal component analysis (PCA) plot of 95 kidney samples included in the primary dataset was the primary method used for outlier detection, among other methods.

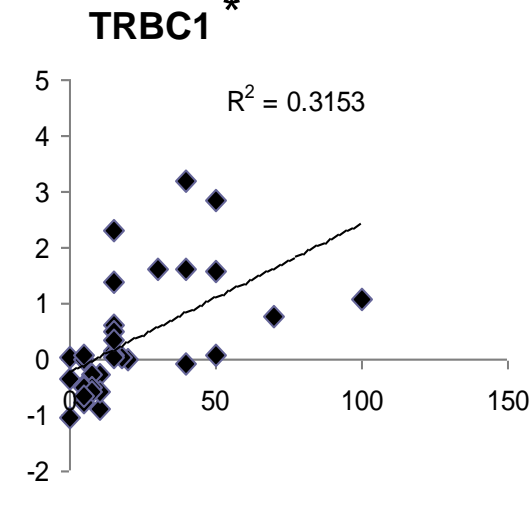
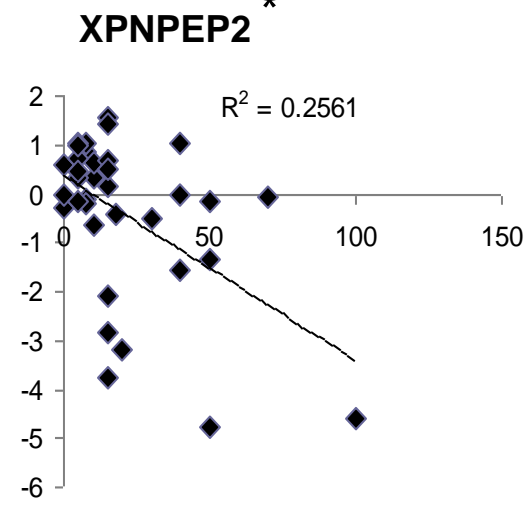
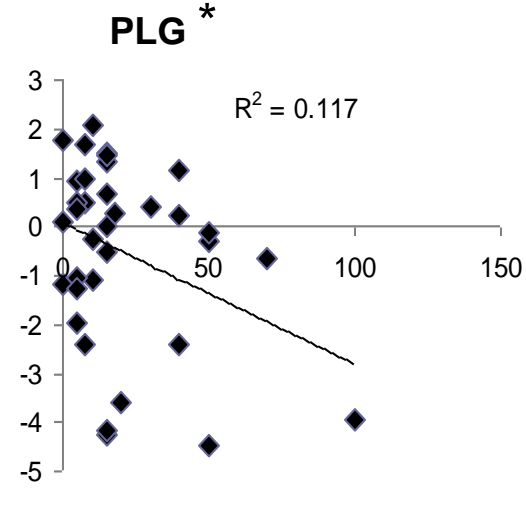
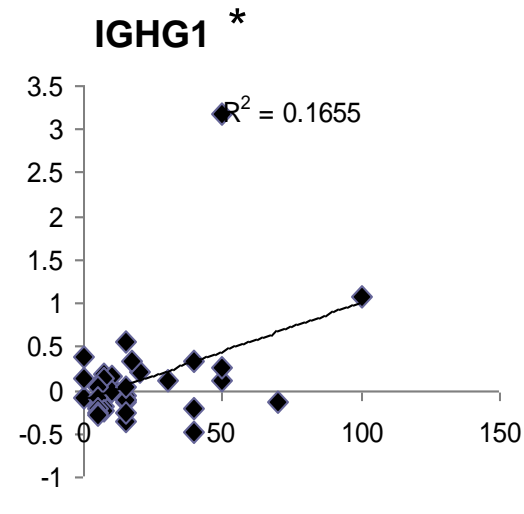
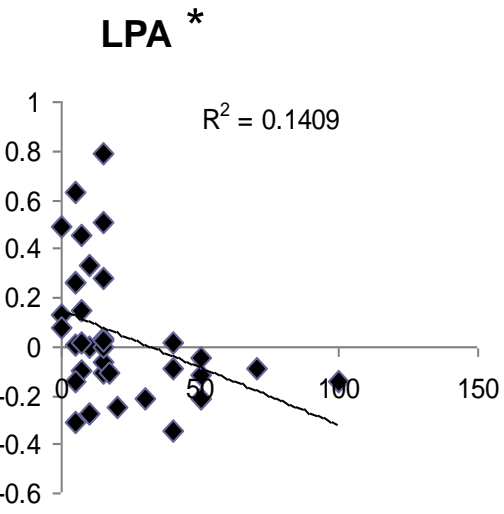
A Top five eGFR-correlated genes

Relative gene expression

Kidney function eGFR ml/min/1.73m²

Top five fibrosis-correlated genes

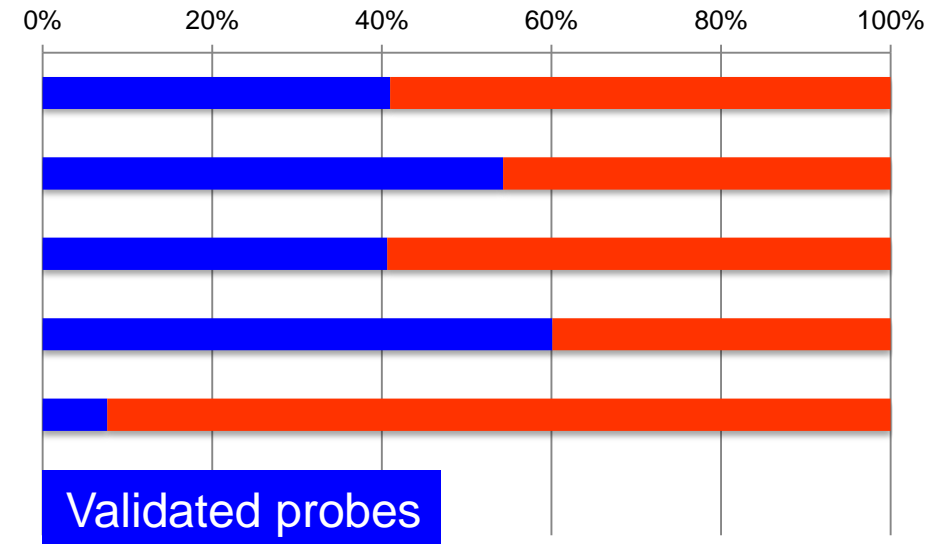
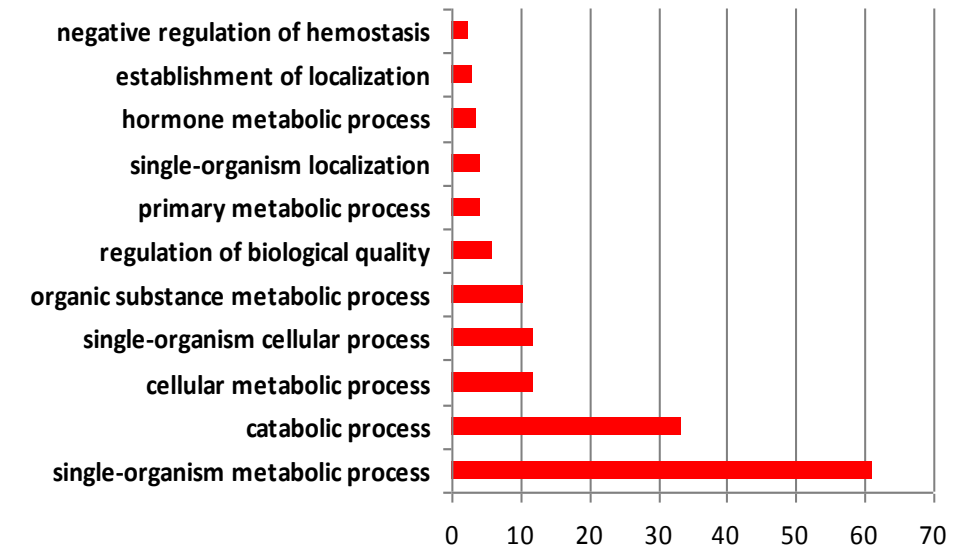
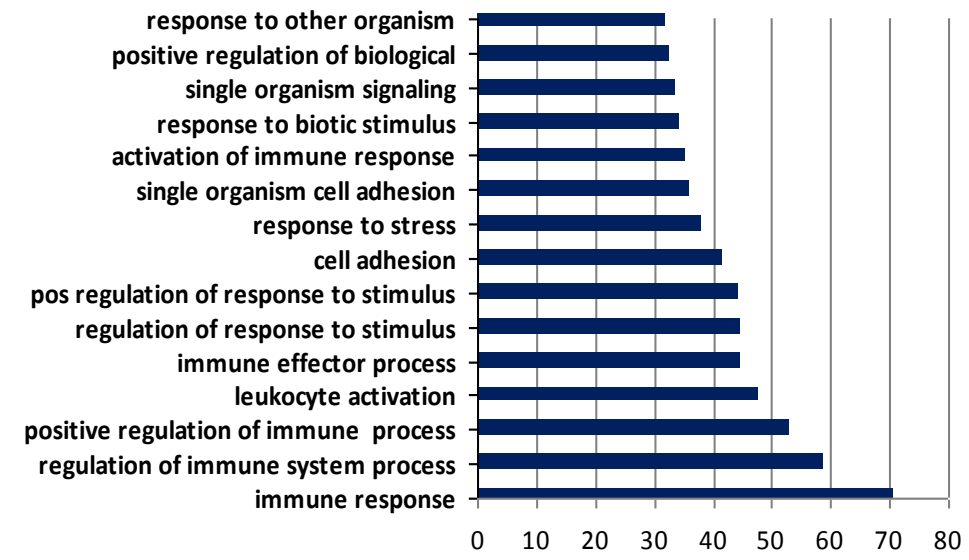
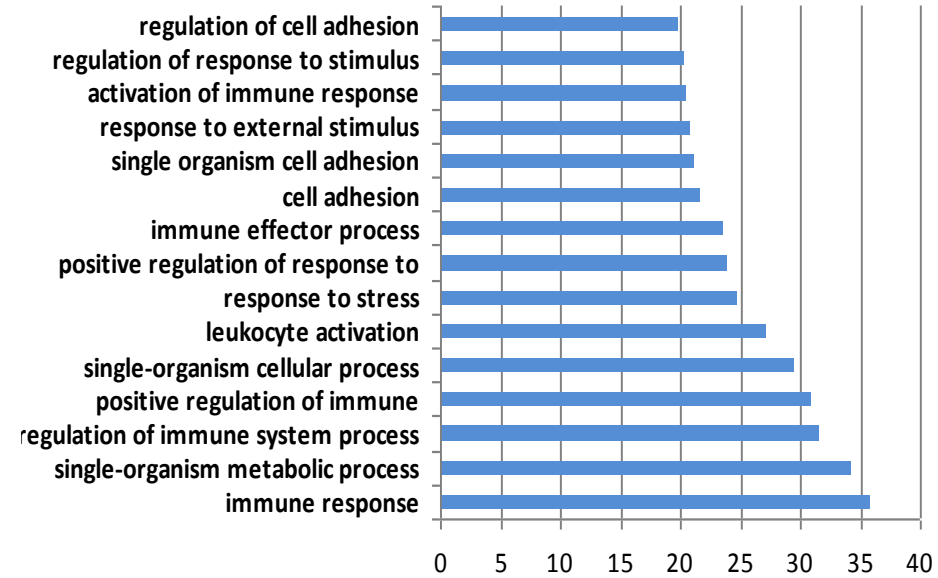
Relative gene expression



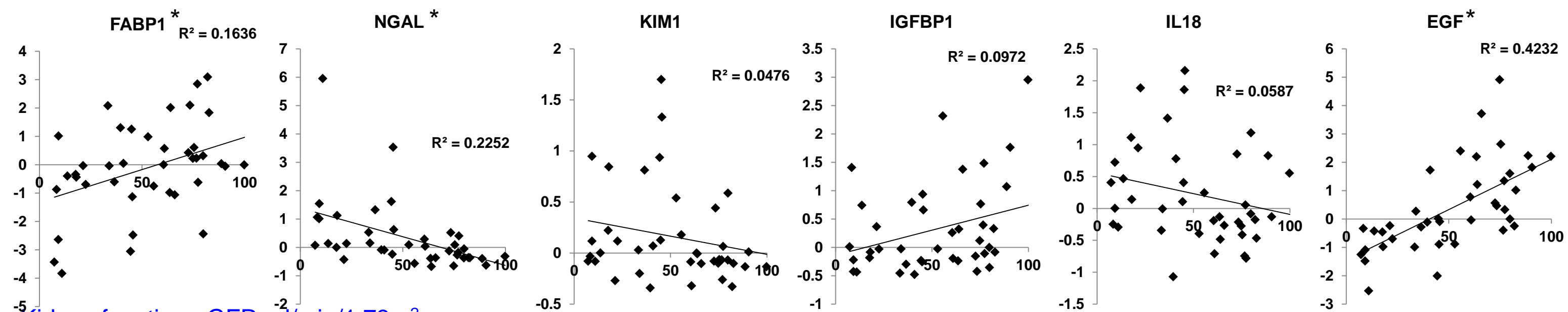
Tubulointerstitial fibrosis (%)

B

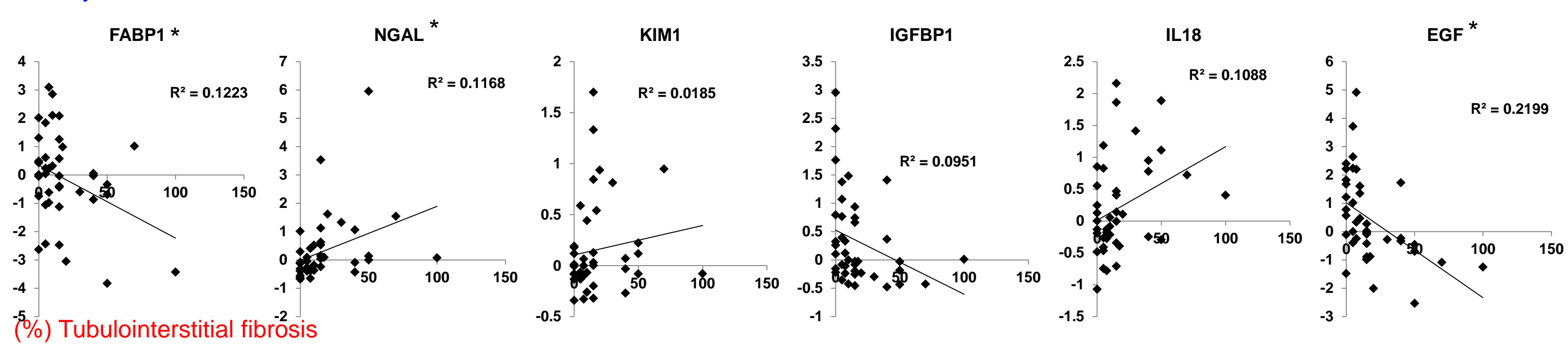
	Primary data	Validated
GE~Fibrosis	5128	2101
GE~GFR	3156	1714
GE~Fibrosis+DM+HTN+age+gender+race	3189	1296
GE~GFR+DM+HTN+age+gender+race	647	389
GE~Fibrosis+GFR+DM+HTN+age+gender+race	1654	126
GE~GFR+Fibrosis+DM+HTN+age+gender+race	0	0

**C**

Supplementary Figure 2

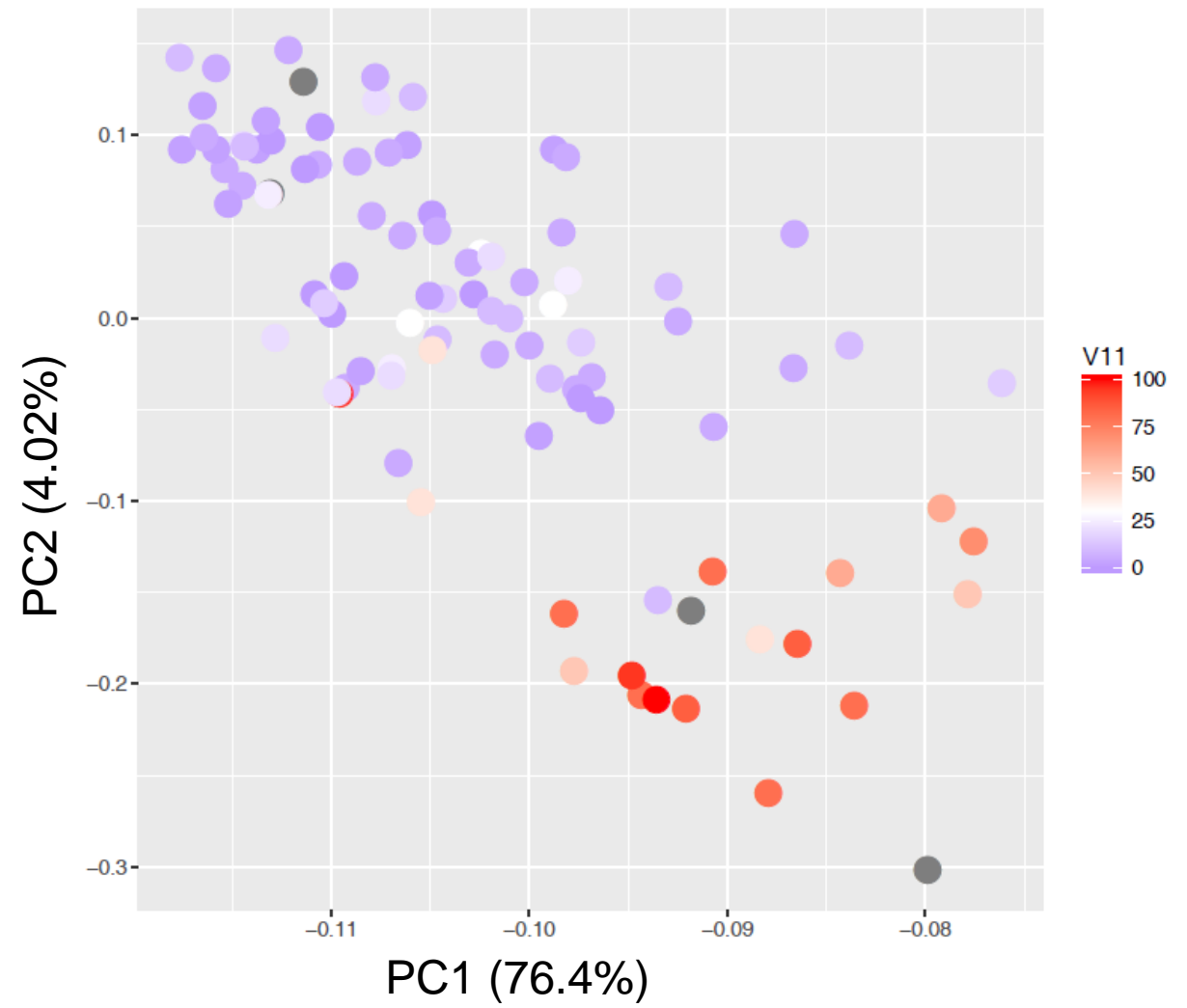


Kidney function eGFR ml/min/1.73m²



(%) Tubulointerstitial fibrosis

Supplementary Figure3



highly variable genes 5000