Research Article

Life Conflux

Transcription Factors as Early Diagnostic Biomarkers for Chronic Kidney Disease: A Comprehensive Analysis

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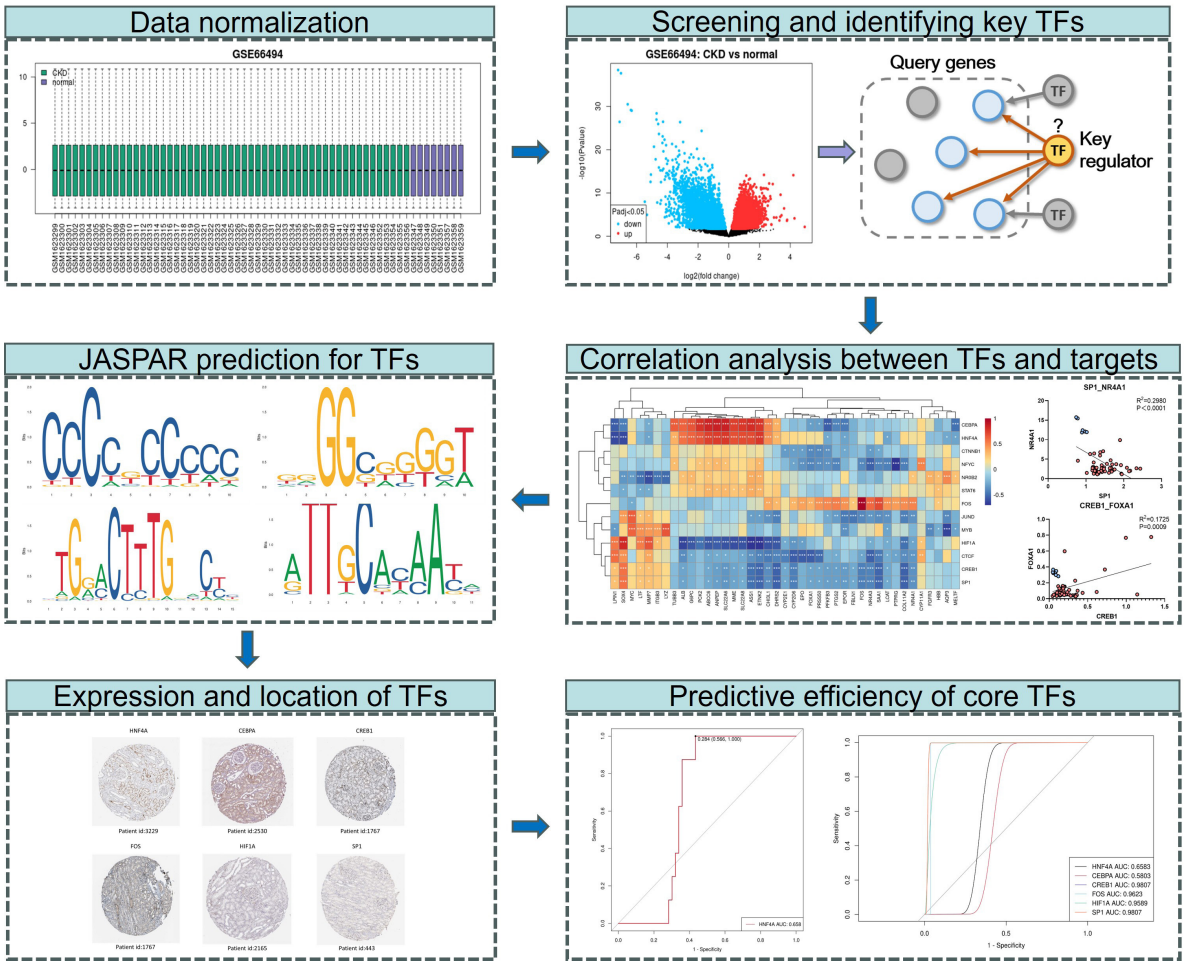
Graphical Abstract



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Transcription Factors as Early Diagnostic Biomarkers for Chronic Kidney Disease: A Comprehensive Analysis

Wei Zhou [1†], Qingqing Jia [2†], Shujun Wu [3†], Hanyan Meng [1], Xinyu Wang [4], Mingzhu Jiang [3], Jianhua Mao [1*]

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Abstract

Background: Chronic kidney disease (CKD) is a global health concern with significant implications for public health and mortality rates, projected to become the fifth leading cause of death by 2040. The search for early diagnostic targets for CKD is imperative. In this study, we concentrated on identifying key transcription factors (TFs) for the early diagnosis of CKD and established a regulatory network between these TFs and their corresponding target genes.

Methods: We conducted microarray data analysis and Gene Set Enrichment Analysis (GSEA) to identify differentially expressed genes (DEGs) and the associated pathways in CKD. We further explored the potential regulatory TFs among DEGs using the TRRUST v2 database and validated the TF-target regulatory relationships through correlation analysis and the JASPAR database. The protein expression of the identified TFs in renal tissues was also assessed.

Results: The analysis identified six TFs, namely HNF4A, CEBPA, CREB1, FOS, HIF1A, and SP1, which demonstrated potential as diagnostic biomarkers for CKD. These TFs showed differentially expressed patterns in CKD and were found to have multiple regulatory relationships with DEGs, indicating their crucial role in the disease process. ROC analysis revealed high predictive efficiency for four of these TFs (CREB1, FOS, HIF1A, and SP1), while the combined predictive efficiency of all TFs was exceptionally high.

Conclusion: Our findings highlight the role of transcription factors in the pathophysiological process of CKD and identify several key TFs with potential for clinical translation as early diagnostic biomarkers for the disease. Further validation and exploration are warranted to leverage the potential clinical utility of these TFs in the early diagnosis and prognosis of CKD.

Keywords: Chronic kidney disease; Transcription factor; Biomarker; Data analysis

Introduction

Chronic kidney disease (CKD) has emerged as a significant healthcare issue, affecting individuals across all age groups worldwide, which is expected to become the fifth leading cause of death by 2040 [1-2]. Despite the different etiologies of CKD, its prolonged and incurable process ultimately results in end-stage kidney disease (ESKD), which requires renal replacement therapy [3]. CKD is an independent risk factor for acute kidney injury (AKI), and AKI further aggravates the development and process of CKD [2, 4].

Renal fibrosis is the most important pathological feature of ESKD, which is characterized by glomerulosclerosis, interstitial fibrosis, and immune cell infiltration in the kidney [5-7]. Renal fibrosis is accompanied by pathological accumulation of extracellular matrix (ECM) proteins, including collagens and fibronectin [8]. However, excessive deposition of ECM in the kidney usually means the late irreversible stage of ESKD. A significant limitation of conventional renal function assessment, which depends on serum creatinine, BUN, and urine-specific gravity, is its inability to reliably detect subclinical renal dysfunction, despite its effectiveness in reflecting changes in glomerular filtration rate [9]. Therefore, the search for early diagnostic targets for CKD is urgently needed.

Transcriptional factors (TFs) play a crucial role in recognizing unique DNA sequences to regulate chromatin structure and

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gene transcription, thereby establishing a complex system essential for controlling the expression of the kidney genome [10]. Recent studies have indicated that dysregulation of human TFs is closely related to the onset and progression of CKD [11-12]. It is well known that each TF, functioning as an upstream regulatory signal, can regulate multiple downstream target genes, which affects different biological processes and signaling pathways. Therefore, the changes in the expression of TFs deserve attention as potential early signals for CKD. Previous studies have identified some TFs mediating the pathogenesis of CKD, including RUNX2, HIF1A, KLF4, P65, IRF1, SMADs and so on [13-19]. Thus, some key TFs closely associated with CKD have the potential to be the biomarkers for early diagnosis.

In this research, we reanalyzed a classic microarray dataset from Nephroseq database (https://www.nephroseq.org/) to achieve TFs for early diagnosis of CKD [20]. In addition, we established the regulatory network between diagnostic TFs and corresponding target genes. Finally, we evaluated the diagnostic efficiency of these TFs.

Materials and Methods

Microarray Data Analysis

The microarray assay consisting of 8 control kidney samples and 53 CKD kidney samples (GSE66494) was reanalyzed using the online tool "GEO2R". The operation procedure was followed by the official instructions, as options were set to default settings. Differential expression genes (DEGs) were characterized by "adjust P value < 0.05".

Gene Set Enrichment Analysis (GSEA) Analysis

The gene symbols and corresponding $\log_2$FC values from GSE66494 were used for GSEA analysis based on the online tool [21]. GSEA analysis and plotting were performed using the clusterProfile package (version 3.10.1) and the enrichplot package (version 1.2.0).

Identification of differentially expressed transcription factors (TFs)

The top 500 DEGs of CKD patients were entered into TRRUST v2 [22] to obtain potential regulatory TFs in the next step. Among these TFs, some were also DEGs, which can be recognized by the venny tool as we described before [23]. In addition, the TF-target regulatory relationships were further validated by correlation analysis and the JASPAR database [24]. The correlation analysis was conducted by using two different online tools from omicstudio (https://www.omicstudio.cn/tool/59; The Spearman's method was employed) and hiplot (https://hiplot.com.cn/cloud-tool/drawing-tool/detail/646; Ward.D2 method was employed). The overlapping results from the above correlation analyses were used for subsequent validation.

Statistical analysis

The transcriptome expression value of selected genes was used for the linear correlation analysis based on the Graphpad software. The receiver operator characteristic (ROC) was performed by R software.

Results

Analysis Process

Firstly, DEGs were identified from microarray data from the GEO database. Then, GSEA analysis was conducted. Subsequently, the regulatory TFs of the top 500 DEGs were predicted by TRRUST database. Among these TFs, some were differentially expressed TFs, whose regulation of corresponding target genes was verified via linear correlation analysis and JASPAR database. Lastly, the diagnostic efficiency of the selected TFs was evaluated using ROC curve.

Identification of DEGs Between Normal and CKD Samples and KEGG Analysis

We selected GSE66494 dataset to conduct deep data mining, because many DEGs from the dataset had been proved to be important pathogenic genes related to CKD, such as PXR, ROCK2, as our research team and other researchers identified before [25-27]. Gene expression levels were compared between the CKD and control samples. The results from GEO2R were shown in Figure 1 A-D. Considering the continuous updates of the KEGG database, we conducted functional analysis based on the newest background genesets using GSEA method. A series of up-regulated and down-regulated pathways were shown in Figure 1E, and these can be summarized be summarized as four categories, including down-regulated energy metabolism, up-regulated proinflammatory and immune infiltration, profibrotic and proliferative pathways and renal dysfunction. As is widely known, renal interstitial fibrosis is the most significant pathological manifestation in CKD patients at the end stage [28]. Activated TGFβ/smads signaling and wnt/β-catenin signaling are canonical pathways associated with renal fibrosis [13, 29-30]. The CKD cluster is characterized by a pronounced pro-fibrotic and pro-inflammatory transcriptomic signature. Therefore, the dataset met the standard for further analysis.

Screening and Identifying Key TFs among DEGs

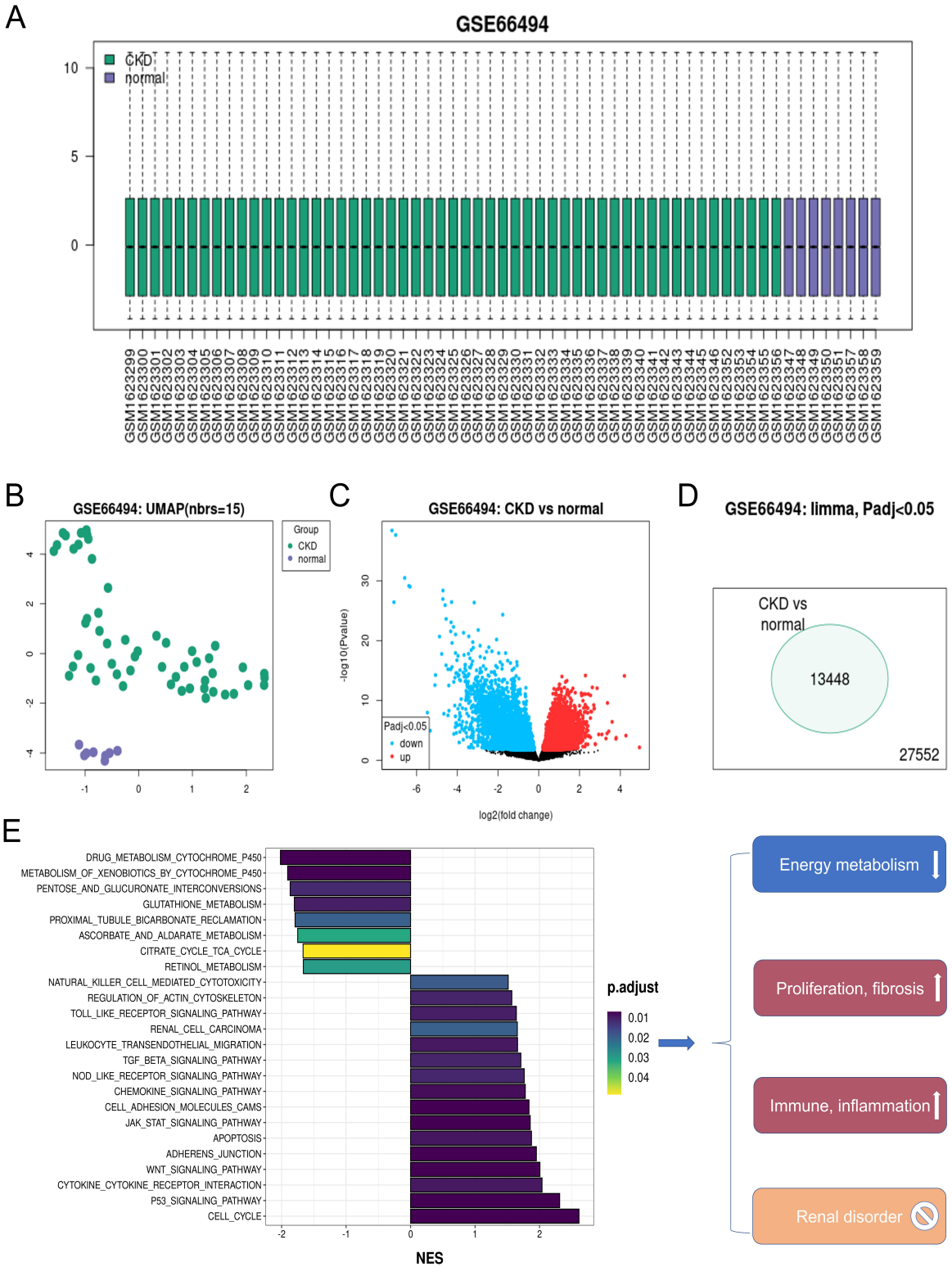
As the microarray dataset reflects changes in transcription levels, we looked up the upstream regulatory TFs for these mRNA changes. TRRUST2.0 is a manually curated database containing 8,444 TF-target regulatory relationships of 800 human TFs [22]. All of the regulatory networks were from recorded literature, which meant they were more reliable than bioinformatics prediction and high-throughput sequencing data. Then, 38 probable regulatory TFs were achieved from TRRUST meeting the criteria "p < 0.05" (Supplementary Figure 1). Among these TFs, 20 were differentially expressed in CKD group (Figure 2A). Furthermore, the above TFs with less than 3 target genes were excluded, only 13 TFs were used for the next validation (Figure 2B).

The Expression of Screening TFs and the Linear Correlation Between TFs and Matching Targets

Among these 13 TFs, heatmap showed that 7 were significantly up-regulated, while the others were significantly down-regulated (Figure 3A). Each TF had its own target gene, which was achieved from TRRUST database. Furthermore, we adopted two ways to conduct the correlation between TFs and corresponding target genes (Figure 3B & C). Each TF directly inter-

acts with the promoter region of one or multiple target genes, thereby influencing the expression of mRNA in those genes. This suggests a potential linear correlation between the TF and its corresponding target genes. We found that many TFs had positively or negatively related target genes (Figure 3D-R) containing HNF4A, CEBPA, CREB1, FOS, HIF1A and SP1. Among these TFs, HIF1A, SP1 and CREB1 were up-regulated in human CKD kidney tissue, while the others were down-regulated.

Figure 1. Differential gene expression in the GSE66494 dataset and the KEGG pathways involved. A. Boxplot of dataset. **B.** UMAP plot of dataset. **C.** Volcano plot of dataset. **D.** The amounts of differential genes of dataset. **E.** The up-regulated and down-regulated pathways of dataset based on GSEA analysis.



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The Potential Binding Sites of Key TFs

JASPAR database provided potential binding sites between TFs and target genes. According to the previous analysis, we focused on the specific TFs and their corresponding binding sites. From Figure 4A, SP1 had 6 binding sites with the promoter region of FOS, 5 binding sites with COL11A2, 1 binding site with PRSS50, 2 binding sites with NR4A1, 1 binding site with CHI3L1, 3 binding sites with FBLN1, 2 binding sites with EPOR and 5 binding sites with LCAT. CREB1 had only 1 binding site with FOXA1. HNF4A had 2 binding sites with the promoter region of ABCC6, 1 with SLC22A6, 1 with MMP7. CEBPA had 2 binding sites with PCK2. FOS had 1 binding site with FOXA1. HIF1A had 5 binding sites with ASS1. The high-frequency bind-

Figure 2. The differentially expressed TFs in CKD kidney. A. The venny diagram between predicted TFs and DEGs in the CKD kidney. **B.** Differentially expressed TFs with more than 3 target genes and their corresponding protein coding in the UniProt database.

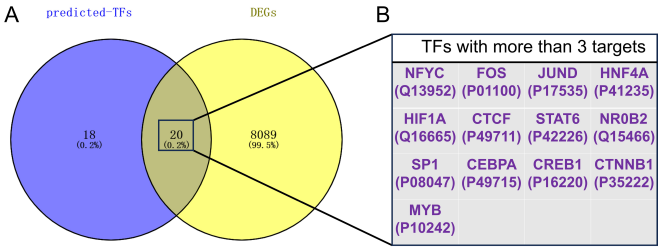
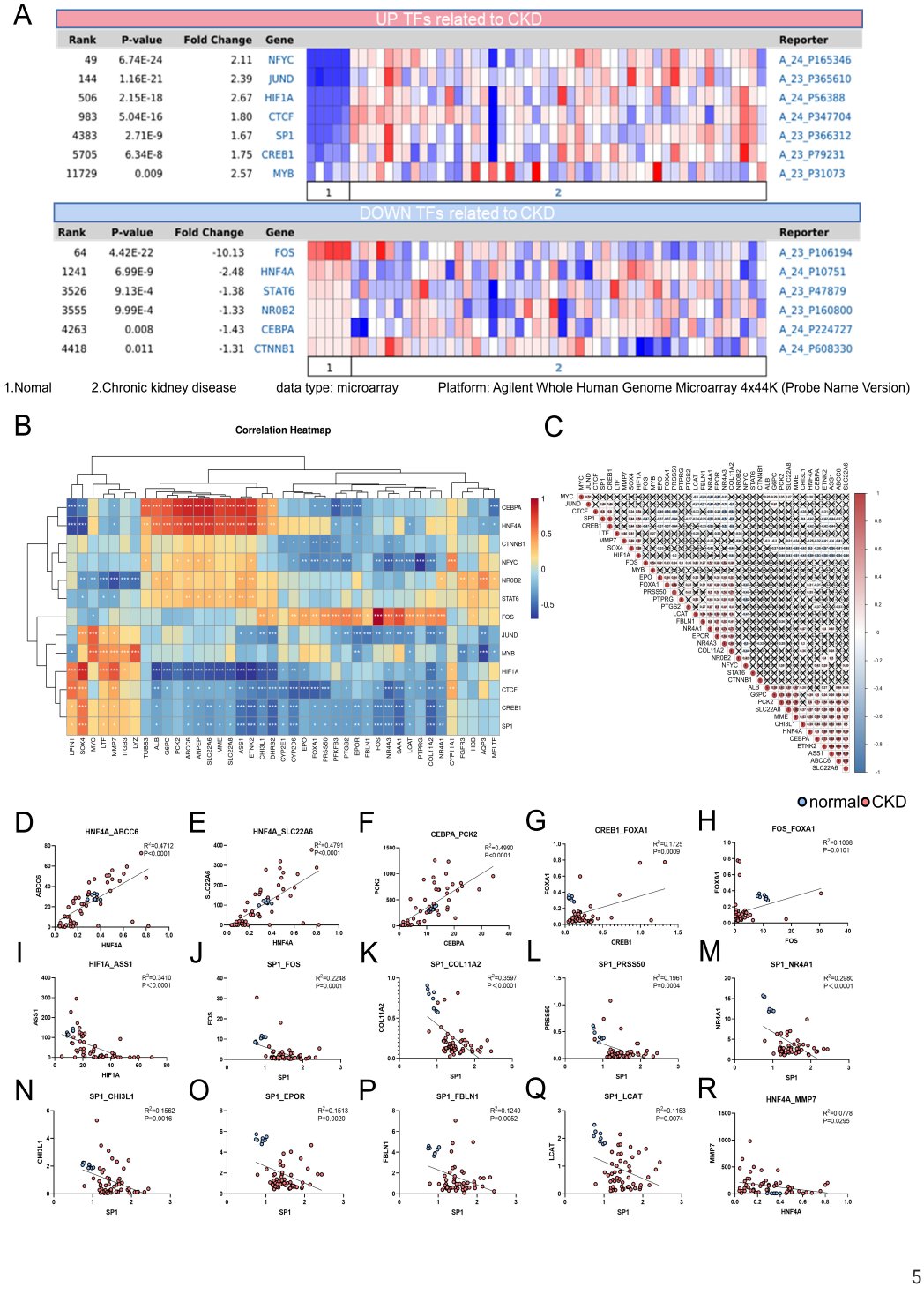


Figure 3. The up-regulated and down-regulated TFs in CKD and their relative linear analysis with corresponding target genes. A. Heatmap based on Nephroseq database reveals the up-regulated and down-regulated TFs in CKD. **B-C.** The linear analysis between TFs and their corresponding targets via two different methods. **D-R.** The linear analysis between each TF and each target gene.



ing base sequences corresponding to each transcription factor were shown in Figure 4B-K.

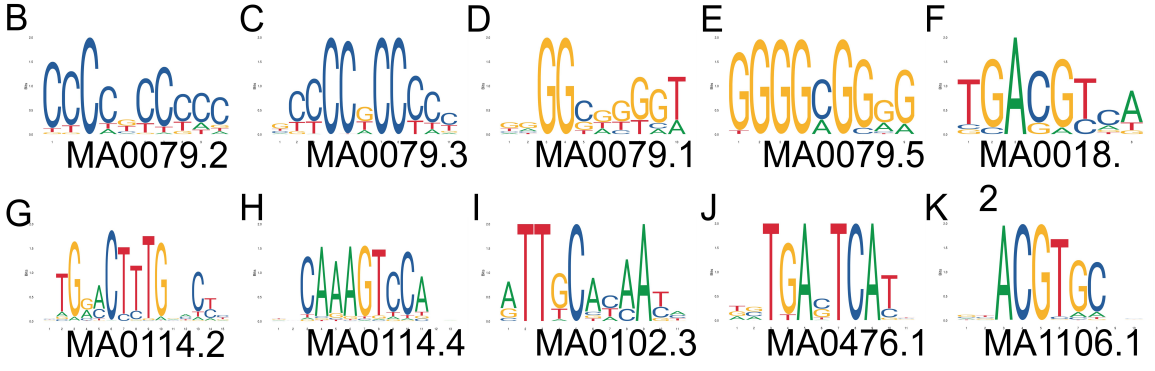
The protein expression of hub TFs in renal tissues

We observed hub TFs in the normal kidney tissue based on the Human Protein Atlas Database. All of the selected TFs were expressed at a protein level in the normal kidney. However, they were distributed in different areas of the kidney. HNF4A was located mainly in the nuclear area of renal tubules (Figure 5A). CEBPA was expressed in both nucleus and cytoplasm of

Figure 4. The binding sites between selected TFs and target genes. A. The combing prediction between TFs and target sequences by JASPAR. **B-E.** The binding sites information for SP1. F. The binding sites information for CREB1. **G-H.** The binding sites information for HNF4A. **I.** The binding sites information for CEBPA. **J.** The binding sites information for FOS. **K.** The binding sites information for HIF1A. The larger the letter, the greater the frequency of the corresponding base.

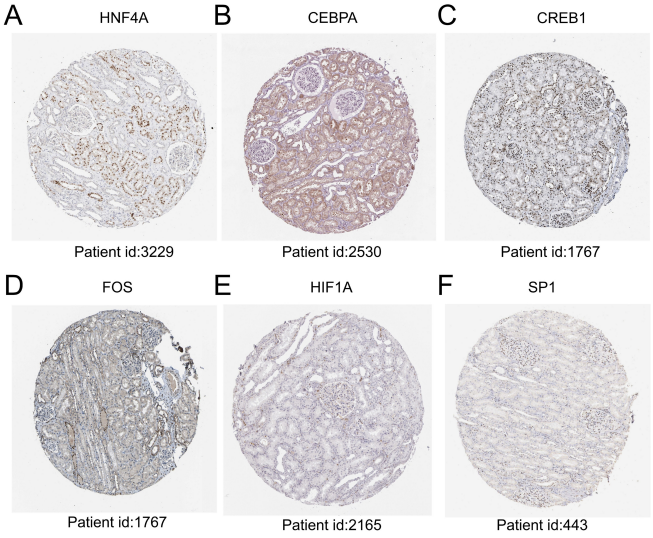
A

Transcription factor	Target gene	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
Total 18 putative site(s) on the positive strand were predicted with relative profile score threshold 95%								
MA0079.2.SP1	FOS	14.453586	0.995298923	NC_000014.9:75276828-75278828	1582	1591	+	CCCCTCCCCC
MA0079.3.SP1	FOS	15.43146	0.975286119	NC_000014.9:75276828-75278828	1581	1591	+	TCCCCTCCCCC
MA0079.2.SP1	FOS	13.213753	0.964074552	NC_000014.9:75276828-75278828	159	168	+	CCCCGCCTCC
MA0079.2.SP1	FOS	13.213753	0.964074552	NC_000014.9:75276828-75278828	1601	1610	+	CCCCGCCTCC
MA0079.3.SP1	FOS	14.486494	0.963397361	NC_000014.9:75276828-75278828	158	168	+	TCCCCGCCTCC
MA0079.3.SP1	FOS	14.459636	0.963059453	NC_000014.9:75276828-75278828	1600	1610	+	CCCCCGCCTCC
MA0079.1.SP1	COL11A2	11.045893	0.972161372	NC_000006.12:c33162694-33160694	1783	1792	+	GAGGCGGGGT
MA0079.1.SP1	COL11A2	11.045893	0.972161372	NC_000006.12:c33162694-33160694	1801	1810	+	GGGGCTGGGT
MA0079.3.SP1	COL11A2	15.093589	0.971035308	NC_000006.12:c33162694-33160694	869	879	+	CCCCCGCCCCT
MA0079.3.SP1	COL11A2	14.962341	0.969384064	NC_000006.12:c33162694-33160694	874	884	+	GCCCCTCCTCC
MA0079.2.SP1	COL11A2	13.027086	0.959373479	NC_000006.12:c33162694-33160694	875	884	+	CCCCTCCTCC
MA0079.3.SP1	PRSS50	13.716568	0.95371081	NC_000003.12:c46712117-46710117	1392	1402	+	TTCCCTCCCCC
MA0079.2.SP1	NR4A1	14.453586	0.995298923	NC_000012.12:52020832-52022832	1093	1102	+	CCCCTCCCCC
MA0079.3.SP1	NR4A1	15.43146	0.975286119	NC_000012.12:52020832-52022832	1092	1102	+	TCCCCTCCCCC
MA0079.5.SP1	CHI3L1	14.750445	0.975201446	NC_000001.11:c203178931-203176931	1059	1067	+	GGGGAGGGG
MA0079.2.SP1	FBLN1	13.213753	0.964074552	NC_000022.11:45500883-45502883	1939	1948	+	CCCCGCCTCC
MA0079.3.SP1	FBLN1	15.706597	0.978747657	NC_000022.11:45500883-45502883	1938	1948	+	GCCCCGCCTCC
MA0079.5.SP1	FBLN1	13.402603	0.951780456	NC_000022.11:45500883-45502883	1732	1740	+	GGGGAGGAG
Total 8 putative site(s) on the positive strand were predicted with relative profile score threshold 90%								
MA0018.2.CREB1	FOXA1	9.00289	0.906041171	NC_000014.9:c37589552-37587552	349	356	+	TGACATCA
MA0079.1.SP1	EPOR	9.171796	0.906789836	NC_000019.10:c11377207-11375207	1670	1679	+	GAGGGTGGGT
MA0079.2.SP1	EPOR	10.835842	0.904188444	NC_000019.10:c11377207-11375207	1760	1769	+	CCCTGCCTCC
MA0079.5.SP1	LCAT	12.212311	0.931097155	NC_000016.10:c67939750-67937750	129	137	+	GGGGCGGTG
MA0079.5.SP1	LCAT	12.212311	0.931097155	NC_000016.10:c67939750-67937750	140	148	+	GGGGCGGTG
MA0079.3.SP1	LCAT	11.298021	0.923282724	NC_000016.10:c67939750-67937750	99	109	+	GCTCCACCCAC
MA0079.1.SP1	LCAT	9.226104	0.908684185	NC_000016.10:c67939750-67937750	140	149	+	GGGGCGGTGA
MA0079.1.SP1	LCAT	9.026768	0.90173102	NC_000016.10:c67939750-67937750	138	147	+	GGGGGGCGGT
Total 7 putative site(s) on the positive strand were predicted with relative profile score threshold 85%								
MA0114.2.HNF4A	ABCC6	8.896688	0.853294207	NC_000016.10:c16149565-16147565	753	767	+	GAGGACTTGGTTCTT
MA0114.4.HNF4A	ABCC6	11.323141	0.872754521	NC_000016.10:c16149565-16147565	1104	1116	+	ACCAAATTCCAGC
MA0114.2.HNF4A	SLC22A6	10.119499	0.869570966	NC_000011.10:c62976597-62974597	140	154	+	CTTGCCTTTGCCCCT
MA0114.4.HNF4A	MMP7	11.524467	0.876765433	NC_000011.10:c102520508-102518508	228	240	+	TGGAAAGTCCAAT
MA0102.3.CEBPA	PCK2	7.1550646	0.88370774	NC_000014.9:24092171-24094171	1191	1201	+	GTTTCCTCATT
MA0102.3.CEBPA	PCK2	6.1691127	0.871895949	NC_000014.9:24092171-24094171	1865	1875	+	GTTACATCATG
MA0476.1.FOS	FOXA1	5.975023	0.868628017	NC_000014.9:c37589552-37587552	3	13	+	GGAGACTCATG
Total 5 putative site(s) on the positive strand were predicted with relative profile score threshold 80%								
MA1106.1.HIF1A	ASS1	6.545462	0.846239267	NC_000009.12:130442707-130444707	1003	1012	+	CCACGTGGCT
MA1106.1.HIF1A	ASS1	5.385243	0.818920892	NC_000009.12:130442707-130444707	1367	1376	+	GGACTTGCTC
MA1106.1.HIF1A	ASS1	4.8551283	0.80643888	NC_000009.12:130442707-130444707	1604	1613	+	GCAGGTGCCA
MA1106.1.HIF1A	ASS1	4.7103024	0.803028827	NC_000009.12:130442707-130444707	32	41	+	CTAGGTGCTG
MA1106.1.HIF1A	ASS1	4.5892386	0.800178276	NC_000009.12:130442707-130444707	18	27	+	CCACCTGCTC



renal tubules (Figure 5B). CREB1 distributed in the nucleus of both glomerulus and renal tubules (Figure 5C). Interestingly, FOS was almost expressed in the whole kidney (Figure 5D). On the contrary, HIF1A was expressed at low protein levels in the glomerulus (Figure 5E). SP1 mainly distributed in the nucleus of glomerulus (Figure 5F).

Figure 5. Immunohistochemistry of the hub TFs based on the Human Protein Atlas database. A. The protein expression of HNF4A in the normal kidney tissue. **B.** The protein expression of CEBPA in the normal kidney tissue. **C.** The protein expression of CREB1 in the normal kidney tissue. **D.** The protein expression of FOS in the normal kidney tissue. **E.** The protein expression of HIF1A in the normal kidney tissue. **F.** The protein expression of SP1 in the normal kidney tissue.



Predictive efficiency of core TFs in CKD patients

ROC analysis was employed to evaluate the predictive efficiency of the six genes mentioned. Four of their AUC values were greater than 0.9, including CREB1, FOS, HIF1A and SP1 (Figure 6C-F), while the AUC value of HNF4A and CEBPA were just 0.658 and 0.5802 (Figure 6A & B), and the summary result was shown in Figure 6G. The combined predictive efficiency of the above TFs was shown in Figure 6H, whose AUC is equal to 1.

Discussion

CKD is a kind of progressive disease whose clinical assessment is usually based on laboratory examination and pathological examination. Over the past years, proteinuria, eGFR, Scr, BUN and some other indexes have reflected the function of kidney. However, when these indexes show significant pathological changes, the kidney has progressed to the end stage. Therefore, a strategy for early diagnosis of CKD needs to be developed urgently.

With the rapid development of the technology of multi-omics, molecular diagnosis has been applied to clinical practice. Many researchers have found some key biomarkers highly related to CKD. Zhang et al identify that XDH is positively correlated with kidney damage [31]. MMP2 and MMP9, which are closely related to glomerulonephritis as we have identified before, are also important biomarkers for CKD [23, 32].

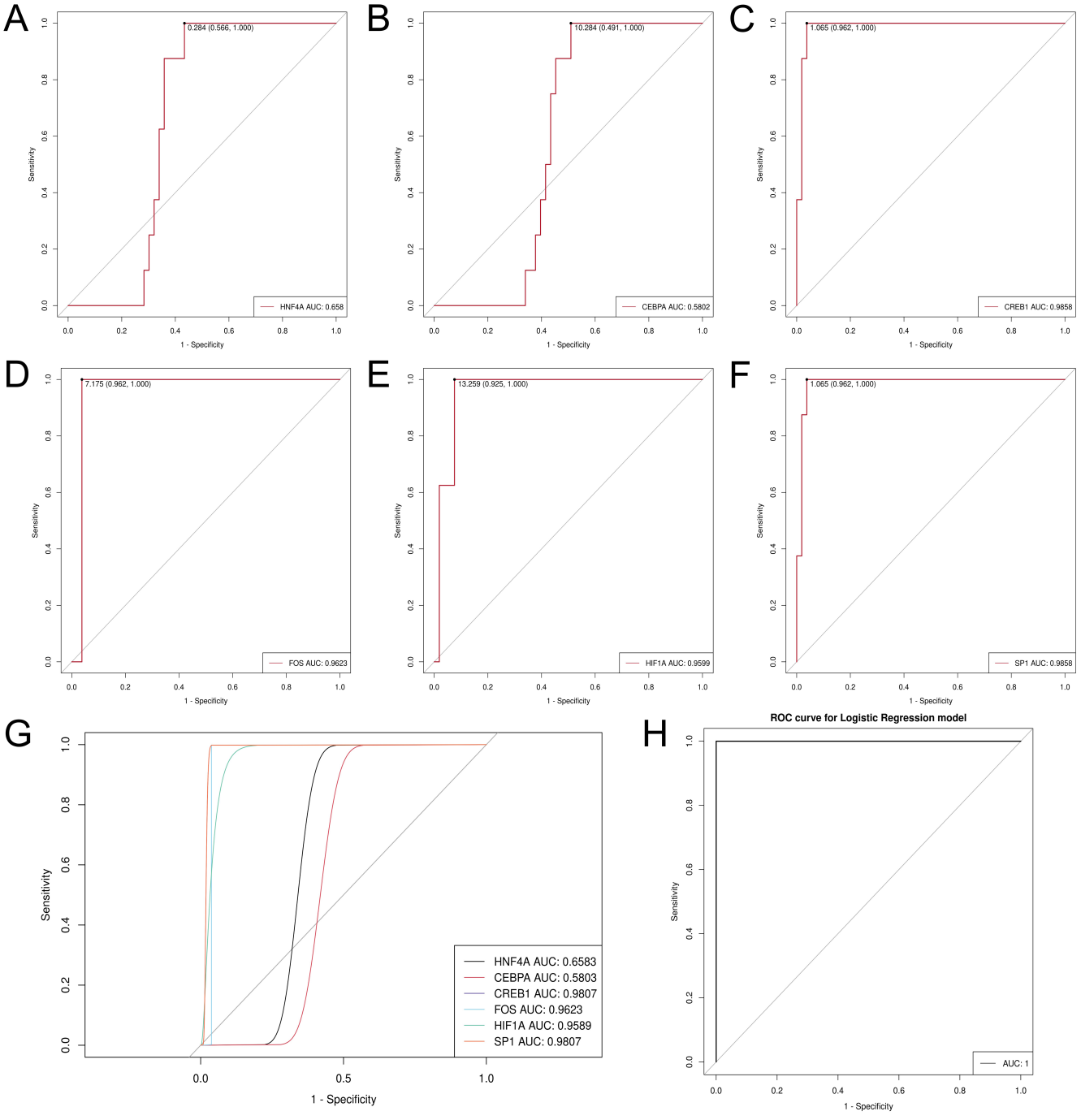
Different from the former diagnostic models, in this study, we focused on searching some diagnostic biomarkers for CKD from transcription factors because of their upstream regulatory effects. We used TRRUST database to predict the regulatory TFs for DEGs and got a series of TFs, among which some were also differentially expressed genes. Further analysis revealed that 6 of them had multiple regulatory relationships with DEGs including HNF4A, CEBPA, CREB1, FOS, HIF1A and SP1, which were supported by linear correlation analysis and evidence from JASPAR database. HNF4A, namely hepatocyte nuclear factor 4-alpha, is associated with the differentiation of proximal tubules, whose deletion or mutation will result in Fanconi renotubular syndrome [33-35]. HNF4A is also down-regulated in the unilateral ureteral obstruction model, which is a classic model used for researching CKD [36]. Additionally, liver-specific HNF4A-deficient mice progress to liver fibrosis, which can be rescued by applicability of HNF4A mRNA therapeutics [37-38]. CEBPA, namely CCAAT/enhancer-binding protein alpha, was down-regulated in our analysis. Interestingly, conversely, it is reported to be up-regulated in the UUO kidney [39]. However, another study supports that the expression of CEBPA is repressed by TGFβ, which contributed to the initiation of endothelial-to-mesenchymal transition in the endothelium [40]. Cyclic AMP-responsive element-binding protein 1 (CREB1) can be induced by TGFβ, which can result in matrix metalloproteinase and fibronectin accumulation [41-43]. FOS, also called protein c-FOS, is increased in the UUO model for 12 days [44]. FOS is a vital component of TGFβ/SMADs signaling, which mediates cell proliferation [45-46]. However, our analysis shows that FOS is down-regulated in human CKD renal tissues. These discrepant results could be attributed to differences in species or to biases arising from the unequal sample sizes between the control and disease groups in the clinical cohort. More samples may need to be included in order to test whether FOS can be a biomarker for CKD at the early stage. HIF1A, also named hypoxia-inducible factor 1-alpha, can promote renal fibrosis in some kidney diseases [47-48]. Therapeutic strategy targeting HIF-1α can protect the kidney from AKI to CKD progression [49]. SP1 is increased in glomerular or proximal tubular tissues in glomerulonephritis and obstructive nephropathy, whose expression is positively correlative with p-Smad2/3 [50]. In addition, the expression of SP1 is positively related to collagen I [51]. Interestingly, the TF SP1 has more binding sites than numerous other TFs as Figure 4 shows. Based on our earlier review [52], SP1 possesses a considerably long amino acid sequence, thereby enabling the potential for more extensive DNA binding. Furthermore, SP1 is evolutionarily an ancient gene, implying that it may have more diverse biological roles.

Furthermore, the above TFs separately have their own target genes. These target genes, including FOS, COL11A2, PRSS50, NR4A1, CHI3L1, FBLN1, FOXA1, EPOR, LCAT, ABCC6, SLC22A6, MMP7, PCK2 and ASS1, are also differentially expressed in human CKD kidney. Among these genes, some are reported to be related to renal fibrosis, such as MMP7, NR4A1, LCAT and so on [53-55]. Some correlations between TFs and downstream target genes reflect the intricate web of transcriptional regulation, characterized by its one-to-many architecture. The net influence of a TF on a given gene is frequently the result of a regulatory calculus involving the summation of multiple positive inputs or the antagonism between opposing regulatory signals. This complexity inherently defies a purely linear

representation (Figure 3H, Q, R). At the same time, ROC analysis reveals that transcription factor CREB1, FOS, HIF1A and SP1 have higher diagnostic efficacy than HNF4A and CEBPA. Based on the results from Figure 3 and 6, SP1, CREB1 and HIF1A seem to have stronger evidence for further clinical transformation.

However, the study has some limitations. First, as the TF-target regulatory network is based on the published literature, quite a few TFs are not reported in TRRUST. Therefore, there may be other TFs which are able to be used for early diagnosis of CKD. Second, our findings just come from numerous data analysis and documentary evidence, some experiments ought to be performed for validation. For instance, the binding affinity between TFs and corresponding DNA sequence should depend on electrophoretic mobility shift assay or chromatin immunoprecipitation. And also, dual-luciferase reporter assay is necessary for analyzing the gene expression regulated by TFs in the kidney cell model. Third, CKD patients have different

Figure 6. The diagnostic efficacy of 6 key TFs and their combined predictive efficiency in CKD. A. ROC analysis of HNF4A in CKD. **B.** ROC analysis of CEBPA in CKD. **C.** ROC analysis of CREB1 in CKD. **D.** ROC analysis of FOS in CKD. **E.** ROC analysis of HIF1A in CKD. **F.** ROC analysis of SP1 in CKD. **G.** The collected results of the above single result. **H.** The combined predictive efficiency for the above six TFs.



primary diseases. This research does not divide CKD patients into diverse subgroups. Fourth, Single-cell transcriptomics data may provide more comprehensive gene expression information than the microarray data used in this study [56-57]. We will overcome these shortcomings and make a deep exploration in the next work.

Conclusion

In summary, transcription factors play an important role in the pathophysiological process of chronic kidney disease. We have identified 6 TFs closely associated with CKD based on a comprehensive method containing HNF4A, CEBPA, CREB1, FOS, HIF1A and SP1. According to the literature evidence and deep data analysis, we conclude that SP1, CREB1 and HIF1A may have greater potential for clinical translation.

Abbreviations

AKI, acute kidney injury; AUC, area under the curve; BUN, blood urea nitrogen; CKD, chronic kidney disease; CREB1, cAMP-responsive element-binding protein 1; DEGs, differentially expressed genes; ECM, extracellular matrix; eGFR, estimated glomerular filtration rate; ESKD, end-stage kidney disease; GEO, Gene Expression Omnibus; GSEA, gene set enrichment analysis; HIF1A, hypoxia-inducible factor 1-alpha; KEGG, Kyoto Encyclopedia of Genes and Genomes; MMP, matrix metalloproteinase; ROC, receiver operating characteristic; Scr, serum creatinine; SP1, specificity protein 1; TF, transcription factor; TGFβ, transforming growth factor beta; TRRUST, Transcriptional Regulatory Relationships Unraveled by Sentence-based Text-mining; UUO, unilateral ureteral obstruction.

Author Contributions

Jianhua Mao designed the research. Wei Zhou, Qingqing Jia and Shujun Wu performed bioinformatic analysis and wrote the manuscript. Xinyu Wang, Mingzhu Jiang and Hanyan Meng helped to solve the clinical problems and contributed to data collection. All authors read and approved the final manuscript.

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Ethics Approval and Consent to Participate

Not Applicable.

Competing Interests

All the authors declared that they have no competing interests.

Data Availability

The datasets analysed during the current study are available in the GEO Database (GSE66494, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE66494). In addition, the datasets analyzed during the current study are available from the corresponding author on reasonable request.

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