

Supplementary Material

Integration of Genetic Testing and Pathology for the Diagnosis of Adults with FSGS

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Supplementary Table 1. Additional Baseline Clinical Characteristics of the Sequenced Cohort.

	Percentage (%) of Available Data	Number of Patients
Age of onset of kidney disease (years) (% of available data)		161
0-12	10	17
12-18	6	9
>18	84	135
Proteinuria at onset		126
Dipstick positive	32	40
300 mg-2 g/ 24 hours	12	15
> 2 g/24 hours	56	71
Nadir plasma albumin (g/dl) (% of available data)		128
>35	43	56
30-34	20	25
25-29	13	17
20-24	8	10
<19	16	20
FSGS histologic subtype		
Not otherwise specified	80	126
Tip	8	126
Perihilar	7	126
Collapsing	2	126
Cellular	1	126
Inadequate to classify	2	126
Progression to kidney failure from disease onset (years) (% of patients with kidney failure)		71
< 5 years	24	17
5-10 years	31	22
> 10 years	45	32
	Percentage (%) of Available Data	Total Number of Available Patients
Patients with reportedly normal creatinine clearance at the onset of disease	65	103
Patients with family history of kidney disease	16	193
History of smoking	43	127
Frequent NSAID use	12	121

193 individuals from 179 families had exome sequencing performed but data was not available for all participants. Number of individuals in which data is available or satisfying the criteria is indicated in the last column. NSAID = non-steroid anti-inflammatory drug.

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Supplementary Table 2. List of Genes Associated with FSGS and Related Phenotypes.

Gene	Inheritance	Accession ID	Mean Depth of Coverage across All Samples
FSGS/steroid-resistant nephrotic syndrome			
<i>ACTN4</i>	AD	NM_004924	57X
<i>ADCK4</i>	AR	NM_024876	54X
<i>ALG1</i>	AR	NM_019109	59X
<i>ALG13</i>	XLR	NM_018466	49X
<i>ANLN</i>	AD	NM_018685	83X
<i>APOL1</i>	assoc.	NM_003661	94X
<i>ARHGAP24</i>	AD	NM_031305	87X
<i>ARHGDI1</i>	AR	NM_004309	70X
<i>AVIL</i>	AR	NM_006576	79X
<i>CD151</i>	AR	NM_004357	54X
<i>CD2AP</i>	AD/AR	NM_012120	62X
<i>CFH</i>	AR	NM_000186	103X
<i>COL4A3</i>	AD/AR	NM_000091	61X
<i>COL4A4</i>	AD/AR	NM_000092	63X
<i>COL4A5</i>	X-linked	NM_033380	35X
<i>COQ2</i>	AR	NM_015697	59X
<i>COQ6</i>	AR	NM_182476	67X
<i>CRB2</i>	AR	NM_173689	44X
<i>CUBN</i>	AR	NM_001081	77X
<i>DGKE</i>	AR	NM_003647	75X
<i>E2F3</i>	AD	NM_001949	74X
<i>EMP2</i>	AR	NM_001424	53X
<i>INF2</i>	AD	NM_032714	45X
<i>ITGA3</i>	AR	NM_002204	73X
<i>ITGB4</i>	AR	NM_000213	64X
<i>KANK1</i>	AR	NM_015158	82X
<i>KANK2</i>	AR	NM_015493	71X
<i>KANK4</i>	AR	NM_181712	75X
<i>LAGE3</i>	AR	NM_006014	29X
<i>LAMA5</i>	AR	NM_005560	41X
<i>LAMB2</i>	AR	NM_002292	82X
<i>LMNA</i>	AD	NM_005572	39X
<i>LMX1B</i>	AD	NM_002316	47X
<i>MAGI2</i>	AR	NM_012301	67X

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<i>MYH9</i>	AD	NM_002473	60X
<i>MYO1E</i>	AR	NM_004998	78X
<i>NPHS1</i>	AR	NM_004646	55X
<i>NPHS2</i>	AR	NM_014625	70X
<i>NUP107</i>	AR	NM_020401	75X
<i>NUP205</i>	AR	NM_015135	85X
<i>NUP93</i>	AR	NM_014669	85X
<i>NXF5</i>	XLR	NM_032946	82X
<i>OCRL</i>	XLR	NM_000276	67X
<i>OSGEP</i>	AR	NM_017807	77X
<i>PAX2</i>	AD	NM_003990	77X
<i>PDSS2</i>	AR	NM_020381	71X
<i>PLCE1</i>	AR	NM_016341	92X
<i>PMM2</i>	AR	NM_000303	84X
<i>PODXL</i>	AD	NM_005397	61X
<i>PTPRO</i>	AR	NM_030667	80X
<i>SCARB2</i>	AR	NM_005506	68X
<i>SGPL1</i>	AR	NM_003901	82X
<i>SMARCAL1</i>	AR	NM_014140	80X
<i>SYNPO</i>	AD	NM_007286	56X
<i>TP53RK</i>	AR	NM_033550	47X
<i>TPRKB</i>	AR	NM_016058	49X
<i>TRPC6</i>	AD	NM_004621	75X
<i>WDR73</i>	AR	NM_032856	79X
<i>WT1</i>	AD	NM_024426	47X
<i>XPO5</i>	AR	NM_020750	84X
<i>ZMPSTE24</i>	AR	NM_005857	88X
CAKUT			
<i>BMP4</i>	AD	NM_130850	82X
<i>BMP7</i>	AR	NM_001719	54X
<i>CHD1L</i>	AD	NM_004284	79X
<i>DSTYK</i>	AD	NM_015375	78X
<i>EYA1</i>	AD	NM_172059	84X
<i>FGF20</i>	AR	NM_019851	75X
<i>FOXC1</i>	AD	NM_001453	23X
<i>FRAS1</i>	AD/AR	NM_025074	78X
<i>FREM2</i>	AD/AR	NM_207361	102X
<i>GATA3</i>	AD	NM_002051	83X
<i>GREB1L</i>	AD	NM_001142966	88X
<i>GRIP1</i>	AR	NM_021150	79X
<i>HNF1B</i>	AD	NM_000458	64X

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<i>ITGA8</i>	AR	NM_003638	75X
<i>RET</i>	AD	NM_020630	62X
<i>ROBO2</i>	AD	NM_002942	73X
<i>SALL1</i>	AD	NM_002968	86X
<i>SIX1</i>	AD	NM_005982	67X
<i>SIX5</i>	AD	NM_175875	26X
<i>SLIT2</i>	AR	NM_004787	74X
<i>SOX17</i>	AD	NM_022454	43X
<i>SRGAP1</i>	AD	NM_020762	81X
<i>TNXB</i>	AD	NM_032470	36X
<i>TRAP1</i>	AR	NM_016292	73X
<i>UPK3A</i>	AD	NM_006953	48X
<i>WNT4</i>	AD	NM_030761	86X
Nephronophthisis			
<i>ANKS6</i>	AR	NM_173551	49X
<i>CCDC41</i>	AR	NM_016122	62X
<i>CEP164</i>	AR	NM_014956	53X
<i>CEP290</i>	AR	NM_025114	52X
<i>DCDC2</i>	AR	NM_016356	89X
<i>GLIS2</i>	AR	NM_032575	50X
<i>IFT172</i>	AR	NM_015662	66X
<i>INVS</i>	AR	NM_183245	93X
<i>IQCB1</i>	AR	NM_001023571	56X
<i>MAPKBP1</i>	AR	NM_014994	70X
<i>NEK8</i>	AR	NM_178170	75X
<i>NPHP1</i>	AR	NM_000272	81X
<i>NPHP3</i>	AR	NM_153240	74X
<i>NPHP4</i>	AR	NM_015102	62X
<i>RPGRIP1L</i>	AR	NM_015272	80X
<i>SDCCAG8</i>	AR	NM_006642	76X
<i>TMEM67</i>	AR	NM_153704	50X
<i>TTC21B</i>	AD/AR	NM_024753	68X
<i>WDR19</i>	AR	NM_025132	85X
<i>ZNF423</i>	AD/AR	NM_015069	109X
Other			
<i>CLCN5</i>	XLR	NM_000084	66X
<i>UMOD</i>	assoc.	NM_003361	57X

Supplementary Table 3. Likely Pathogenic Variants in COL4A Genes.

Patient # (Family ID)	Sex	Ethnicity	Age at Disease Onset	Age at kidney failure	Exon (Intron) Number	Nucleotide Change	Protein Effect	Allele Frequency	Zygotity	References
Likely Pathogenic <i>COL4A3</i> Variants										
2378 (s)	M	EUR	22	23	29	c.2172delA	Gly724fs	0	Het	
7939 (s)	F	EUR	29	n/a (33)	1	c.84delC	Ser28fs	0	Het	
Likely Pathogenic <i>COL4A4</i> Variants										
7505 (F29)	F	EAS	24	n/a (40)	10	c.603G>A	Trp201stop	0	Het	
2526 (s)	M	EUR	Unk	45	8	c.509G>A	Gly170Glu	0	Het	¹
2566 (s)	M	EUR	21	53	(25)	c.1988-2A>C	Disrupts splice acceptor	0	Het	
2687 (s)	F	EUR	23	42	(26)	c.2057-1G>A	Disrupts splice acceptor	0	Het	
Likely Pathogenic <i>COL4A5</i> Variants										
2545 (s)	F	EUR	Unk	Unk	(9)	c.545_546+2delAAgt	Affects splicing	0	Het	

The following minor allele frequency (MAF) cut-offs as determined in gnomAD (<http://gnomad.broadinstitute.org/>) were used for dominant and recessive disease genes respectively: 0.00005 and 0.005 (accessed 2018 Feb 22). (F) designates family pedigree number while (s) indicates a sporadic case. Het indicates heterozygous. References indicate previously reported pathogenic variants affecting the same codon. Age at kidney failure was indicated as n/a for patients without kidney failure, followed by their age at time of analysis in parentheses. Unk indicates that data were unavailable. EUR indicates European while EAS indicates East Asian. The *COL4A5* mutation in 2545 was predicted to affect splicing at the wild-type donor site by Human Splicing Finder 3.1 (<http://www.umd.be/HSF3/>).

Supplementary Table 4. Likely Pathogenic Variants in non-COL4A Genes.

Patient # (Family ID)	Sex	Ethnicity	Age at Disease Onset	Age at kidney failure	Gene Symbol	Inheritance	Exon (Intron) Number	Nucleotide Change	Protein Effect	Allele Frequency	Zygosity	References
Likely Pathogenic Podocyte Gene Variants												
2202 (F2)	F	EUR	11	12	<i>TRPC6</i>	AD	2	c.326G>A	Gly109Asp	0	Het	²
2195 (F2)	F	EUR	26	32	<i>TRPC6</i>	AD	2	c.326G>A	Gly109Asp	0	Het	²
2469 (F3)	F	EUR	24	47	<i>PODXL</i>	AD	7	c.1376_1379del	Lys459fs	0	Het	
2470 (F3)	F	EUR	7	23	<i>PODXL</i>	AD	7	c.1376_1379del	Lys459fs	0	Het	
2504 (s)	F	EUR	27	36	<i>TRPC6</i>	AD	2	c.523C>T	Arg175Trp	0	Het	³
2572 (s)	M	EUR	17	24	<i>INF2</i>	AD	4	c.542T>C	Val181Ala	0	Het	⁴
7939 (s)	F	EUR	29	n/a (33)	<i>LMX1B</i>	AD	6	c.879delG	Leu293fs	0	Het	
Likely Pathogenic CAKUT Gene Variants												
1791 (s)	M	EUR	21	Unk	<i>BMP4</i>	AD	4	c.774dupA	Pro259fs	0	Het	
2653 (s)	F	EUR	28	37	<i>PAX2</i>	AD	3	c.369_370insTA	Ile123fs	0	Het	
7535 (s)	F	EUR	Unk	Unk	<i>EYA1</i>	AD	14	c.1318C>T	Arg440Trp	2.44E-05	Het	⁵
Likely Pathogenic Variants in Other Genes												
7019 (s)	M	EUR	Unk	Unk	<i>CLCN5</i>	AR	10	c.1535G>T	Gly512Val	0	Hemi	⁶
7276 (s)	M	EUR	27	n/a (32)	<i>LAMA5</i>	AR	(45)	c.6065-1G>T	Disrupts splice acceptor	0	Homo	
7902 (s)	F	EUR	33	n/a (43)	<i>CEP290</i>	AR	54	c.7346C>A	Ser2449stop	0	Homo	

The following minor allele frequency (MAF) cut-offs as determined in gnomAD (<http://gnomad.broadinstitute.org/>) were used for dominant and recessive disease genes respectively: 0.00005 and 0.005 (accessed 2018 Feb 22). (F) designates family pedigree number while (s) indicates a sporadic case. Het indicates heterozygous, hemi indicates hemizygous, and homo indicates homozygous. References indicate previously reported pathogenic variants affecting the same codon. Age at kidney failure was indicated as n/a for patients without kidney failure, followed by their age at time of analysis in parentheses. Unk indicates that data were unavailable. EUR indicates European. 2195 and 2202 are mother and daughter; 2469 and 2470 are mother and daughter.

Supplementary Table 5. Possibly Pathogenic Variants.

Patient # (Family ID)	Sex	Ethnicity	Age at Disease Onset	Age at ESRD	Gene Symbol	Inheritance	Exon (Intron) Number	Nucleotide Change	Protein Effect	Allele Frequency	Zygosity	References
Possibly Pathogenic Podocyte Gene Variants												
7482 (F28)	M	EAS	28	n/a (36)	<i>TRPC6</i>	AD	2	c.643C>T	Arg215Trp	8.15E-06	Het	⁷
2475 (s)	F	EUR	29	32	<i>WT1</i>	AD	8	c.1312C>T	Leu438Phe	0	Het	
6699 (s)	F	EUR	32	n/a (50)	<i>WT1</i>	AD	10	c.1502G>A	Arg501His	0	Het	
7276 (s)	M	EUR	27	n/a (32)	<i>INF2</i>	AD	3	c.500A>C	His167Pro	0	Het	
7938 (s)	M	EUR	33	n/a (53)	<i>WT1</i>	AD	7	c.1099G>T	Asp367Tyr	0	Het	
Possibly Pathogenic CAKUT Gene Variants												
2583 (s)	M	EUR	23	42	<i>PAX2</i>	AD	4	c.413T>A	Ile138Asn	0	Het	
2639 (s)	M	EAS	18	36	<i>PAX2</i>	AD	3	c.275C>T	Thr92Met	0	Het	
Potentially Compound Heterozygous Variants												
2698 (s)	F	Admixed	51	68	<i>CD2AP</i>	AR	8	c.902A>T	Lys301Met	1.77E-04	Het	⁸
							3	c.274G>A	Ala92Thr	0	Het	
2708 (s)	M	Admixed	40	Unk	<i>ANKS6</i>	AR	6	c.1322A>G	Gln441Arg	6.83E-04	Het	⁹
							10	c.1883C>T	Ser628Phe	2.26E-04	Het	
2758 (s)	M	EUR	4	n/a (20)	<i>NUP93</i>	AR	11	c.1162C>T	Arg388Trp	8.23E-04	Het	¹⁰
							17	c.2065T>A	Phe689Ile	0	Het	
7596 (s)	F	EUR	2	n/a (19)	<i>CUBN</i>	AR	45	c.6928_6934delT AACCTC	Glu2310Cysfs	1.77E-04	Het	¹¹
							51	c.7968_7969delinsGTTATATAA GGTATAACA	Leu2656_Pro2657delinsPheValIleProTyrIleThr	3.61E-05	Het	

The following minor allele frequency (MAF) cut-offs as determined in gnomAD (<http://gnomad.broadinstitute.org/>) were used for dominant and recessive disease genes respectively: 0.00005 and 0.005 (accessed 2018 Feb 22). (F) designates family pedigree number while (s) indicates a sporadic case. Het indicates heterozygous. References indicate previous reports of the variant. Age at kidney failure was indicated as n/a for patients without kidney failure, followed by their age at time of analysis in parentheses. Unk indicates that data were unavailable. EUR indicates European while EAS indicates East Asian.

Supplementary Table 6. Previously Reported Variants with Uncertain Pathogenic Significance.

Patient # (Family ID)	Sex	Ethnicity	Age at Disease Onset	Age at Kidney Failure	Gene Symbol	Inheritance	Exon (Intron) Number	Nucleotide Change	Protein Effect	Allele Frequency	Zygoty	References
1613 (F1)	M	EUR	24	42	<i>NUP93</i>	AR	11	c.1162C>T	Arg388Trp	8.23E-04	Het	10
2517 (F4)	M	Admixed	Unk	14	<i>ZMPSTE24</i>	AR	7	c.794A>G	Asn265Ser	1.22E-05	Het	12
6463 (F13)	F	EUR	Unk	Unk	<i>TTC21B</i>	AR	14	c.1697A>G	His566Arg	6.68E-04	Het	13
5772 (s)	F	Admixed	44	61	<i>NPHS1</i>	AR	12	c.1610C>T	Thr537Met	9.68E-04	Het	14
7291 (s)	M	Admixed	38	n/a (50)	<i>COQ2</i>	AR	5	c.890A>G	Tyr297Cys	4.11E-06	Het	15
7596 (s)	F	EUR	2	n/a (19)	<i>NPHS1</i>	AR	14	c.1868G>T	Cys623Phe	3.61E-05	Het	14
7982 (s)	M	EUR	40	n/a (64)	<i>NPHP3</i>	AR	(8)	c.2694-2_2694-1delAG	Disrupts splice acceptor	2.78E-04	Het	16

The following minor allele frequency (MAF) cut-offs as determined in gnomAD (<http://gnomad.broadinstitute.org/>) were used for dominant and recessive disease genes respectively: 0.00005 and 0.005 (accessed 2018 Feb 22). (F) designates family pedigree number while (s) indicates a sporadic case. Het indicates heterozygous. References indicate previous reports of the variant. Age at kidney failure was indicated as n/a for patients without kidney failure, followed by their age at time of analysis in parentheses. Unk indicates that data were unavailable. EUR indicates European. 2517 has an additional pathogenic variant in *LMX1B* (c.668G>A, p.R223Q). 7596 has additional possibly pathogenic variants in *CUBN* (c.6928_6934delTAACCTC, p.E2310Cfs; c.7968_7969delinsGTTATATAAGGTATAACA, p.L2656_P2657delinsFVIPYIT).

Supplementary Table 7. Additional Clinical Characteristics for Patient Subgroups.

	COL4A (n=12)	Other genetic (n=12)	Non-proven genetic (n=169)
Age of onset of kidney disease (years)			
0-12	10	12	10
12-18	0	13	6
>18	90	75	84
Ethnicity			
European	92	50	64
African	0	0	4
East Asian	0	25	12
Admixed	8	25	20
Proteinuria at onset			
Dipstick positive	25	38	32
300 mg-2 g/ 24 hours	13	12	12
> 2 g/24 hours	62	50	56
Nadir plasma albumin (g/dl)			
>35	57	27	44
30-34	14	43	18
25-29	29	15	12
20-24	0	15	8
<19	0	0	18
Normal creatinine clearance at disease onset	67	83	77
History of smoking	50	25	46
Frequent NSAID use	14	0	12
FSGS histologic subtype			
Not otherwise specified	100	50	77
Tip	0	0	9
Perihilar	0	0	8
Collapsing	0	25	2
Cellular	0	0	1
Inadequate	0	25	3
Kidney failure	46	44	50
Number of years to kidney failure from diagnosis			
< 5 years	0	60	23
5-10 years	50	40	29
> 10 years	50	0	48
Kidney transplant (% of transplant in patients with kidney failure)	100	75	54
Recurrence of disease after kidney transplant (within the first year)	0	0	13
Graft failure after one year	20	67	32

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All patients in the *COL4A* subgroup received a kidney transplant, which was significantly different from the no proven genetic basis group ($p=0.05$). Numbers shown are percentages of available data. Total number of biopsies for each subgroup: COL4A (9), other genetic (4), non-proven genetic (113).

Supplementary Table 8. Tables demonstrating ages at disease onset and estimated mean survival/age of kidney failure by subgroup, with sexes analyzed separately.

			95% CI	
	Age of onset / all cohort	Std error	Lower	Upper
COL4A	36	3	29	42
Genetic	26	5	17	37
No proven genetic	34	1	32	37

			95% CI	
	Kidney failure / all cohort	Std error	Lower	Upper
COL4A	58	5	49	69
Genetic	43	6	31	55
No proven genetic	62	2	58	66

			95% CI	
	Age of onset / females	Std error	Lower	Upper
COL4A	27	4	19	35
Genetic	24	6	12	36
No proven genetic	36	3	31	41

			95% CI	
	Kidney failure / females	Std error	Lower	Upper
COL4A	48	4	40	56
Genetic	NA	NA	NA	NA
No proven genetic	64	3	57	70

			95% CI	
	Age of onset / males	Std error	Lower	Upper
COL4A	36	4	27	44
Genetic	27	7	14	40
No proven genetic	34	2	30	37

			95% CI	
	Kidney failure / males	Std error	Lower	Upper
COL4A	66	0	66	66
Genetic	33	8	17	48
No proven genetic	63	3	57	70

Genetic refers to other genetic causes not including *COL4A*. For *COL4A* subgroup, only one male patient developed kidney failure at last follow up. No females in the other genetic group developed kidney failure at last follow up. There were no statistically significant differences between males and females in any pairwise comparison. Std error = standard error; CI = confidence interval; NA = not applicable.

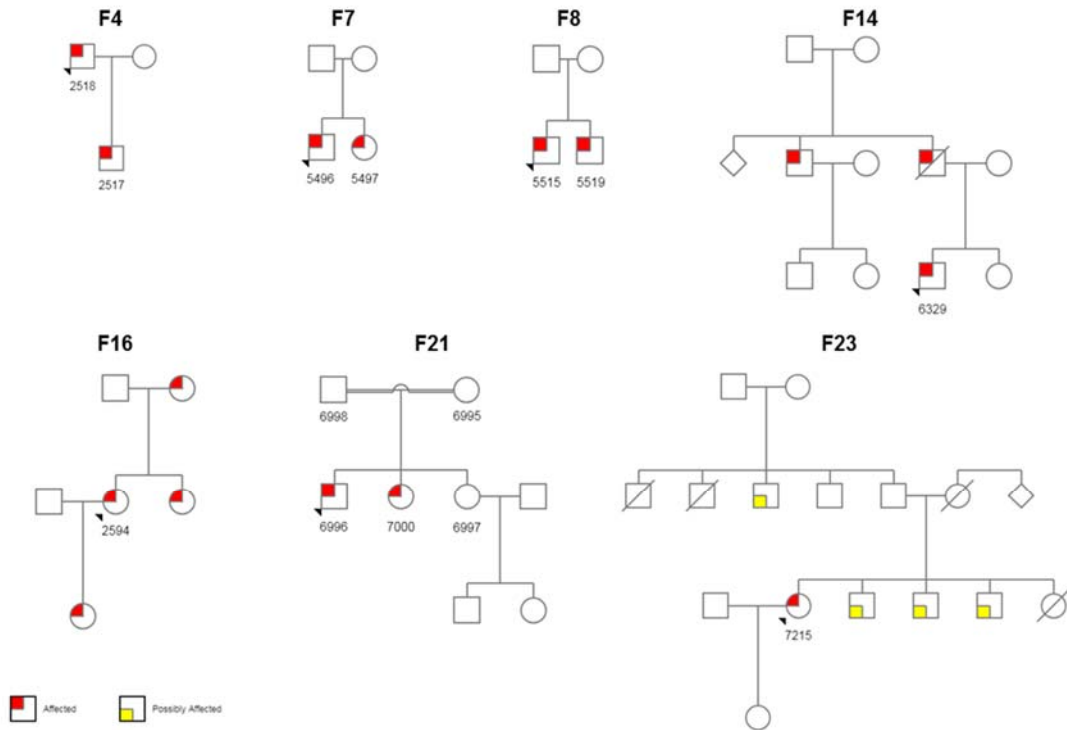
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Supplementary Table 9. Clinical characteristics of COL4A, other genetic cause and no proven genetic cause subgroups.

	COL4A (12)	Other genetic (12)	No proven genetic (169)
% male	5/12	8/12	98/169
Mean age of onset of kidney disease	36	26	34
% with hematuria	6/10	2/8	20/70
% of patients with family history of kidney disease	5/11	4/9	19/155
% partial remission	2/7	3/10	25/95
% complete remission	0/7	0/10	19/95
% no remission	1/7	2/10	14/95
% unknown status of remission	4/7	5/10	37/95
% kidney failure	5/11	4/9	63/127
% with only global glomerulosclerosis on light microscopy	1/9	2/4	10/113
% glomerular basement membrane abnormalities on electron microscopy	5/9	1/4	30/113
% with >50% podocyte foot process effacement on electron microscopy	9/9	3/4	81/113
Number of patients where pathology report with electron microscopy description is available	9	4	113
Mean age at kidney failure (years)	58	43	62
% kidney transplant in patients with kidney failure	5/5	3/4	34/63
% of recurrence of disease after kidney transplant (within the first year)	0/5	0/3	4/31

Absolute numbers presented. Denominator represents number of individuals for which data is available.

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Supplementary Figure 1. Pedigrees of families with definitely pathogenic variants. In F21, 6996 has a likely pathogenic variant (*NPHS1* R976S) while other samples have not been tested yet. In all other families shown, individuals with ID's are known to have the respective pathogenic variant. Pedigree information is not available for F9. Arrows indicate probands.

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