

Supplemental Table 1a. Power Analysis for the combined FSGS and HIVAN cohort. The power calculations assume a cohort of 65 cases and 74 controls, two-sided alpha 0.05, minor allele frequency 0.2, and baseline disease risk of 1%. Power calculations were conducted using Quanto v.1.2.4 software.

Additive OR	Study Power Additive Model
2.0	70.5%
3.0	98.1%
4.0	99.9%

Recessive OR	Study Power Recessive Model
4.0	57.3%
6.0	84.5%
8.0	95.1%

Supplemental Table 1b. Power Analysis for the IgAN cohort. The power calculations assume a cohort of 35 cases and 74 controls, two-sided alpha 0.05, minor allele frequency 0.2, and baseline disease risk of 1%.

Additive OR	Study Power Additive Model
2.0	55.1%
3.0	92.3%
4.0	98.9%

Recessive OR	Study Power Recessive Model
4.0	44.7%
6.0	72.3%
8.0	87.4%

Supplemental Table 2. Pairwise linkage disequilibrium measures between the markers tested: r^2 above the diagonal, D' below the diagonal. Both LD measures calculated based on a joint sample of 65 cases (HIVAN + FSGS) and 74 controls.

D'		APOL1			MYH9		
		rs73885319	rs60910145	rs71785313	rs11912763	rs4821481	rs5750250
APOL1	rs73885319		0.924	0.135	0.354	0.174	0.180
	rs60910145	0.984		0.129	0.404	0.167	0.173
	rs71785313	1.000	1.000		0.016	0.037	0.096
MYH9	rs11912763	0.725	0.756	0.422		0.127	0.148
	rs4821481	0.895	0.898	0.664	0.931		0.592
	rs5750250	0.768	0.769	0.896	0.848	0.912	

Supplemental Table 3. Sliding Window Haplotype Analysis.

3-SNP window						
SNP window	Haplotype	Freq. cases	Freq. controls	CHISQ	DF	Omnibus P-value
rs73885319 rs60910145 rs71785313	ATD	0.244	0.127	35.46	3	9.7E-08
	GGI	0.486	0.245			
	GTI	0.005	0.018			
	ATI	0.265	0.609			
rs60910145 rs71785313 rs11912763	TDA	0.041	0.001	38.24	5	3.4E-07
	GIA	0.332	0.158			
	TIA	0.027	0.024			
	TDG	0.206	0.134			
	GIG	0.152	0.092			
	TIG	0.242	0.591			
rs71785313 rs11912763 rs4821481	DGT	0.013	0.013	25.22	5	1.3E-04
	IGT	0.187	0.310			
	DAC	0.050	0.003			
	IAC	0.345	0.178			
	DGC	0.185	0.119			
	IGC	0.220	0.377			
rs11912763 rs4821481 rs5750250	GTA	0.185	0.311	22.80	4	1.4E-04
	GCA	0.036	0.117			
	GTG	0.016	0.016			
	ACG	0.393	0.166			
	GCG	0.369	0.390			
2-SNP window						
SNP window	Haplotype	Freq. cases	Freq. controls	CHISQ	DF	Omnibus P-value
rs73885319 rs60910145	GG	0.485	0.245	17.52	2	1.6E-04
	GT	0.008	0.020			
	AT	0.508	0.735			
rs60910145 rs71785313	TD	0.246	0.135	33.39	2	5.6E-08
	GI	0.485	0.250			
	TI	0.269	0.615			
rs71785313 rs11912763	DA	0.059	0.006	24.60	3	1.9E-05
	IA	0.341	0.176			
	DG	0.188	0.129			
	IG	0.413	0.689			
rs11912763 rs4821481	GT	0.201	0.323	16.41	2	2.7E-04
	AC	0.395	0.181			
	GC	0.405	0.497			
rs4821481 rs5750250	TA	0.192	0.311	14.89	3	1.9E-03
	CA	0.038	0.128			
	TG	0.015	0.014			
	CG	0.754	0.547			

I= insertion, D= deletion at rs71785313

Supplemental Table 4. Association analysis of *APOL1* and *MYH9* SNPs with risk of ESRD in IgAN patients.

SNP	BP	Allele	IgAN ESRD (N=9)	IgAN No ESRD (N=23)	OR	P-value
rs73885319	36661906	G	0.364	0.152	3.18	0.049 *
rs60910145	36662034	G	0.364	0.152	3.18	0.049 *
rs71785313	36662046	D	0.136	0.217	0.57	0.43
rs11912763	36684722	A	0.364	0.174	2.71	0.08
rs4821481	36695942	T	0.455	0.318	1.79	0.28
rs5750250	36708483	A	0.546	0.409	1.73	0.29

Supplemental Table 5. Primer sequences.

Gene	SNP	Forward primer	Reverse primer
<i>APOL1</i>	rs73885319 rs60910145 rs71785313	AGCTGAAAGCGGTGAACAG	CATATCTCTCCTGGTGGCTG
<i>MYH9</i>	rs11912763	GAGTCACTGAACCCCGAGAC	GAGCAGAGCGAGGAGAAGAAG
	rs4821481	TGAGGGCTTCTGCTTAACTG	AACCCACAGTGACCAACAC
	rs5750250	GGCTGACACCTTTACCCAAG	ATCTCCCGTGGCAGGATC

Supplemental Figure 1. *Myh9* expression in whole kidney from B6 mice, *Myh9* haploinsufficient (B6-*Myh9*^{+/-}) and HIV transgenic mice (TgB6-*Myh9*^{+/-}) at 4-5 months of age. Expression is adjusted to a B6 sample, N = 4-5 per group. * p<0.04 vs. B6 mice.

