

Supplementary Table 2. Distribution of frequencies of the interferon lambda-related genotype in the controls and CKD patients in the model of inheritance in the entire CKD cohort

Gene	SNP number	Function	Model of inheritance							
			Codominant genetic model		Dominant genetic model		Recessive genetic model		Log-additive genetic model	
			OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value	OR (95% CI)	p-value
<i>IFNL3</i>	rs148543092	Missense	2.76	0.007*	2.76	0.009*				
			(1.32-5.79)		(1.32-5.79)					
<i>IFNL2</i>	rs8103362	Missense	-		-					
			2.76	0.007*	2.60	0.01*			2.31	0.02*
			(1.32-5.79)		(1.25-5.41)			(1.14-4.69)		
<i>IFNAR2</i>	rs1051393	Missense	-		-					
			1.31	0.35	1.50	0.14	1.69	0.07	1.42	0.04*
			(0.74-2.34)		(0.87-2.58)		(0.97-2.95)	(1.01-1.99)		
			2.02	0.04*						
			(1.03-3.96)							
<i>TLR9</i>	rs187084	NearGene-5'	1.50	0.19	1.73	0.05	1.75	0.04*	1.51	0.02*
			(0.82-2.74)		(0.98-3.05)		(1.03-2.97)		(1.08-2.11)	
			2.27	0.02*						
			(1.16-4.44)							
<i>IL-22</i>	rs2227513	NearGene-5'	3.73	0.09	3.73	0.09				
			(0.80-17.38)		(0.80-17.38)					
			-							

CI, confidence interval; CKD, chronic kidney disease; OR, odds ratio; SNP, single nucleotide polymorphisms.

*p < 0.05.