

Supplemental Figure Legends

Supplemental Figure 1. Distribution of MBL levels according to *MBL2* genotypes

in patients with IgAN and healthy controls. Bar plot showing the distribution of

MBL levels in IgAN patients and healthy controls with different *MBL2* genotypes.

The number of patients with different *MBL2* genotypes is indicated by the n below the

plot. When MBL levels were compared between IgAN patients and healthy controls

with same genotypes, * indicated $p < 0.05$ while ** indicated $p < 0.01$.

Supplemental Table 1. Distribution of allele and genotype frequencies of *MBL2* gene variants in IgAN patients and healthy controls.

Variant	Genotype	Count (frequency)		p-value	Allele	Count (frequency)		p-value
		IgAN	Healthy controls			IgAN	Healthy controls	
c.-550G>C (rs11003125)	CC	151 (20.2)	108 (22.1)	0.392	C	656 (43.8%)	455 (46.5%)	0.182
	GC	354 (47.3)	239 (48.9)		G	842 (56.2%)	523 (53.5%)	
	GG	244 (32.6)	142 (29.0)					
c.-427A>C (rs11003124)	AA	577 (77.0)	375 (76.7)	0.971	A	1316 (87.9%)	858 (87.7%)	0.929
	AC	162 (21.6)	108 (22.1)		C	182 (12.1%)	120 (12.3%)	
	CC	10 (1.3)	6 (1.2)					
c.-349A>G (rs7084554)	AA	577 (77.0)	375 (76.7)	0.971	A	1316 (87.9%)	858 (87.7%)	0.929
	AG	162 (21.6)	108 (22.1)		G	182 (12.1%)	120 (12.3%)	
	GG	10 (1.3)	6 (1.2)					
c.-336A>G (rs36014597)	AA	577 (77.0)	375 (76.7)	0.971	A	1316 (87.9%)	858 (87.7%)	0.929
	AG	162 (21.6)	108 (22.1)		G	182 (12.1%)	120 (12.3%)	
	GG	10 (1.3)	6 (1.2)					
c.-324_-329 delAAAGAG (rs10556764)	AAAGAG/AAAGAG	577 (77.0)	375 (76.7)	0.971	AAAGAG	1316 (87.9%)	858 (87.7%)	0.929
	AAAGAG/del	162 (21.6)	108 (22.1)		del	182 (12.1%)	120 (12.3%)	
	del/del	10 (1.3)	6 (1.2)					
c.-221G>C (rs7096206)	CC	21 (2.8)	8 (1.6)	0.372	C	181 (12.1%)	113 (11.6%)	0.691
	GC	139 (18.6)	97 (19.8)		G	1317 (87.1%)	865 (88.4%)	
	GG	589 (78.6)	384 (78.5)					
c.-70C>T (rs11003123)	CC	577 (77.0)	375 (76.7)	0.971	C	1316 (87.9%)	858 (87.7%)	0.929
	TC	162 (21.6)	108 (22.1)		T	182 (12.1%)	120 (12.3%)	
	TT	10 (1.3)	6 (1.2)					
c.4C>T (rs7095891)	CC	577 (77.0)	375 (76.7)	0.971	C	1316 (87.9%)	858 (87.7%)	0.929

	TC	162 (21.6)	108 (22.1)		T	182 (12.1%)	120 (12.3%)	
	TT	10 (1.3)	6 (1.2)					
c.223C>T (rs5030737)	CC	747 (99.7)	488 (99.8)	0.827*	C	1496 (99.9%)	977 (99.9%)	0.655*
	TC	2 (0.3)	1 (0.2)		T	2 (0.1%)	1 (0.1%)	
	TT	0 (0.0)	0 (0.0)					
c.230G>A (rs1800450)	AA	16 (2.1)	10 (2.0)	0.083	A	210 (14.0)	164 (16.8%)	0.062
	AG	178 (23.8)	144 (29.4)		G	1288 (86.0%)	814 (83.2%)	
	GG	555 (74.1)	335 (68.5)					
c.239G>A (rs1800451)	AA	0 (0.0)	0 (0.0)	0.419*	A	1 (0.1%)	0 (0%)	0.605*
	AG	1 (0.1)	0 (0.0)		G	1497 (99.9%)	978 (100%)	
	GG	748 (99.9)	489 (100.0)					

Note: * p value was calculated by Fisher's exact test.

Supplemental Table 2. Distribution of the *MBL2* A allele/O allele group in IgAN patients and healthy controls.

Variant	IgAN	Healthy controls	p-value
Genotype	Count (frequency)	Count (frequency)	0.100
AA	552 (73.3)	334 (68.3%)	
AO	181 (24.2%)	145 (29.7%)	
OO	16 (2.1%)	10 (2.0%)	
Allele/Allele group	Count (frequency)	Count (frequency)	0.073
A	1285 (85.8%)	813 (83.1%)	
O	213 (14.2%)	165 (16.9%)	

Supplemental Table 3. Distribution of haplotype frequencies of the *MBL2* gene in IgAN patients and healthy controls.

Haplotype	Count		Frequency		p-value	Odds ratio (95% CI)
	IgAN	Healthy controls	IgAN	Healthy controls		
LYPB	205	161	0.137	0.165	0.06	0.799 (0.633, 1.010)
LXPA	176	113	0.117	0.116	0.864	0.977 (0.753, 1.268)
LYP A	96	61	0.064	0.062	0.943	0.988 (0.704, 1.386)
LYQA	178	120	0.119	0.123	0.584	0.931 (0.720, 1.203)
HYP A	827	519	0.552	0.531	0.249	reference
Rare	16	4	0.011	0.004	0.101	2.510 (0.835, 7.550)
HYPB	5	3	0.003	0.003	-	-
HYPD	2	1	0.001	0.001	-	-
HXPA	5	0	0.003	0.000	-	-
HYQA	3	0	0.002	0.000	-	-
LYQC	1	0	0.001	0.000	-	-

Supplemental Table 4. Power for genetic association analysis between variants/haplotypes in *MBL2* and IgAN susceptibility.

Variants/haplotypes	Genetic analysis	Power
c.-550G>C (rs11003125)	genotype frequencies comparison (GG/GC/CC)	0.608
	allele frequencies comparison (G/C)	0.818
c.-427A>C (rs11003124)	genotype frequencies comparison (AA/AC/CC)	0.029
	allele frequencies comparison (A/C)	0.071
c.-349A>G (rs7084554)	genotype frequencies comparison (AA/AG/GG)	0.029
	allele frequencies comparison (A/G)	0.071
c.-336A>G (rs36014597)	genotype frequencies comparison (AA/AG/GG)	0.029
	allele frequencies comparison (A/G)	0.071
c.-324_-329 delAAAGAG (rs10556764)	genotype frequencies comparison (II/ID/DD)	0.029
	allele frequencies comparison (I/D)	0.071
c.-221G>C (rs7096206)	genotype frequencies comparison (GG/GC/CC)	0.628
	allele frequencies comparison (G/C)	0.309
c.-70C>T (rs11003123)	genotype frequencies comparison (CC/CT/TT)	0.029
	allele frequencies comparison (C/T)	0.071
c.4C>T (rs7095891)	genotype frequencies comparison (CC/CT/TT)	0.029
	allele frequencies comparison (C/T)	0.071
c.223C>T (rs5030737)	genotype frequencies comparison (CC/CT/TT)	0.175
	allele frequencies comparison (C/T)	0.000
c.230G>A (rs1800450)	genotype frequencies comparison (GG/GA/AA)	0.917
	allele frequencies comparison (G/A)	0.938
c.239G>A (rs1800451)	genotype frequencies comparison (GG/GA/AA)	0.684
	allele frequencies comparison (G/A)	0.000
variants combination in Exon1	genotype frequencies comparison (AA/AO/OO)	0.900
	allele frequencies comparison (A/O)	0.927
haplotypes	haplotype frequencies comparison (LYPB/LXPA/LYPA/LYQA/HYPA/Rare)	0.771

Supplemental Table 5. Primers used for PCR and PCR-SSP.

Method	Forward primer		Reverse primer		Annealing temperature	Amplified fragment	Amplified genotypes
	Primer name	Primer sequence (5' to 3')	Primer name	Primer sequence (5' to 3')			
PCR	MBL2F	TTGCCAGTGGTTTTGACTC	MBL2R	CAGGCAGTTTCCTCTGGAAG	54°C	990 bp (from -677 to 313)	all
PCR-SSP	MBL2-P-U-F	GGAGGAGGATTCAAGGCAAG	MBL2-P-U-R	TGTCTGTAGGAGCTTCCTCTTT	54°C	399 bp (from -705 to -307)	HL/YY/PQ/AA
	MBL2-A-U-F	GGGATGGAAAGCAGAAATCA	MBL2-A-U-R	CCCCTTTCTCCCTTGGTGTC	60°C	1178 bp (from -929 to 249)	HL/YY/PP/AB
							HL/YY/PQ/AB
							LL/XY/PP/AB
							LL/YY/PQ/AB
	MBL2-C-U-F	GAGTGGGATGGAAAGCAGAA	MBL2-C-U-R	ACCTGGTCCCCCTTTTCTC	62°C	1191 bp (from -933 to 258)	HL/YY/PQ/AC
	MBL2F	TTGCCAGTGGTTTTGACTC	MBL2-X-U-R	AGACTATAAACATGCTTTCG	54°C	476 bp (from -677 to -202)	HL/XY/PP/AA
MBL2-X-D-F	CATTGTCTCACTGCCACC	MBL2-X-D-R	TCATATCCCAGGCAGTTTC	60°C	562 bp (from -240 to 322)	LL/XY/PQ/AA	

Supplemental Figure 1

