

Supplementary Table 1. Clinical and pathological characteristics of iMN patients with and without anti-PLA2R antibodies.

Clinical parameter	Overall	Anti-PLA2R positive (n=173)	Anti-PLA2R negative (n=88)	P
Gender (male/female)	147/114	101/72	46/42	0.35
Age (yr)	48.74±15.61	50.91±15.88	44.48±14.28	0.002
Serum albumin (g/L)	25.89±5.87	24.89±5.35	27.86±6.37	<0.0001
Proteinuria (g/24h)	5.93±4.83	6.79±5.34	4.26±3.04	<0.0001
Serum creatinine (μmol/L)	70.84±25.11	73.04±26.81	66.51±20.86	0.03
eGFR	117.20±38.60	113.25±38.18	125.17±38.38	0.02
Triglyceride (mmol/L)	2.79±2.12	2.68±1.87	2.73±2.55	0.85
Total cholesterol (mmol/L)	7.25±2.34	7.32±2.34	7.10±2.34	0.49
Pathology stage, n (%)				
I-MN	134(51.3%)	81(46.8%)	53(60.2%)	0.07
II-MN	112(42.9%)	83(48.0%)	29(33.0%)	
III-MN	15(5.7%)	9(5.2%)	6(6.8%)	

eGFR=175*POWER(Scr/88.1,-1.234)*POWER(Age,-0.179)

Supplementary Table 2. Association results for HLA class II allele analysis in Chinese patients with iMN

	Allele frequency in cases	Allele frequency in controls	OR	P
DRB1*1501	0.3755	0.1469	4.65	1.67×10^{-21}
DRB1*0901	0.03065	0.1494	0.16	1.29×10^{-13}
DQB1*0602	0.3238	0.1544	2.82	2.84×10^{-10}
DQB1*0303	0.04215	0.1444	0.24	7.54×10^{-10}
DQA1*0301	0.0249	0.1102	0.19	2.43×10^{-9}
DRB1*0301	0.1207	0.0384	3.96	3.95×10^{-9}
DQA1*0302	0.03065	0.1035	0.28	3.53×10^{-6}
DQA1*0102	0.4004	0.2621	2.11	1.55×10^{-5}
DPB1*0402	0.05192	0.1064	0.42	0.00502
DQB1*0501	0.03065	0.06928	0.39	0.01351
DQA1*0201	0.04789	0.08598	0.49	0.03962
DQB1*0605	0.009579	0	26.01	0.05294
DRB1*0803	0.01533	0.04591	0.35	0.10199
DQA1*0505	0.113	0.06678	1.78	0.10843
DRB1*1201	0.01724	0.04508	0.35	0.15093
DQB1*0401	0.01533	0.0384	0.4	0.29328
DQA1*0401	0.003831	0.01503	0.18	0.37346
DRB1*1454	0	0.01169	0.08	0.37996
DRB1*0405	0.01724	0.04257	0.41	0.38934
DQB1*0302	0.02299	0.04591	0.47	0.49727
DQA1*0501	0.1207	0.08932	1.49	0.58263
DQB1*0609	0	0.009182	0.1	0.88542
DPB1*3301	0	0.03685	0.02	1
DRB1*0407	0	0.001669	0.46	1
DRB1*0801	0	0.001669	0.46	1

DRB1*1106	0	0.001669	0.46	1
DQB1*0203	0.001916	0.0008347	2.32	1
DQB1*0305	0.001916	0.0008347	2.32	1
DRB1*0907	0.001916	0.0008347	2.32	1
DRB1*1103	0.001916	0.0008347	2.32	1
DPB1*10001	0	0.001675	0.46	1
DPB1*1101	0	0.001675	0.46	1
DPB1*2002	0	0.001675	0.46	1
DPB1*20401	0	0.001675	0.46	1
DPB1*2401	0	0.001675	0.46	1
DPB1*5701	0	0.001675	0.46	1
DPB1*6801	0	0.001675	0.46	1
DPB1*4801	0.001923	0.0008375	2.32	1
DPB1*3801	0.003846	0	11.65	1
DRB1*0410	0.001916	0.001669	1.39	1
DPB1*3601	0.001923	0.001675	1.39	1
DPB1*0302	0	0.002513	0.33	1
DPB1*0601	0	0.002513	0.33	1
DPB1*3501	0	0.002513	0.33	1
DPB1*4101	0	0.002513	0.33	1
DPB1*4501	0	0.002513	0.33	1
DQA1*0506	0	0.003339	0.26	1
DPB1*2001	0	0.00335	0.26	1
DPB1*2101	0.003846	0.001675	2.32	1
DPB1*10501	0.001923	0.002513	1.39	1
DPB1*1901	0.005769	0.0008375	5.45	1
DRB1*1407	0.003831	0.002504	1.66	1
DRB1*1503	0.003831	0.002504	1.66	1

DRB1*1504	0.007663	0.0008347	7.06	1
DPB1*1601	0	0.004188	0.21	1
DPB1*2301	0	0.004188	0.21	1
DPB1*2402	0	0.004188	0.21	1
DPB1*10401	0.005769	0.001675	3.26	1
DPB1*1001	0.003846	0.002513	1.66	1
DRB1*0404	0	0.005008	0.18	1
DPB1*2601	0.001923	0.004188	0.63	1
DRB1*0402	0.005747	0.003339	1.29	1
DRB1*0102	0.003831	0.004174	1.05	1
DPB1*1801	0	0.005863	0.15	1
DRB1*1403	0.003831	0.005008	0.89	1
DRB1*1404	0.005747	0.005843	1.08	1
DPB1*0101	0.003846	0.0067	0.68	1
DRB1*0802	0.005747	0.006678	0.68	1
DQB1*0402	0.009579	0.005843	1.4	1
DRB1*1312	0.005747	0.008347	0.85	1
DQA1*0503	0.01149	0.007513	1.6	1
DQA1*0508	0.005747	0.01085	0.6	1
DQA1*0105	0.007663	0.01002	0.83	1
DRB1*1104	0.01724	0.008347	2.14	1
DRB1*0403	0.003831	0.01503	0.31	1
DQB1*0604	0.009579	0.01336	0.77	1
DPB1*13501	0.01538	0.01173	1.47	1
DRB1*0401	0.007663	0.01586	0.53	1
DPB1*1401	0.01731	0.01256	1.37	1
DRB1*1001	0.009579	0.01669	0.61	1
DQB1*0603	0.02299	0.01252	1.75	1

DRB1*1301	0.02299	0.01419	1.55	1
DRB1*0101	0.01149	0.02254	0.56	1
DPB1*0901	0.03269	0.01424	2.26	1
DRB1*0406	0.01149	0.02504	0.41	1
DRB1*1602	0.01916	0.0217	0.95	1
DRB1*1401	0.0249	0.0192	1.35	1
DRB1*1302	0.01533	0.03172	0.49	1
DRB1*1502	0.02874	0.03005	1.01	1
DPB1*1701	0.01923	0.03518	0.58	1
DPB1*0202	0.02885	0.0335	0.82	1
DRB1*1405	0.03257	0.03255	1.03	1
DQA1*0101	0.02874	0.03589	0.84	1
DPB1*1301	0.03462	0.03434	1.06	1
DQA1*0303	0.0249	0.04257	0.59	1
DQB1*0202	0.03448	0.04341	0.82	1
DPB1*0301	0.03846	0.04606	0.89	1
DQA1*0601	0.03448	0.04841	0.68	1
DQA1*0104	0.06513	0.04257	1.6	1
DRB1*1202	0.03257	0.05676	0.59	1
DQB1*0601	0.06322	0.05008	1.23	1
DQB1*0502	0.06322	0.05342	1.21	1
DQB1*0503	0.05939	0.06427	0.87	1
DRB1*1101	0.07854	0.06344	1.31	1
DQA1*0103	0.07854	0.06427	1.11	1
DRB1*0701	0.05364	0.08765	0.61	1
DPB1*0401	0.1596	0.134	1.36	1
DQB1*0301	0.1648	0.1836	0.77	1

Supplementary Table 3. Analysis of gene-gene interactions: odds ratios for iMN according to SNP rs3749117 (PLA2R1) and HLA-DRB1*1501/DRB1*0301 combinations.

SNP rs3749117 (PLA2R1)		HLA-DRB1*1501		HLA-DRB1*0301	
		(-)	(+)	(-)	(+)
CC (Low risk)	No. of cases/controls	3/22	0/8	2/28	1/2
	Odds ratio (95% CI)	1	-	1	-
	P-value	(ref)	0.56	(ref)	0.26
TC (Moderate risk)	No. of cases/controls	23/138	16/39	26/155	13/22
	Odds ratio (95% CI)	-	-	-	8.27 (1.69-40.57)
	P-value	1.0	0.16	0.38	0.007
TT (High risk)	No. of cases/controls	47/139	106/51	122/179	31/11
	Odds ratio (95% CI)	-	15.24 (4.36-53.29)	9.54 (2.23-40.80)	39.46 (8.04-193.66)
	P-value	0.21	1.58×10⁻⁷	1.07×10⁻⁴	7.72×10⁻⁹

Supplementary Table 4. Analysis of gene-gene interactions: odds ratios for iMN according to SNP rs35771982 (PLA2R1) and HLA-DRB1*1501/DRB1*0301 combinations.

rs35771982(PLA2R1)		HLA-DRB1*1501		HLA-DRB1*0301	
		(-)	(+)	(-)	(+)
CC (Low risk)	No. of cases/controls	3/22	0/8	2/28	1/1
	Odds ratio (95% CI)	-	-	-	-
	P-value	(ref)	0.56	(ref)	0.18
GC (Moderate risk)	No. of cases/controls	23/138	16/39	26/156	13/21
	Odds ratio (95% CI)	-	-	-	8.67 (1.76-42.61)
	P-value	1.0	0.16	0.38	0.003
GG (High risk)	No. of cases/controls	47/140	106/51	122/179	31/12
	Odds ratio (95% CI)	-	15.24 (4.36-53.29)	9.54 (2.23-40.80)	36.17 (7.44-175.90)
	P-value	0.21	1.58×10⁻⁷	1.07×10⁻⁴	1.23×10⁻⁸

Supplementary Table 5. Study power as a function of disease allele frequency and odd ratios.

Allele frequency	OR for a risk allele							
	1.2	1.4	1.6	1.8	2.0	3.0	4.0	5.0
0.1%	0.06	0.07	0.08	0.09	0.12	0.21	0.22	0.40
0.5%	0.06	0.08	0.11	0.14	0.17	0.35	0.53	0.67
1%	0.07	0.10	0.14	0.19	0.39	0.54	0.77	0.99
3%	0.08	0.16	0.26	0.38	0.51	0.90	0.99	1.00
5%	0.10	0.21	0.37	0.54	0.92	1.00	1.00	1.00
10%	0.13	0.33	0.57	0.77	0.99	1.00	1.00	1.00
15%	0.16	0.42	0.70	0.88	1.00	1.00	1.00	1.00

Supplementary Figure 1. The structure of DR2b-peptide 285 (SKTVEVW(M/V)GLNQLDE)-TCR with amino acid substitution M292V. Gray cartoon is peptide, cyan cartoon is MHC DR2b molecule, and magenta cartoon is TCR molecule. Blue stick is methionine, and aubergine stick is valine. Amino acid substitution of M292V in peptide 285 [SKTVEVW(M/V)GLNQLDE] does not influence the presentation modeling by DR2b. S, serine; K, lysine; T, threonine; V, valine; E, glutamic acid; W, tryptophan; M, methionine; G, glycine; L, leucine; N, asparagine; Q, glutamine; D, aspartic acid.

