

SUPPLEMENTARY TABLES

Supplementary Table 1. Sequences of primer and probe for TaqMan genotyping assay of HLA 3'UTR variants

HLA 3'UTR variants	Sequence (5'-3')
rs1710	Primer F: CCTTTGTGACTTCAAGAACCCTGA R: GAAGGAATGCAGTTCAGCATGAG Probe VIC-TCTCTGCAGAAAGAG-NFQ FAM-TCTCTGCACAAAGAG-NFQ
rs1063320	Primer F: CCTTCCCCAATCACCTTTCCT R: TCTCTCAAATTCAGGAATCTTCTCCTT Probe VIC-TTATAGCTCAGTGGACCACA-NFQ FAM-TAGCTCAGTGCACCACA-NFQ
rs2770	Primer F: AAGAAGTTGCAGCTCAGT R: TGTGTTTCCTCCCCAGT Probe VIC-TCTGTCTCAACTTTATGTG-NFQ FAM-TCTGTCTCAACTTTACGTG-NFQ

Supplementary Table 2. Association between genotypes of rs1710 and rs2770 and baseline serum levels of HBV DNA and HBsAg in 1655 HBeAg-seronegative CHB patients genotyped for both variants by HBV genotype

	Genotype B (n=1137)				Genotype C (n=518)			P value
	No (%)	No (%)	No (%)	p value	No (%)	No (%)	No (%)	
rs1710 (HLA-G) C>G	CC	CG	GG		CC	CG	GG	
HBV DNA level								
(copies/mL)								
Undetectable	61 (15.0)	70 (13.3)	25 (12.3)	0.28	38 (20.0)	55 (21.7)	13 (17.3)	0.27
300-9999	148 (36.4)	193 (36.6)	67 (33.0)		95 (50.0)	108 (42.7)	30 (40.0)	
10000-99999	110 (27.0)	146 (27.7)	60 (29.6)		38 (20.0)	58 (22.9)	18 (24.0)	
100000-999999	60 (14.7)	80 (15.2)	44 (21.7)		9 (4.7)	20 (7.9)	5 (6.7)	
≥100000	28 (6.9)	38 (7.2)	7 (3.5)		10 (5.3)	12 (4.7)	9 (12.0)	
Mean± SD (log)	4.32 ± 1.20	4.31 ± 1.11	4.40 ± 1.07	0.65	3.91 ± 1.04	4.07 ± 1.06	4.35 ± 1.41	0.03
HBsAg level (IU/mL)								
<100	92 (22.6)	118 (22.4)	44 (21.7)	0.72	28 (14.7)	34 (13.4)	10 (13.3)	0.96
100-999	173 (42.5)	222 (42.1)	77 (37.9)		48 (25.3)	59 (23.3)	17 (22.7)	
≥1000	142 (34.9)	187 (35.5)	82 (40.4)		114 (60.0)	160 (63.2)	48 (64.0)	
Mean± SD (log)	2.48 ± 1.06	2.53 ± 0.94	2.52 ± 1.11	0.79	2.89 ± 1.23	2.96 ± 1.24	2.91 ± 1.27	0.85

rs2770 (HLA-B) A>G	AA	AG	GG		AA	AG	GG	
HBV DNA level								
(copies/mL)								
Undetectable	51 (9.5)	81 (17.1)	24 (19.4)	<0.0001	44 (19.3)	51 (22.2)	11 (18.3)	0.15
300-9999	174 (32.3)	183 (38.6)	51 (41.1)		91 (39.9)	112 (48.7)	30 (50.0)	
10000-99999	168 (31.2)	114 (24.1)	34 (27.4)		63 (27.6)	40 (17.4)	11 (18.3)	
100000-999999	110 (20.4)	66 (13.9)	8 (6.5)		19 (8.3)	11 (4.8)	4 (6.7)	
≥100000	36 (6.7)	30 (6.3)	7 (5.7)		11 (4.8)	16 (7.0)	4 (6.7)	
Mean± SD (log)	4.44 ± 1.09	4.25 ± 1.16	4.08 ± 1.16	0.004	4.16 ± 1.04	3.98 ± 1.18	3.97 ± 1.19	0.29
HBsAg level (IU/mL)								
<100	115 (21.3)	114 (24.1)	25 (20.2)	0.20	35 (15.4)	31 (13.5)	6 (10.0)	0.86
100-999	211 (39.2)	204 (43.0)	57 (46.0)		52 (22.8)	57 (24.8)	15 (25.0)	
≥1000	213 (39.5)	156 (32.9)	42 (33.9)		141 (61.8)	142 (61.7)	39 (65.0)	
Mean± SD (log)	2.53 ± 1.04	2.49 ± 0.99	2.50 ± 1.02	0.82	2.93 ± 1.26	2.88 ± 1.29	3.13 ± 0.89	0.36

Supplementary Table 3. Association of genotypes of rs1710 and rs2770 with the seroclearance of HBeAg and HBV DNA in CHB patients

HLA variant	Crude rate ratio (95% CI)	p value	Adjusted rate ratio (95% CI)	p value
Seroclearance of HBeAg				
rs1710 (HLA-G) C>G				
Additive model	0.99 (0.94-1.05)	0.76	1.00 (0.94-1.05)	0.85
rs2770 (HLA-B) A>G				
Additive model	0.98 (0.93-1.04)	0.48	0.98 (0.93-1.04)	0.53
Seroclearance of HBV DNA				
rs1710 (HLA-G) C>G				
Additive model	1.01 (0.93-1.10)	0.79	1.04 (0.95-1.14)	0.38
rs2770 (HLA-B) A>G				
Additive model	1.04 (0.96-1.14)	0.35	0.96 (0.87-1.05)	0.32

^a For association with seroclearance of HBeAg, the rate ratio was adjusted for HBV genotype and serum level of HBV DNA at study entry among HBeAg-seropositive patients. For association with seroclearance of HBV DNA, the rate ratio was adjusted for HBV genotype, and serum levels of HBV DNA and HBsAg at study entry among HBeAg-seronegative patients.