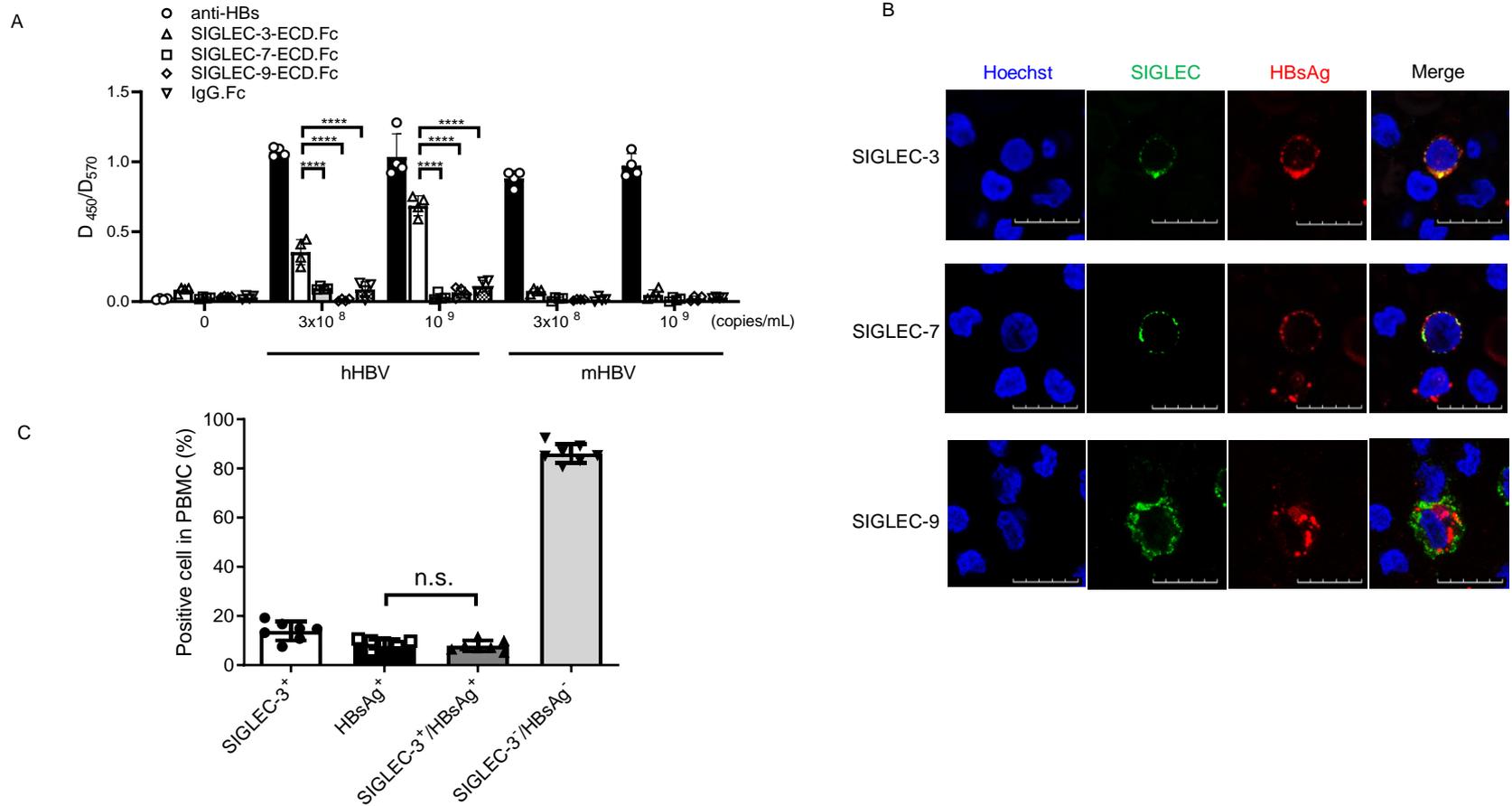


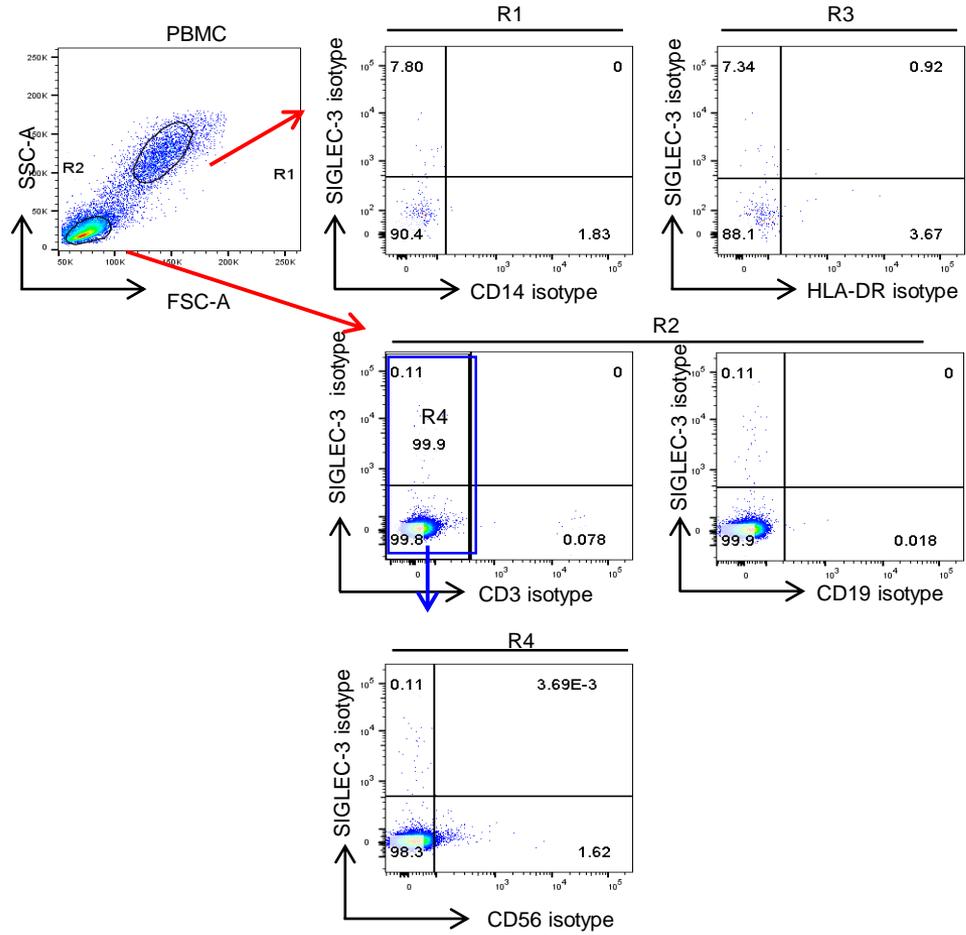
Supplemental Figure 1



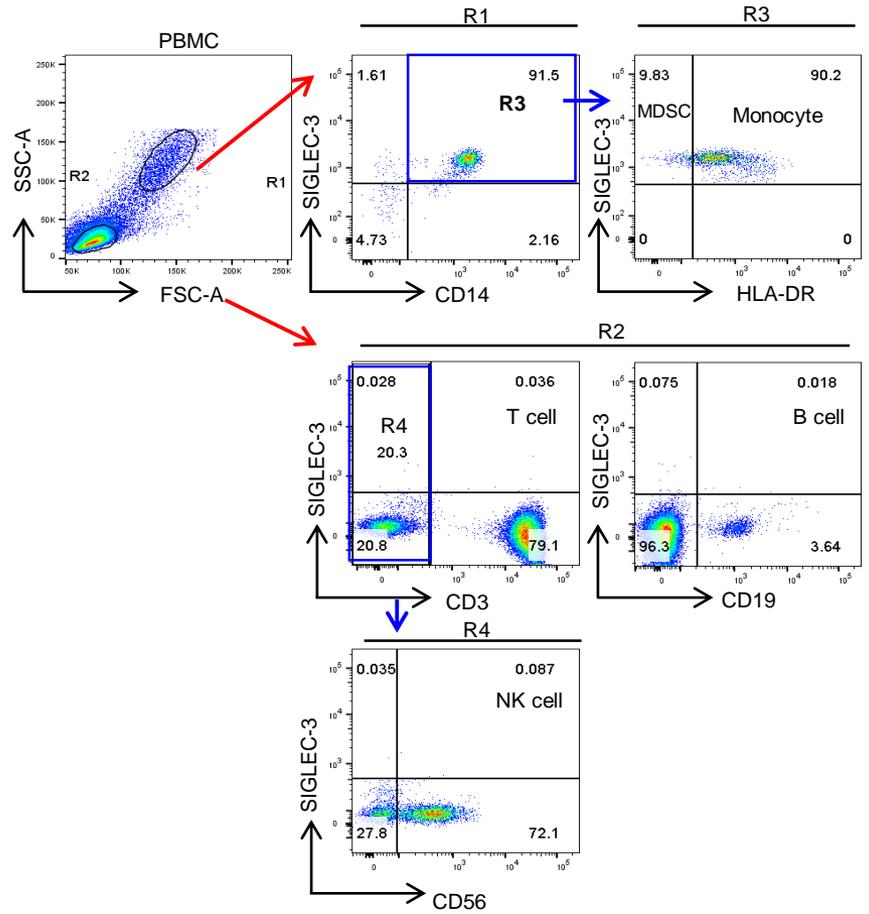
Supplemental Figure 1

(A) Determination of hHBV and mHBV interaction with SIGLEC-ECD.Fc by ELISA (n=4). SIGLEC-ECD.Fc fusion proteins (5 μ g) were coated on microtitre plates, followed by the addition of hHBV or mHBV at 4 $^{\circ}$ C for 12 hr with protein-free blocking buffer. After washing with PBST, HBsAg associated with SIGLEC-ECD.Fc were detected by addition of rabbit anti-HBsAg antibody (RT, 2 hr) and HRP-conjugated anti-rabbit antibody (RT, 2 hr) subsequently, followed by coloration reacting using tetramethylbenzidine (TMB) (One way ANOVA). (B) Co-localization of SIGLEC and hHBV under confocal microscopy (green: SIGLEC, red: HBsAg, blue: Hoechst 33342) Scale bars: 10 μ m. Peripheral blood mononuclear cells were isolated from CHB patients and stained with mouse anti-SIGLEC-3 (NBP2-32819, Novus), rabbit anti-SIGLEC-7 mAb (ab111619, Abcam), or mouse anti-SIGLEC-9 (351502, Biolegend) and goat anti-HBsAg antibodies, followed by incubation with Alexa Fluor 488-conjugated (green) goat anti-mouse mAb or Alexa Fluor 555-conjugated (green) donkey anti-rabbit mAb and Alexa Fluor 647-conjugated (red) donkey anti-goat mAb. (C) The frequency of colocalization of SIGLEC-3 and HBsAg (n = 6-7) were quantified using Metamorph[®] software. Data are expressed as means \pm s.d., n.s.: no significant (One-way ANOVA). (A) (C) are represented in independent samples

A



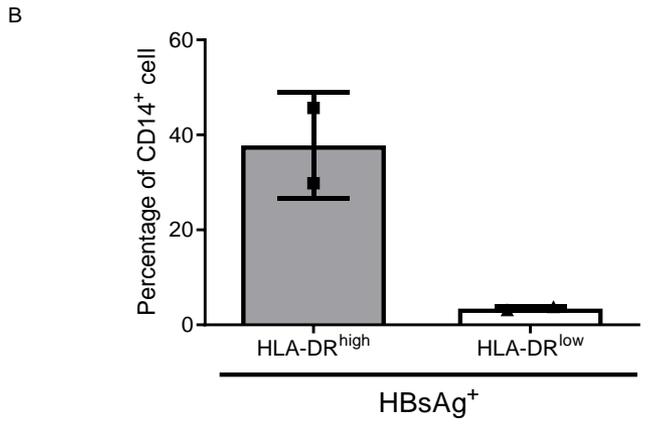
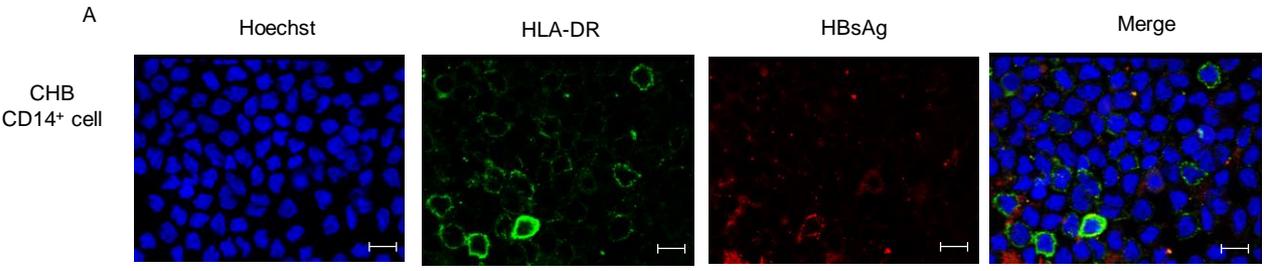
B



Supplemental Figure 2

Characterization of SIGLEC-3 expression in PBMCs. Human PBMCs isolated from healthy donors or CHB patients were stained with different panels of antibodies and SIGLEC-3⁺ cells were analyzed by flow cytometry. (A) The gating strategy of isotype control. (B) The gating strategy is shown in the followings: T cells (CD3⁺ SSC^{low}), B cells (CD19⁺ SSC^{low}), NK cells (CD3⁻ CD56⁺ SSC^{low}), monocytes (CD14⁺ SIGLEC-3⁺ HLA-DR⁺), MDSC (CD14⁺ SIGLEC-3⁺ HLA-DR^{low}). MDSC: Myeloid-derived suppressor cells

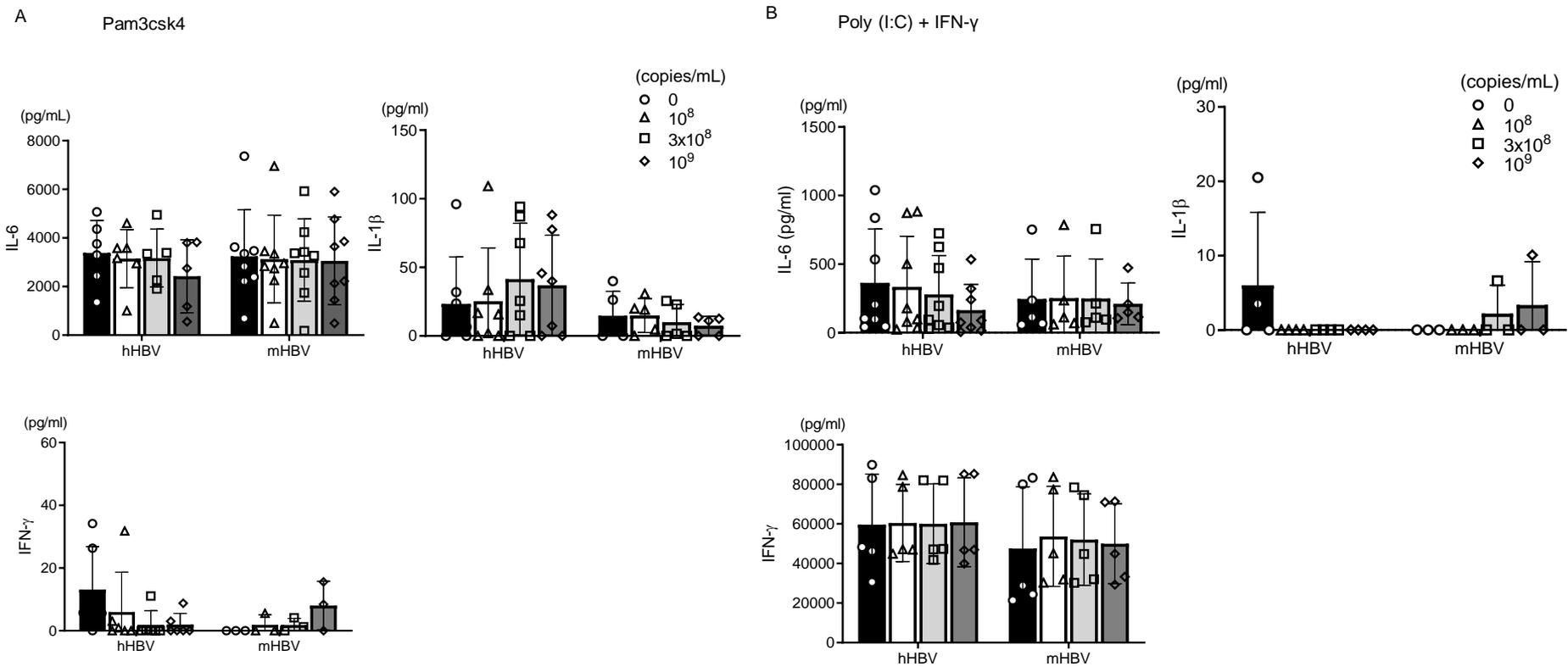
Supplemental Figure 3



Supplemental Figure 3

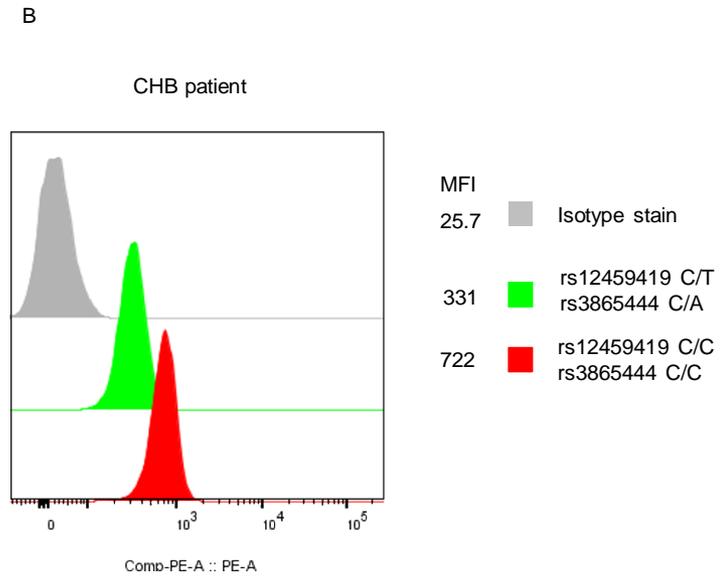
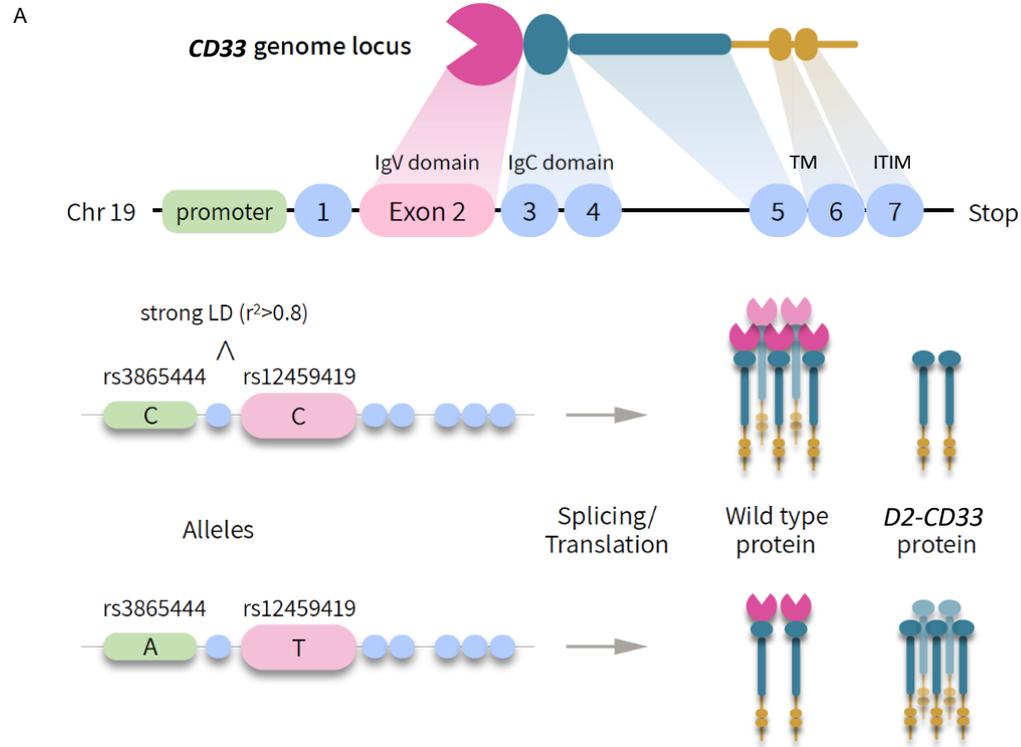
HBV binds to CD14⁺ cells in PBMCs. (A) CD14⁺ cells isolated from fresh blood of CHB patients were incubated with anti-HLA-DR mAb (green), anti-HBsAg mAb (red), and Hoechst 33342 (blue) at 4 °C for 1 hr. The binding of HBsAg on CD14⁺HLA-DR^{high} or CD14⁺HLA-DR^{low} cells was observed under a confocal microscopy (Leica TCS SP8 X). Nucleus: Hoechst (blue), HLA-DR: rabbit anti-HLA-DR mAb (Ab257320) and Alexa Fluor 555-conjugated donkey anti-rabbit mAb (green), HBsAg: goat anti-HBsAg (BS-1557G) and Alexa Fluor 647-conjugated (red) donkey anti-goat mAb. Scale bars: 10 μm. (B) Percentage of CD14⁺HBsAg⁺HLA-DR^{high} and CD14⁺HBsAg⁺HLA-DR^{low} from CHB patients (n=2). The fluorescence intensity was captured under a confocal microscope (LEICA TCX SP8 X) and analyzed by Metamorph® software. HLA-DR^{high} (scale: 5.7-95.3); HLA-DR^{low}: (scale: < 5.7). The percentage of HLA-DR^{high} vs. ^{low} is (89.9% vs. 10.1% counted from 2209 cells). Data are expressed as means ± s.d.

Supplemental Figure 4



Supplemental Figure 4

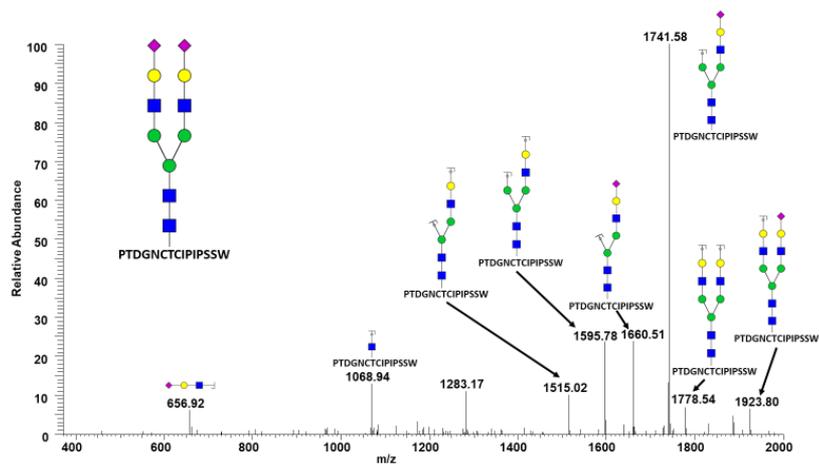
Cytokine secretion in TLR ligand-stimulated moDC under HBV virion incubation. MoDC from healthy donors were pretreated with hHBV or mHBV in different doses for 24 hr before incubation with Pam3csk4 (A) or poly(I:C) and interferon- γ (B) for another 24 hr. Cytokine levels in the supernatant were determined by ELISA. Data are expressed as means \pm s.d.; (Two-way ANOVA) (n=3-8).



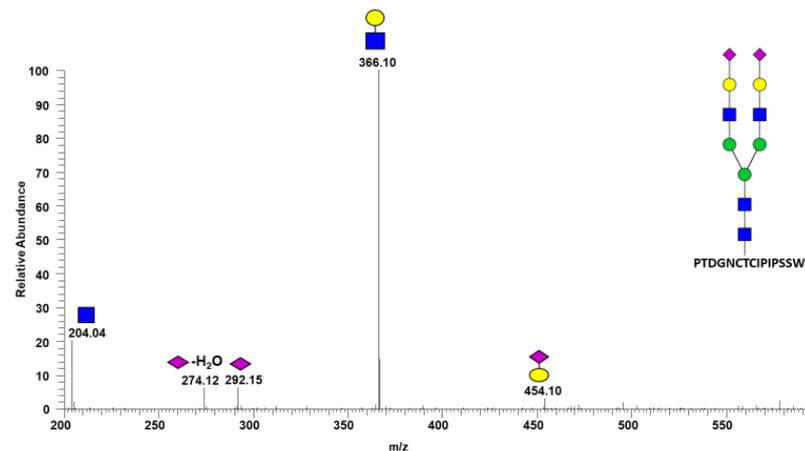
Supplemental Figure 5

Influence of *SIGLEC-3* (*CD33*) polymorphic alleles in the production of wild type and exon-2 skip mutant. There are two types of *SIGLEC-3* monomer. The wild type protein has the IgV sialic acid binding domains (pink), while D2-CD33 protein generated by exon 2-skip does not contain the IgV domain, thereby cannot bind to sialoglycan. Exon 2 skipping efficiency increases in the two co-segregated rs12459419 T allele and rs3865444 A alleles located in the promoter region. LD: Linkage disequilibrium. TM: Transmembrane. ITIM: Immunoreceptor tyrosine-based inhibitory motif. (B) Human PBMCs were isolated from CHB patients with different types of *SIGLEC-3* SNPs rs12459419/rs3865444. Cells were stained with anti-*SIGLEC-3* (clone WM53) and analyzed by FACS. CD14⁺ cells were gated and mean fluorescence intensity (MFI) of *SIGLEC-3* was shown.

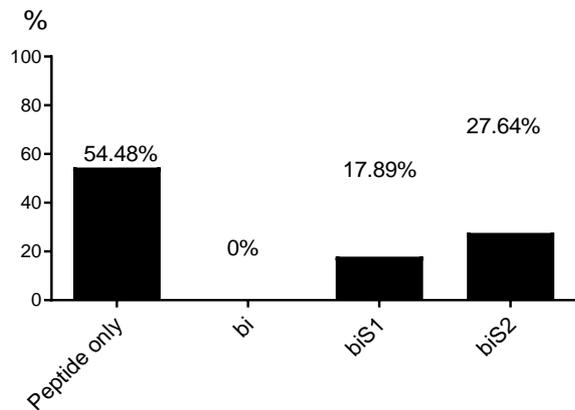
A



B



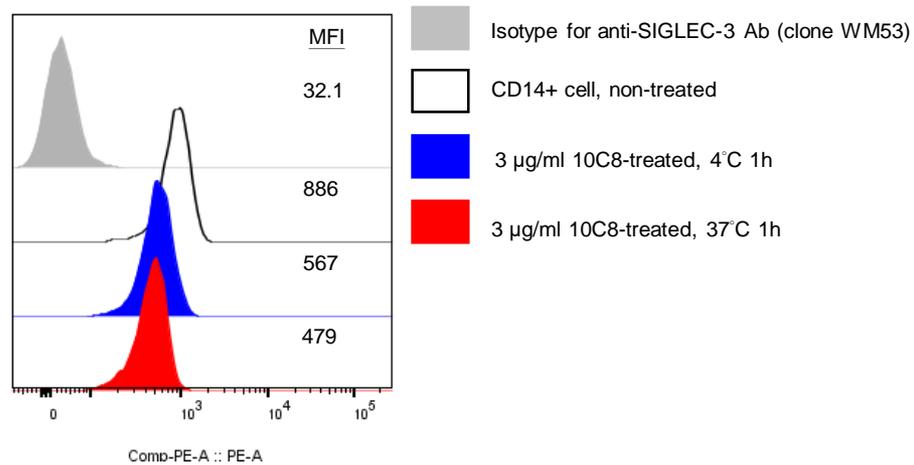
C



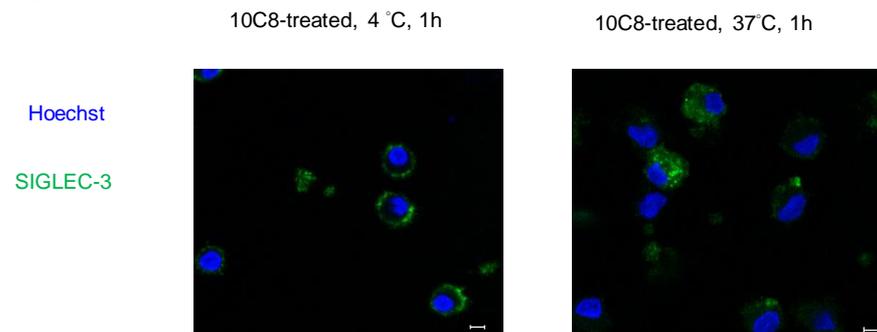
Supplemental Figure 6

Glycans at Asn-146 of HBsAg. (A) Glycan structure at Asn-146 of peptide “P₁₄₂TDGN₁₄₆CTCIPISSW₁₅₆” derived from HBsAg (Genotype B) by Tandem Mass spectrum analysis. ◆ Neu5Ac, ● Galactose, ■ GlcNAc, ● Mannose (B) Determination of Neu5Ac linkage to Galactose by Pseudo-MS³ spectra. (C) Percentage of biantennary sialoglycans in peptide “P₁₄₂TDGN₁₄₆CTCIPISSW₁₅₆” from hHBsAg. bi (biantennary glycan with no terminal Neu5Ac), biS1 (single Neu5Ac), biS2 (two Neu5Ac). Experiments were performed and repeated three times with the same results.

A

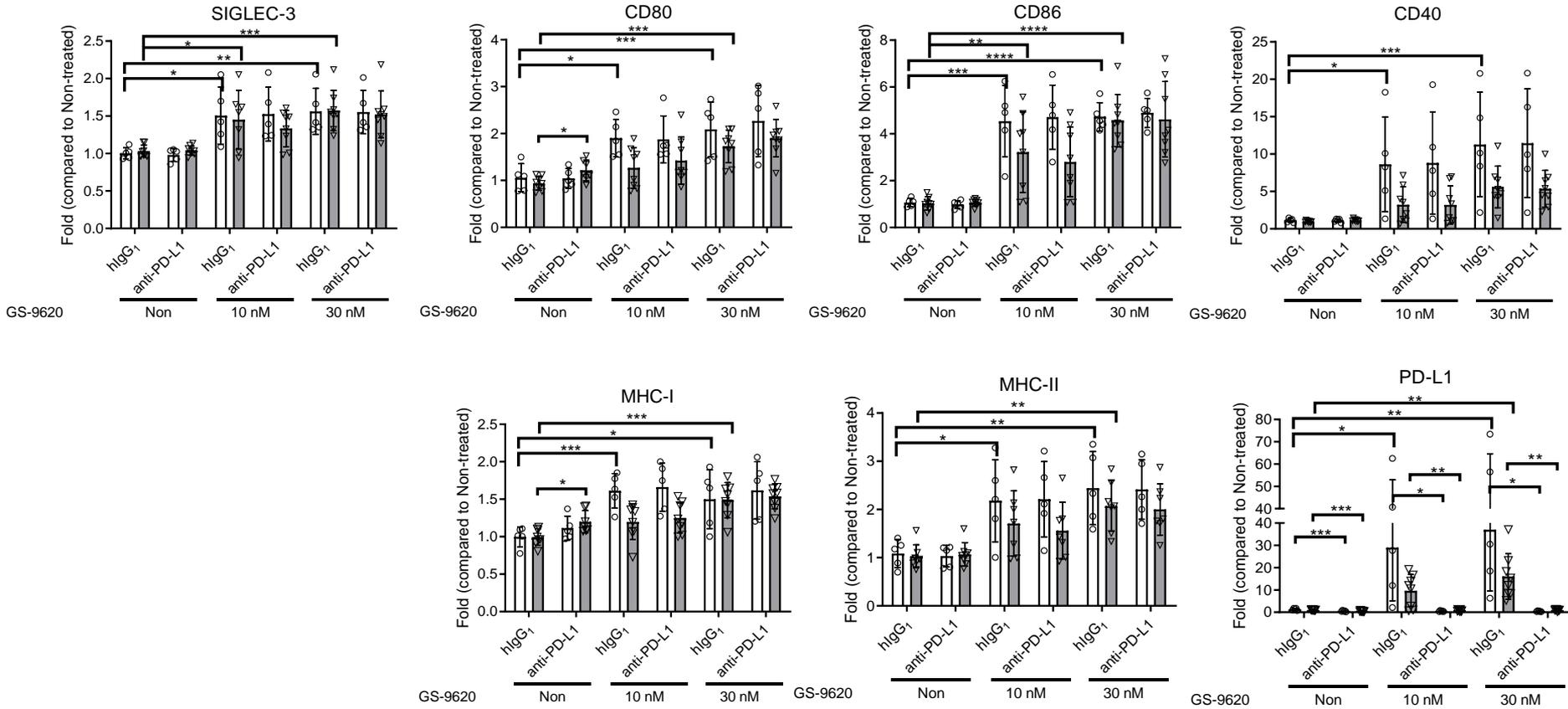


B

**Supplemental Figure 7**

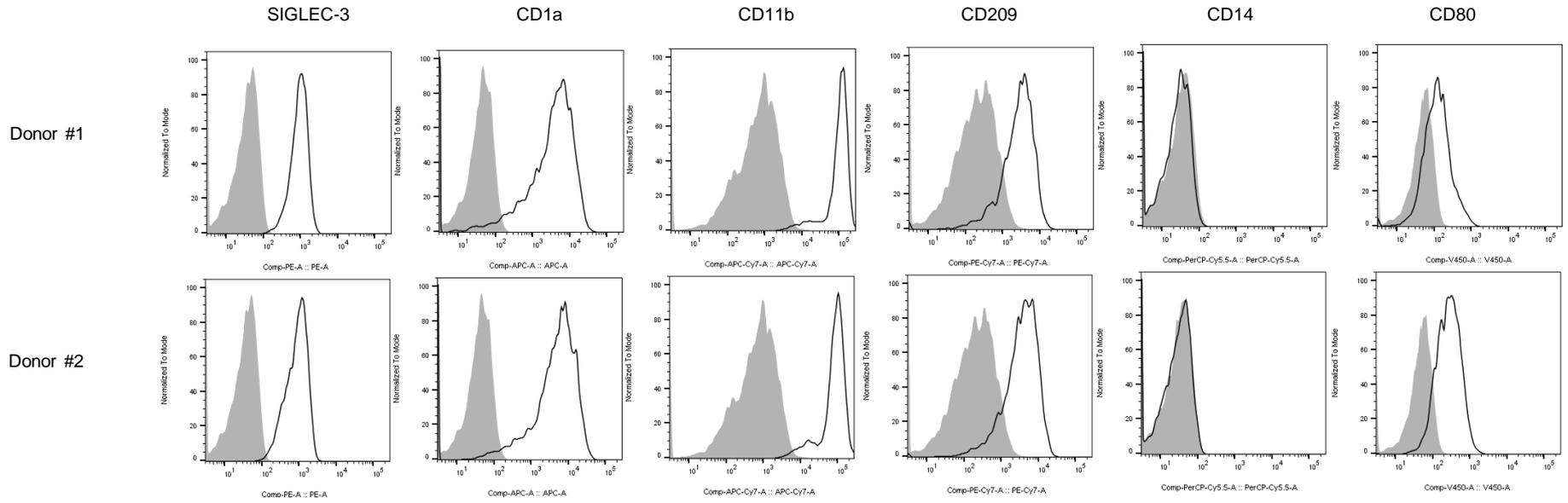
(A) Internalization of SIGLEC-3 by 10C8 in human CD14⁺ monocytes. Human CD14⁺ monocytes isolated from PBMC were incubated on ice 4°C for 15 min then treated with 3 $\mu\text{g/ml}$ of 10C8 and transferred to 37°C or on ice 4°C for another 1h. The cells then were stained with PE-conjugated anti-SIGLEC-3 antibody (clone WM53, Biolegend) and analyzed by FACSVerse. (B) 10C8 induce SIGLEC-3 internalization in human monocyte-derived dendritic cell. Human monocyte-derived dendritic cells were incubated on ice for 15 min then treated with 3 $\mu\text{g/ml}$ 10C8 and transferred to 37°C or on ice for another 1h to examine whether 10C8 induce internalization of surface SIGLEC-3. The cells then were fixed, permeabilized, and stained with Alexa Fluor 647 conjugated goat anti-hIgG (green). Nuclei were visualized with Hoechst (blue). Scale bars: 5 μm . Experiments were performed and repeated three times with the similar results.

○ Healthy donor
 ▼ CHB patient



Supplemental Figure 8

Surface marker expression in PBMC from CHB patients after anti-PD-L1 treatment. PBMCs from healthy donor (n = 5) or CHB patient (n = 7) were pretreated with anti-PD-L1 antibody (Atezolizumab, Roche) or hlgG1 as isotype control (3 µg/ml) for 1 h before 10 nM or 30 nM GS-9620 treatment. 24 h later, cells were resuspended and stained with SIGLEC-3, CD80, CD86, CD40, MHC-I, MHC-II, and PD-L1 antibodies as indicated in materials and methods. Cells were analyzed by flow cytometry and the mean fluorescence intensity of surface marker on CD14⁺ cells were analyzed by FlowJo. All data are expressed as means ± s.d. * p<0.05, ** p<0.01, ***: p<0.001, ****: p<0.0001 (One way ANOVA).



Supplemental Figure 9

Phenotype of CD14⁺ monocyte-derived dendritic cell (moDC) by flow cytometry. CD14⁺ cells isolated from PBMCs were cultured with GM-CSF and IL-4 to differentiate to dendritic cells for 6-7 days. Cells were stained with SIGLEC-3, CD1a, CD11b, CD209, CD14, and CD80 antibodies and analyzed by flow cytometry. Staining results from two healthy donors were shown.

Supplemental Table 1

mHBV			
Immobilized Fc-Lectin (nm)	Ka (1/Ms)	Kd (1/s)	KD (M)
Anti-HBs	8.12 (± 0.01) x 10⁶	2.55 (± 0.29) x 10⁻⁵	3.14 (±0.36) x 10⁻¹²
SIGLEC-3	N/A	N/A	N/A
SIGLEC-7	N/A	N/A	N/A
SIGLEC-9	N/A	N/A	N/A
hIgG₁	N/A	N/A	N/A

Supplemental Table 1. Determination of HBV-SIGLEC.Fc binding affinity by Bio-layer interferometry (BLI).

Kinetic interaction of mHBV virion with SIGLEC-ECD.Fc fusion protein coated on Biosensor (ForteBio) was performed at room temperature and analyzed by Octet® HTX (ForteBio). Binding affinity between SIGLEC-ECD.Fc fusion proteins and mHBV as compared to immobilized anti-HBV antibodies. Ka: Rate constants for the association. Kd: Rate constants for dissociation. KD: Equilibrium dissociation constant. Results are expressed as means ± s.d. from three independent experiments.

Supplemental Table 2

SNP rs12459419

Variables	Univariate analysis		Multivariate analysis	
	Hazard Ratio (95% CI)	P Value	Hazard Ratio (95% CI)	P Value
Age: < 40 vs ≥ 40 years old	0.369 (0.306 – 0.445)	<0.0001	0.299 (0.246 – 0.365)	<0.0001
Gender: Woman vs Man	0.393 (0.330 – 0.467)	<0.0001	0.491 (0.408 – 0.590)	<0.0001
Liver cirrhosis: No vs Yes	0.083 (0.072 – 0.096)	<0.0001	0.161 (0.137 – 0.189)	<0.0001
HBeAg: negative vs positive	0.220 (0.191 – 0.255)	<0.0001	0.550 (0.436 – 0.694)	<0.0001
HBV DNA (log ₁₀ IU/mL)	1.446 (1.401 – 1.493)	<0.0001	1.238 (1.171 – 1.308)	<0.0001
HBsAg (log ₁₀ IU/mL)	1.539 (1.441 – 1.645)	<0.0001	1.041 (0.965 – 0.123)	0.3014
ALT: < 45 vs ≥ 45 IU/L	0.317 (0.258 – 0.388)	<0.0001	0.878 (0.649 – 1.187)	0.3959
AST: < 45 vs ≥ 45 IU/L	0.255 (0.183 – 0.275)	<0.0001	0.892 (0.651 – 1.222)	0.4760
rs12459419: C vs T	1.173 (0.965 – 1.424)	0.1083	1.256 (1.027 – 1.535)	0.0266

SNP rs3865444

Variables	Univariate analysis		Multivariate analysis	
	Hazard Ratio (95% CI)	P Value	Hazard Ratio (95% CI)	P Value
Age: < 40 vs ≥ 40 years old	0.369 (0.306 – 0.445)	<0.0001	0.300 (0.247 – 0.366)	<0.0001
Gender: Woman vs Man	0.398 (0.335 – 0.474)	<0.0001	0.500 (0.417 – 0.601)	<0.0001
Liver cirrhosis: No vs Yes	0.083 (0.072 – 0.096)	<0.0001	0.161 (0.137 – 0.188)	<0.0001
HBeAg: negative vs positive	0.223 (0.193 – 0.257)	<0.0001	0.563 (0.446 – 0.711)	<0.0001
HBV DNA (log ₁₀ IU/mL)	1.447 (1.402 – 1.494)	<0.0001	1.239 (1.172 – 1.309)	<0.0001
HBsAg (log ₁₀ IU/mL)	1.544 (1.444 – 1.649)	<0.0001	1.046 (0.970 – 1.129)	0.2450
ALT: < 45 vs ≥ 45 IU/L	0.318 (0.260 – 0.390)	<0.0001	0.877 (0.648 – 1.186)	0.3931
AST: < 45 vs ≥ 45 IU/L	0.224 (0.183 – 0.275)	<0.0001	0.888 (0.648 – 1.218)	0.4627
rs3865444: C vs A	1.164 (0.957 – 1.416)	0.1280	1.251 (1.022 – 1.532)	0.0303

Supplemental Table 2. Association of factors with HCC incidence in patients with CHB

Association factors include age, gender, LC, HBeAg, baseline serum level of HBV DNA, baseline serum level of HBsAg, baseline serum level of ALT, baseline serum level of AST, SNP rs12459419, and rs3865444.

The incidence of HCC were analyzed by multivariate Cox proportional hazard regression analysis.

Supplemental Table 3

SNP rs12459419

Variables	Univariate analysis		Multivariate analysis	
	Hazard Ratio (95% CI)	P Value	Hazard Ratio (95% CI)	P Value
Age: < 40 vs ≥ 40 years old	0.539 (0.458 – 0.635)	<0.0001	0.436 (0.368 – 0.517)	<0.0001
Gender: Woman vs Man	0.372 (0.314 – 0.441)	<0.0001	0.394 (0.330 – 0.469)	<0.0001
HBeAg: negative vs positive	0.297 (0.257 – 0.342)	<0.0001	0.758 (0.608 – 0.945)	0.0139
HBV DNA(log ₁₀ IU/mL)	1.351 (1.312 – 1.391)	<0.0001	1.285 (1.223 – 1.350)	<0.0001
HBsAg (log ₁₀ IU/mL)	1.367 (1.291 – 1.447)	<0.0001	1.012 (0.947 – 1.082)	0.7146
ALT: < 45 vs ≥ 45	0.296 (0.244 – 0.359)	<0.0001	0.772 (0.580 – 1.029)	0.0775
AST: < 45 vs ≥ 45 IU/L	0.237 (0.195 – 0.289)	<0.0001	0.629 (0.464 – 0.851)	0.0026
rs12459419: C vs T	0.995 (0.833 – 1.187)	0.9541	1.043 (0.870 – 1.250)	0.6503

SNP rs3865444

Variables	Univariate analysis		Multivariate analysis	
	Hazard Ratio (95% CI)	P Value	Hazard Ratio (95% CI)	P Value
Age: < 40 vs ≥ 40 years old	0.543 (0.461 – 0.639)	<0.0001	0.437 (0.369 – 0.518)	<0.0001
Gender: Woman vs Man	0.374 (0.315 – 0.443)	<0.0001	0.400 (0.336 – 0.476)	<0.0001
HBeAg: negative vs positive	0.300 (0.260 – 0.346)	<0.0001	0.774 (0.621 – 0.965)	0.0228
HBV DNA(log ₁₀ IU/mL)	1.350 (1.311 – 1.390)	<0.0001	1.286 (1.224 – 1.351)	<0.0001
HBsAg (log ₁₀ IU/mL)	1.369 (1.293 – 1.450)	<0.0001	1.017 (0.951 – 1.087)	0.6302
ALT: < 45 vs ≥ 45	0.296 (0.244 – 0.359)	<0.0001	0.769 (0.577 – 1.025)	0.0769
AST: < 45 vs ≥ 45 IU/L	0.237 (0.195 – 0.289)	<0.0001	0.628 (0.464 – 0.851)	0.0026
rs3865444: C vs A	1.001 (0.837 – 1.197)	0.9895	1.061 (0.883 – 1.275)	0.5271

Supplemental Table 3. Association of factors with liver cirrhosis incidence in patients with CHB

Association factors include age, gender, HBeAg, baseline serum level of HBV DNA, baseline serum level of HBsAg, baseline serum level of ALT, baseline serum level of AST, SNP rs12459419, and rs3865444. The incidence of liver cirrhosis were analyzed by multivariate Cox proportional hazard regression analysis.

Supplemental Table 4

SNP rs12459419

Variables	Total	rs12459419 (T/T)	rs12459419 (C/T)	rs12459419 (C/C)	P Value
Median ± IQR or N (%)	3554 (100%)	141 (3.97%)	1000 (28.14%)	2413 (67.90%)	
Age	45 ± 17	44 ± 16	44 ± 17	45 ± 17	0.1000^A
Gender					0.0983^C
Man	2189 (61.59%)	85 (60.28%)	644 (64.40%)	1460 (60.51%)	
Woman	1365 (38.41%)	56 (39.72%)	356 (35.60%)	953 (39.49%)	
Genotype					0.1222^C
B	1686 (47.43%)	58 (42.34%)	477 (50.11%)	1151 (49.87%)	
C	908 (25.54%)	48 (35.04%)	255 (26.79%)	605 (26.21%)	
B&C	95 (2.67%)	1 (0.73%)	33 (3.47%)	61 (2.64%)	
HBeAg					0.3323^C
No	3010 (84.69%)	113 (80.14%)	850 (85%)	2047 (84.83%)	
Yes	544 (15.31%)	28 (19.86%)	150 (15%)	366 (15.17%)	
HBV DNA(log₁₀ IU/mL)	3.69 ± 2.58	3.76 ± 5.15	3.73 ± 2.60	3.68 ± 2.57	0.9564^A
HBsAg (log₁₀ IU/mL)	2.86 ± 1.52	3.05 ± 1.47	2.82 ± 1.49	2.87 ± 1.54	0.4660^A
ALT: IU/L	12 ± 14	12 ± 11	13 ± 14	12 ± 14	0.7497^A
AST: IU/L	15 ± 10	15 ± 11	16 ± 9	15 ± 10	0.6681^A
Cirrhosis					0.9693^C
No	3146 (88.51%)	125 (88.65%)	882 (88.20%)	2135 (88.48%)	
Yes	412 (11.59%)	16 (11.35%)	118 (11.80%)	278 (11.52%)	
HCC					0.3403^C
No	3177 (87.70%)	129 (91.49%)	903 (90.30%)	2145 (88.89%)	
Yes	377 (10.60%)	12 (8.51%)	97 (9.70%)	268 (11.11%)	
Average age of LC diagnosed	54 ± 14	52 ± 11	55 ± 14	54 ± 15	0.9927^A
Average age of HCC diagnosed	63 ± 13	64 ± 12	63 ± 13	63 ± 14	0.7289^A

A: ANOVA test and C: Chi-squared test.

SNP: rs3865444

Variables	Total	rs3865444 (A/A)	rs3865444 (C/A)	rs3865444 (C/C)	P Value
Median ± IQR or N (%)	3555 (100%)	138 (3.89%)	979 (27.66%)	2438 (68.45%)	
Age	45 ± 17	44 ± 16	44 ± 18	45 ± 17	0.1546 ^A
Gender					0.1472 ^C
Man	2187 (61.52%)	86 (62.32%)	627 (64.04%)	1474 (60.46%)	
Woman	1368 (38.48%)	52 (37.68%)	352 (35.96%)	964 (39.54%)	
Genotype					0.2743 ^C
B	1686 (49.62%)	58 (43.28%)	467 (50.05%)	1161 (49.81%)	
C	909 (26.75%)	43 (32.09%)	256 (27.44%)	610 (26.17%)	
B&C	95 (2.80%)	2 (1.49%)	32 (3.43%)	61 (2.62%)	
HBeAg					0.3747 ^C
No	3012 (84.73%)	111 (80.43%)	829 (84.68%)	2072 (84.99%)	
Yes	543 (15.27%)	27 (19.57%)	150 (15.32%)	366 (15.01%)	
HBV DNA(log ₁₀ IU/mL)	3.69 ± 2.58	3.88 ± 2.58	3.73 ± 2.64	3.67 ± 2.56	0.8214 ^A
HBsAg (log ₁₀ IU/mL)	2.86 ± 1.52	3.05 ± 1.53	2.84 ± 1.49	2.87 ± 1.53	0.7316 ^A
ALT: IU/L	12 ± 14	12 ± 14	13 ± 14	12 ± 14	0.7807 ^A
AST: IU/L	15 ± 10	15 ± 10	16 ± 9	15 ± 10	0.5877 ^A
Cirrhosis					0.9979 ^C
No	3143 (88.41%)	122 (88.41%)	865 (88.36%)	2156 (88.43%)	
Yes	412 (11.59%)	16 (11.59%)	114 (11.64%)	282 (11.57%)	
HCC					0.3797 ^C
No	3178 (89.40%)	126 (91.30%)	884 (90.30%)	2168 (88.93%)	
Yes	377 (10.60%)	12 (8.70%)	95 (9.70%)	270 (11.07%)	
Average age of LC diagnosed	54 ± 14	53 ± 11	55 ± 14	54 ± 15	0.9956 ^A
Average age of HCC diagnosed	63 ± 13	64 ± 13	63 ± 13	63 ± 14	0.7099 ^A

A: ANOVA test and C: Chi-squared test

Supplemental Table 4. Baseline patient characteristics

Baseline patient characteristics of patients with CHB enrolled from the REVEAL-HBV database. A: ANOVA test. C: Chi-squared test.

Supplemental Table 5

PBMC	Antibody (3 µg/ml)	GS-9620	CHB	CHB	P value
			rs12459419 C/C rs3865444 C/C (n = 5)	rs12459419 C/T rs3865444 C/A (n = 2)	
Fold change of SIGLEC-3 MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	0.17 ± 0.03	0.18 ± 0.01	0.8523
		10 nM	0.17 ± 0.04	0.13 ± 0.03	0.6638
		30 nM	0.11 ± 0.03	0.14 ± 0.01	0.3272
Fold change of CD80 MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	1.25 ± 0.03	1.32 ± 0.02	0.1433
		10 nM	1.31 ± 0.1	1.17 ± 0.02	0.6789
		30 nM	1.14 ± 0.08	1.06 ± 0.02	0.7899
Fold change of CD86 MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	2.12 ± 0.11	1.47 ± 0.02	0.0036**
		10 nM	1.83 ± 0.37	1.1 ± 0.13	0.1192
		30 nM	1.22 ± 0.15	0.9 ± 0.13	0.1930
Fold change of CD40 MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	1.38 ± 0.15	1.17 ± 0.06	0.2381
		10 nM	1.54 ± 0.25	1.23 ± 0.32	0.4987
		30 nM	1.94 ± 0.43	1.00 ± 0.03	0.0952
Fold change of MHC-I MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	1.2 ± 0.03	1.19 ± 0.07	0.9149
		10 nM	1.25 ± 0.10	1.06 ± 0.11	0.3092
		30 nM	1.11 ± 0.04	1.05 ± 0.11	0.6829
Fold change of MHC-II MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	2.17 ± 0.33	1.49 ± 0.01	0.1095
		10 nM	1.73 ± 0.36	1.16 ± 0.06	0.1891
		30 nM	1.94 ± 0.43	0.91 ± 0.03	0.0735
Fold change of PD-L1 MFI after 10C8 treatment (compared to hIgG1-treated)		0 nM	2.66 ± 1.13	1.28 ± 0.28	0.2980
		10 nM	3.2 ± 1.52	1.19 ± 0.06	0.2572
		30 nM	2.27 ± 0.57	1.01 ± 0.06	0.0919

Supplemental Table 5. Surface marker expression of CD14⁺ cell from CHB patients with different *SIGLEC-3* SNPs rs12459419/rs3865444

Fold change of cell surface marker (SIGLEC-3, CD80, CD86, MHC-I, MHC-II, PD-L1 and CD40) expression of CD14⁺ cells from CHB patients' PBMCs with major allele (rs12459419 C/C/rs3865444 C/C) versus minor allele (rs12459419 C/T /rs3865444C/A). Samples were treated with 10C8 in the presence or absence of GS-9620.

Supplemental Table 6

PBMC	Antibody (3 µg/ml)	GS-9620	CHB	CHB	P value
			rs12459419 C/C rs3865444 C/C (n = 6)	rs12459419 C/T rs3865444 C/A (n = 2)	
Fold change of IFN- α after 10C8 treatment		10 nM	1.00 \pm 0.00	0.95 \pm 0.42	0.9264
		30 nM	2.10 \pm 0.40	0.38 \pm 0.38	0.0641
Fold change of TNF- α after 10C8 treatment		10 nM	1.49 \pm 0.58	0.39 \pm 0.00	0.1164
		30 nM	1.91 \pm 0.18	0.87 \pm 0.42	0.2034
Fold change of IL-6 after 10C8 treatment		10 nM	0.67 \pm 0.25	1.68 \pm 1.06	0.5109
		30 nM	2.48 \pm 0.81	0.91 \pm 0.05	0.1104
Fold change of IP-10 after 10C8 treatment		10 nM	6.36 \pm 3.91	1.00 \pm 0.00	0.2288
		30 nM	1.22 \pm 0.17	1.11 \pm 0.32	0.7959

Supplemental Table 6. Cytokine level of PBMCs from CHB patients with different *SIGLEC-3* SNPs rs12459419/rs3865444

Fold change of cytokine levels (IFN- α , TNF- α , IL-6 and IP-10) from CHB patients' PBMCs with major allele (rs12459419 C/C/rs3865444 C/C) versus minor allele (rs12459419 C/T /rs3865444C/A). Samples were treated with 10C8 in the presence or absence of GS-9620.

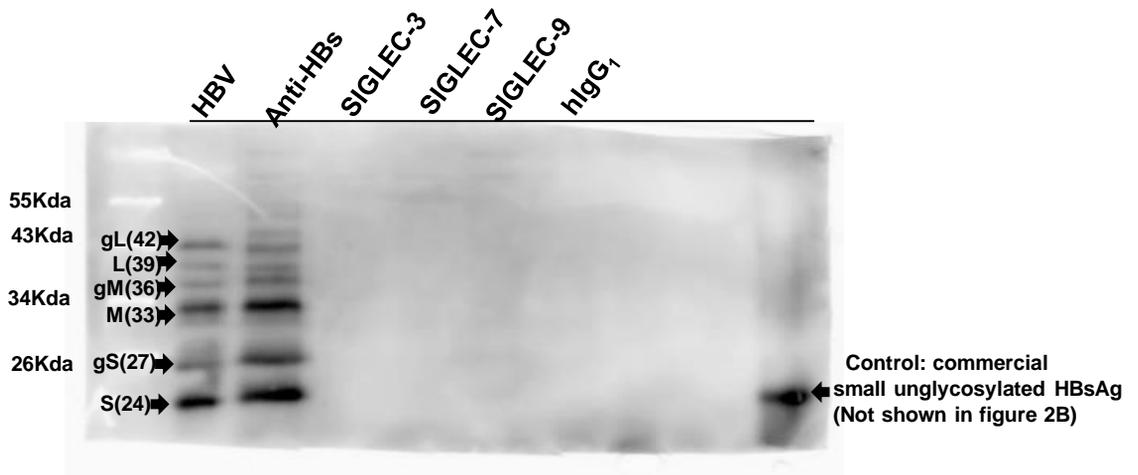
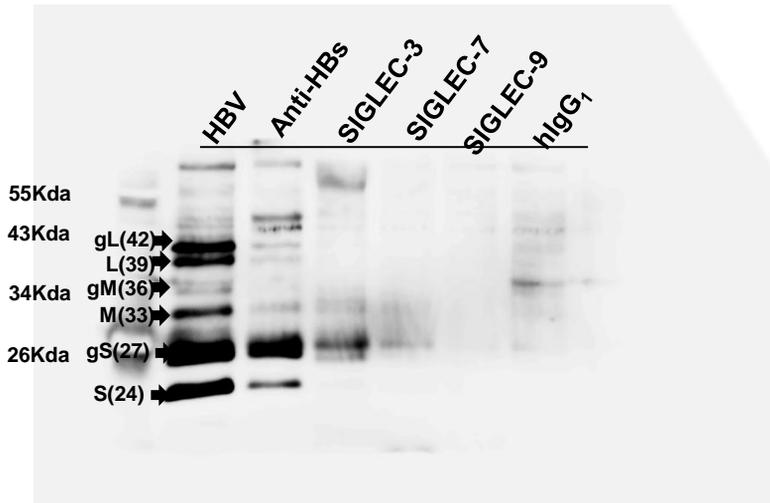
Supplemental Table 7

Antibodies	Fluorescence	Clone	Company	Cata #
CD11b	APC-Cy7	M1/70	Biolegend	101226
CD14	APC-Cy7	63D3	Biolegend	367108
CD14	PerCP-Cy5.5	M5E2	Biolegend	301824
CD19	PE	HIB19	Biolegend	302208
CD1a	APC	HI149	BD	559775
CD209	PE-Cy7	9E9A8	Biolegend	330114
CD3	APC	HIT3a	Biolegend	300306
CD40	PerCP-Cy5.5	5C3	Biolegend	334316
CD56	Alexa Fluor 488	B159	BD	561905
CD80	Brilliant Violet 421	2D10	Biolegend	305222
CD86	PE-Cy7	BU63	Biolegend	374210
HBsAg	unconjugated	polyclonal	Bioss	BS-1557G
HBsAg	HRP	polyclonal	Bioss	BS-1557G-HRP
HLA-DR	unconjugated	polyclonal	Abcam	Ab257320
HLA-DR	APC	L243	Biolegend	307610
MHC-I	Brilliant Violet 510	W6/32	Biolegend	311436
MHC-II	FITC	Tü39	Biolegend	361706
PD-L1	APC	29E.2A3	Biolegend	329922
SHP-1	unconjugated	polyclonal	Cell Signaling Technology	3759S
SHP-2	unconjugated	polyclonal	Cell Signaling Technology	3397S
SIGLEC-3	unconjugated	6C5/2	R&D systems	MAB1137
SIGLEC-3	unconjugated	C33/68	Novus	NBP2-32819
SIGLEC-3	APC	6C5/2	R&D systems	FAB1137A
SIGLEC-3	PE	WM53	Biolegend	303404
SIGLEC-3	PerCP-Cy5.5	WM53	Biolegend	303414
SIGLEC-7	unconjugated	polyclonal	Novus	AF1138
SIGLEC-7	unconjugated	194212	R&D systems	MAB1138
SIGLEC-7	unconjugated	polyclonal	Abcam	ab111619
SIGLEC-9	unconjugated	191240	R&D systems	MAB1139
SIGLEC-9	unconjugated	polyclonal	R&D systems	AF1139
SIGLEC-9	unconjugated	K8	Biolegend	351502
GAPDH	unconjugated	6C5	Sigma	MAB374
Donkey anti-	Alexa Fluor	polyclonal	Thermo	A-11056

Goat IgG (H+L)	546		Scientific	
Donkey anti-mouse (H+L)	Alexa Fluor 647	polyclonal	Abcam	ab150107
Goat anti-mouse (H+L)	Alexa Fluor 488	polyclonal	Abcam	ab150113
Donkey anti-Rabbit IgG (H+L)	Alexa Fluor 555	polyclonal	Thermo Scientific	A-31572
Streptavidin-HRP			Sigma	RABHRP3

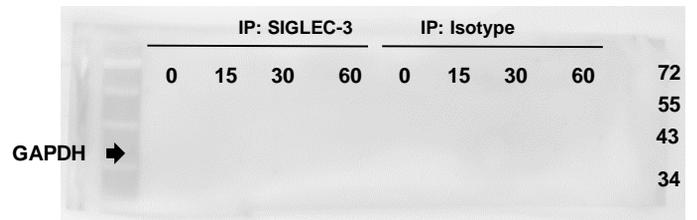
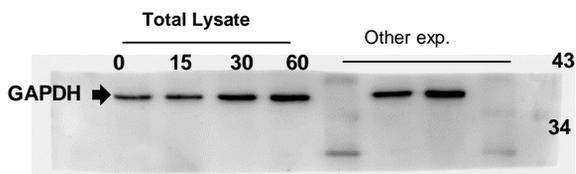
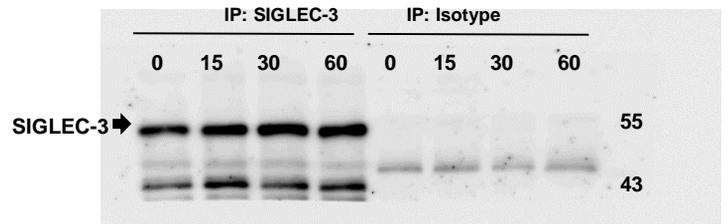
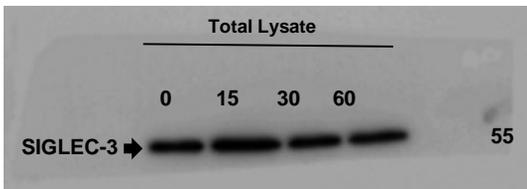
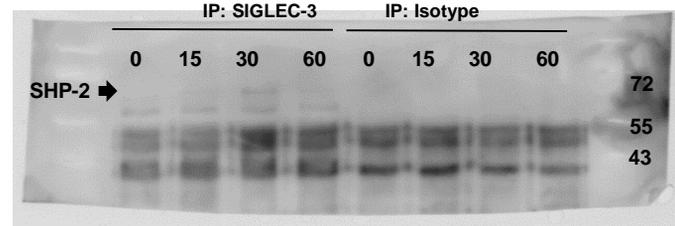
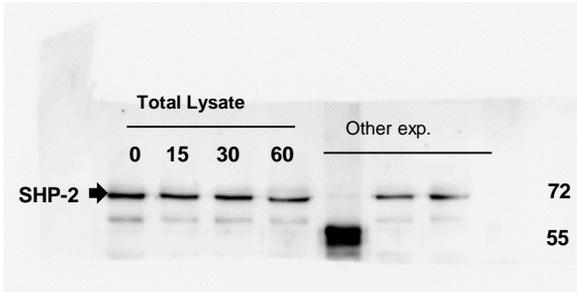
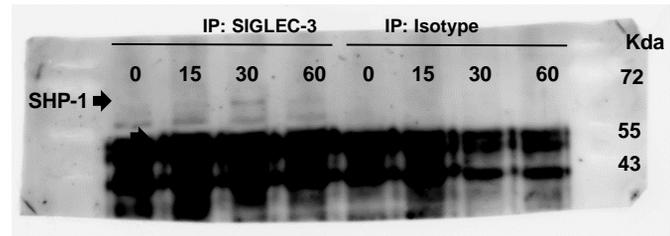
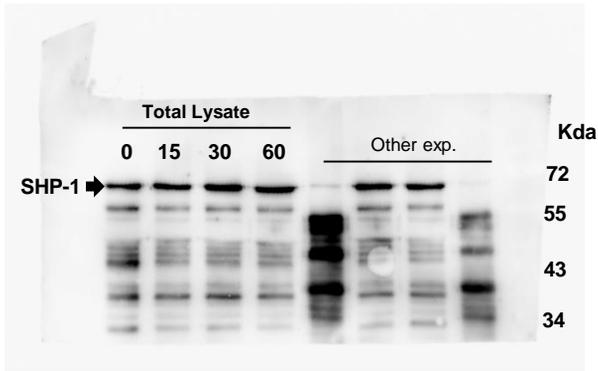
Supplemental Table 7. Antibody list

Full unedited gel for Figure 2A and 2B



gL: glycosylated large HBsAg
 L: Large HBsAg
 gM: glycosylated middle HBsAg
 M: Middle HBsAg
 gS: glycosylated small HBsAg
 S: Small HBsAg

Full unedited gel for Figure 4C



Full unedited gel for Figure 5F

