Supplemental Table 1. Patient characteristics for population analysis

	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNA[a] (IU/ml)	ALT (U/L)	HBeAg+
Healthy	12	10/2	40	9/3	NT	NT	NT
HBV Low	14	9/5	45	11/3	3.17E+04	54	6/14
HBV High	14	9/5	37	11/3	1.88E+08	115	14/14

[a] Data expressed as Median
NT = not tested

Supplemental table 2. Patient characteristics for MLR experiments

	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNA[a] (IU/ml)	ALT (U/L)	HBeAg+
Healthy	5	3/2	39	4/1	NT	NT	NT
HBV Low	5	3/2	50	5/0	4.24E+03	43	0/5
HBV High	5	3/2	43	5/0	2.54E+08	63	5/5
Flare	5	5/0	43	5/0	1.40E+06	620	4/1

[a] Data expressed as Median
NT = not tested

Supplemental table 3. Patient characteristics for CD14 MN HBsAg staining

	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNA[a] (IU/ml)	ALT (U/L)	HBeAg+
Healthy	11	9/2	40	8/3	NT	NT	NT
HBsAg+	12	11/1	43	10/2	3.00E+04	114	2/12
HBsAg-	7	6/1	45	5/2	9.31E+05	59	4/7

[a] Data expressed as Median
NT = not tested

Supplemental table 4. Patient characteristics for ex vivo cross-presentation

	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNA[a] (IU/ml)	ALT (U/L)	HBeAg+
Healthy	4	4/0	44	2/2	NT	NT	NT
HBV	7	4/3	41	1/6	1.45E+06	79	4/7

[a] Data expressed as Median
NT = not tested

Supplemental table 5. Patient characteristics for moDC cross-presentation experiments

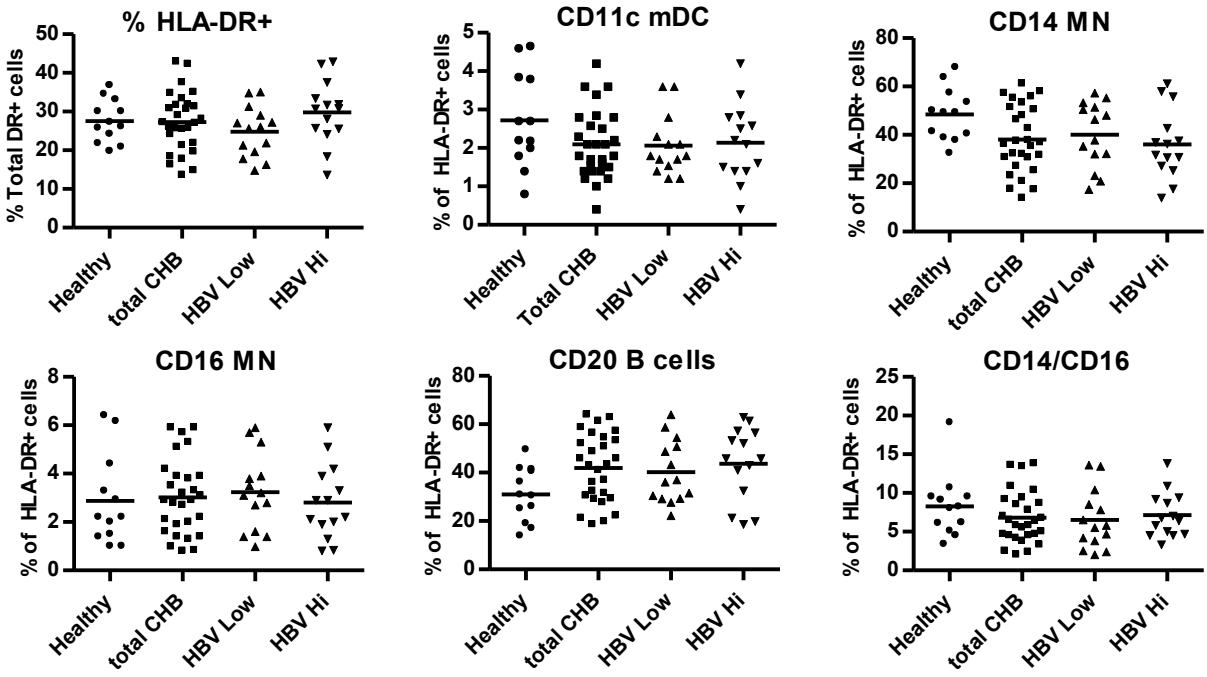
	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNA[a] (IU/ml)	ALT (U/L)	HBeAg+
Healthy	4	4/0	43	2/2	NT	NT	NT
HLA mismatch	5	4/1	35	5/0	1.63E+03	65	1/5
HLA match	9	8/1	42	4/5	9.63E+03	78	2/9

[a] Data expressed as Median
NT = not tested

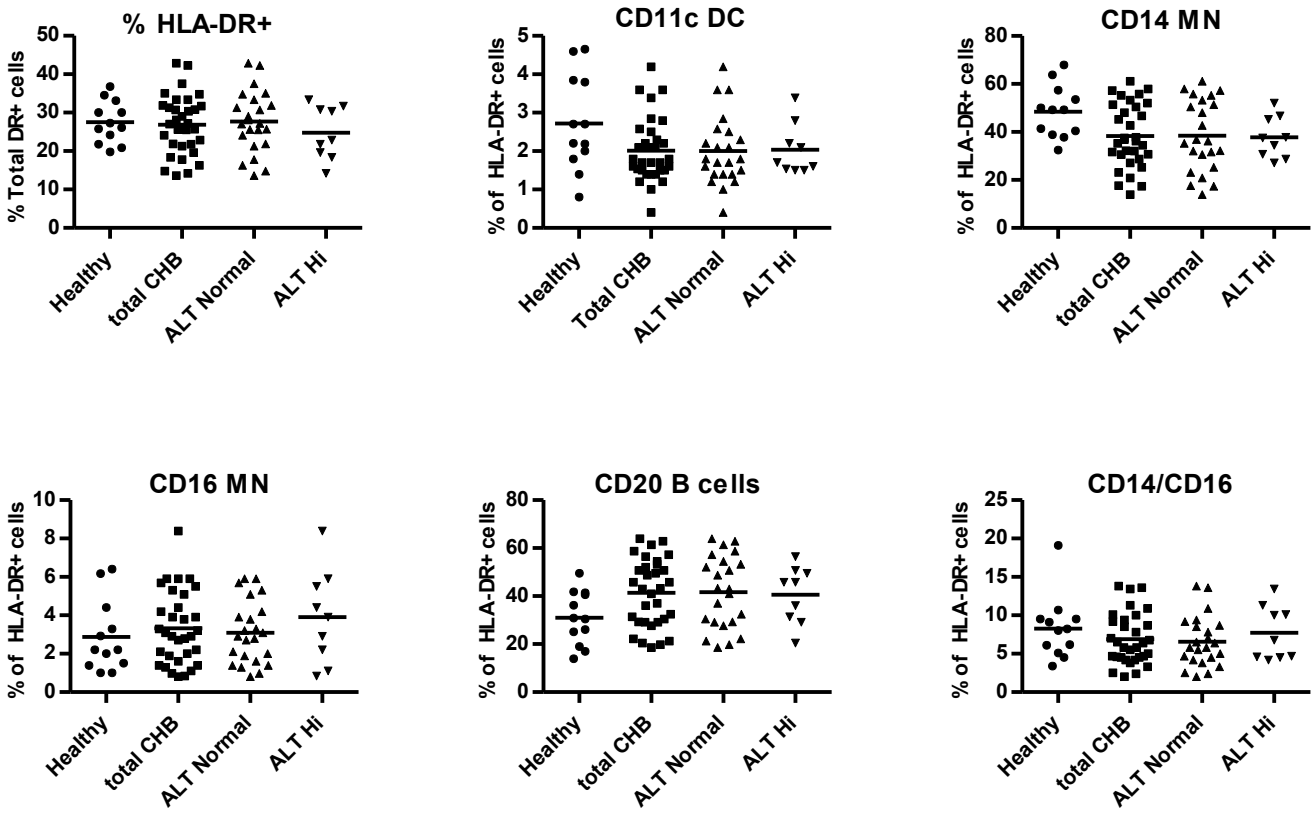
Supplemental Table 6. Patient characteristics for autolgous expansion

	Number	Gender (M/F)	Age (mean)	Ethnicity (Asian/Caucasian)	HBV DNAa (IU/ml)	ALT (U/L)	HBeAg+
Peptide Responder	16	13/3	46.3	10/6	1158	45	5/16
Peptide non-responder	4	2/2	51.7	1/3	200	23	1/4
4-DC responder	6	4/2	43.3	5/1	94.5	35.5	2/6
4-DC non-responder	14	13/3	49.2	6/8	12965	43.2	4/14
15-DC responder	7	6/1	48	5/2	8700	44.8	4/7
15-DC nonresponder	7	6/1	46.7	3/4	1158	52.1	2/7

[a] Data expressed as Median

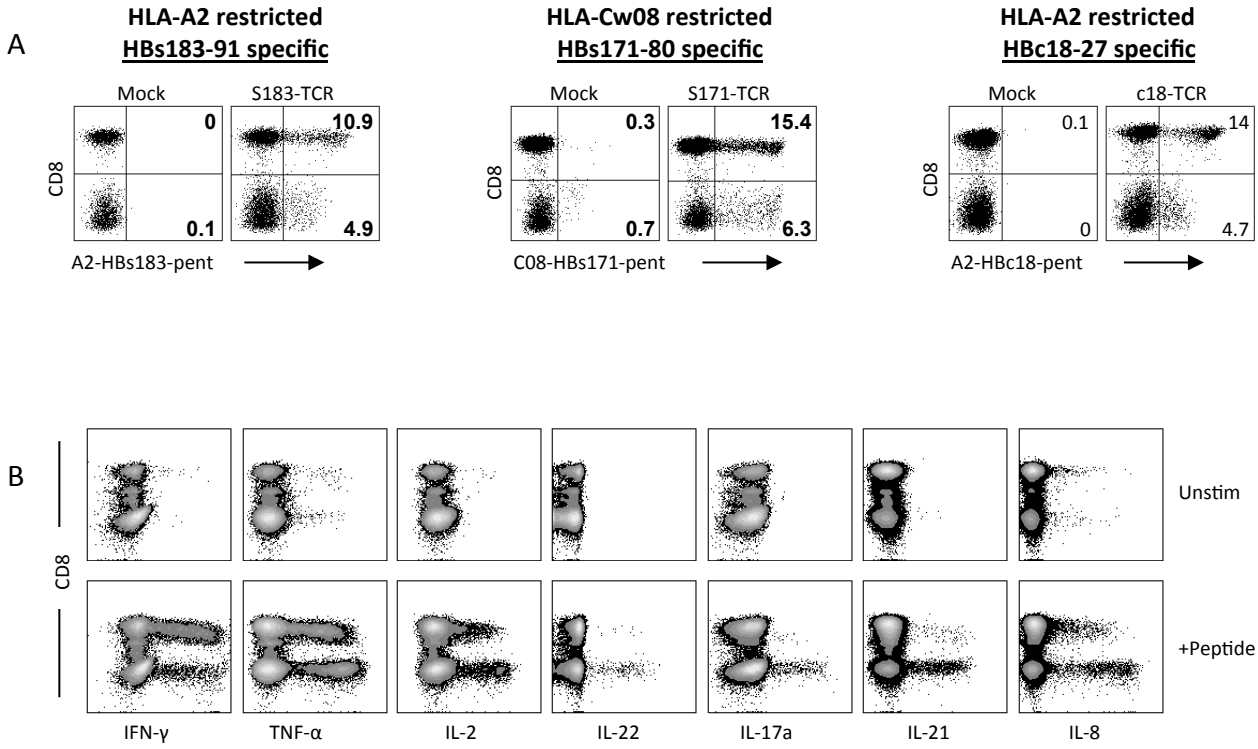


Supplemental Figure 1. Frequency of APC populations are not significantly affected by by viral load. Frequency of HLA-DR+ cells in the total PBMC and the frequency of specific APC populations as a proportion of the HLA-DR+ cells. Patients were categorized based on the level of HBV DNA; HBV low ≤ 10^6 copies/ml and HBV hi > 10^6 copies/ml. There were no statistically significant difference determined by 1 way ANOVA and Tukey post-test analysis.



Supplemental Fig 2. Frequency of APC populations are not significantly affected by liver inflammation. The frequency of total HAL-DR+ cells were calculated for each healthy donor and chronic HBV patient. The different APC populations were then calculated as a percentage of the total HLA-DR+ cells to normalize between patients. Chronic HBV patients were segregated based on the level of alanine amino transferase (ALT) in their serum, an enzyme released upon liver damage and inflammation. Patients were grouped into ALT normal and ALT high; defined as >120 U/L or greater than 2 times upper limit of normal (≤40 U/L). There were no statistically significant difference determined by 1 way ANOVA and Tukey post-test analysis.

Supplemental Fig 2. Gehring et al.



Supplemental Fig 3. Characterization of the HBV-specific T cell receptor (TCR) redirected T cells used for functional cross-presentation assays. A) Primary human T cells from a single healthy donor were transduced with either HLA-A2 restricted HBs183-91- (s183-TCR) or HBc18-27-specific (c18-TCR) or HLA-Cw08 restricted HBs171-80-specific (s171-TCR) TCRs. TCR expression was monitored using matching HLA-A2 pentamers (s183-TCR & c18-TCR) and HLA-C08 tetramers kindly provided by Gijsbert Grotenbreg at the National University of Singapore. Clear pentamer/tetramer positive populations were evident, compared to mock transduced T cells, for all three TCRs. B) Functional profile of s183-TCR T cells. S183-TCR T cells were stimulated overnight with HLA-A2+ T2 loaded with 1 µg/ml HBs183-91 peptide in the presence of 2 µg/ml brefeldin A. Cells were then stained with antibodies for CD3, CD4, CD8, IFN-γ, IL-2, TNF-α, IL-22, IL-17, IL21, IL-8, Mip1β, IL-4 and IL-10. Unpulsed T2 cells (top row) show the background production of each cytokine. Peptide specific activation (bottom row) demonstrates that these transduced T cell populations can make at least 7 different cytokines. IFN-γ was chosen to monitor cross-presentation in functional assays because it was the dominant cytokine produced by TCR redirected CD8 T cells. CD8 T cells were isolated by using the untouched CD8 T cell isolation kit (Miltenyi) and used in cross-presentation assays.