

Online Supplementary Table I

Patient	Age	Sex	HLA-A2	Viral load (IUx10 ⁶ /ml)	ALT (IU/L)	Serology	cDNA arrayed (purified*)	Bim		Mcl-1 10 day	Rescue (VAD)	
								ex vivo	10 day		ex vivo	10 day
Resolved												
R1	NA	F	+	N	NA	HBsAg-	Y*	N	Y	Y	N	Y
R2	NA	M	+	N	<50	HBsAg-	N	N	Y	Y	N	Y
R3	50	M	+	N	NA	HBsAg-	N	N	N	N	N	Y
R4	41	NA	+	N	NA	HBsAg-	Y	N	Y	Y	N	Y
R5	32	M	+	N	10	HBsAg-	N	N	Y	Y	N	Y
R6	38	M	+	N	<50	HBsAg-	Y	N	Y	Y	N	Y
R7	26	M	+	N	32	HBsAg-	N	Y	Y	Y	N	N
R8	35	M	+	N	<50	HBsAg-	N	N	Y	Y	N	N
R9	39	M	+	N	74	HBsAg-	N	N	Y	Y	N	N
R10	NA	F	+	N	NA	HBsAg-	Y*	N	N	N	N	N
R11	NA	M	+	N	NA	HBsAg-	Y	N	N	N	N	N
R12	NA	F	+	N	NA	HBsAg-	Y	N	Y	Y	N	N
R13	42	M	+	N	17	HBsAg-	N	Y	N	N	N	N
R14	69	M	+	N	NA	HBsAg-	Y	N	N	N	N	N
R15	49	M	+	N	NA	HBsAg-	Y	N	N	N	N	N
R16	64	M	+	N	NA	HBsAg-	Y	N	N	N	N	N
R17	24	M	+	N	<50	HBeAg-	N	Y	N	N	N	N
R18	NA	NA	-	N	15	HBeAg-	N	Y	N	N	N	N
R19	31	M	-	N	31	HBeAg-	N	Y	N	N	N	N
Chronic												
C1	25	M	+	0.42	270	HBeAg+	N	N	Y	Y	N	Y
C2	49	F	+	1.1	151	HBeAg-	N	N	Y	Y	N	Y
C3	31	M	+	0.00018	92	HBeAg-	N	N	Y	Y	N	N
C4	29	F	+	0.0011	NA	HBeAg-	N	N	Y	N	N	N
C5	38	M	+	510	206	HBeAg+	N	N	Y	Y	N	Y
C6	28	F	+	7.9	261	HBeAg+	N	N	Y	Y	N	Y
C7	50	F	+	0.22	63	HBeAg-	N	N	Y	Y	N	Y
C8	NA	M	+	>10	<50	HBeAg+	N	Y	N	N	Y	Y
C9	NA	M	+	>10	<50	HBeAg+	Y*	N	N	N	N	Y
C10	NA	M	+	0.00057	<50	HBeAg-	N	N	N	N	N	Y
C11	44	M	+	0.065	49	HBeAg-	N	Y	N	N	Y	Y
C12	43	M	+	33	250	HBeAg+	N	N	N	N	N	Y
C13	31	M	+	0.0045	NA	HBeAg-	N	N	Y	Y	N	Y
C14	45	M	+	BLQ	25	HBeAg-	N	Y	N	N	N	N
C15	35	M	+	220	42	HBeAg+	N	Y	Y	Y	Y	N
C16	31	M	+	>10	<50	HBeAg+	Y	Y	N	N	Y	N
C17	42	F	+	NA	17	HBeAg-	N	N	Y	Y	N	N
C18	45	M	+	110	32	HBeAg-	N	N	Y	Y	N	N
C19	71	M	+	2,900	22	HBeAg-	N	N	Y	Y	N	N
C20	30	F	+	770	31	HBeAg-	N	N	Y	Y	N	N
C21	33	F	+	BLQ	17	HBeAg-	N	N	Y	Y	N	N
C22	NA	M	+	>10	NA	HBeAg+	Y	N	N	N	N	N
C23	31	M	-	330	39	HBeAg+	N	N	N	N	N	N
C24	35	F	-	260	554	HBeAg+	N	Y	N	N	N	N
C25	42	M	-	95	183	HBeAg+	N	Y	N	N	N	N

NA= not available; N= negative

Online Supplementary Table II
Significance analysis of Microarrays shortlist

76 positive significant genes

Gene Name	Unigene ID (Hs.) *	Score(d)	Fold Change
<i>Bcl-2 interacting mediator</i>	140648	5.20	6.63
EST	330442	4.97	4.81
Complement component 3	1203320	4.96	5.81
Complement component 3	1203320	4.64	5.08
Secreted frizzled-related protein 1	7306	4.54	3.75
N-acetylglucosaminidase, alpha	50727	4.37	4.09
Myelin associated glycoprotein	1780	4.32	8.56
Insulin-like growth factor binding protein	77326	4.23	9.25
Extracellular matrix protein 2	35094	4.09	3.08
Coiled-coil domain containing 52	477144	4.02	4.42
Growth arrest & DNA-damage-inducible, gamma	9701	3.91	4.15
Contactin	143434	3.91	2.79
Frizzled homolog 2	81217	3.90	2.86
Serine (or cysteine) proteinase inhibitor, clade A	297681	3.84	3.74
Cytochrome c oxidase subunit Va	434076	3.80	3.68
Ki-ras	ND	3.77	3.57
Dystrobrevin, alpha	336678	3.76	2.23
Integrin, alpha 6	227730	3.72	4.22
Procollagen (type III) N-endopeptidase	183138	3.70	2.69
Ribosomal protein S4, Y-linked	180911	3.62	3.48
Matrix metalloproteinase 17	159581	3.62	4.28
Forkhead box G1B	386249	3.60	3.32
Matrix metalloproteinase 13	2936	3.57	2.98
Connective tissue growth factor	75511	3.52	7.34
<i>Cathepsin B</i>	297939	3.50	3.33
Profilin 1	75721	3.49	4.12
Chloride channel 4	199250	3.47	2.77
<i>Suppressor of cytokine signalling</i>	405946	3.47	4.51
Uracil-DNA glycosylase	78853	3.45	2.49
Pyrroline-5-carboxylate reductase 1	79217	3.45	3.50
Gamma-aminobutyric acid (GABA) A receptor	45740	3.44	3.40
STAT6	ND	3.42	2.84
Cut-like 1, CCAAT displacement protein	147049	3.41	2.74
<i>OX-40</i>	129780	3.40	3.00
Rho GTPase-activating protein	111138	3.37	4.11
Lysophosphatidic acid G-protein-coupled R.2	75794	3.37	3.31
Tryptase beta 1	405479	3.36	3.09
Apolipoprotein A-I	93194	3.35	7.50
<i>Mitogen-activating protein kinases 4 2</i>	82979	3.34	3.34
Catenin (cadherin-associated protein)	80220	3.34	3.30
Acyl-Coenzyme A oxidase 3, pristanoyl	12773	3.33	3.39
Folate receptor 2	24194	3.32	2.94
DNA (cytosine-5-)-methyltransferase 1	202672	3.31	4.62
Glycine receptor, beta	32973	3.31	4.68
EST	(N55083)	3.31	3.13
Gap junction protein, beta 1	333303	3.29	3.80

EST	(R59352)	3.28	2.67
EST	(R37350)	3.27	3.11
Amyloid B (A4) precursor protein-binding m.3	17528	3.26	3.87
Human insulin-like growth factor binding	635441	3.26	6.13
Cysteine-rich, angiogenic inducer, 61	8867	3.25	4.89
Transcription factor 21	78061	3.25	3.13
Hypothetical protein LOC27351	570455	3.23	4.16
Chromosome X open reading frame 12	23119	3.22	3.03
Ribosomal protein S4, Y linked	180911	3.22	3.08
Ras homolog gene family, member E	6838	3.21	3.52
Frizzled homolog 4	19545	3.19	3.80
Hypothetical protein LOC138046 isoform 1	121663	3.18	2.33
Transcription factor AP-2 beta	33102	3.17	3.33
MET	ND	3.16	3.31
Fibroblast growth factor 2	284244	3.15	4.01
Suppressor of cytokine signaling 1	50640	3.15	3.45
EST	(AI356286)	3.13	3.04
Baculoviral IAP repeat-containing 3	127799	3.13	4.51
Palmitoyl-protein thioesterase 2	81737	3.12	3.75
Lactotransferrin	105938	3.12	2.92
Angiopoetin 1	ND	3.12	3.14
Acyl-Coenzyme A oxidase 3, pristanoyl	12773	3.11	3.32
Telomerase-associated protein 1	232070	3.11	3.47
Rho/Rac guanine nucleotide exchange factor 2	337774	3.11	3.27
Secreted frizzled-related protein 1	7306	3.11	2.49
D component of complement (adipsin)	155597	3.11	2.27
OX-40	129780	3.09	3.00
Solute carrier family 3	239106	3.09	4.24
EST	(R53362)	3.09	2.30
EST	(R32170)	3.09	3.15

ND = not defined; EST = expressed sequence tag; * (Genebank ID provided where Unigene ID unavailable)

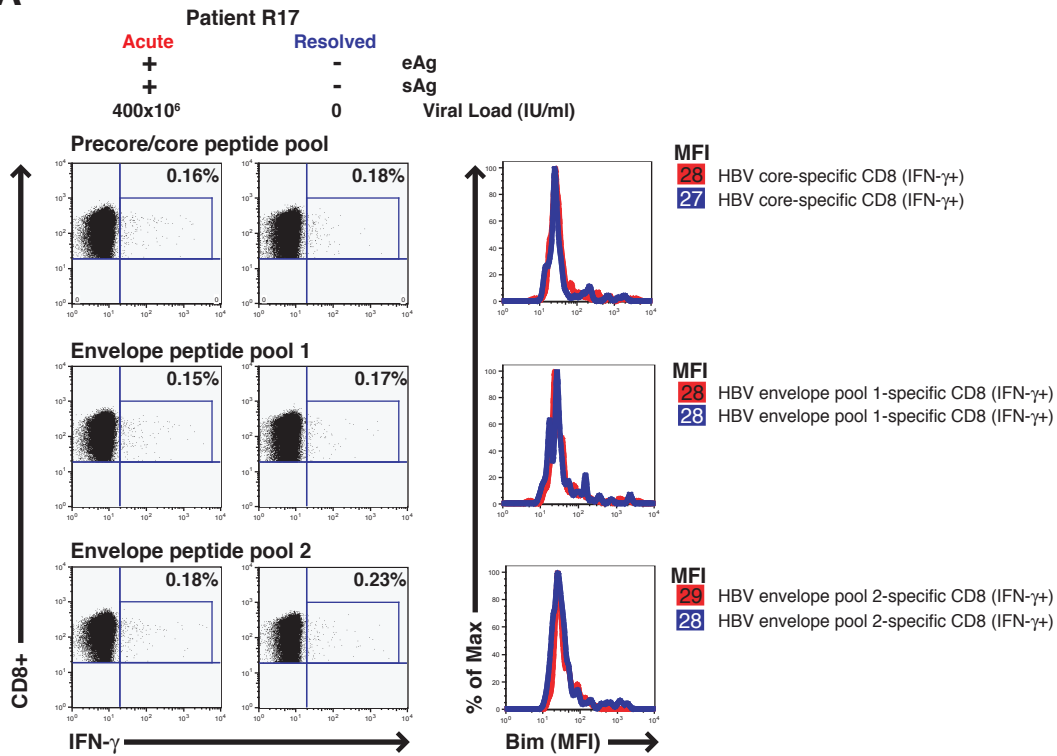
29 negative significant genes

Gene Name	Unigene ID	Score(d)	Fold Change
Diacylglycerol O-acyltransferase homolog 1	288627	-4.44	0.33
GTP-binding protein Rho7	603111	-4.39	0.29
Interferon, gamma	856	-4.12	0.16
Sjogren's syndrome nuclear autoantigen 1	18528	-3.95	0.43
Zinc finger RNA binding protein	173518	-3.80	0.32
E2F transcription factor 1	96055	-3.77	0.30
Huntingtin interacting protein	107019	-3.74	0.45
Human D9 splice variant B mRNA, complete	37616	-3.71	0.35
Flightless I homolog	83849	-3.70	0.40
Hypothetical protein MGC14480	37616	-3.69	0.37
Hypothetical protein FLJ10432	143187	-3.69	0.37
Fibroblast growth factor i.c. binding protein	7768	-3.63	0.46
Phosphomevalonate kinase	30954	-3.62	0.42
Growth arrest & DNA-damage-inducible, alpha	80409	-3.59	0.38
Integrin beta 3 binding protein	82084	-3.58	0.40
Flightless I homolog	83849	-3.57	0.37
ATP-binding cassette, sub-family F	153612	-3.55	0.52
Vestigial like 1	9030	-3.55	0.50
CD37 antigen	153053	-3.54	0.27
Glycine dehydrogenase	380791	-3.52	0.27
Phosphorylase kinase, gamma 2	196177	-3.49	0.39
SET domain containing 1A	297483	-3.46	0.30
Hypothetical protein XP_375359	97805	-3.43	0.36
Hypothetical protein MGC5356	197755	-3.43	0.35
Postreplication repair protein hRAD18p	21320	-3.42	0.33
KIAA0368 protein	3852	-3.40	0.45
Phosphorylase, glycogen	75658	-3.40	0.38
Integrin-linked kinase	6196	-3.40	0.38
Small nuclear ribonucleoprotein polypeptide A	173255	-3.39	0.46

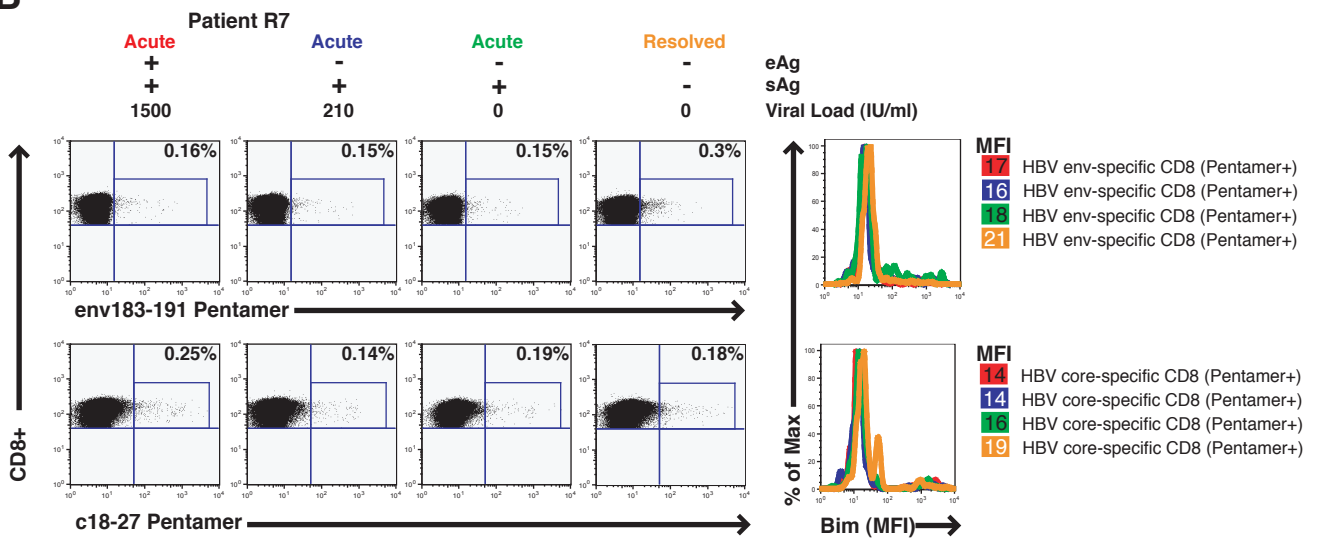
ND = not defined; EST = expressed sequence tag; * (Genebank ID provided where Unigene ID unavailable)

Online Supplementary Figure - Bim expression during acute HBV infection

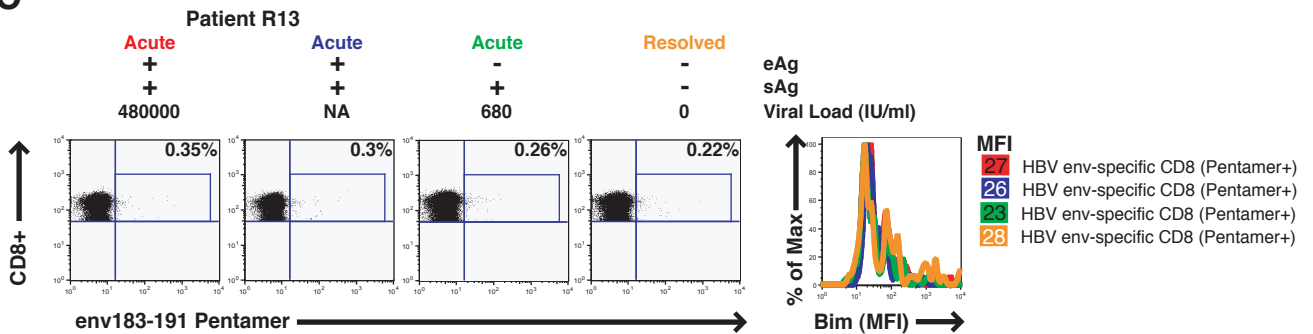
A



B



C



Online Supplementary Figure: Bim expression during acute HBV infection.

(A) FACS dot plots show identification of HBV-specific CD8 responses using pools of overlapping peptides for core and envelope in an HLA-A2 negative patient with acute symptomatic HBV infection (R17, see online patient table I). Above the dot plots are the evolution of serology and viral load from acute to resolution phases of the infection, and the right panel shows the overlay of the MFI for Bim expression within the HBV-specific CD8 for the different time points. (B) As for (A) but for an HLA-A2+ patient (R7) sampled through the course of acute HBV infection using HLA-A2/core18-27 and env183-91 tetramers. (C) As for (A) for an HLA-A2+ patient (R13) sampled through the course of acute HBV infection using the HLA-A2/env183-91 tetramers.