

# Supplementary Materials

## **Hepatitis B virus spliced variants are associated with an impaired response to interferon therapy**

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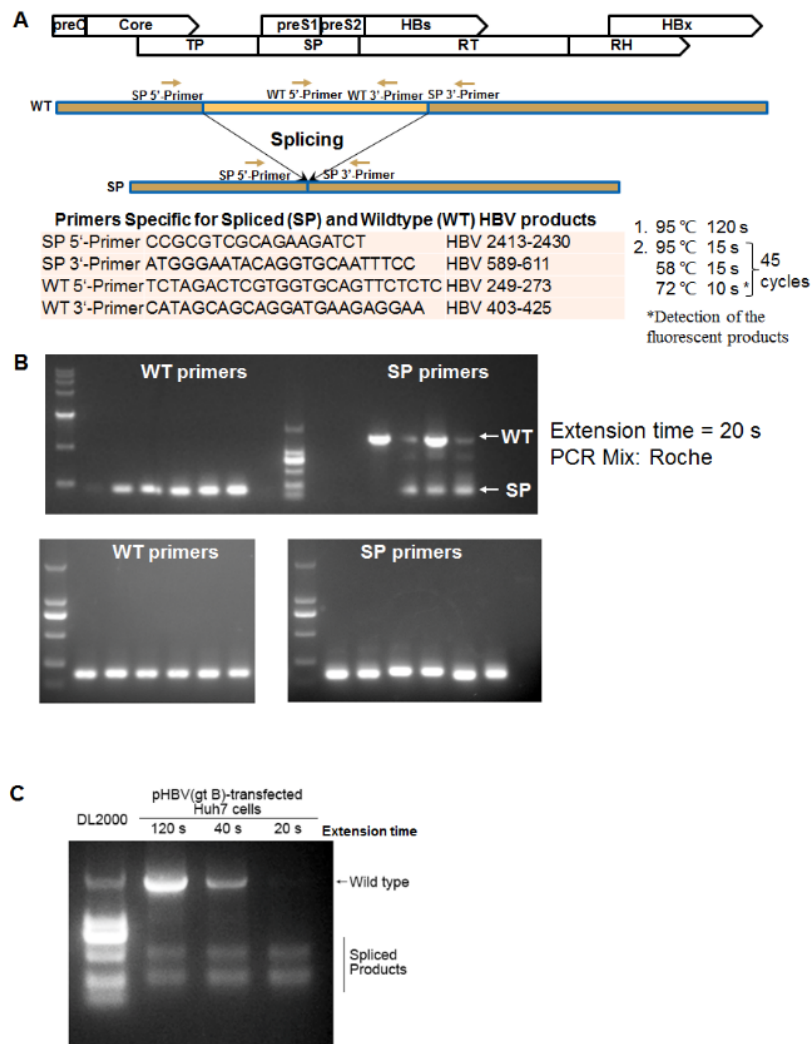
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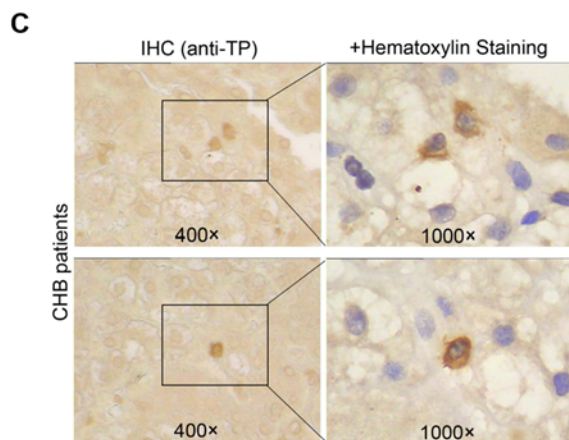
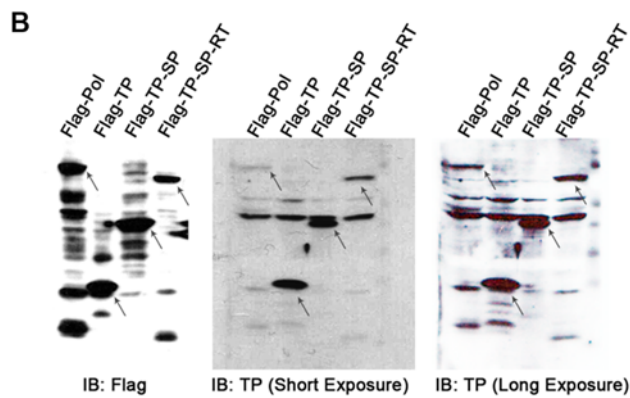
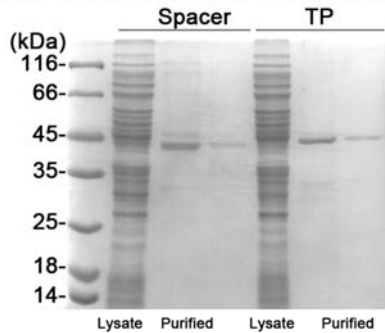
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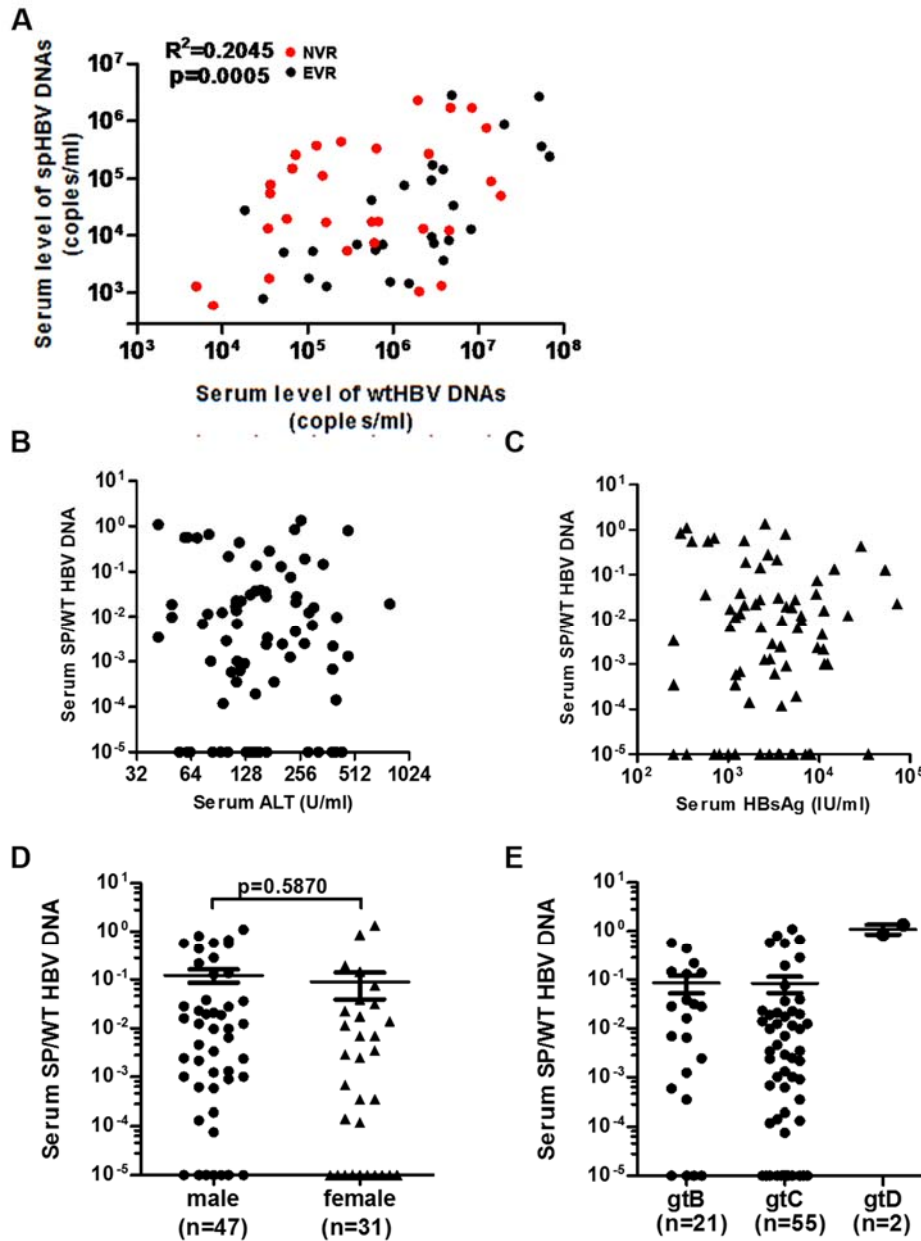
**Fig S1. Optimization of the PCR protocol for WT and SP HBV DNAs amplification.**

(A) Schematic of the designed primers for detecting WT- and SP-HBV DNAs. (B) The HBV DNAs extracted from the sera of CHB patients were analyzed by PCR followed by agarose gel electrophoresis with primers specific for WT or SP. The extension time during PCR was 20 s (the upper panel) or 10 s (the lower panel). The data showed that protocol setting extension time as 10 s was suitable for amplify specific WT- and SP- HBV DNAs, during which there was no nonspecific amplification of WT products with SP primers. (C) The cDNAs reverse-transcribed from the total RNAs extracted from Huh7 cells transfected with pHBV1.3 were analyzed by PCR followed by agarose gel electrophoresis. The data showed that the shorter extension time led to less amplified products of wtHBV (~2 kb) but did not much affect the amounts of the amplified products of spHBV(~0.3-0.5 kb), which may be a result of the characteristic of the polymerase (1 kb/min) used in PCR.

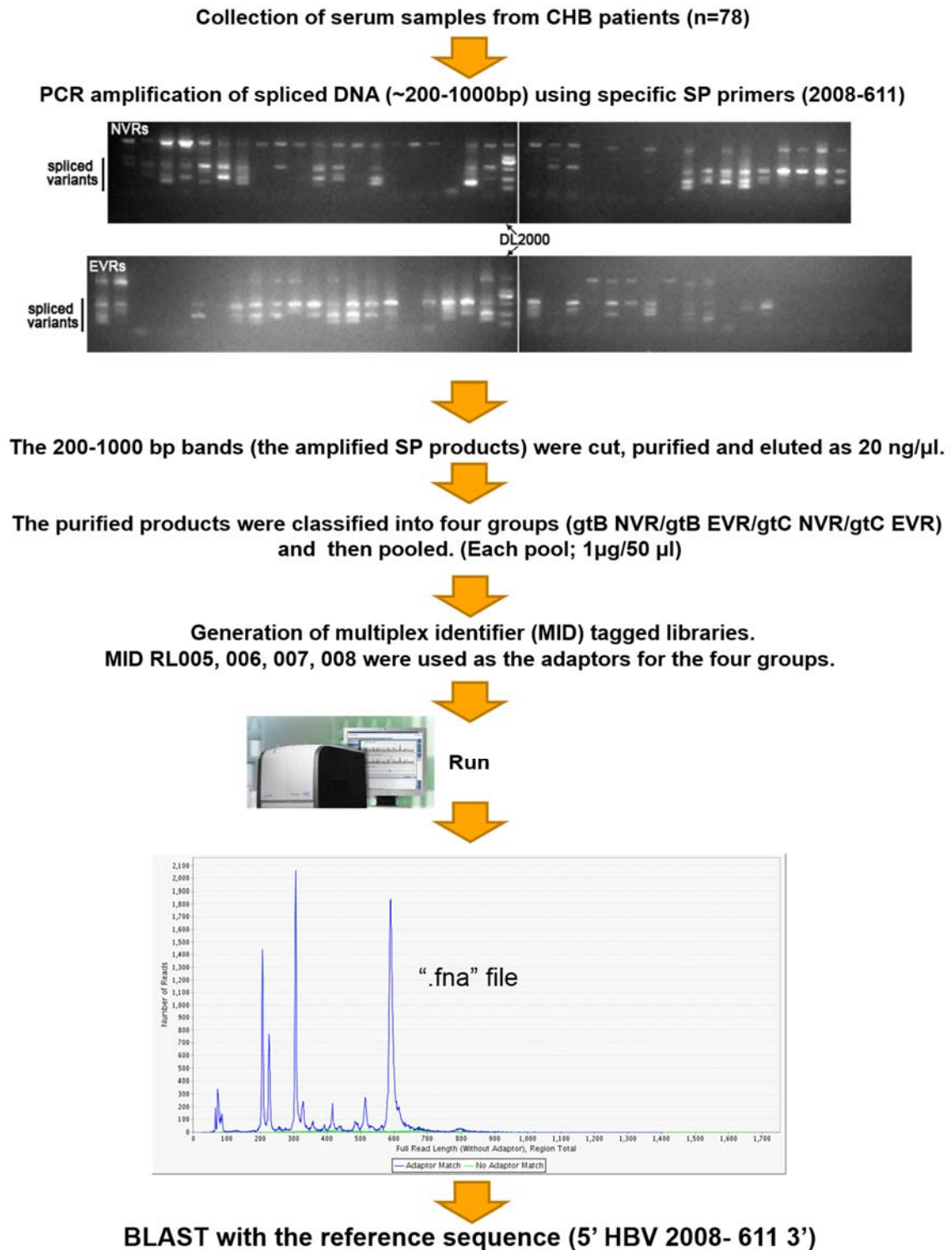
**A** TP -fEcoRI GCGGAATTCATGCCCCCTATCTTATCAACA  
 TP -rXhoI GAACTCGAGCTACTCGTGTCCCAAGAATATG  
 SP -fBamHI ATTGGATCCCTACAGCATGGGAGGTTGGTC  
 SP -rXhoI GCGCTCGAGCTATTCGAGAAGATTGACGATAT



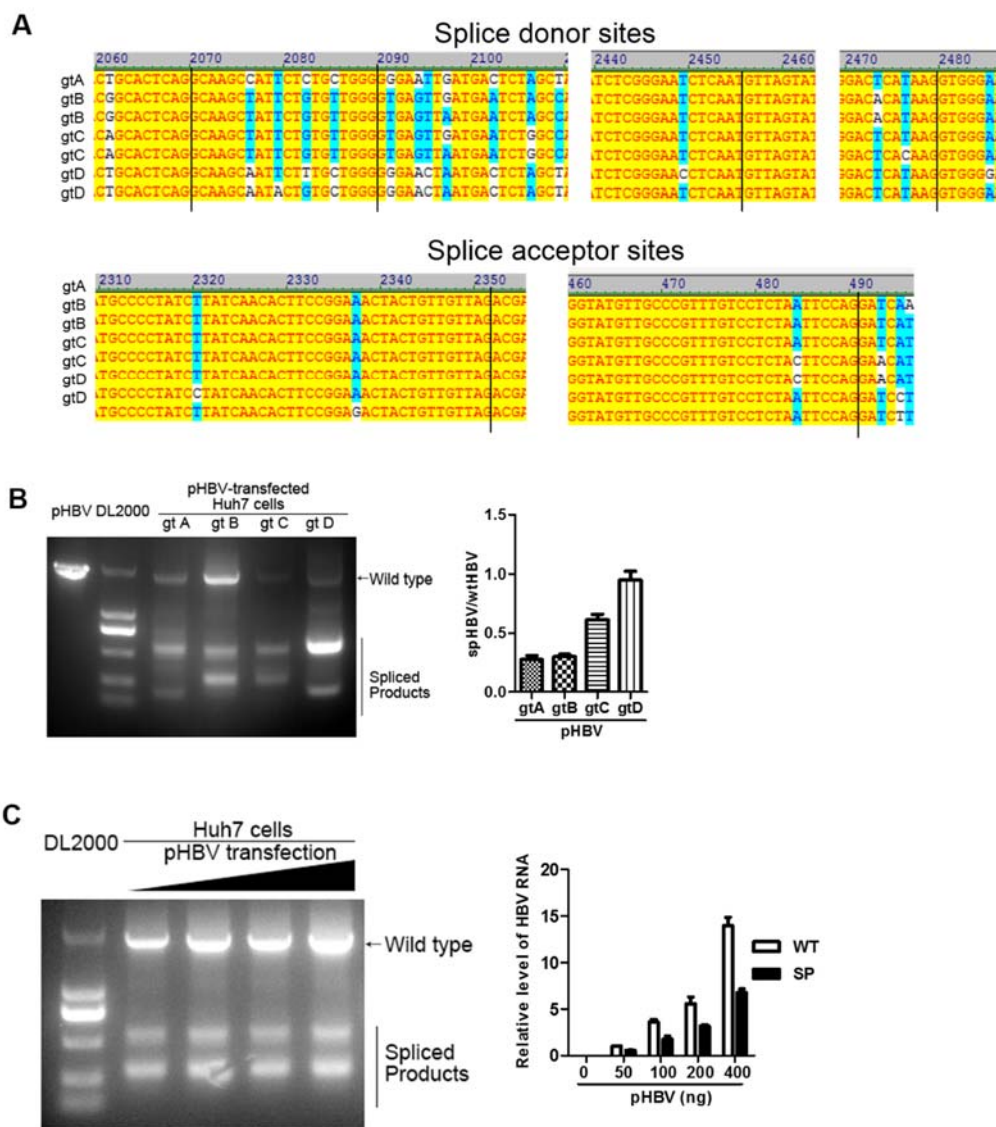
**Fig S2. Preparation of the antibodies against TP and Spacer regions of viral polymerase.** (A) Detection of the purified GST-Spacer and GST-TP proteins expressed in the E. coli BL21 by SDS-PAGE followed by coomassie staining. (B) Huh7 cells transfected with the indicated plasmids were extracted to detect the expression of full length- and truncated-Pol by western blotting with anti-Flag Abs or anti-TP Abs. (C) Detection of HBV proteins expression in liver biopsies from CHB patients by immunohistochemistry with anti-TP antibodies.



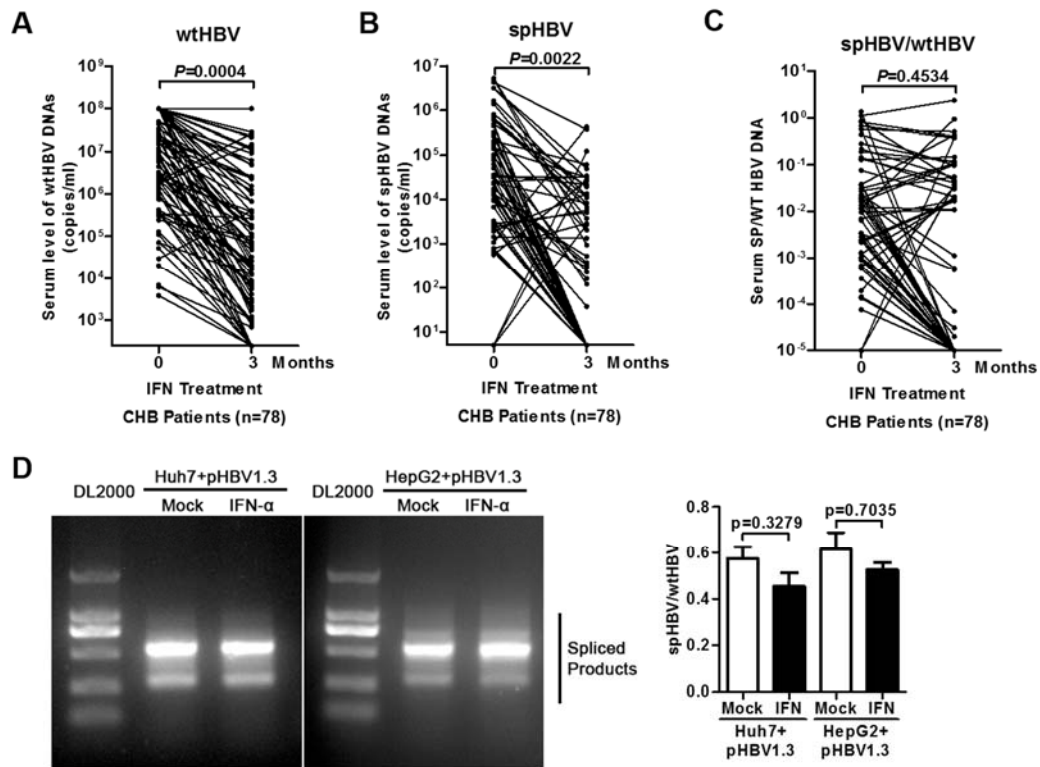
**Fig S3. The correlation between spHBV variants and HBsAg, ALTs, genders or viral genotypes.** (A) The level of spHBV and wtHBV DNAs in sera from the NVRs and EVRs before IFN therapy were quantified by qPCR. The relationship between spHBV DNAs and wtHBV DNAs in samples with spHBV > 100 copies/ml was analyzed using Spearman's correlation. The correlation between the proportions of spHBV and the level of ALT (B) or HBsAg (C) in the sera from the 82 patients before IFN therapy. The ratio of spHBV to wtHBV DNAs in the serum samples was compared between males and females (D) (Student's t-tests) or among different genotypes (E).



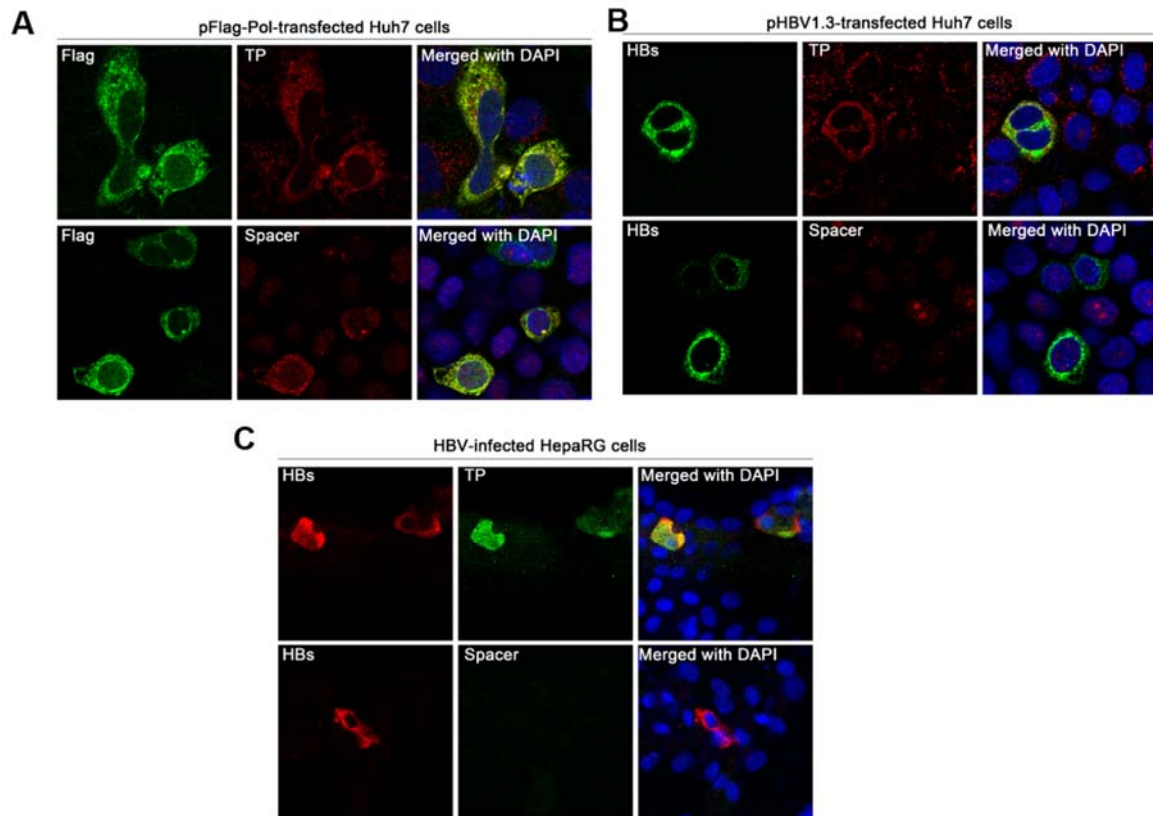
**Fig S4. Work Flow of the 454 sequencing analysis of the spHBV variants in the sera of CHB patients.**



**Fig S5. HBV splicing is associated with the viral genotypes.** (A) The sequence alignment of the donor and acceptor sites among different HBV genotypes. (B) The cDNAs reverse-transcribed from the total RNAs extracted from Huh7 cells transfected with HBV constructs with different genotypes were analyzed by PCR followed by agarose gel electrophoresis (the left panel) and realtime PCR (the right panel). (C) The cDNAs reverse-transcribed from the total RNAs extracted from Huh7 cells transfected with different amounts of pHBV1.3 were analyzed by PCR followed by agarose gel electrophoresis (the left panel) and realtime PCR (the right panel). The data showed that the intracellular level of both the wt- and sp-HBV RNAs closely associated with the amounts of transfected plasmids, but there was no significant difference on the ratio of spHBV to wtHBV RNAs among cells transfected with different amounts of pHBV1.3.

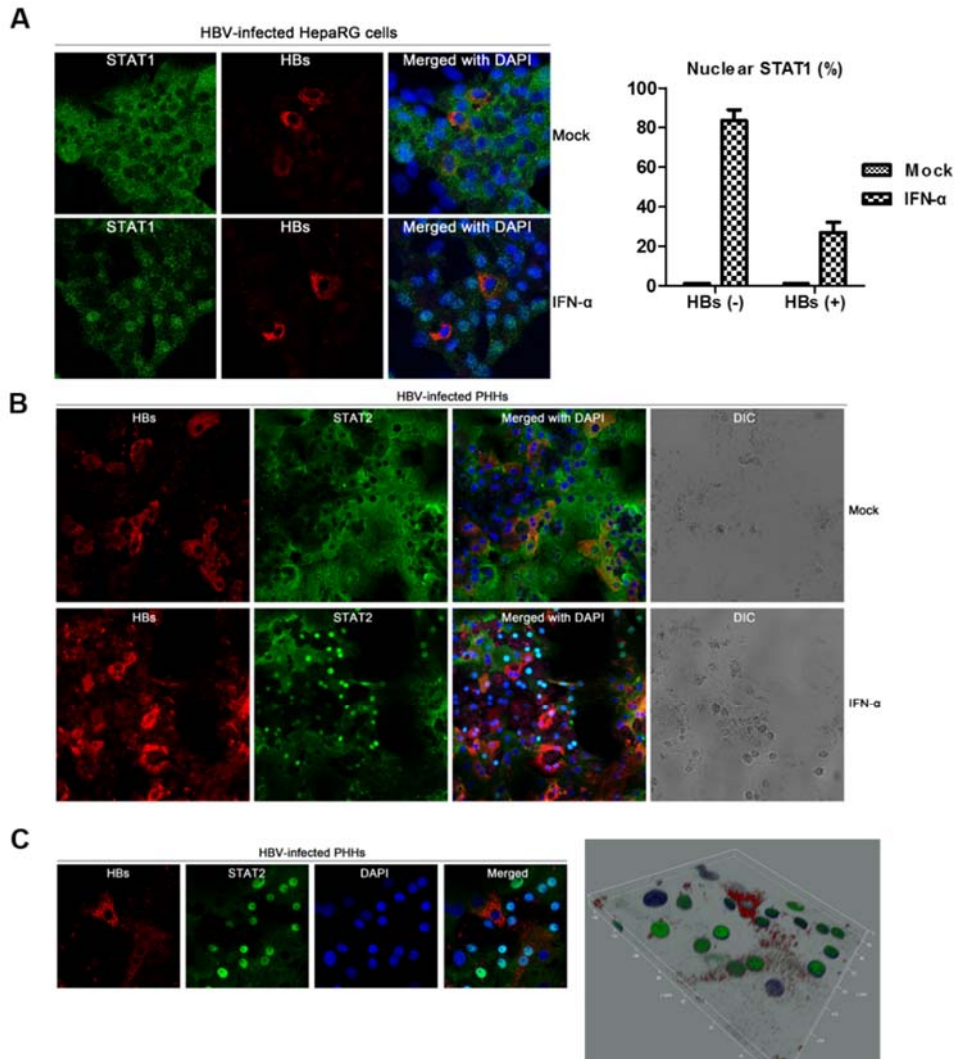


**Fig S6. Effect of IFN treatment on the expression of the spHBV variants.** Comparison of the absolute amount of wtHBV(A), spHBV(B), and the ratios of spHBV/wtHBV(C) DNA between paired samples from CHB patients before and after 3 months of IFN therapy. The cDNAs reverse-transcribed from the total RNAs extracted from mock- or IFN- $\alpha$  treated Huh7 or HepG2 cells transfected with pHBV1.3 were analyzed by PCR followed by agarose gel electrophoresis (the upper panel) and realtime PCR (the lower panel). The data, which represents results of three independent experiments performed in triplicates, was analyzed using Student's t-tests (D). To determine whether IFN treatment could affect HBV splicing, we compared the change of the amounts of spHBV and wtHBV in CHB patients following IFN therapy. Twelve weeks of IFN therapy resulted in varying degrees of reduction of both spHBV DNA level and wtHBV DNA level, and decreased the total detection rate of the serum spHBV, particularly in EVRs. Although the absolute amounts of spHBV and wtHBV decreased, the spHBV/wtHBV ratio was not much affected by IFN treatments, in both the NVRs and EVRs group. Similar results were obtained in replication-competent HBV constructs-transfected Huh7 and HepG2 cells, suggesting that IFN could globally reduce the viral DNA, including the spHBV DNA and wtHBV DNA, but did not much affect the proportions of spHBV variants among the total detected HBV genomes.

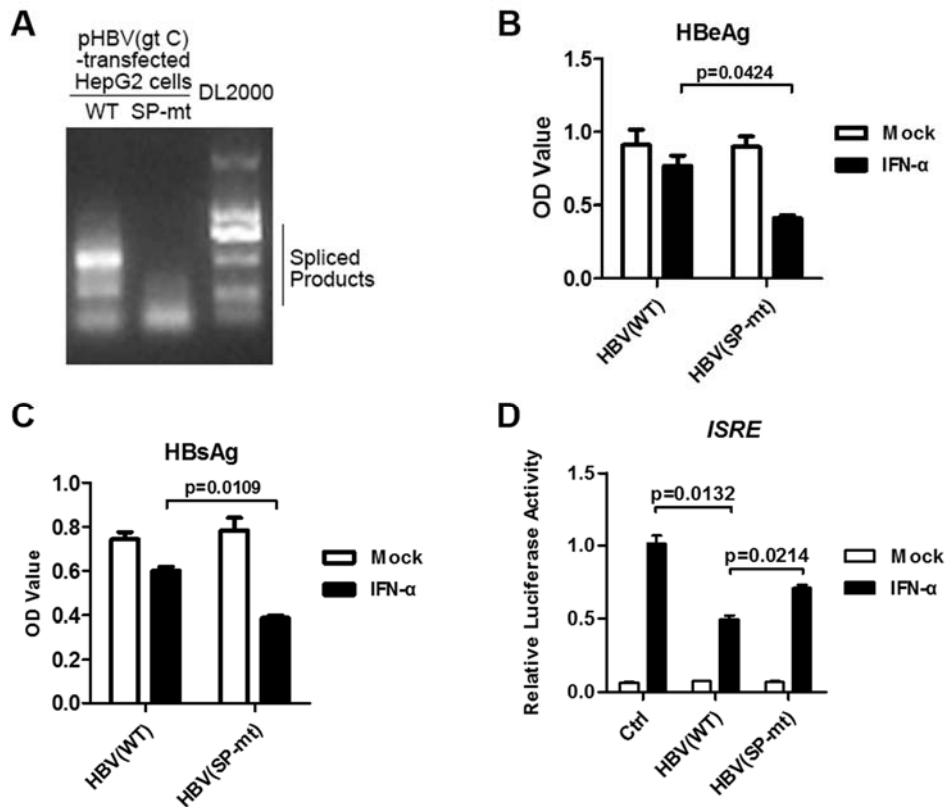


**Fig S7. Detection of viral proteins expression using immunofluorescence with anti-TP and anti-SP antibodies.** (A, B) Huh7 cells transfected with pFlag-Pol or pHBV1.3 were fixed, immunofluorescence stained with indicated antibodies, and analyzed using a confocal laser scanning microscope. (C) Ten days post HBV infection of the HepaRG cells, immunofluorescence assay was performed with indicated antibodies.



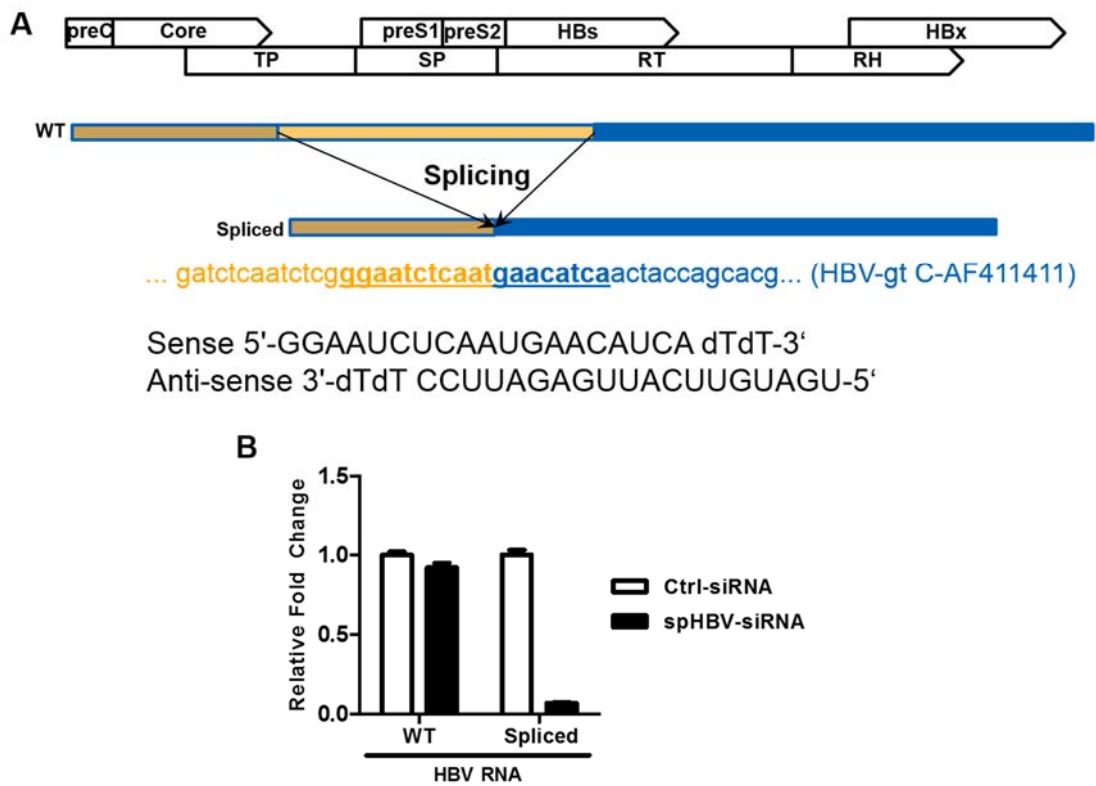


**Fig S8. Impaired IFN-induced STAT1/2 nuclear accumulation in HepaRG cells and HBV-infected PHHs.** (A) HepaRG cells plated in the chamber coverglass slides were treated with pooled sera from CHB patients overnight. 10 days post HBV infection, the cells were mock-treated or treated with IFN- $\alpha$  for 0.5 h, followed by the immunofluorescence assay with antibodies against HBs and STAT1 (the left panel). The percentage of cells with nuclear STAT1 from three independent fields covering approximately 100 HBs negative and 30 HBs positive cells was calculated (mean $\pm$ SD) (the right panel). The experiments were performed three independent times in triplicates. (B) PHH cells were plated in the collagen I-pre-coated chamber coverglass slides. 10 days post HBV infection, the cells were treated with or without IFN- $\alpha$  for 0.5 hours, followed by the immunofluorescence assay with antibodies against HBs and STAT2. (C) The PHH cells with HBV viral protein expression showed an impaired STAT2 nuclear-translocation upon IFN treatment compared to those cells without HBV. The three-dimensional view of one of the representative field of IFN-treated PHHs were obtained by reconstruction of z-series sectioned fluorescent images using Leica Confocal Software.



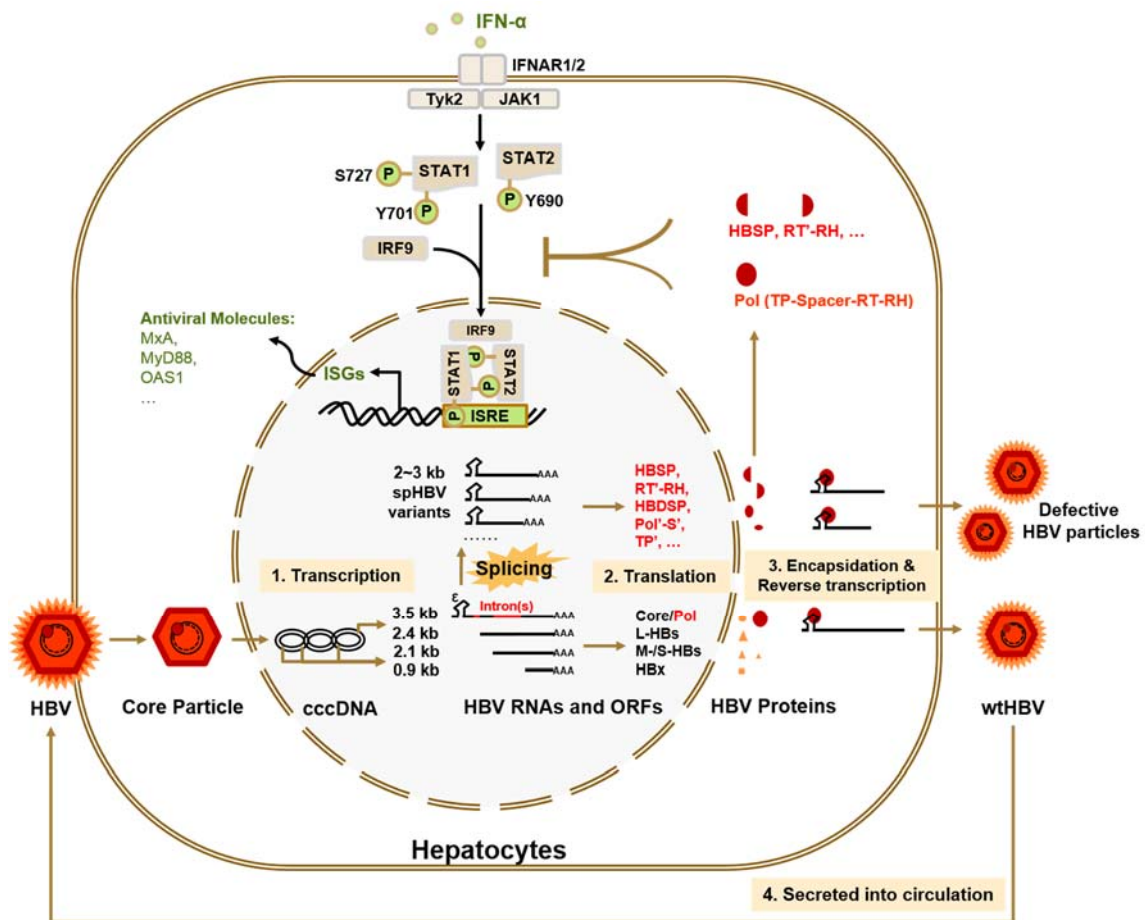
**Fig S9. Mutation of the common splice sites of HBV impaired its anti-IFN activities in HepG2 cells.**

The cDNAs reverse-transcribed from the total RNAs extracted from pHBV1.3- or pHBV1.3-SP-mt-transfected HepG2 cells were analyzed by PCR followed by agarose gel electrophoresis (A). The level of HBeAg and HBsAg in culture supernatants 48 h post transfection was analyzed by ELISA (B, C). HepG2 cells transfected with the indicated plasmids were mock- or IFN- $\alpha$ -treated for 12 hours and then harvested for luciferase reporter assay (D). The data was analyzed using Student's t-tests.



**Fig S10. siRNA specifically targeting the major spHBV RNAs**

(A) Schematic of the designed siRNA that specifically targets the major spliced HBV RNAs. (B) Huh7 cells were co-transfected with pHBV and control siRNAs or siRNAs targeting spHBV RNAs. 48 h post transfection, the RNAs were extracted for real-time PCR using indicated primers to determine the level of wildtype and spliced HBV RNAs.



**Fig S11. Model of HBV splicing-generated products-mediated inhibition on IFN signaling.**

**Table S1. Species and frequency of HBV spliced variants detected in the sera from CHB patients.**

Types of HBV spliced variants	Exon Counts	3' splice acceptor sites	5' splice donor sites	Frequencies of HBV spliced variants (%)			
				NVRs		EVRs	
				gtB	gtC	gtB	gtC
SP1	2	488/489	2447/2448	43.59	48.60	40.96	40.25
SP2	3	2349/2350, 488/489	2067/2068, 2447/2448	17.18	17.62	23.13	23.70
SP3	2	488/489	2067/2068	9.95	7.61	9.79	9.90
SP4	3	2349/2350, 488/489	2087/2088, 2447/2448	7.99	7.52	7.69	7.15
SP5	2	488/489	2087/2088	9.84	5.42	5.66	4.68
SP6	2	488/489	2471/2472	0.42	0.26	0.11	0.25
SP7	3	2936/2937, 488/489	2447/2448, 3020/3021	0.03	0.02	0.01	0.02
SP8	4	2349/2350, 2936/2937, 488/489	2067/2068, 2447/2448, 3020/3021	6.13	6.51	7.30	7.73
SP9	2	281/282	2447/2448	0.00	0.00	0.00	0.00
SP10	3	2349/2350, 281/282	2067/2068, 2447/2448	0.72	0.92	0.80	0.46
SP11	2	281/282	2471/2472	0.00	0.00	0.00	0.00
SP12	3	2235/2236, 281/282	2067/2068, 2447/2448	0.02	0.05	0.02	0.03
SP13	2	488/489	3020/3021	0.00	0.00	0.00	0.00
SP14	2	2936/2937	2447/2448	0.00	0.00	0.00	0.00
SP15*	3	2235/2236, 488/489	2067/2068, 2447/2448	1.28	1.07	1.19	1.39
SP16*	3	2349/2350, 488/489	2067/2068, 2471/2472	1.38	2.61	2.01	3.19
SP17*	2	281/282	2067/2068	1.47	1.80	1.33	1.25



<b>0 week</b>	<b>SP detection rate (positive/total)</b>	<b>AVG of SP/WT</b>	<b>Two-tailed t-test</b>
NVRs (<2 log)	31/37	0.203832576	p=0.00215
EVRs (>2 log)	29/41	0.024805674	
<b>12 weeks</b>	<b>SP detection rate (positive/total)</b>	<b>AVG of SP/WT</b>	
NVRs (<2 log)	26/37	0.159418305	p=0.03611
EVRs (>2 log)	11/41	0.018208319	

\* Before IFN treatment; \*\* After 12 weeks of IFN treatment;

“SP-positive” was defined as spHBV positive and spHBV/wtHBV >0.00001;  
The viral load was determined using an HBV DNA quantitative real-time PCR kit (Qiagen) and  
HBV genotyping was performed as previously reported (1).

Table S3. Regression analysis of the factors related to the prognosis of IFN responses

HBs (U/ml)	SP/WT DNA	*Fold Reduction	Gender	Age	ALT(IU/ml)	HBs(Log)	SP/WT DNA (Log)	Fold Reduction (Log)
4900	0.00001	9.788135593	2	40	55	3.69019608	-5	0.990699977
1350	0.038938355	12.32	2	28	155	3.130333768	-1.409622394	1.090610708
5450	0.027930749	21.67741935	1	21	166	3.736396502	-1.553917418	1.336007579
5000	0.018689008	7.662337662	1	32	50	3.698970004	-1.728413739	0.884361286
2850	0.00001	10.02008032	1	38	141	3.45484486	-5	1.000871203
20802	0.012340135	5.334796926	1	36	95	4.318105092	-1.908680077	0.727117892
9230	0.037873477	16.26139818	1	29	145	3.965201701	-1.421664827	1.211157884
700	0.667265235	93.47368421	1	26	80	2.84509804	-0.175701502	1.97068936
3550	0.031206732	7.692307692	2	28	136	3.550228353	-1.505751708	0.886056648
1000	0.00001	10.88737201	1	30	93	3	-5	1.036923063
4250	0.803573363	5.829015544	1	28	472	3.62838893	-0.094974468	0.765595213
1550	0.192109425	16.10062893	2	27	272	3.190331698	-0.716451328	1.206842841
1050	0.006963361	43.78531073	2	24	115	3.021189299	-2.157181059	1.641328436
2250	0.144987527	0.119863014	2	29	343	3.352182518	-0.838669357	-0.921314807
2750	0.282632277	0.07556391	1	25	173	3.439332694	-0.548778242	-1.121685579
2550	1.350975885	42.24021592	2	39	259	3.40654018	0.130647597	1.62572613
250	0.00001	10.1076716	1	38	63	2.397940009	-5	1.004651123
2250	0.00001	16.09195402	2	37	61	3.352182518	-5	1.206608783
9500	0.07576458	17.34693878	2	21	227	3.977723605	-1.120533777	1.239222846
1200	0.011509732	5.442073171	2	28	79	3.079181246	-1.938934772	0.735764377
53122	0.129049604	2.565720294	1	46	201	4.725274418	-0.889243324	0.409209309
250	0.00001	1.279850746	2	28	152	2.397940009	-5	0.107159326
1500	7.57706E-05	19.51456311	1	36	102	3.568201724	-3.87756753	1.290358833
3700	0.00001	65.77981651	2	28	239	2.477121255	-0.06773129	1.818092658
1150	0.00001	5.844262295	1	28	69	2.602059991	-0.252163033	0.766729699
300	0.855595931	0.072413793	1	22	42	2.544068044	0.042144016	-1.140178703
400	0.559547509	8.942028986	1	36	61	3.176091259	-0.241726361	0.951436073
350	1.10190465	6.134453782	1	38	145	3.748188027	-3.71350616	0.787775899
1500	0.573157051	44.05286344	1	29	147	4.167317335	-0.868872759	1.643974143
5600	0.000193417	9.009009009	1	39	166	3.980094314	-2.621970987	0.954677021
15150	0.000132566	20.66115702	1	28	389	4.047274867	-2.662610105	1.315154638
14700	0.135246876	4.651162791	1	22	118	4.460145817	-0.356119229	0.66756154
9552	0.002387971	4.385964912	1	27	50	3.802773725	-2.007267791	0.642065153
11150	0.002174653	8.130081301	1	32	241	4.033423755	-2.334787654	0.910094889
28850	0.440433932	3.546099291	1	26	115	4.093421685	-2.994044286	0.549750892
6350	0.009834045	1	1	28	114	4.859024152	-1.642218892	0
10800	0.004626072	4.587155963	1	26	82	4.058805487	-2.99223795	0.661543506
12400	0.001013808	148.3679525	1	24	305	4.054995862	-1.79343629	2.171340103
72281	0.02279193	100	2	55	403	3.550228353	-5	2
11450	0.001018033	338.6138614	2	18	385	3.717004407	-5	2.529704732
11350	0.016090284	118.1440443	1	40	165	2.748962861	-1.442636355	2.072411834
3550	0.00001	108.8235294	2	28	152	3.887898488	-5	2.036722807
5212	0.00001	232.5396825	2	32	184	2.397940009	-3.452613076	2.366497075
561	0.036088069	184.3478261	1	27	169	2.397940009	-2.474566454	2.265638021
7725	0.00001	148.9130435	2	34	42	2.397940009	-2.461923824	2.17293274
250	0.000352685	103200	1	39	300	3.763427994	-2.19089742	5.013679697
250	0.003353	18083.18264	2	33	387	3.130333768	-3.166484492	4.257274869
250	0.003452043	4508.928571	2	22	121	3.301029996	-1.649043083	3.654073355
5800	0.006443214	81300.81301	1	32	107	3.084933575	-3.231456325	4.910094889
1350	0.000681578	21625.61576	2	31	129	4.541579244	-5	4.334968482
2000	0.022436593	4309.52381	1	25	103	3.537819095	-0.661663917	3.634429284
1216	0.000586872	3095.975232	1	30	408	3.591064607	-2.013589393	3.490797478

Regression Analysis

**OVERALL FIT**

Multiple R 0.3421102  
 R Square 0.1170394  
 Adjusted R Squ 0.0557227  
 Standard Errc 1.2941637  
 Observations: 78

ANOVA		Alpha 0.05				
	df	SS	MS	F	p-value	sig
Regression	5	15.98459	3.196918	1.9087678	0.1034007	no
Residual	72	120.58989	1.6748596			
Total	77	136.57448				

	coeff	std err	t stat	p-value	lower	upper
Intercept	1.3641042	1.2830054	1.06321	0.2912397	-1.19352	3.9217288
Gender	0.1692558	0.3134792	0.5399265	0.5909138	-0.455654	0.7941652
Age	0.0084977	0.0200945	0.4228839	0.6736404	-0.03156	0.0485554
ALT(IU/ml)	0.0021851	0.0011098	1.9689618	<b>0.0528068</b>	-2.72E-05	0.0043975
HBs(Log)	-0.217254	0.2719143	-0.79898	0.4269301	-0.759305	0.3247972
SP/WT DNA (L	-0.167781	0.0923704	-1.816397	<b>0.073472</b>	-0.351918	0.0163557



34800	0.00001	500	2	28	284	3.698970004	-5	2.698970004	2
3450	0.217939567	167.3758865	2	26	143	3.556302501	-5	2.22369289	2
3900	0.009691938	3861.003861	1	29	126	3.638489257	-3.041306239	3.586700236	2
5000	0.00001	5102.040816	1	42	471	3.462397998	-2.880556102	3.707743929	2
3600	0.00001	269.541779	1	25	204	3.574031268	-2.612739686	2.43062609	2
4350	0.000909272	591.7159763	1	36	803	3.638489257	-1.711757283	2.772113295	2
2900	0.00131657	437.6146789	2	55	271	3.579783597	-2.604812707	2.641091881	2
3750	0.002439272	1573.604061	1	33	119	3.511883361	-3.208779131	3.196895468	2
4350	0.019419709	3858.757062	1	25	287	3.802773725	-1.906221867	3.586447437	2
3800	0.002484204	4748.538012	1	49	226	3.397940009	-2.904036175	3.676559919	2
3250	0.000618331	5360	2	29	114	3.079181246	-3.453014229	3.72916479	2
6350	0.012410181	1105.568445	2	31	96	3.58546073	-3.925029501	3.043585635	2
2500	0.00124728	2263.975155	2	38	114	3.130333768	-1.857355096	3.354871657	2
1200	0.000352359	22960	2	20	74	3.361727836	-2.16089402	4.360971884	2
3850	0.000118842	981.5668203	1	33	243	3.176091259	-1.678744662	2.99191987	2
1350	0.013888166	4120	1	32	245	3.352182518	-1.552812908	3.614897216	2
2300	0.006904083	286.2254025	1	31	84	3.908485019	-5	2.456708175	2
1500	0.02095344	178.2608696	1	28	436	3.079181246	-5	2.251056021	2
2250	0.028001874	200	2	26	405	3.230448921	-3.845959519	2.301029996	2
8100	0.00001	134.7150259	2	24	167	2.903089987	-5	2.129416039	2
1200	0.00001	1672	1	26	397	2.544068044	-5	3.223236273	2
1700	0.000142574	444	2	21	113	3.021189299	-1.761828087	2.64738297	2
800	0.00001	350.9225092	2	25	100.00	3.484299839	-2.540893326	2.545211226	2
350	0.00001	207.2	1	31	324	3.847572659	-5	2.316389751	2
1050	0.017305012	273.6	1	25	136	2.84509804	-5	2.437116093	2
3050	0.002878105	152.8	1	46	59	2.77815125	-0.245340181	2.184123354	2
7040	0.00001								
700	0.00001								
600	0.568407525								

2: Female \* Fold Reduction of viral DNA after 3 months therapy  
1: Male

We have applied the multiple linear regression models (<http://www.real-statistics.com/multiple-regression/>) to determine whether independent variables including gender, age, ALT, HBsAg (Log), spHBV/wtHBV (Log) are making a significant contribution to the fold of viral DNA reduction after IFN therapy. Results showed that ALT and the ratio of sp/wt HBV tend to be associated with the responses to IFN treatment. The ratio of sp/wt HBV was statistically associated with the responses to IFN treatment when the patients with undetectable spHBV DNAs were excluded.

Gender	Age	ALT(IU/ml)	HBsAg(Log)	SP/WT DNA (Log)	old Reduction of viral DNA (Log)
2	28	155	3.1303338	-1.409622394	1.090610708
1	21	166	3.7363965	-1.553917418	1.336007579
1	32	50	3.69897	-1.728413739	0.884361286
1	36	95	4.3181051	-1.908680077	0.727117892
1	29	145	3.9652017	-1.421664827	1.211157884
1	26	80	2.845098	-0.175701502	1.97068936
2	28	136	3.5502284	-1.505751708	0.886056648
1	28	472	3.6283889	-0.094974468	0.765595213
2	27	272	3.1903317	-0.716451328	1.206842841
2	24	115	3.0211893	-2.157181059	1.641328436
2	29	343	3.3521825	-0.838669357	-0.921314807
1	25	173	3.4393327	-0.548778242	-1.121685579
2	39	259	3.4065402	0.130647597	1.62572613
2	21	227	3.9777236	-1.120533777	1.239222846
2	28	79	3.0791812	-1.938934772	0.735764377
1	46	201	4.7252744	-0.889243324	0.409209309
2	28	239	2.4771213	-0.06773129	1.818092658
1	28	69	2.60206	-0.252163033	0.766729699
1	22	42	2.544068	0.042144016	-1.140178703
1	36	61	3.1760913	-0.241726361	0.951436073
1	38	145	3.748188	-3.71350616	0.787775899
1	29	147	4.1673173	-0.868872759	1.643974143
1	39	166	3.9800943	-2.621970987	0.954677021
1	28	389	4.0472749	-2.662610105	1.315154638
1	22	118	4.4601458	-0.356119229	0.66756154
1	27	50	3.8027737	-2.007267791	0.642065153
1	32	241	4.0334238	-2.334787654	0.910094889
1	26	115	4.0934217	-2.994044286	0.549750892
1	28	114	4.8590242	-1.642218892	0
1	26	82	4.0588055	-2.99223795	0.661543506
1	24	305	4.0549959	-1.79343629	2.171340103
1	40	165	2.7489629	-1.442636355	2.072411834
2	32	184	2.39794	-3.452613076	2.366497075
1	27	169	2.39794	-2.474566454	2.265638021
2	34	42	2.39794	-2.461923824	2.17293274
1	39	300	3.763428	-2.19089742	5.013679697
2	33	387	3.1303338	-3.166484492	4.257274869
2	22	121	3.30103	-1.649043083	3.654073355
1	32	107	3.0849336	-3.231456325	4.910094889
1	25	103	3.5378191	-0.661663917	3.634429284
1	30	408	3.5910646	-2.013589393	3.490797478
1	29	126	3.6384893	-3.041306239	3.586700236
1	42	471	3.462398	-2.880556102	3.707743929
1	25	204	3.5740313	-2.612739686	2.43062609
1	36	803	3.6384893	-1.711757283	2.772113295
2	55	271	3.5797836	-2.604812707	2.641091881
1	33	119	3.5118834	-3.208779131	3.196895468
1	25	287	3.8027737	-1.906221867	3.586447437
1	49	226	3.39794	-2.904036175	3.676559919
2	29	114	3.0791812	-3.453014229	3.72916479
2	31	96	3.5854607	-3.925029501	3.043585635
2	38	114	3.1303338	-1.857355096	3.354871657
2	20	74	3.3617278	-2.16089402	4.360971884
1	33	243	3.1760913	-1.678744662	2.99191987
1	32	245	3.3521825	-1.552812908	3.614897216
2	26	405	3.2304489	-3.845959519	2.301029996

Regression Analysis

OVERALL FIT

Multiple R 0.5466  
R Square 0.2987  
Adjusted R Square 0.2326  
Standard Error 1.258  
Observations 59

ANOVA

Alpha 0.05

	df	SS	MS	F	p-value	sig
Regression	5	35.727	7.1454	4.5152	0.0017	yes
Residual	53	83.873	1.5825			
Total	58	119.6				

Coefficients

	coeff	std err	t stat	p-value	lower	upper
Intercept	2.5351	1.6067	1.5779	0.1205	-0.687	5.7577
Gender	-0.045	0.3786	-0.12	0.9049	-0.805	0.7139
Age	0.0177	0.0234	0.7562	0.4529	-0.029	0.0646
ALT(IU/ml)	0.0019	0.0012	1.5321	0.1315	-6E-04	0.0044
HBsAg(Log)	-0.714	0.3269	-2.183	0.0335	-1.37	-0.058
SP/WT DNA (Log)	-0.578	0.1567	-3.689	0.0005	-0.892	-0.264

2	21	113	3.0211893	-1.761828087	2.64738297
2	25	100	3.4842998	-2.540893326	2.545211226
1	46	59	2.7781513	-0.245340181	2.184123354

SP/WT HBV DNA>0.00001

**Table S4. Primers for qPCR detection of OAS-1, GAPDH, mMx1, mSTAT1 and mGAPDH**

<b>Gene</b>	<b>Primer Sequences(5'→3')</b>	<b>Length</b>
OAS-1	F- TGCCAGACACGTGTTCCGC R- GAGGAAGACAACCAGGTCAGCG	185 bp
GAPDH	F- GGTATCGTGGAAGGACTCATGA R- ATGCCAGTGAGCTTCCCGTTCAGC	188 bp
mMx1	F- GGATGTGATGCGGAACCT R- AGAAGAATGCTGAAGTATGAGTGA	156 bp
mSTAT1	F- CTTCCACGACCTCCTCTC R- CTCCTTCAGACAGTTGTAGATG	167 bp
mGAPDH	F- AGTATGTCGTGGAGTCTA R- CAATCTTGAGTGAGTTGTC	162 bp

## **References**

1. Naito H, Hayashi S, Abe K. Rapid and specific genotyping system for hepatitis B virus corresponding to six major genotypes by PCR using type-specific primers. *J Clin Microbiol* 2001;39:362-364.