Table S1. Sorting of the 26 HCC studied according to HBsAg status.

HBsAg status	NT/T	SEX	AGE	PATHOLOGY		*TP53* status	p53 immuno-staining	*CTNNB1* status	HCV RNA	HBV			
				TUMOR GRADE	METAVIR SCORE					DNA	Genotype, *serotype*	Mutation (NT/T)	
												BCP	PreCore
-	1	M	46	G4	A2 F4	***G331H***	-	WT	+	+	C, *adr*	WT+**DV**/**DV**	WT/WT
	2	M	40	G1	A0 F2	WT	-	WT	-	+	NA	WT+**DV**/WT+**DV**	WT/WT
	3	F	37	G2	A0 F1	WT	-	WT	-	+	B, *adw2*	NA	NA
	4	M	61	G2-3	A2 F4	WT	-	***T41A***	-	+	C, *adr*	NA/WT	WT/WT
	5	M	73	G3	NA	WT	-	***S37F***	-	+	NA	NA	NA
	6	M	70	G2	NA	WT	-	WT	-	-	-	-	-
	7	M	39	G3-4	A0 F3	WT	-	WT	-	-	-	-	-
	8	F	50	G2-3	A0 F1	WT	20-50%	WT	-	-	-	-	-
	9	F	35	G2-3	NA	WT	<10%	NA	-	-	-	-	-
	10	M	53	G3	A0 F2	WT	10-20%	WT	+	-	-	-	-
+	11	M	34	G4	A1 F4	***R249S***	<10%	WT	+	+	C, *adr*	**DV**/**DV**	WT/WT
	12	M	43	G1-2	A2 F4	***R249S***	<10%	***S41F***	-	+	C, *adr*	NA	NA
	13	M	50	G3-4	A0 F1	***R249S***	<10%	WT	-	+	B, *adw2*	NA	NA
	14	M	44	G3	NA	***R249S***	<10%	WT	-	+	C, *adr*	NA	NA
	15	M	60	G3-4	A2 F4	***P278R***	10-20%	***S33Y***	-	+	C, *NA*	**DV**/WT+**DV**	WT/WT
	16*	M	42	G2	A0 F2	WT	-	NA	-	+	NA	WT+**DV**/WT+**DV**	WT/WT
	17	M	39	G2	A1 F4	WT	-	WT	+	+	NA	NA/**DV**	WT/WT
	18	M	62	G2-3	A1 F3	WT	-	WT	-	+	C, *adr*	**DV**/WT+**DV**	**MUT**/WT
	19*	M	36	G4	A1 F2	WT	-	NA	-	+	C, *NA*	NA	NA
	20	M	37	G3-4	A0 F1	WT	-	WT	-	+	C, *NA*	NA	NA
	21	M	57	G2-3	A1 F3	WT	-	WT	-	+	NA	NA	NA
	22	M	17	G3	NA	***R249S***	<10%	***S33Y***	-	-	NA	NA	NA
	23*	M	40	G2-3	NA	WT	-	NA	-	-	NA	NA	NA
NA	24*	NA	NA	G3-4	A0 F2	***R249S***	<10%	NA	-	+	NA	NA	NA
	25	NA	NA	G1	A0 F4	***R249S***	<10%	***S37F***	-	+	NA	NA	NA
	26	F	48	NA	A0 F1	WT	-	WT	-	+	NA	WT/WT	WT/WT

-=negative, +=positive, NA=not available, NT=non-tumoral tissue, T=tumoral tissue, WT=wild-type, DV=dual variant (*A1764G*/*T1762A*), /=no sample, *=four HBV-positive cases with non-available *CTNNB1* status were excluded in Fig. 3. p53 immunostaining is given for T samples as it was negative for all the NT tissues.#

Table S2. DHPLC conditions for exon 3 of *CTNNB1* gene.

Exon	Temperature (°C)	Acetonitrile gradient (%B)	Positive controls
3	60	52-60	H358S (codon 75: **A**CT-**G**CT)
	60	52-60	HCT116 (codon 45: deleted)
	63	49-57	SW48 (codon 33: T**C**T-T**A**T)

Temperature and gradient analyzes were determined by Transgenomic software. Forward primer (β_f) 5'-ccaatctactaatgctaatactg-3', reverse primer (β_r) 5'-ctgcattctgactttcagtaagg-3'

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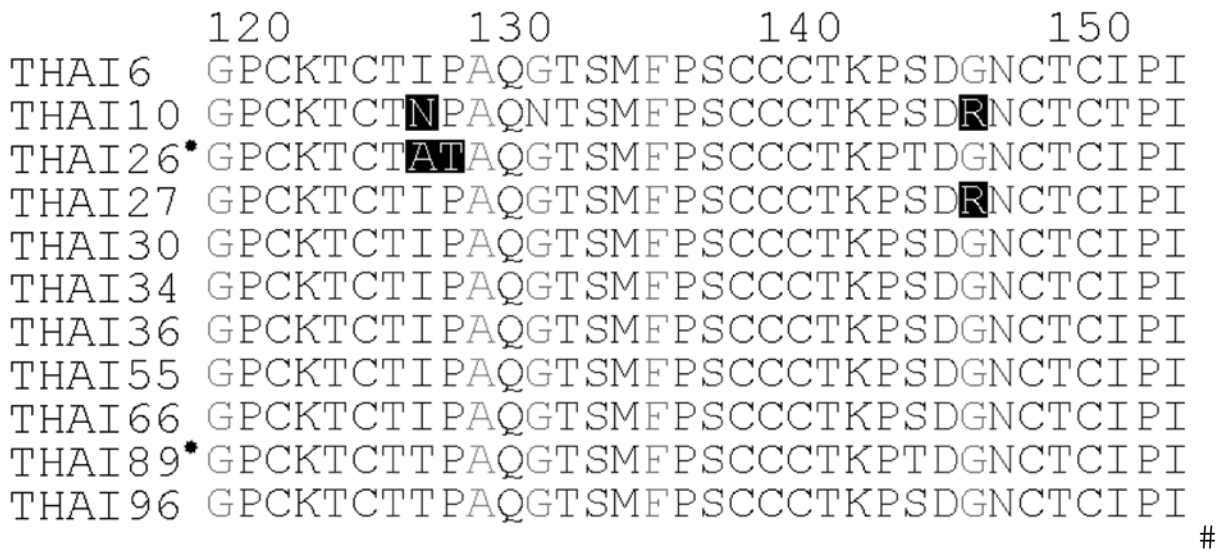

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Figure S3. Alignments of HBsAg in determinant “a” region from 11 HBV patients (classified as genotype C except samples marked with stars which are genotype B). Samples 10, 26 and 27 are occult HBV infections. *R145G* is a common mutation causing false negative results for HBV serological testing using first generation antibodies. Double mutant *A126I* / *T127P* was detected in case 26.

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