

# *New Biomarkers for Chronic Hepatitis B: ready for clinical use?*

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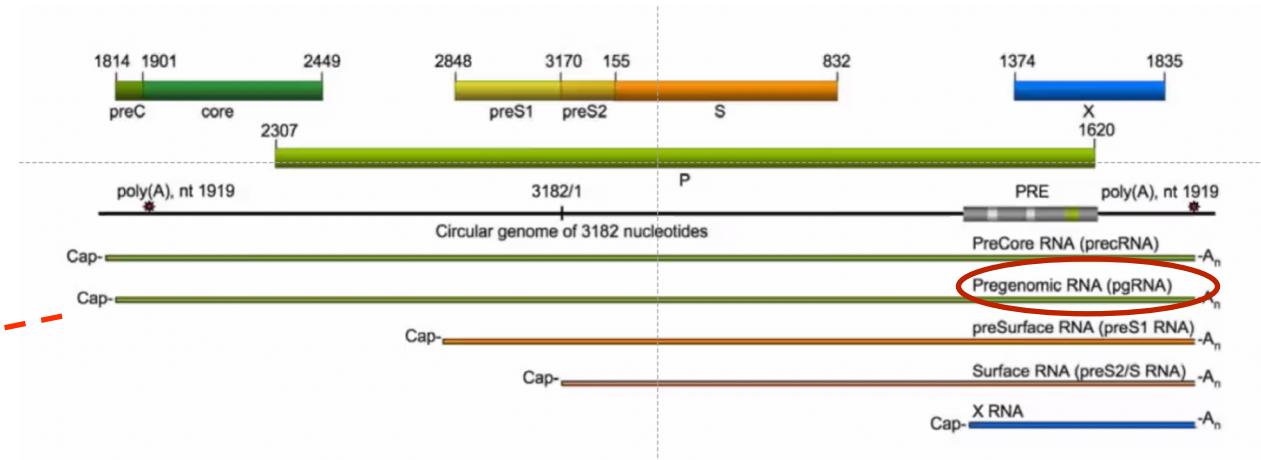
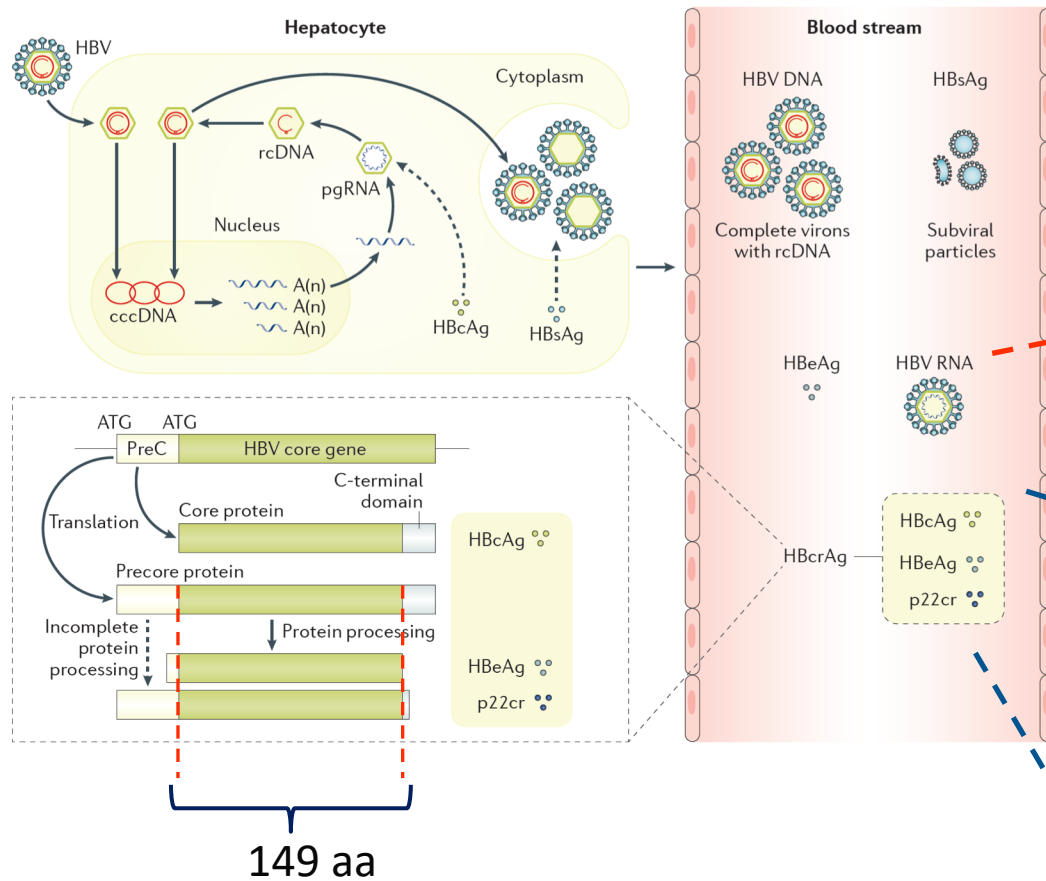
Hong Kong



# What are ideal biomarkers ?

- Non-invasive
- Able to stratify disease stages and risk of complications
- Reflect intrahepatic virologic status e.g. cccDNA content
- Predictive of cure including functional and complete cure
- Assist identification of treatment response including new agents
  - Proof of concept of modes of action
- Assist patient management including
  - Treatment initiation
  - Combination of treatment
  - Treatment cessation

# Conventional and new serum biomarkers

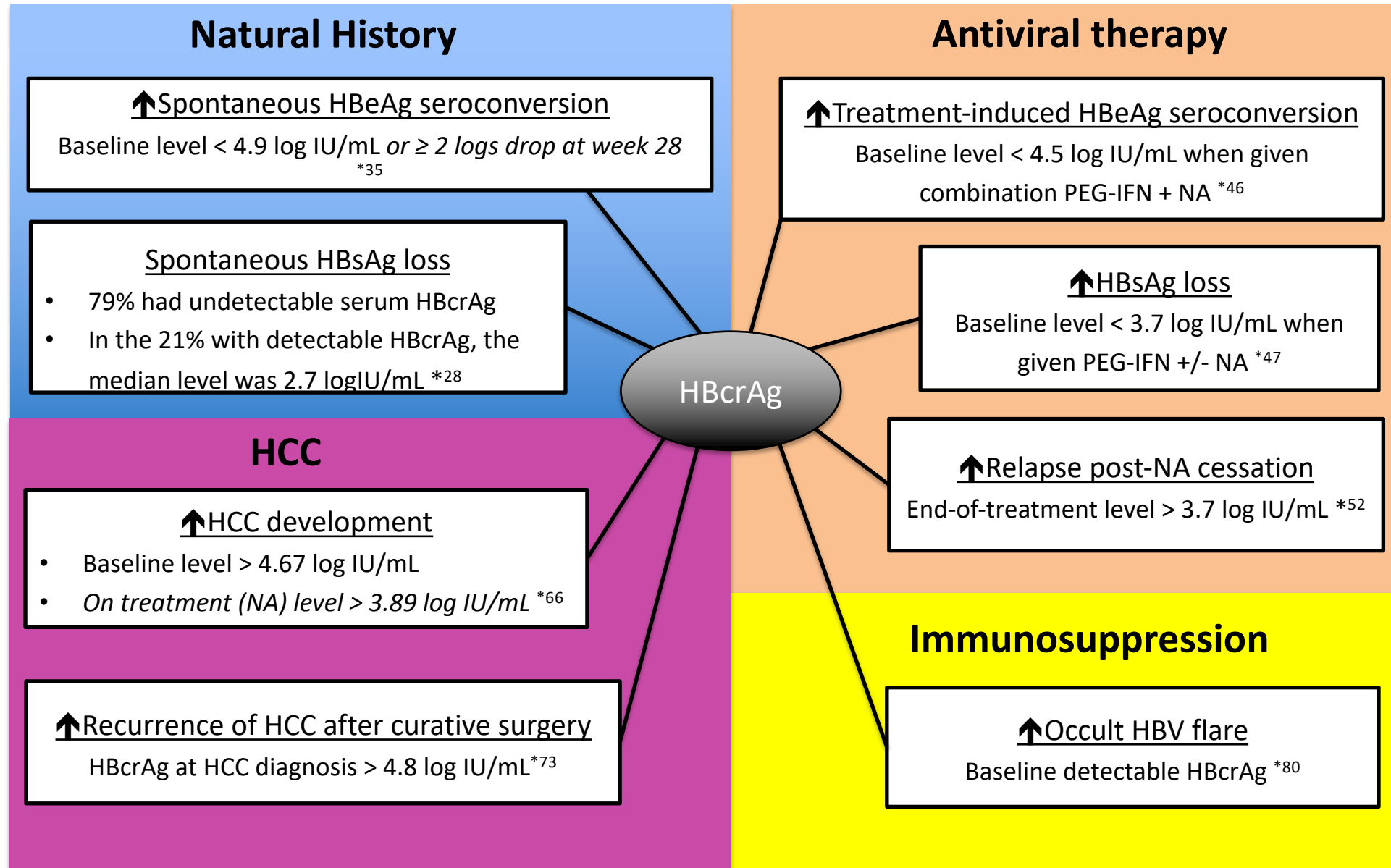


Sommer G & Heise T. *Front Biosci* 2008;13:5533-47



Yuen MF et al., *Nat Rev Dis Primers*. 2018;4:18035

# Multifunctional roles of HBcrAg in chronic hepatitis B





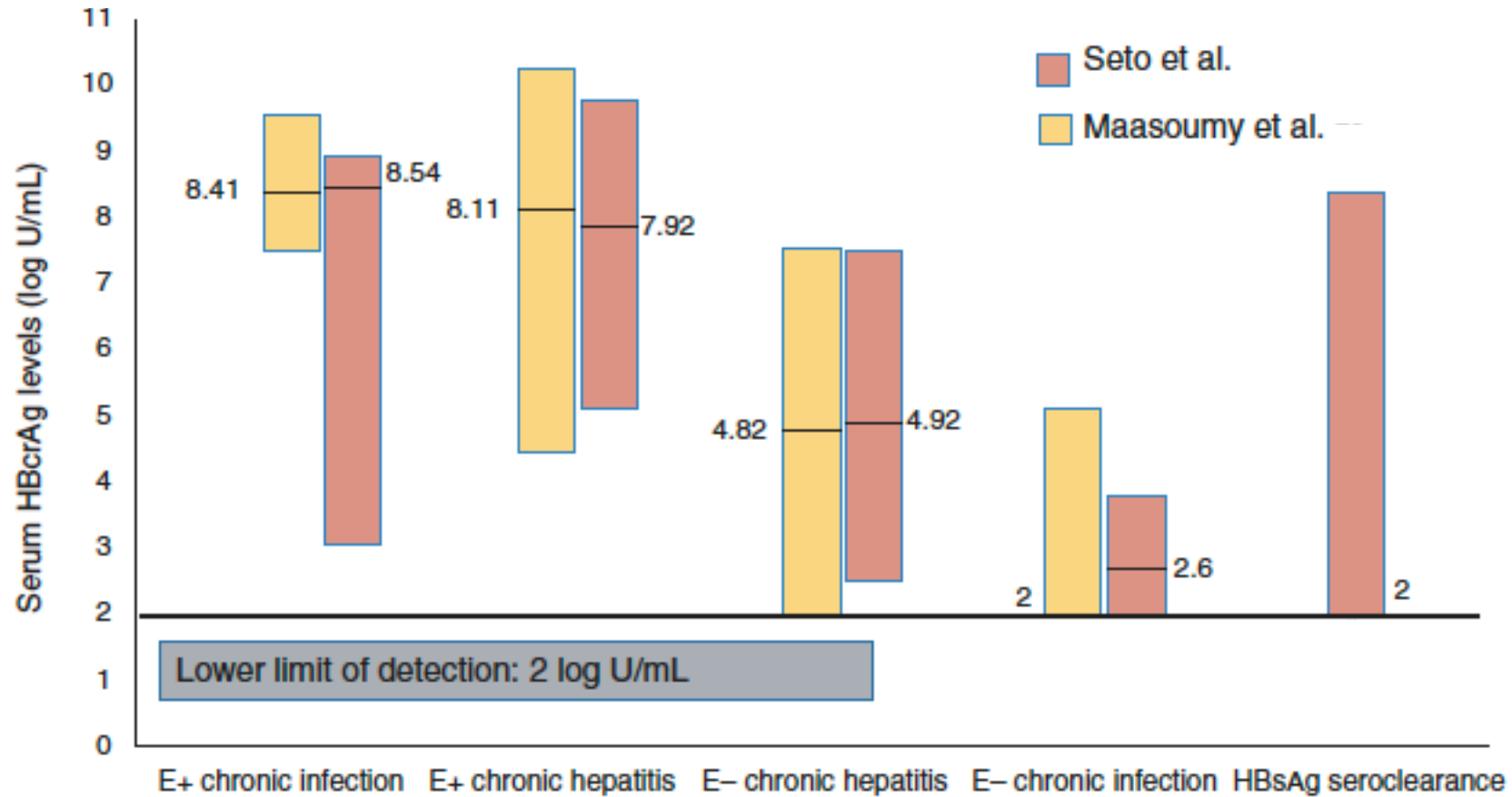
# HBcrAg in chronic hepatitis B disease

- Natural history of CHB
- Correlations with other established markers
- Relationship with HBeAg seroconversion and long-term complications
- Treatment effect
- Role in special populations

# HBcrAg in chronic hepatitis B disease

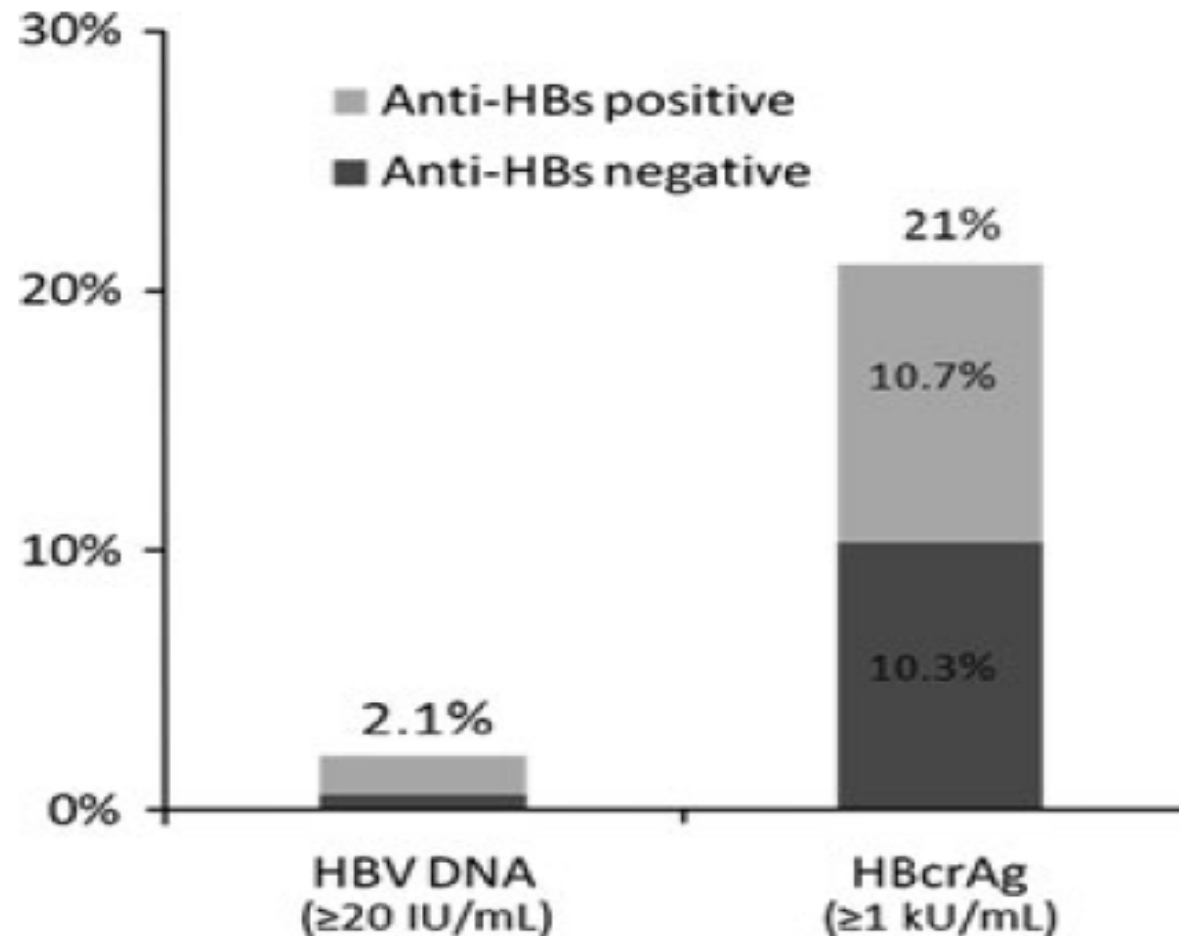
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# HBcrAg in natural history of chronic hepatitis B

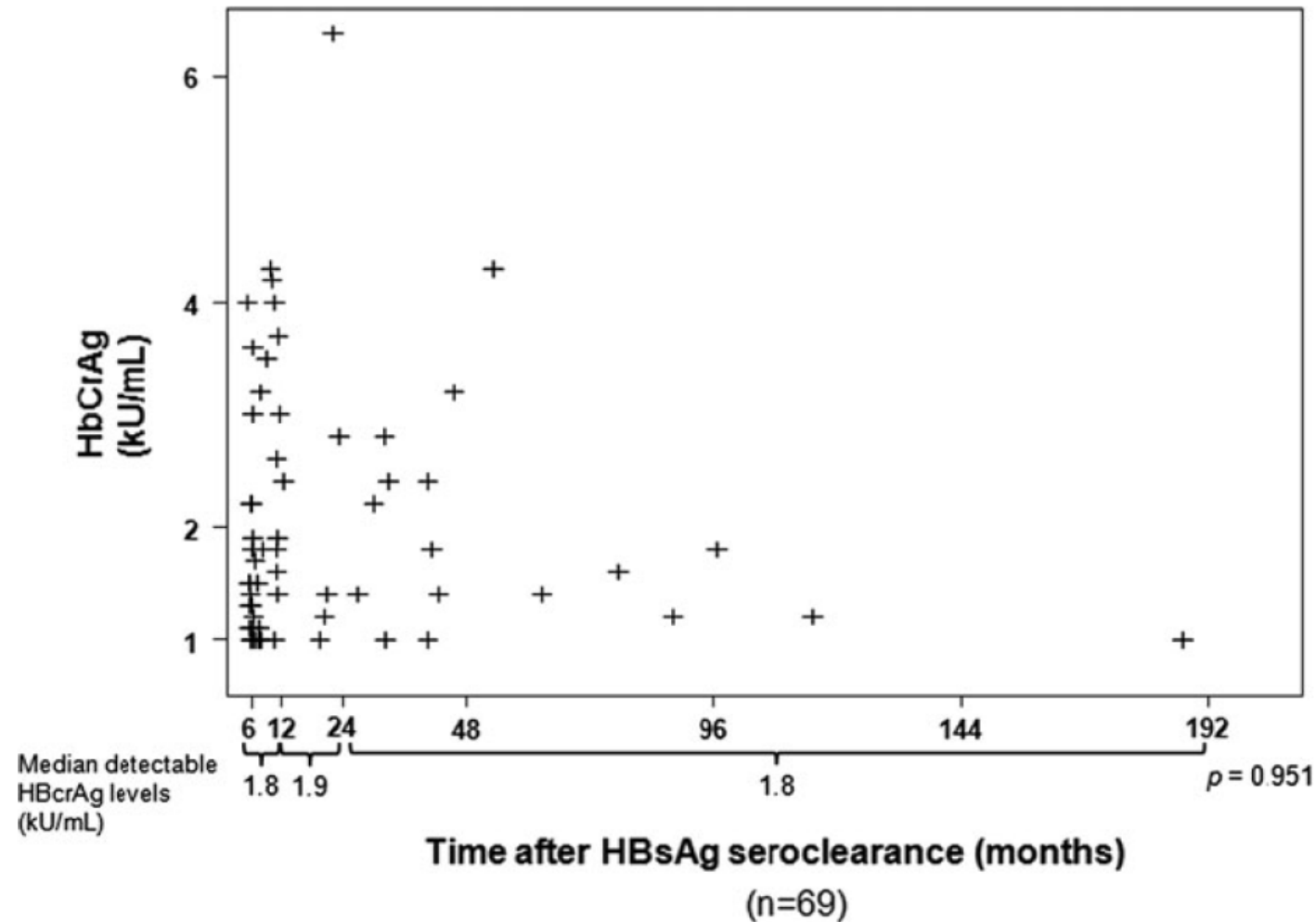


# HBcrAg in chronic hepatitis B with HBsAg seroclearance

Patient population: 329 patients with HBsAg seroclearance



# Detectable HBcrAg over long time after HBsAg seroclearance



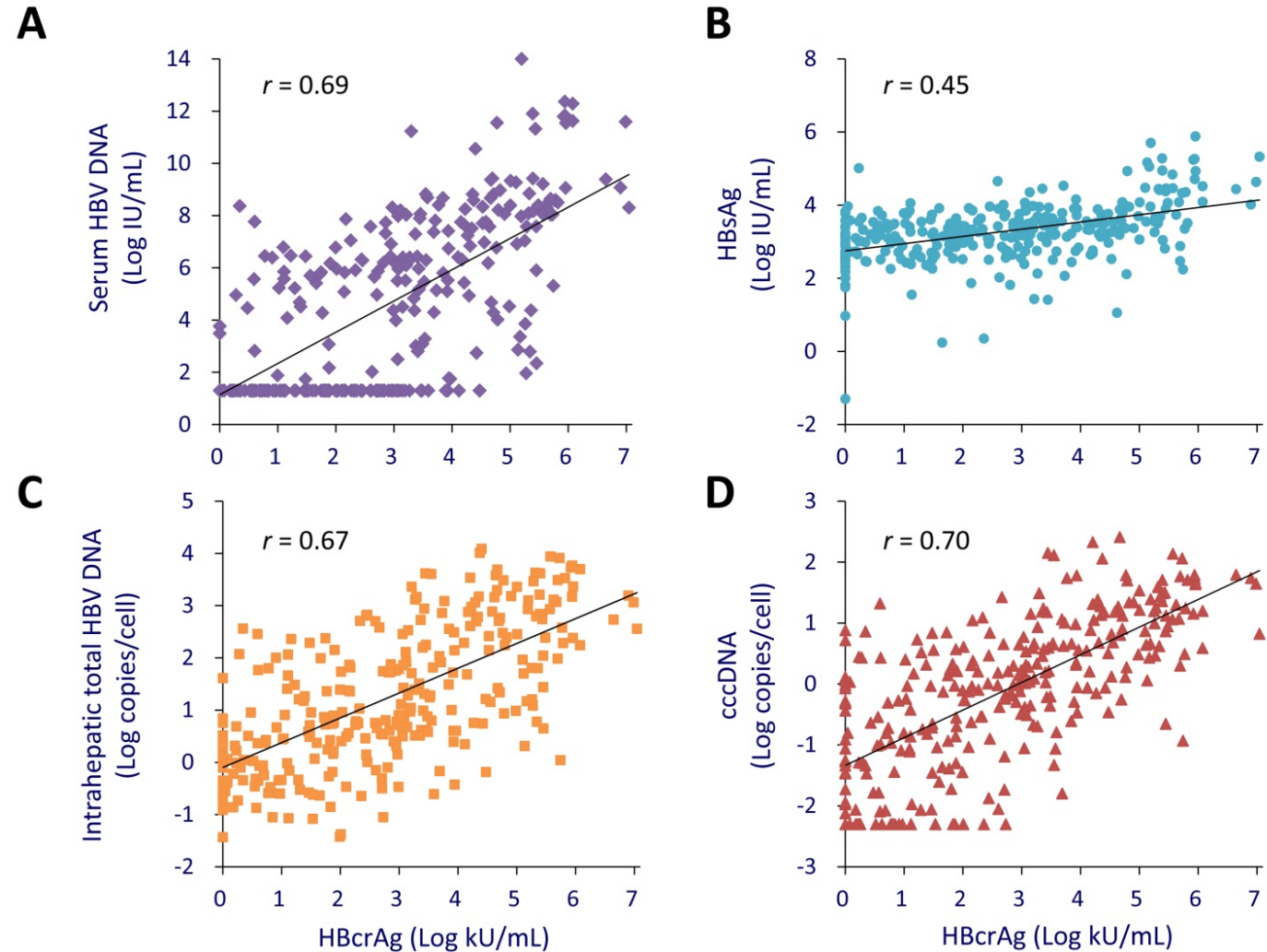
# HBcrAg in chronic hepatitis B disease

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# Correlation between HBcrAg and serum HBV DNA, HBsAg, intrahepatic total HBV DNA, cccDNA

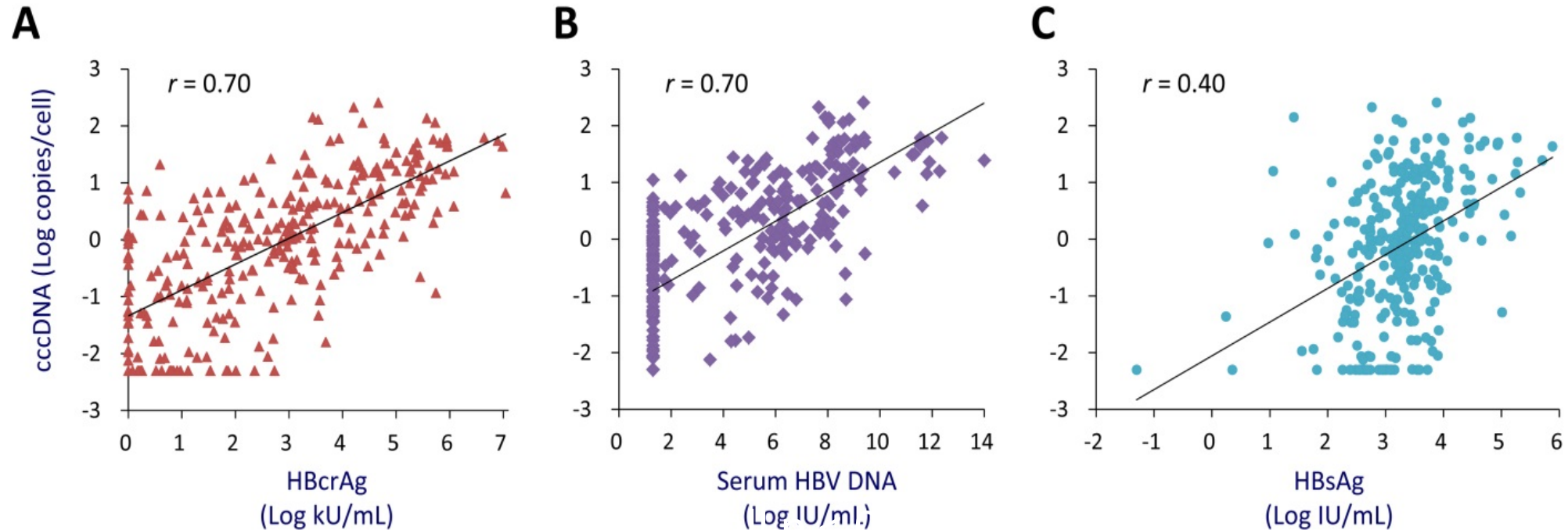
138 patients: 56% HBeAg +ve

— 305 liver samples with corresponding serum samples





# Correlation between cccDNA and serum HBcrAg, HBV DNA, HBsAg



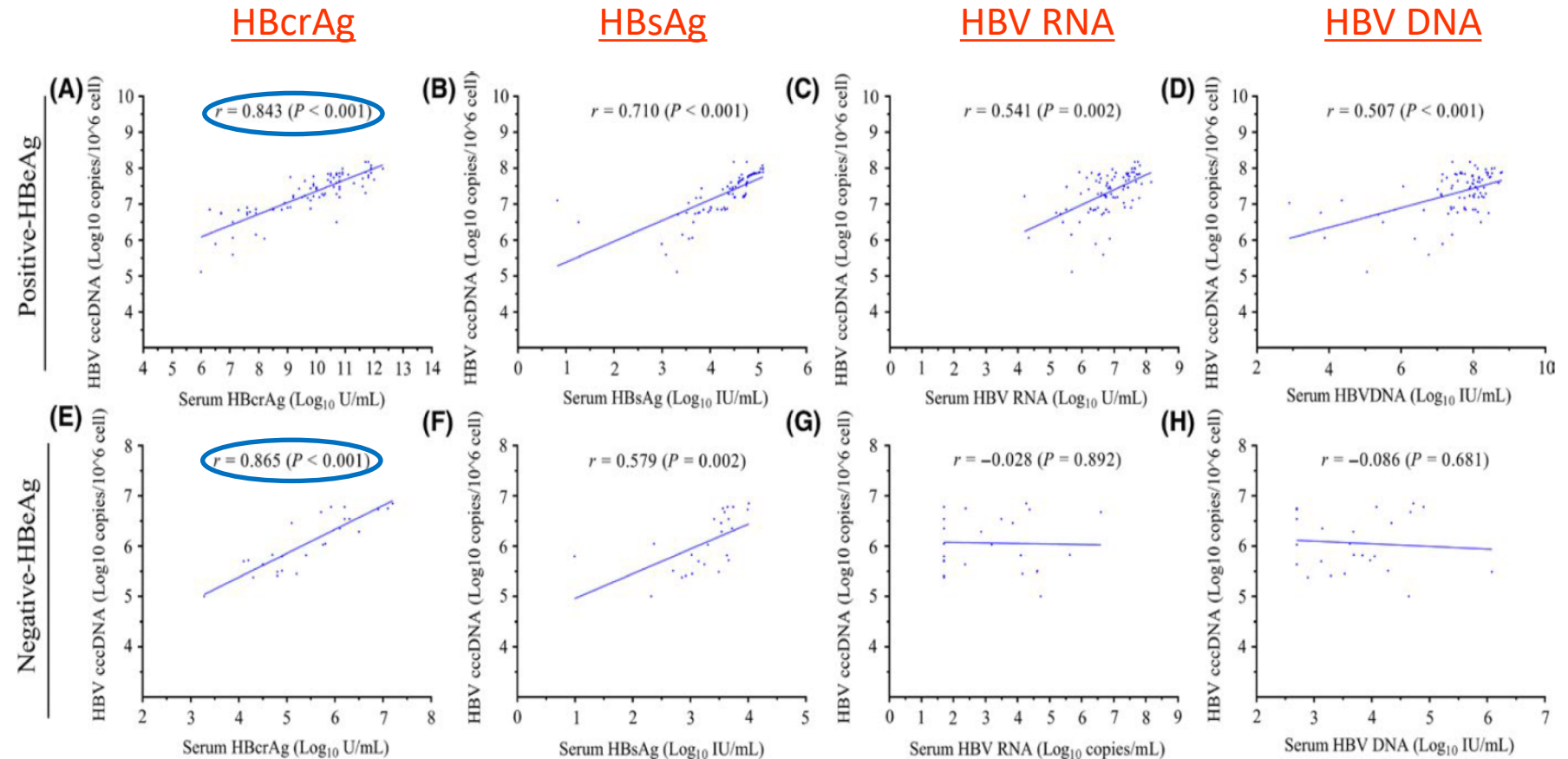
Samples with undetectable serum HBV DNA

- 78% still have detectable HBcrAg
  - HBcrAg still correlated with cccDNA in the liver ( $r=0.42$ ,  $p<0.0001$ )

# Correlation between cccDNA and HBcrAg, HBsAg, HBV DNA, HBV RNA

110 treatment naïve patients

- 85 HBeAg +ve
- 25 HBeAg -ve



# Correlation between serum HBcrAg, HBsAg, HBV DNA and intrahepatic viral markers

Study population: 130 patients (36 HBeAg +ve; 94 HBeAg –ve)

	Liver markers			
	tHBV-DNA	cccDNA	pgRNA	cccDNA transcriptional activity (pgRNA/cccDNA)
ALL <sup>1</sup>				
HBcrAg	R = 0.85; <i>p</i> <0.0001	R = 0.74; <i>p</i> <0.0001	R = 0.75; <i>p</i> <0.0001	R = 0.52; <i>p</i> <0.0001
qHBsAg	R = 0.38; <i>p</i> = 0.003	R = 0.26; <i>p</i> = 0.044	R = 0.35; <i>p</i> = 0.006	R = 0.29; <i>p</i> = 0.023
Serum HBV DNA	R = 0.78; <i>p</i> <0.0001	R = 0.57; <i>p</i> <0.0001	R = 0.41; <i>p</i> <0.0001	R = 0.25; <i>p</i> = 0.015
HBeAg+ chronic hepatitis <sup>2</sup> (n = 32)				
HBcrAg	R = 0.79; <i>p</i> <0.0001	R = 0.80; <i>p</i> <0.0001	R = 0.68; <i>p</i> = 0.004	R = –0.02; <i>p</i> = n.s.
qHBsAg	R = 0.49; <i>p</i> = n.s.	R = 0.33; <i>p</i> = 0.01	R = 0.32; <i>p</i> = n.s.	R = 0.26; <i>p</i> = n.s.
Serum HBV DNA	R = 0.50; <i>p</i> = 0.003	R = 0.29; <i>p</i> = n.s.	R = 0.41; <i>p</i> = 0.07	R = 0.18; <i>p</i> = n.s.
HBeAg– chronic hepatitis <sup>1</sup> (n = 43)				
HBcrAg	R = 0.61; <i>p</i> <0.0001	R = 0.25; <i>p</i> = n.s.	R = 0.81; <i>p</i> <0.0001	R = 0.70; <i>p</i> <0.0001
qHBsAg	R = –0.15; <i>p</i> = n.s.	R = –0.4; <i>p</i> = 0.01	R = –0.02; <i>p</i> = n.s.	R = 0.15; <i>p</i> = n.s.
Serum HBV DNA	R = 0.71; <i>p</i> <0.0001	R = 0.19; <i>p</i> = n.s.	R = 0.79; <i>p</i> <0.0001	R = 0.66; <i>p</i> = 0.0002
HBeAg– chronic infection <sup>1</sup> (n = 18)				
HBcrAg	R = 0.34; <i>p</i> = n.s.	R = 0.47; <i>p</i> = 0.05	R = 0.29; <i>p</i> = 0.09	R = 0.11; <i>p</i> = n.s.
qHBsAg	R = 0.24; <i>p</i> = n.s.	R = –0.03; <i>p</i> = n.s.	R = –0.12; <i>p</i> = n.s.	R = 0.08; <i>p</i> = n.s.
Serum HBV DNA	R = –0.02; <i>p</i> = n.s.	R = 0.27; <i>p</i> = n.s.	R = 0.39; <i>p</i> = n.s.	R = 0.28; <i>p</i> = n.s.

HBcrAg, hepatitis B core-related antigen; HBeAg, hepatitis B e antigen; HBV, hepatitis B virus; pgRNA, pregenomic RNA; qHBsAg, quantitative hepatitis B surface antigen. The correlation coefficient was calculated using Spearman's correlation test. Twotailed *p* value was calculated for a risk threshold  $\alpha = 0.05$ .

<sup>1</sup> Only patients with positive HBcrAg quantification (i.e. >3 LogU/ml) were included in the analysis.

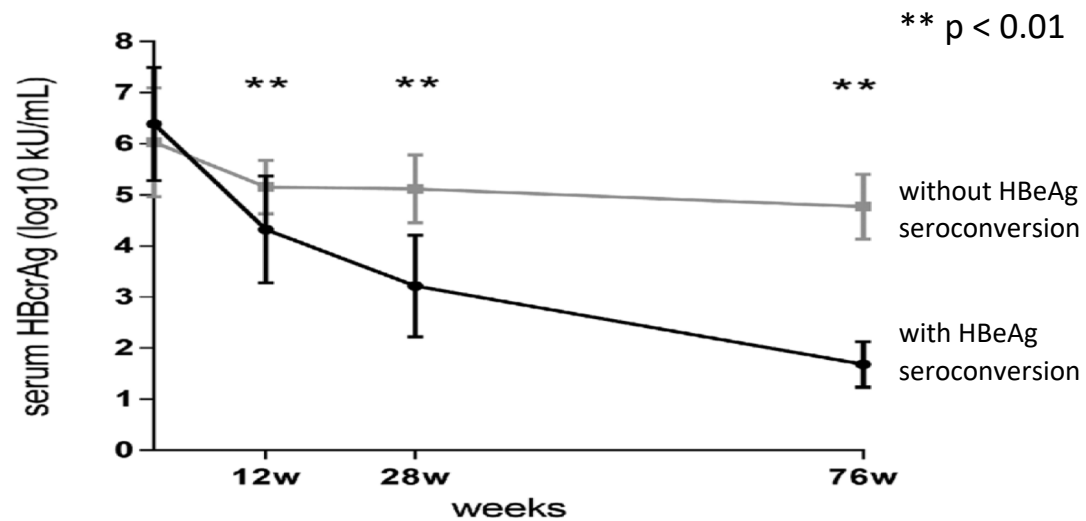
<sup>2</sup> HBeAg+ chronic infection category was composed by only 4 patients (see Table S1), therefore it was not included in the analysis.

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- Treatment effect
- Role in special populations

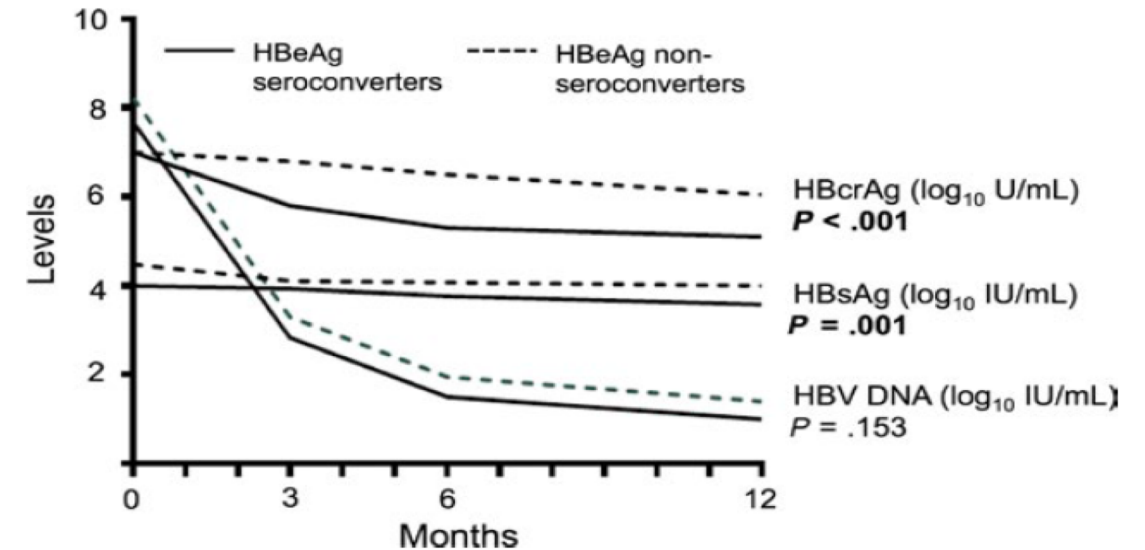
# HBcrAg and spontaneous and Nuc-induced HBeAg seroconversion

Patients without treatment



Song et al. J Med Virol 2017;89:463-468

Patients on nucleos(t)ide analogue



Wang B et al., J Viral Hepat 2018;25(8):886-893

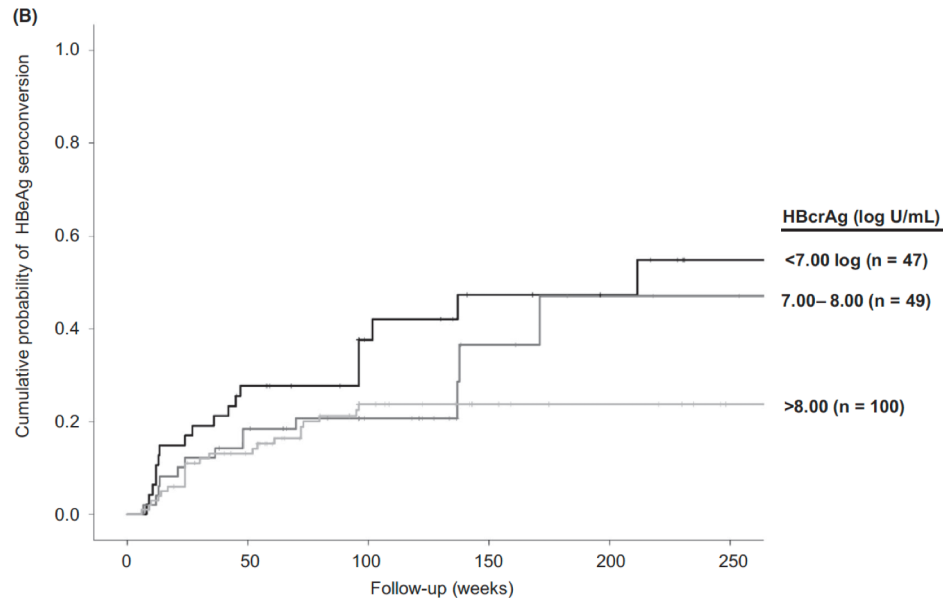
# HBcrAg and Nuc-induced and sustained HBeAg seroconversion

196 HBeAg +ve patients on NUCs

55 achieved HBeAg seroconversion over a median of 34 weeks

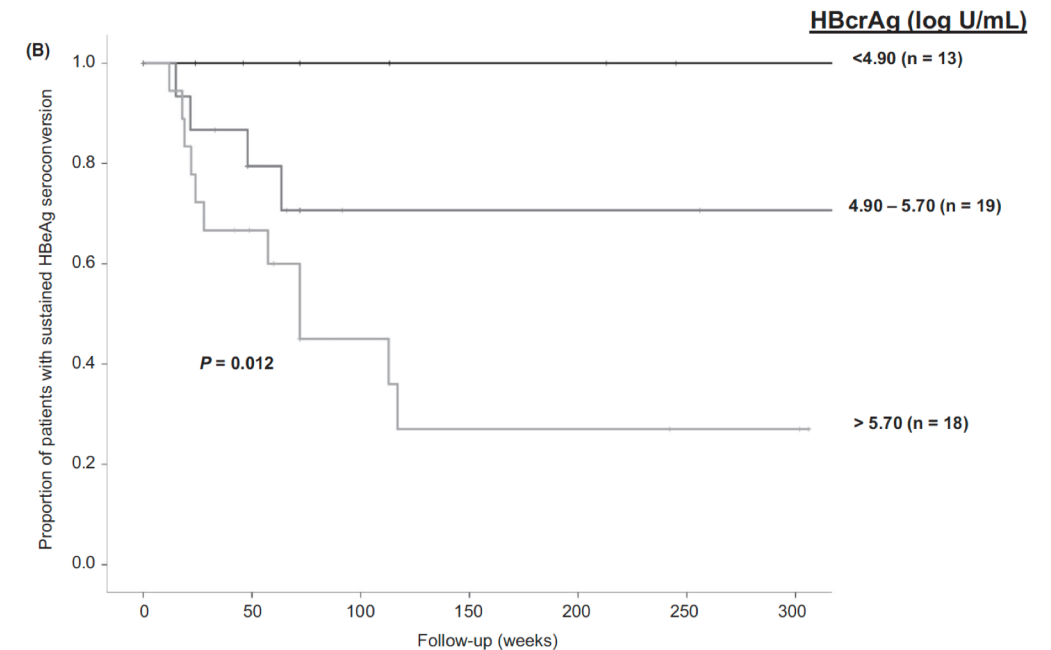
## Baseline HBcrAg level

with HBeAg seroconversion (7.42 log U/mL) vs. without HBeAg seroconversion (7.86 log U/mL)  $p = 0.017$



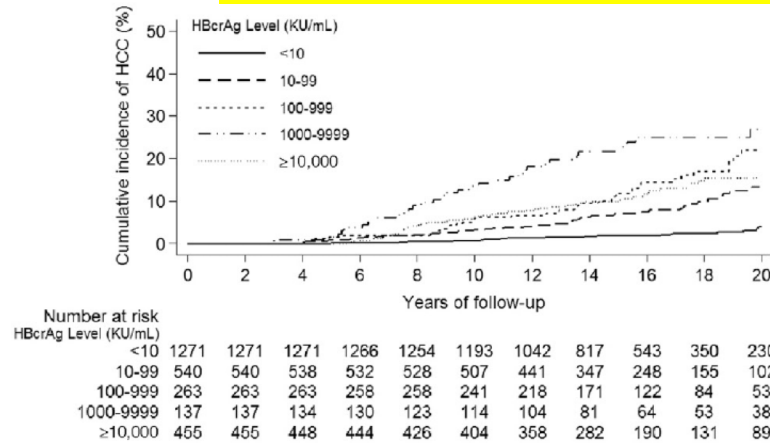
## Lower HBcrAg levels at HBeAg seroconversion

high chance of sustained HBeAg seroconversion after stopping of NUCs

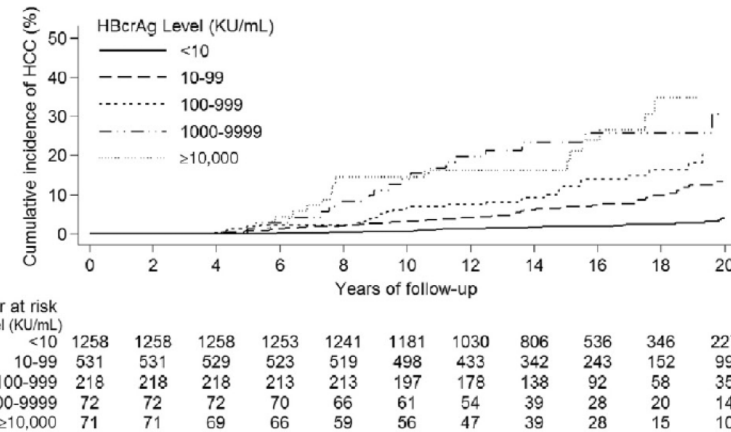


# HBcrAg and HCC development

Whole population n=2,666

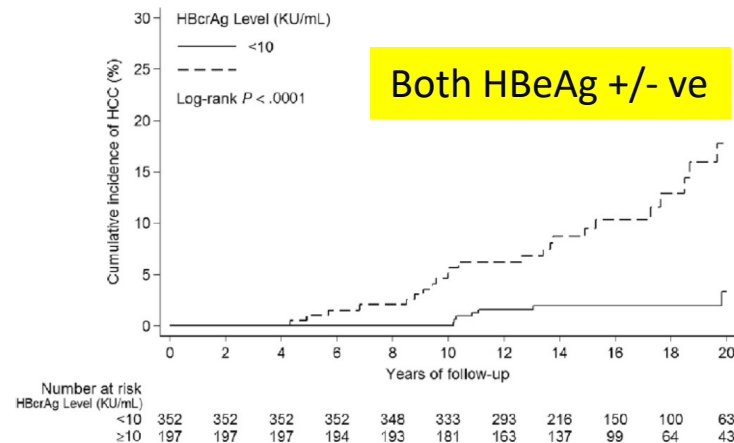


HBeAg -ve n=2,150

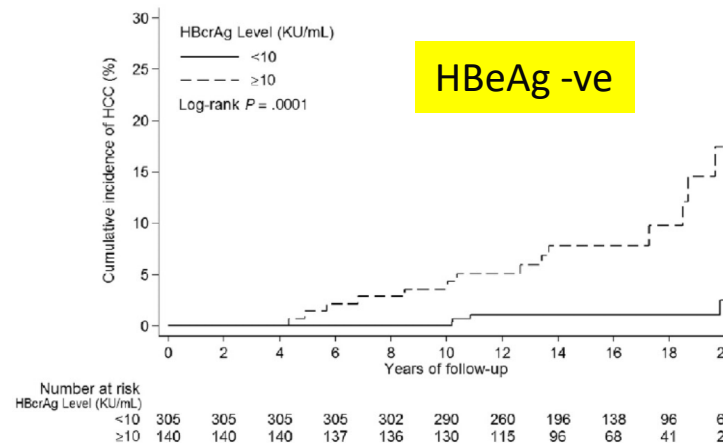


Overall, increasing levels of HBcrAg associated with higher risk of HCC

Patients with IVL (HBV DNA 2,000 – 19,999 IU/mL)



Both HBeAg +/- ve



HBeAg -ve

Among patients with IVL, HBcrAg > 10 KU/mL significantly associated with a higher risk of HCC

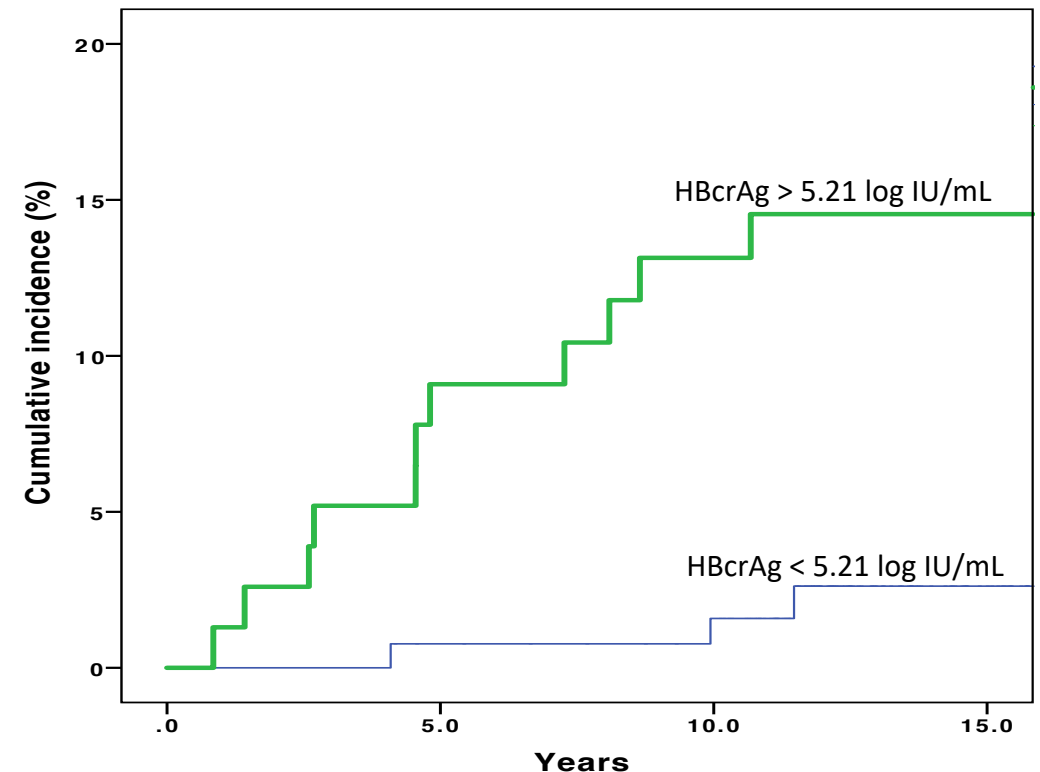


# HBcrAg after spontaneous HBeAg seroconversion: HCC development

- 207 CHB with documented time of HBeAg seroconversion
- HBcrAg and HBsAg measured within 3 years after HBeAg seroconversion

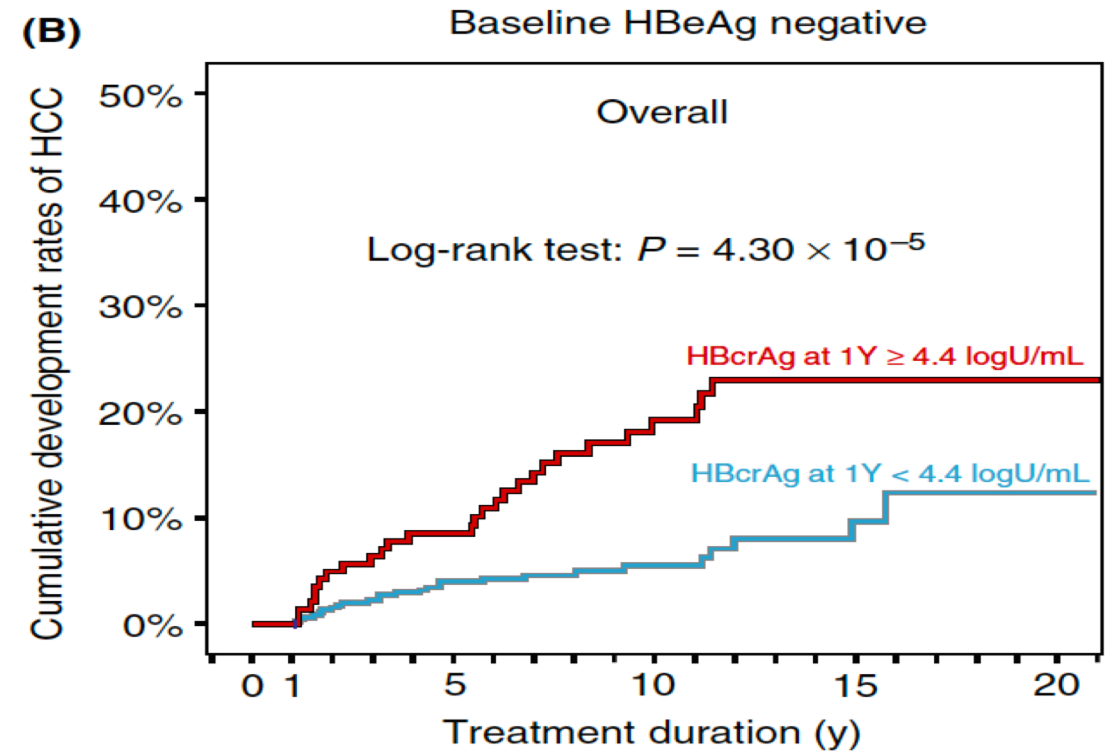
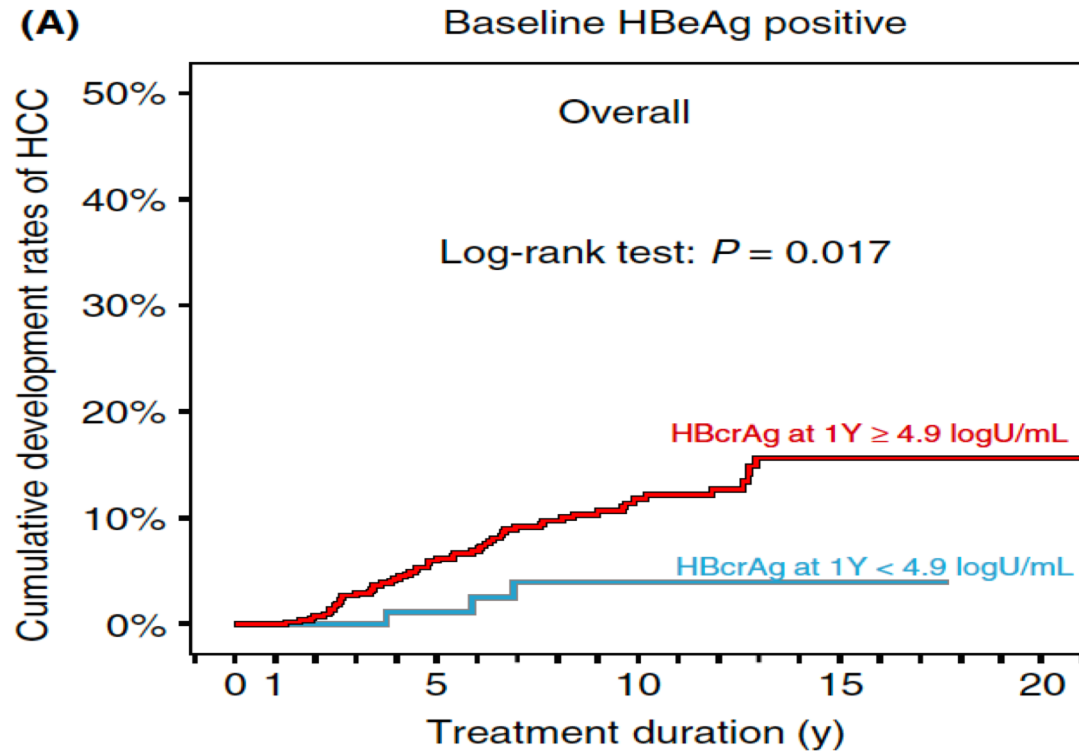
## Multivariable analysis

	Hazard ratio	95% CI	p value
Age (>40 years old)	4.60	1.00-21.04	0.049
Baseline cirrhosis	6.23	1.87-20.72	0.003
HBcrAg (log IU/ml)	1.75	1.06-2.90	0.032



# HBcrAg at year 1 of NUC treatment and HCC

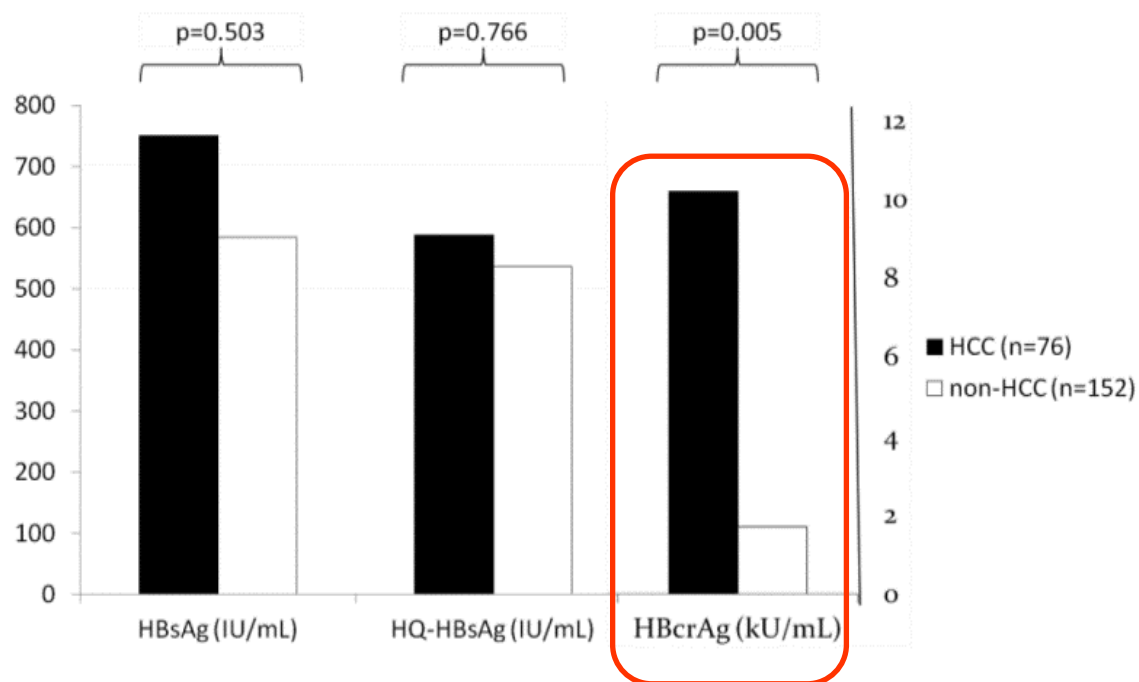
Study population: 1,268 patients on Nucs (667 HBeAg +ve; 601 HBeAg -ve)



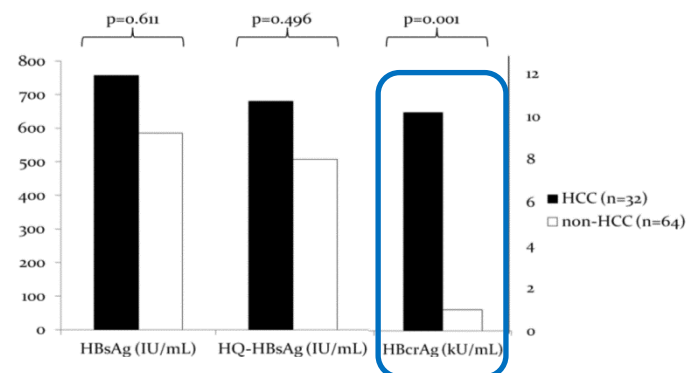
# HBcrAg and HCC in NUC-treated patients with undetectable HBV DNA

Study population: 228 patients on Nucs

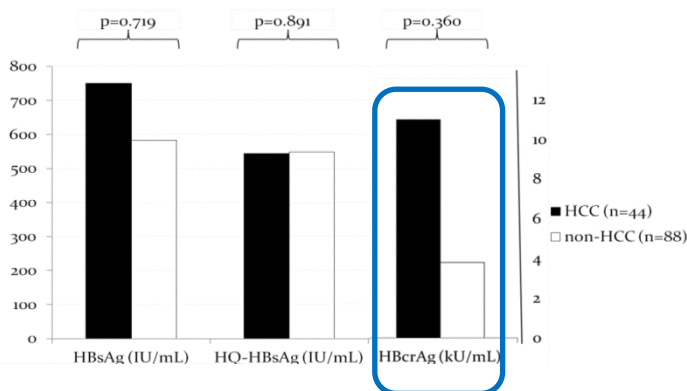
- 76 patients with HCC vs. 152 without HCC



Patients without cirrhosis



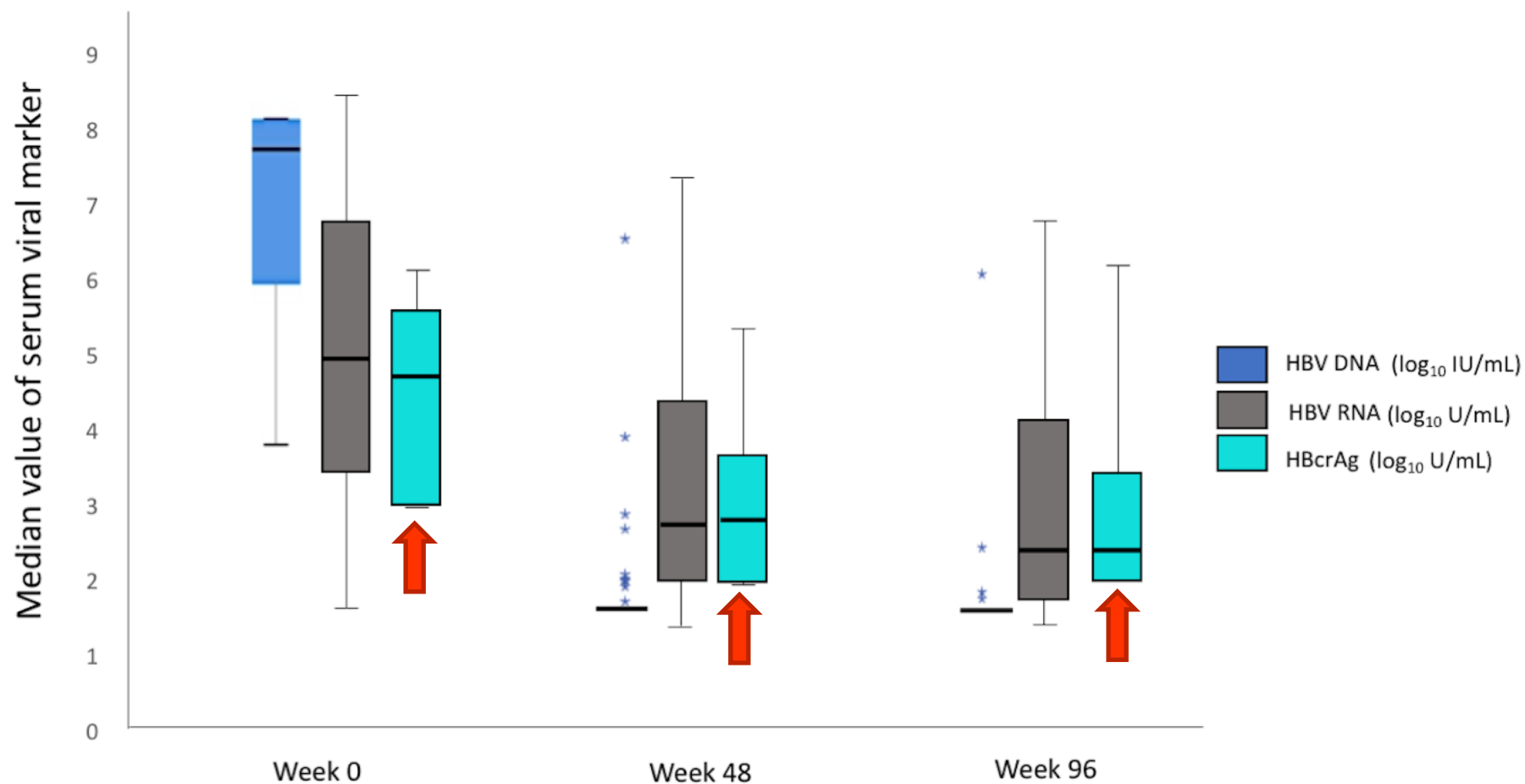
Patients with cirrhosis



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- **Treatment effect**
- Role in special populations

# HBcrAg levels on 2-year TDF/ TAF/ ETV treatment



# HBcrAg levels on long-term entecavir treatment

Treatment - naïve Chinese CHB patients treated for entecavir in the real world setting for up to 7 years

HBcrAg measurement at baseline, year 1, 5 and 7

Annual decline: 0.244 log KU/mL/year ( $p = 0.001$ )

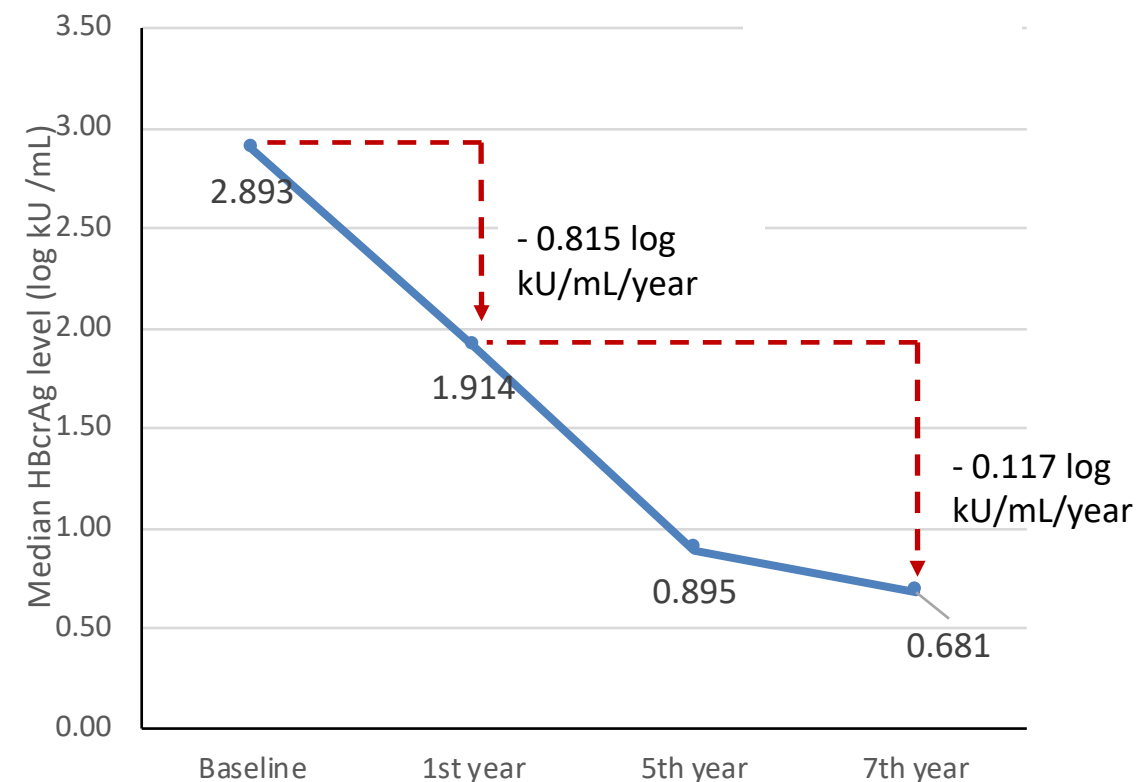
Median levels:

baseline 2.8 Ku/mL

1<sup>st</sup> year 1.9 Ku/mL

5<sup>th</sup> year 0.9 Ku/mL

7<sup>th</sup> year 0.7 Ku/mL



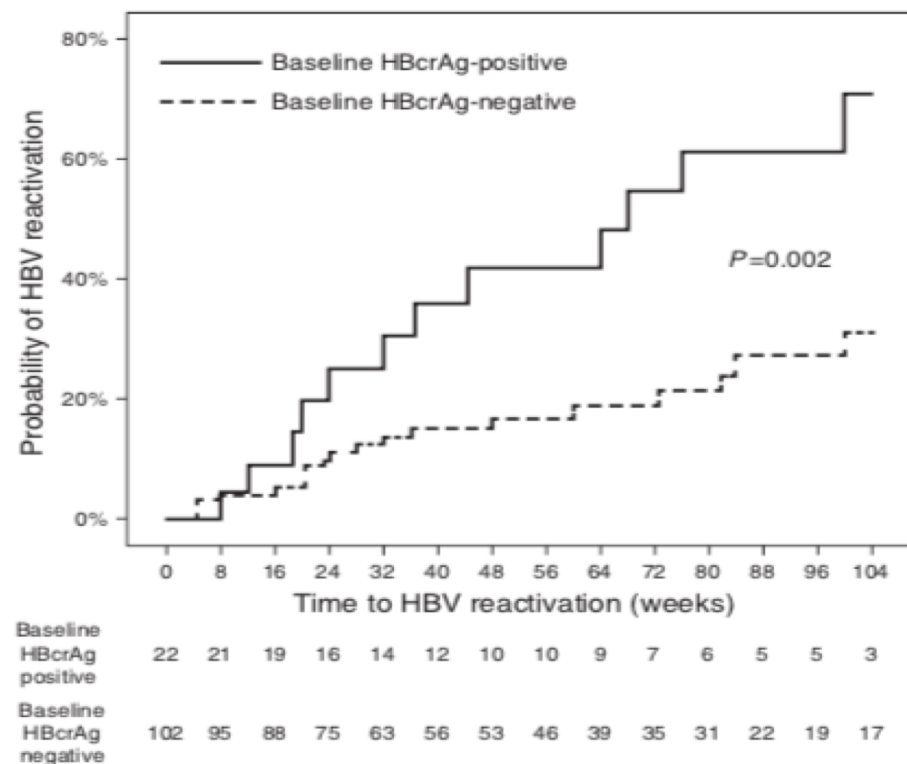
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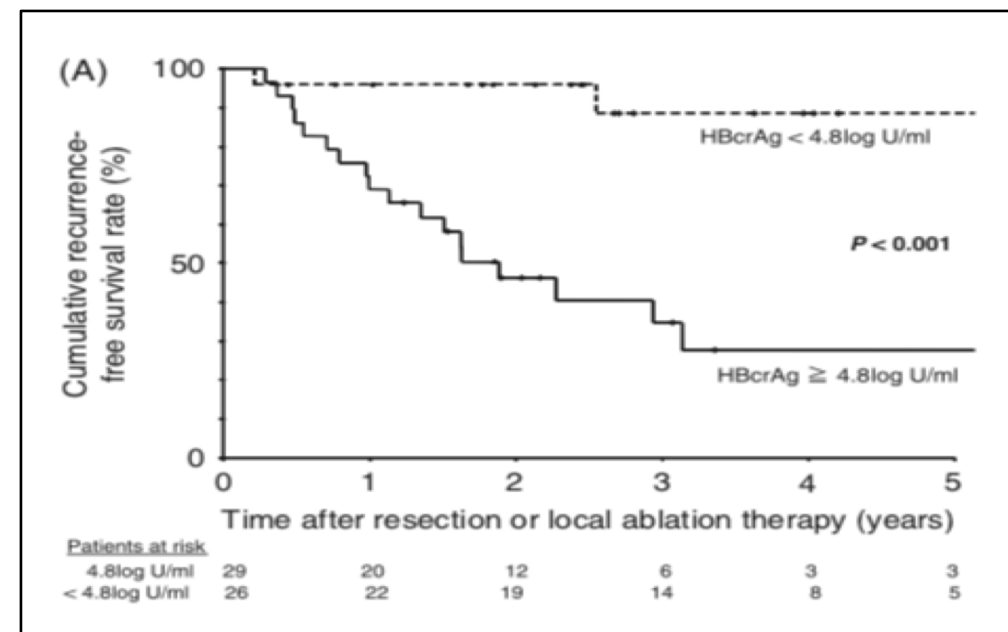
# Role of HBcrAg in special populations

Predicts risk of HBV reactivation in patients receiving rituximab or allogeneic hematopoietic stem cell transplantation



Seto WK et al. Am J Gastroenterol 2016; 111:1788-95

Predicts recurrence free survival after curative treatment of HCC

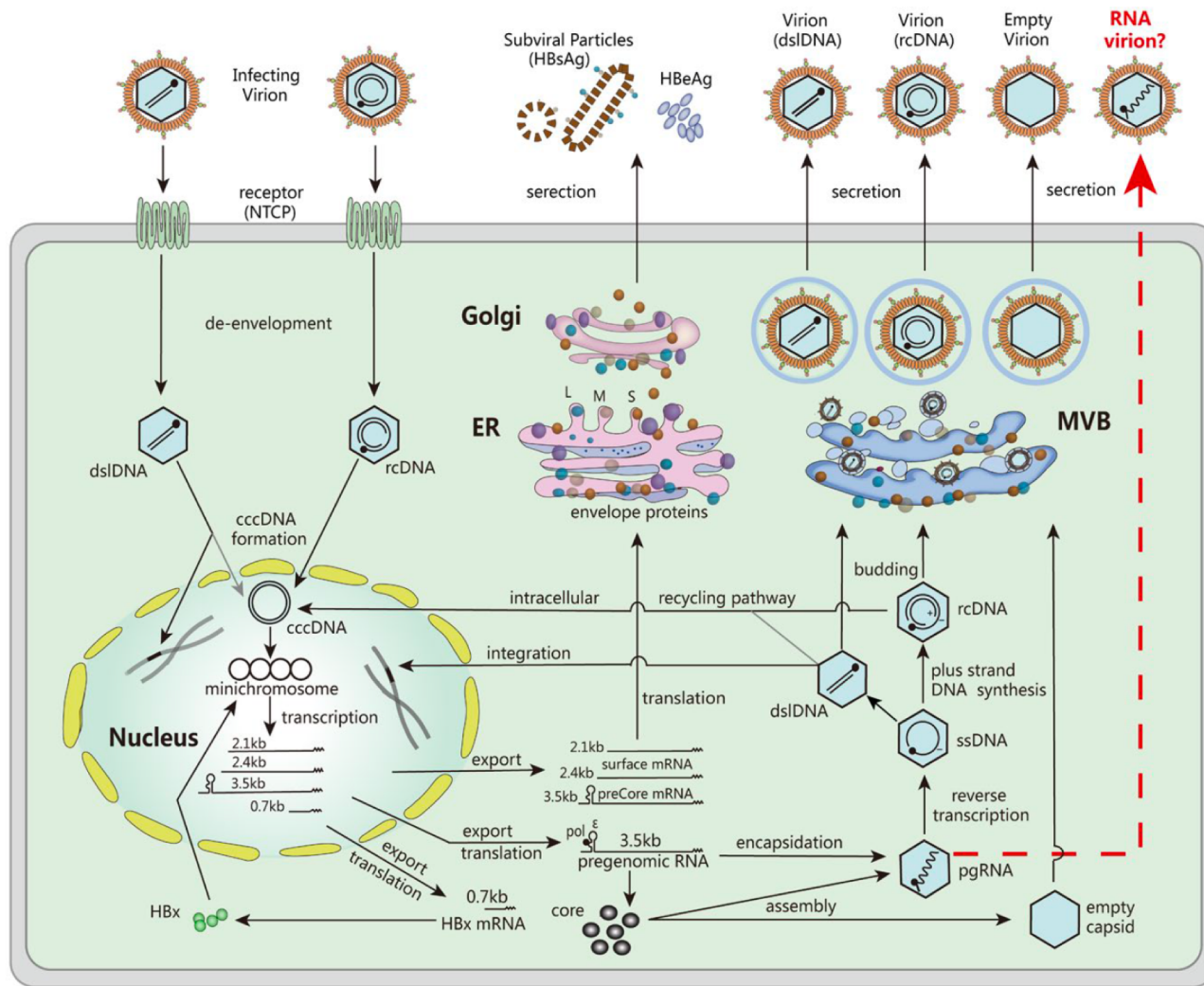


Hosaka T et al. Liver International 2010; 30:1461-70

# Clinical Utility of HBcrAg

- **Monitor tool** for different phases of CHB
- **Detect** occult hepatitis B/ CHB with HBsAg seroclearance
- **Correlate** with the gold standard of viral replication in serum: HBV DNA
- **Highly reflect** the intrahepatic HBV DNA and cccDNA contents
- **Assess** treatment efficacy
- **Associate** with the risk of HCC
- **Predict** disease outcome for immunosuppressive patients and HCC patients

# Different HBV virions and HBV RNA



## HBV RNAs

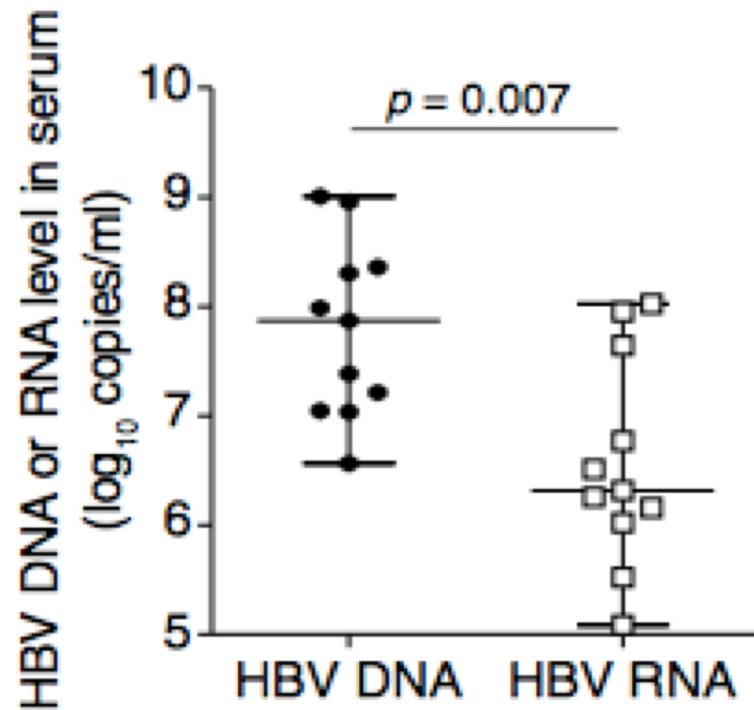
- Only produced from cccDNA by transcription.
- **pgRNA 3.5 kb (species detected in serum)**
- pcRNA 3.5 kb
- surface mRNAs 2.4/2.1 kb
- X mRNA 0.7 kb

**FIG. 1.** HBV life cycle. The major steps in the HBV life cycle including entry, de-envelopment, cccDNA formation, mRNA transcription, protein translation, pgRNA encapsidation, DNA replication, viral particle assembly, and secretion are shown. See text for details. Abbreviations: ER, endoplasmic reticulum; L, large surface protein; M, middle surface protein; MVB, multivesicular body; NTCP, sodium taurocholate cotransporting polypeptide; pol, polymerase; S, small surface protein; ssDNA, single-stranded DNA.

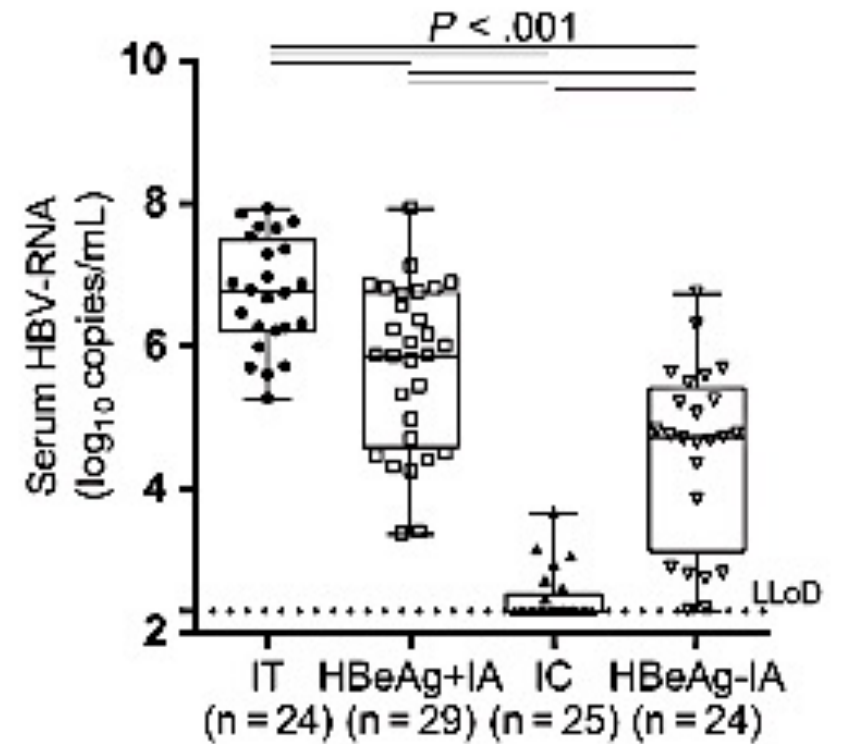
*Liu S et al., Hepatology 2019;69:1816-27*

*EK Butler, et al. Hepatology 2018;68:2106-17*

## HBV RNA in natural history of HBV

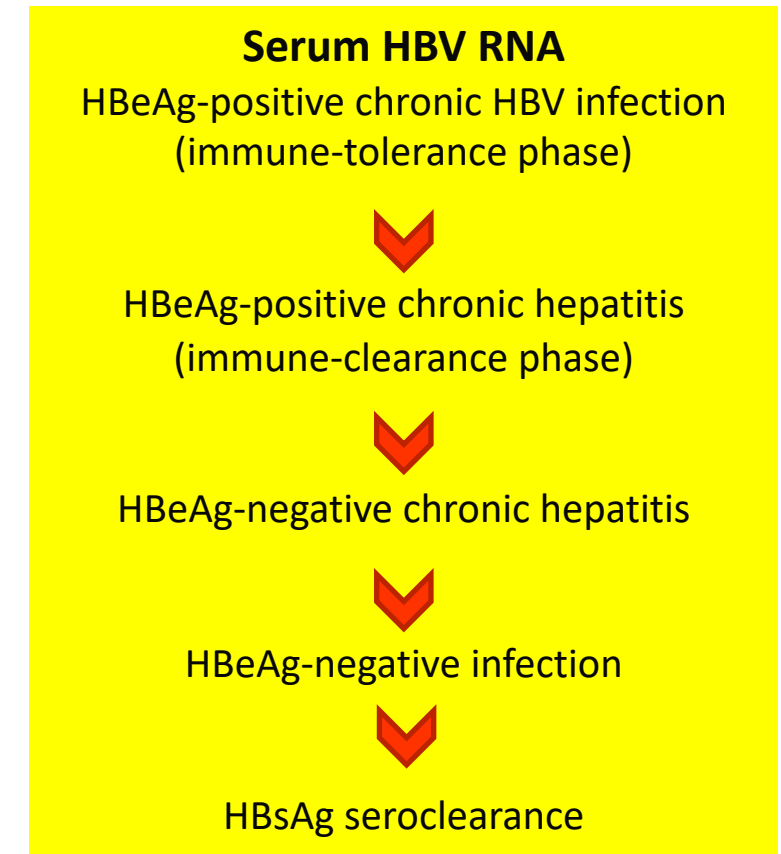
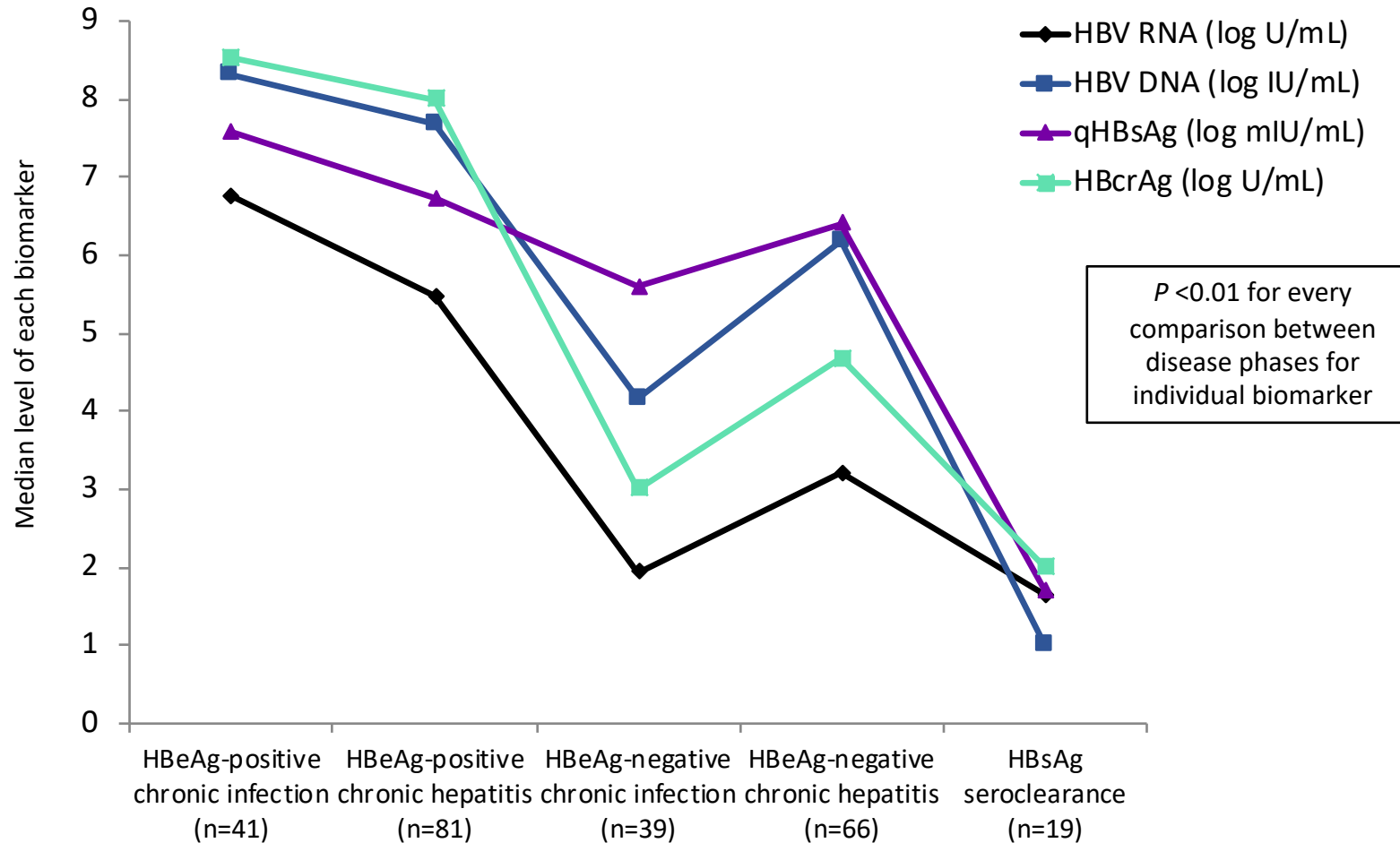


Wang J, et al. *J Hepatol* 2016; 65:700-710

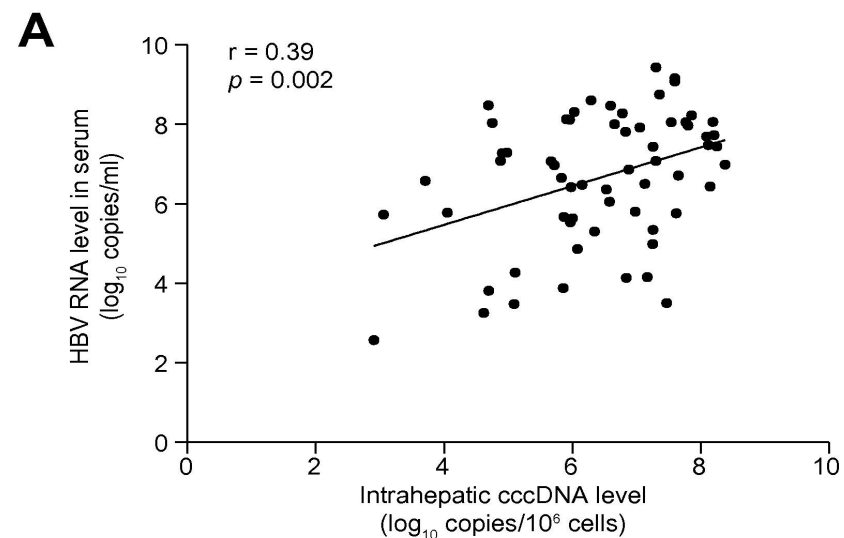


Wang J et al, *J Viral Hepat* 2018;25(9):1038-47

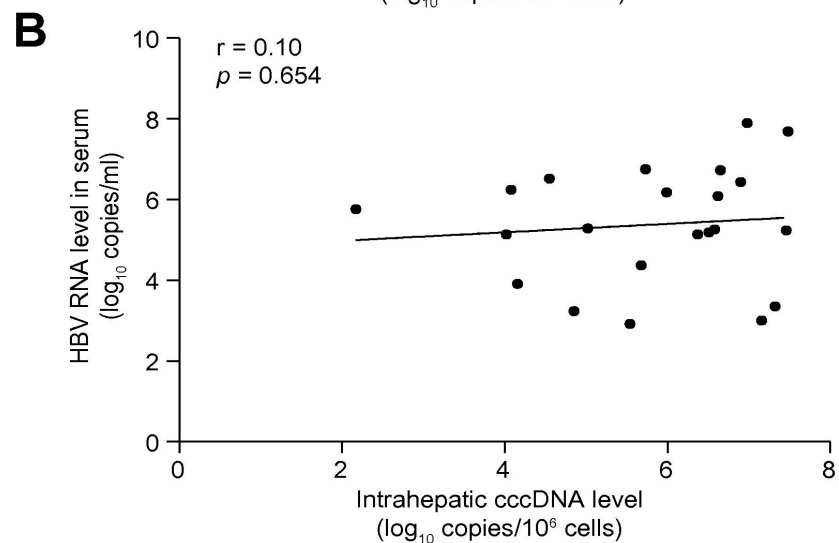
# HBV RNA in natural history of HBV



# Serum HBV RNA correlations with intra-hepatic cccDNA

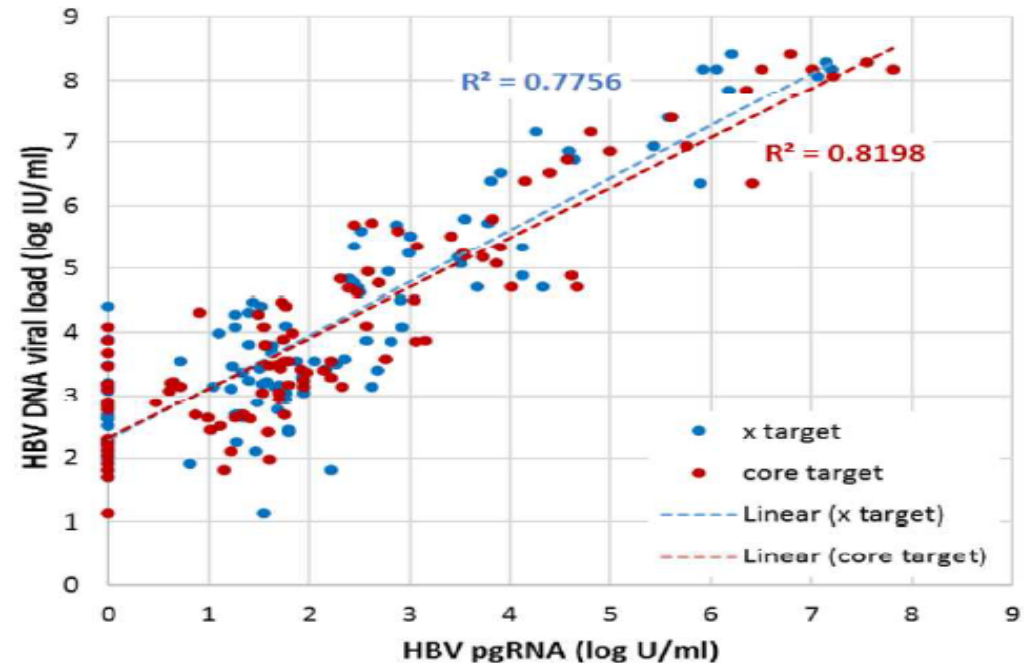
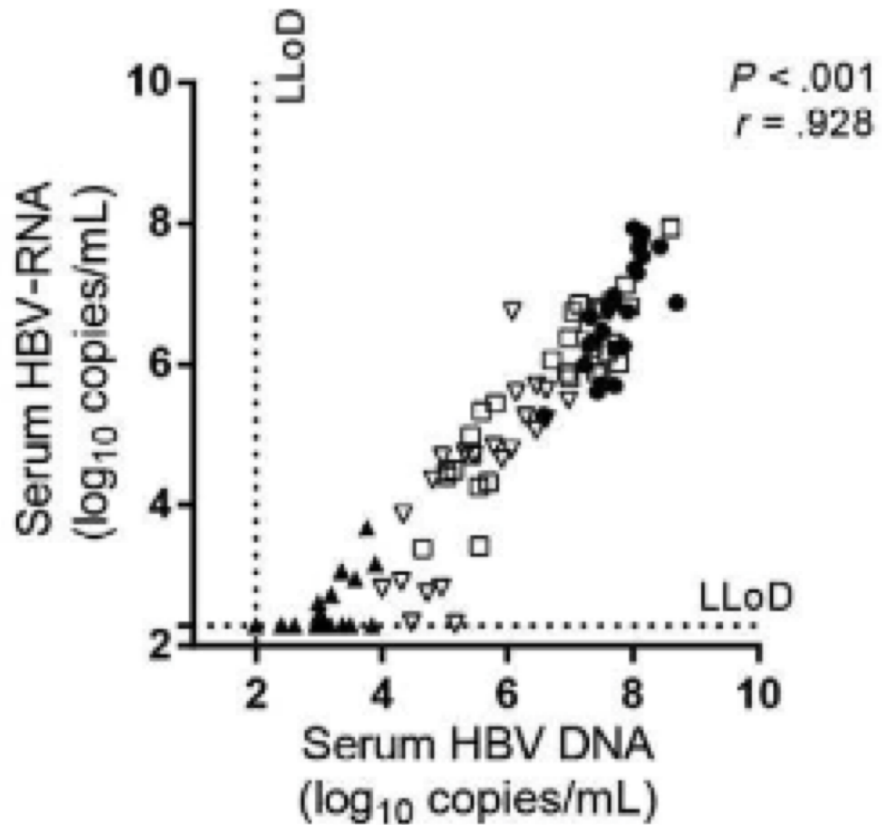


HBeAg positive patients (n=62)



HBeAg negative patients (n=22)

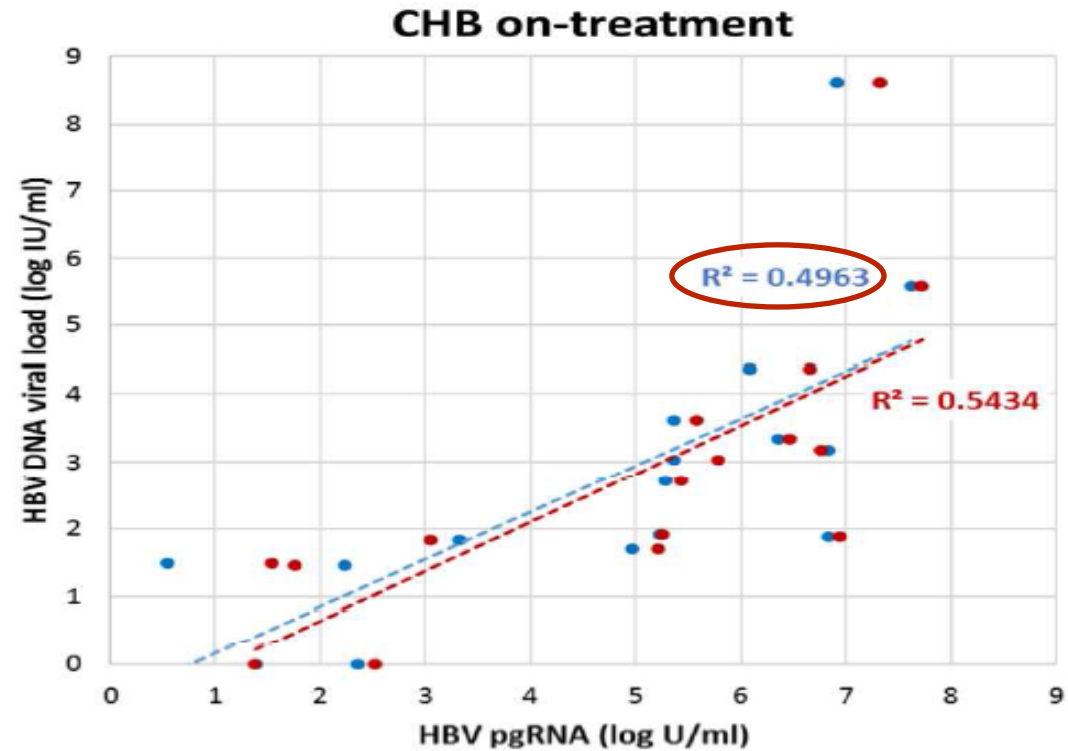
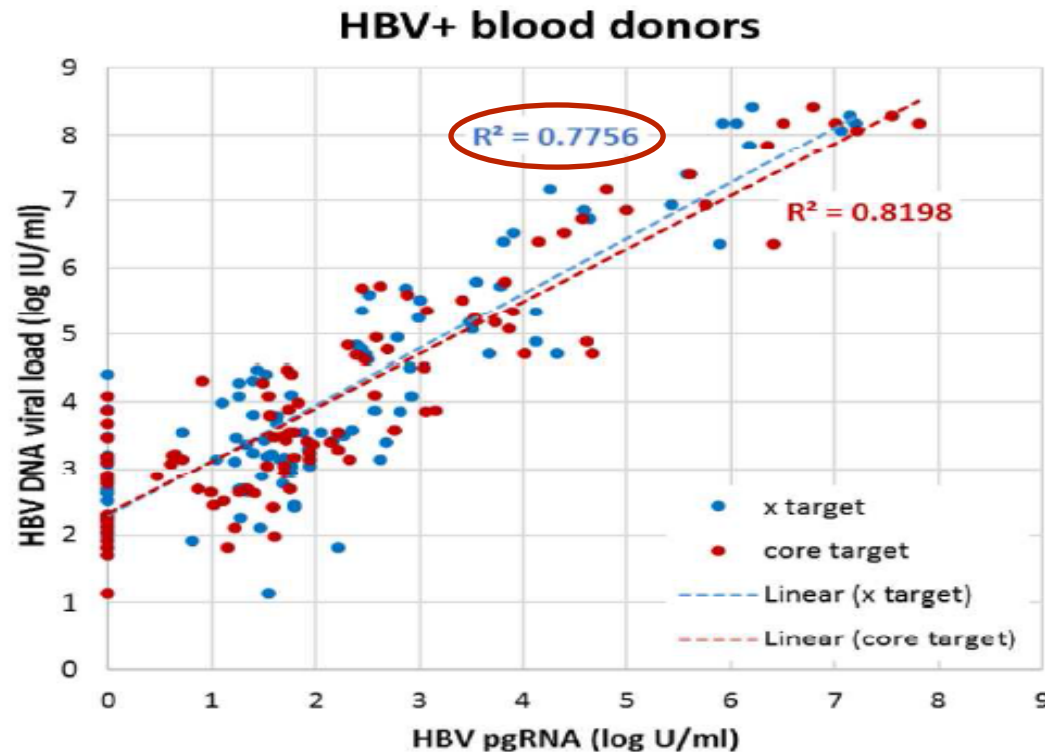
# Serum HBV RNA and serum HBV DNA correlation



- 102 HBsAg+, HBV DNA+ samples (92 had detectable pgRNA)
- HBV DNA > pgRNA by  $1.7 \pm 0.71$  log



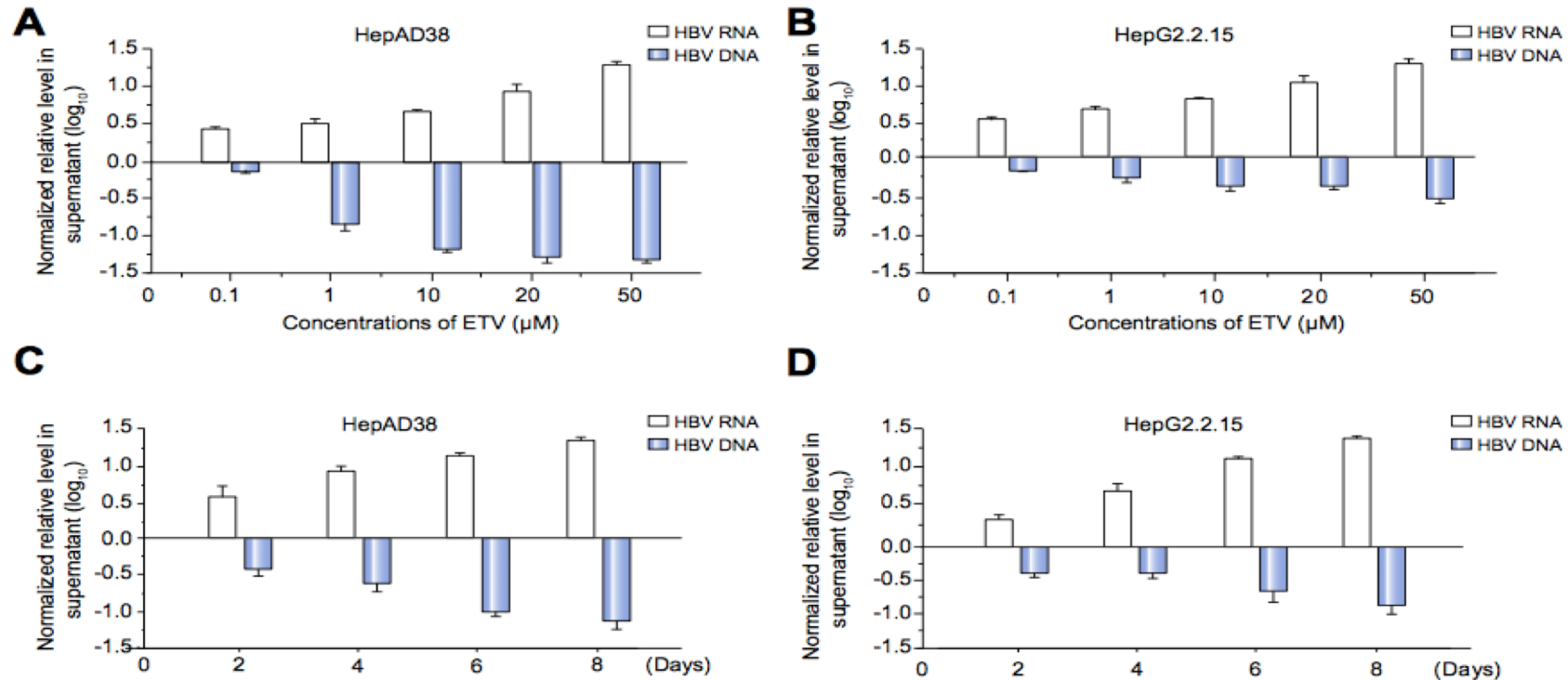
# Correlations between serum HBV RNA and HBV DNA in treatment naive and experienced patients



- **Correlation** between HBV DNA & pgRNA in NA-treated patients **lower** than in untreated patients
- NA-treated patients: pgRNA > HBV DNA

HBV RNA profiles under HBV treatment

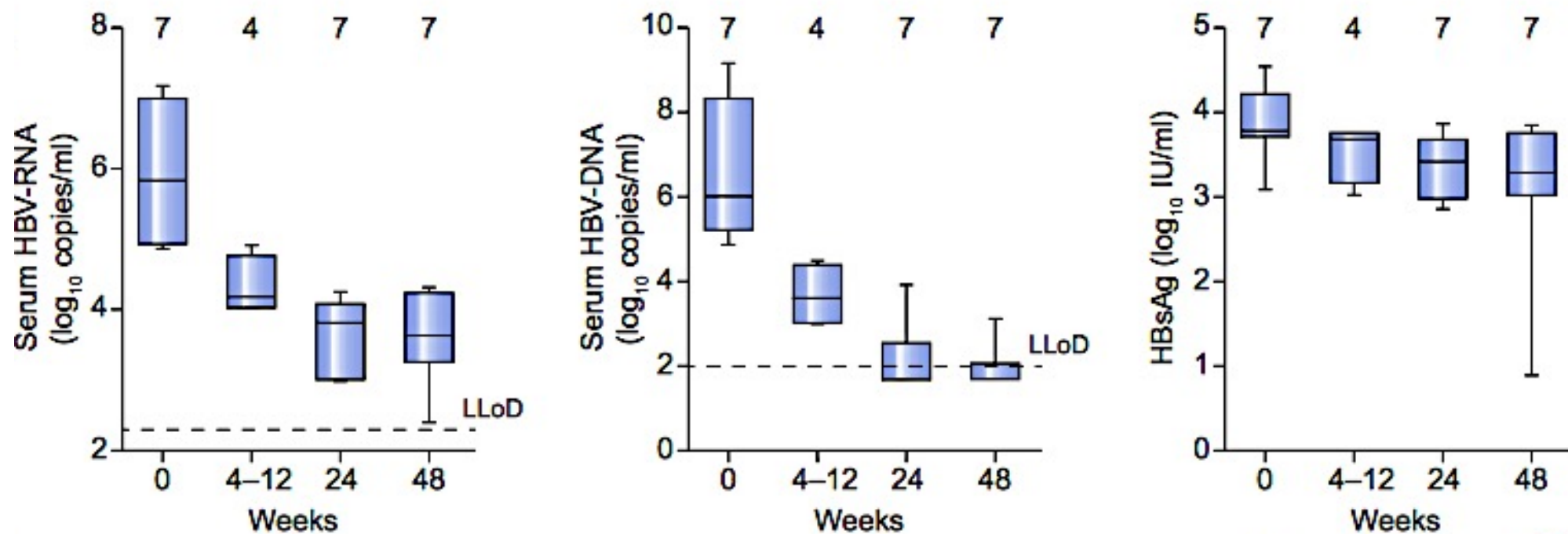
In vitro studies showed that suppression of the reverse transcription activity of HBV DNA polymerase increases the level of HBV pgRNA virions.



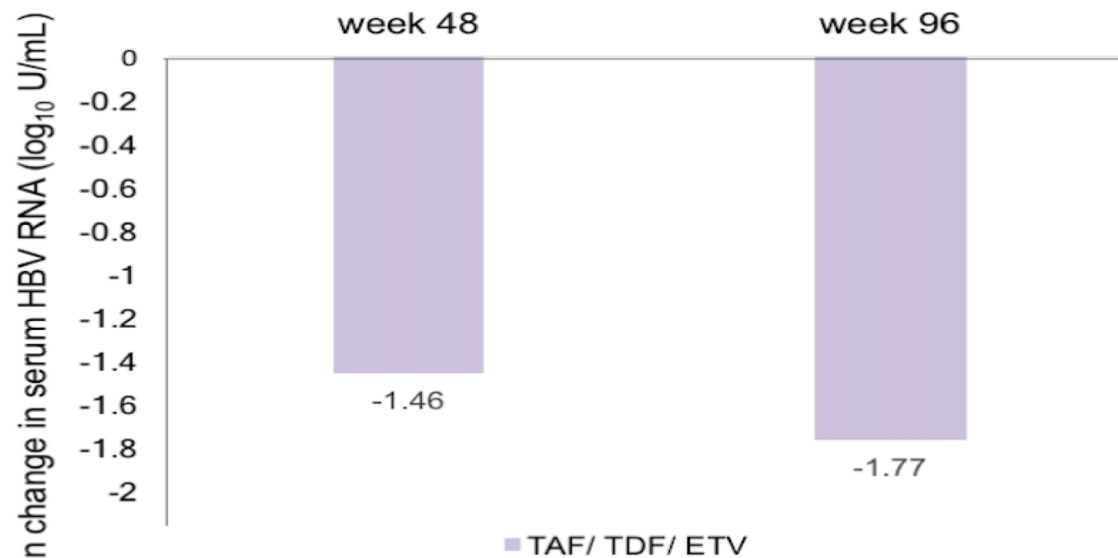
↑ ETV concentration: ↓ HBV DNA levels ↑ HBV RNA levels

↑ ETV duration (up to 8 days): ↓ HBV DNA levels ↑ HBV RNA levels

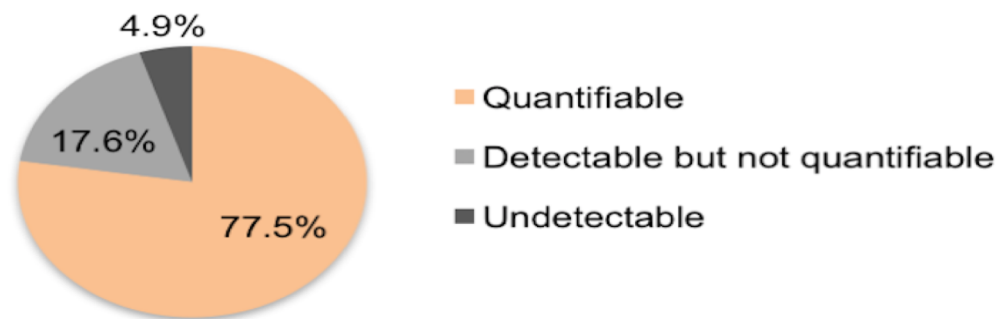
## In vivo dynamic changes of serum HBV RNA with entecavir therapy



## Changes of HBV RNA after 2 years of antiviral treatment



### Serum HBV RNA at week 96 of NA

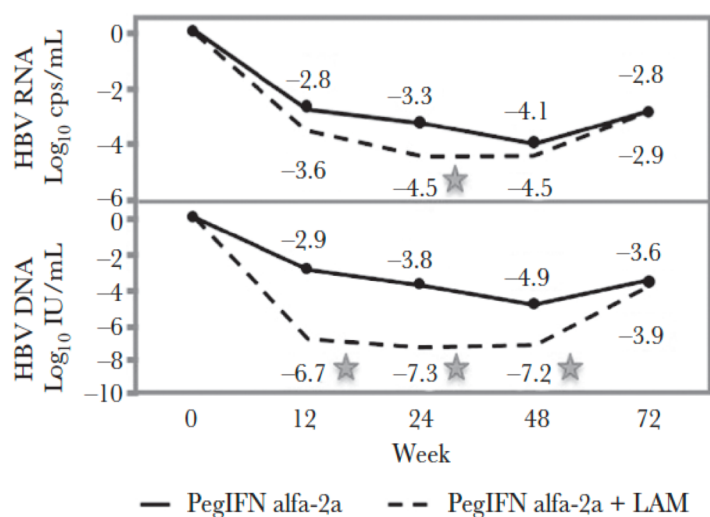


# HBV RNA levels under PegIFN +/- lamivudine

Study population 131

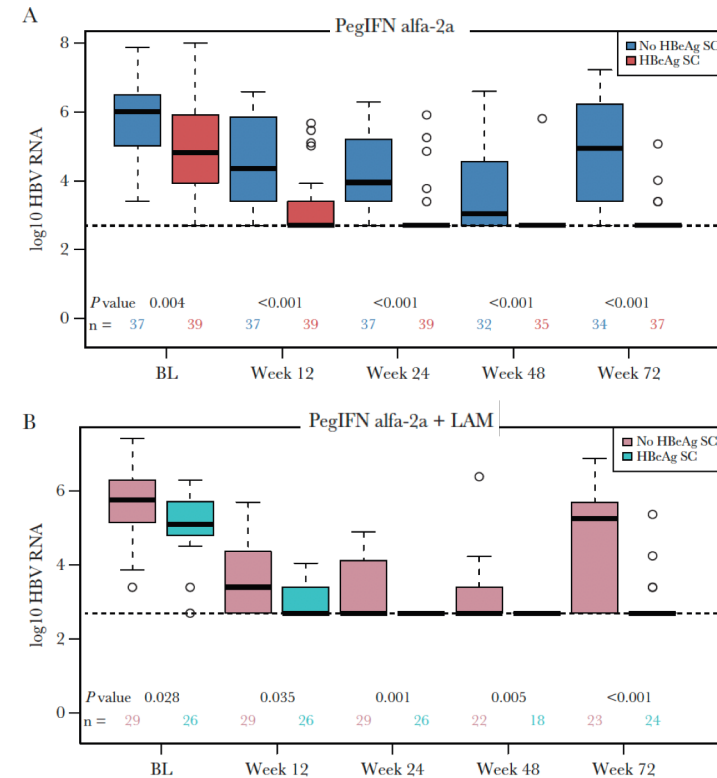
- HBeAg +, ALT ( $> 1 - 10 \times$  ULN)
- 48-week treatment
- PegIFN alpha 2a: 76
- PegIFN alpha 2a + LAM: 55

HBV DNA and RNA during treatment



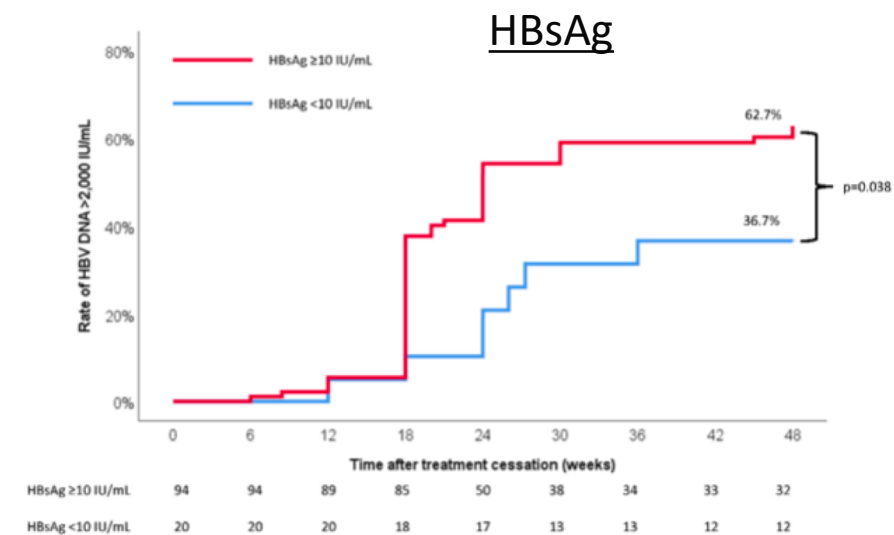
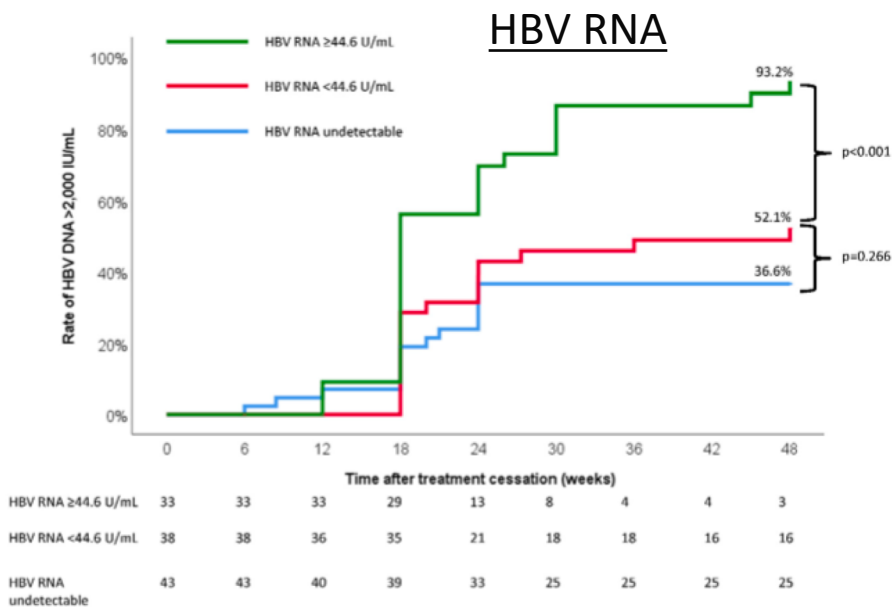
- 1) Both DNA and RNA decreased in both groups
- 2) Reduction of DNA & RNA more pronounced in PegIFN + Lam vs. PegIFN alone

HBeAg seroconversion at 96 weeks

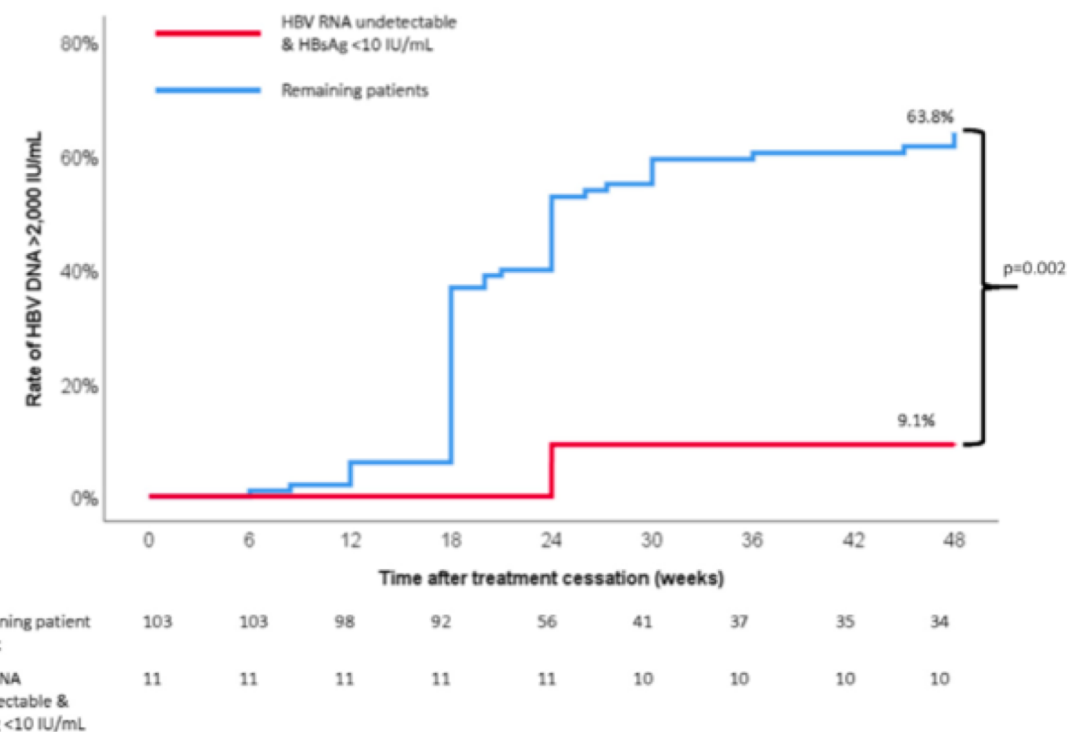


HBV RNA levels were lower at all time points during treatment in patients achieving HBeAg seroconversion

# Role of HBV RNA/ HBsAg to predict disease relapse upon treatment cessation



## HBV RNA + HBsAg



# Clinical Utility of HBV RNA

- Detected in serum as virus-like particles with encapsidated RNA.
- RNA levels differ in different disease phases of CHB
- Present in serum of chronic hepatitis B patients, albeit in lower levels, compared to serum HBV DNA.
- Correlated with serum HBV DNA (correlation became weaker during NA treatment)
- Correlated with intra-hepatic cccDNA (HBeAg-positive mainly) in treatment-naïve patients
- Long term effects of NUCs on HBV RNA remains to be defined.
- May predict response to HBeAg seroconversion (IFN based therapy + NUCs) and disease relapse in patients after NA cessation



Thank you