



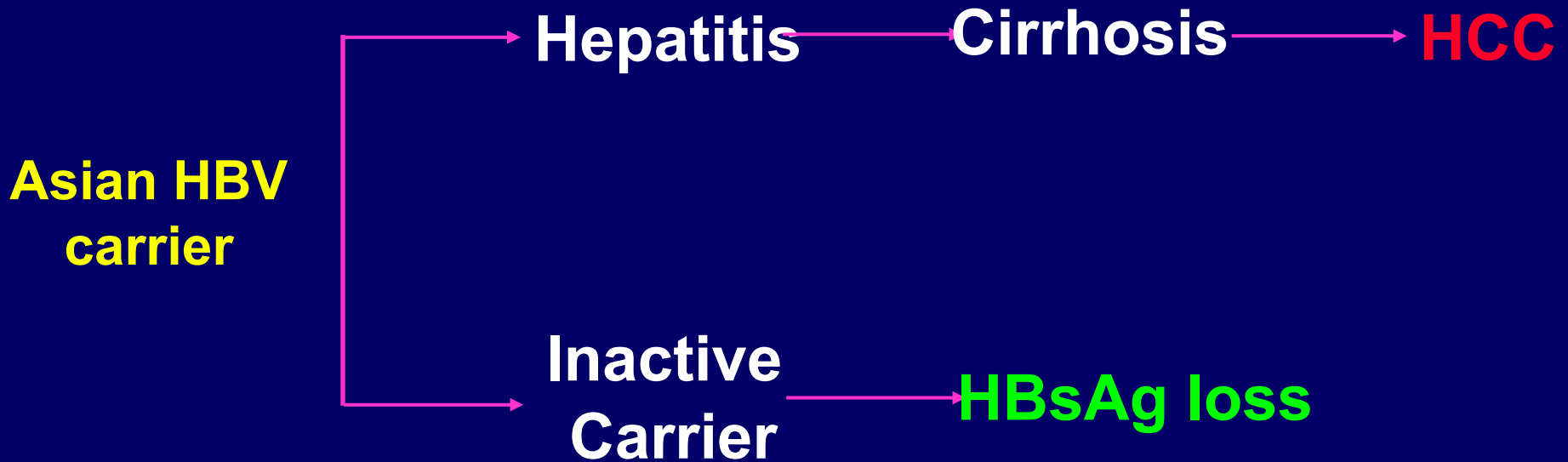
# *What have we learned from HBV clinical cohorts?*

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Hepatitis Research Center,  
Department of Internal Medicine,  
National Taiwan University College of  
Medicine and Hospital***

# Clinical outcomes of Asian HBV carriers

Adverse outcome



Favorable outcome

What are factors affecting long-term outcomes?



# Factors associated with disease progression in Asian HBV carriers

## Viral

Persistent presence of HBeAg

Persistently high HBV-DNA level

HBV genotype C > genotype B

Core promoter mutations\*

High HBsAg level\*\*

## Host

Male gender  
Increasing age

Recurrent ALT flare

Persistently increased ALT levels

Cirrhosis\*

Diabetes\*

## Environment

Heavy drinking

Cigarette smoking\*

Aflatoxin\*

HCV, HDV, or HIV co-infection

\*Factors shown to be associated with an increases risk of HCC only. Abbreviations: ALT, alanine aminotransferase; HBeAg, hepatitis B e antigen; HCC, hepatocellular carcinoma

\*\* In HBV carriers with HBV DNA < 2000 IU/mL



# Outline

- **HBV natural history cohorts**
  - **REVEAL-HBV**
  - **SEARCH-B**
  - **ERADICATE-B**
- **Risk calculator update**
- **Conclusions**

# Summary of three HBV cohorts

Cohort	Study design	Disease stage	Number of participants	Follow-up (y)
REVEAL-HBV	Community -based cohort	Including HBeAg-positive and -negative phases	3653	11.4
SEARCH-B	Hospital-based cohort	Early HBeAg negative phase	390	7.4
ERADICATE-B	Hospital-based cohort	Including HBeAg-positive and -negative phases	2688	14.7

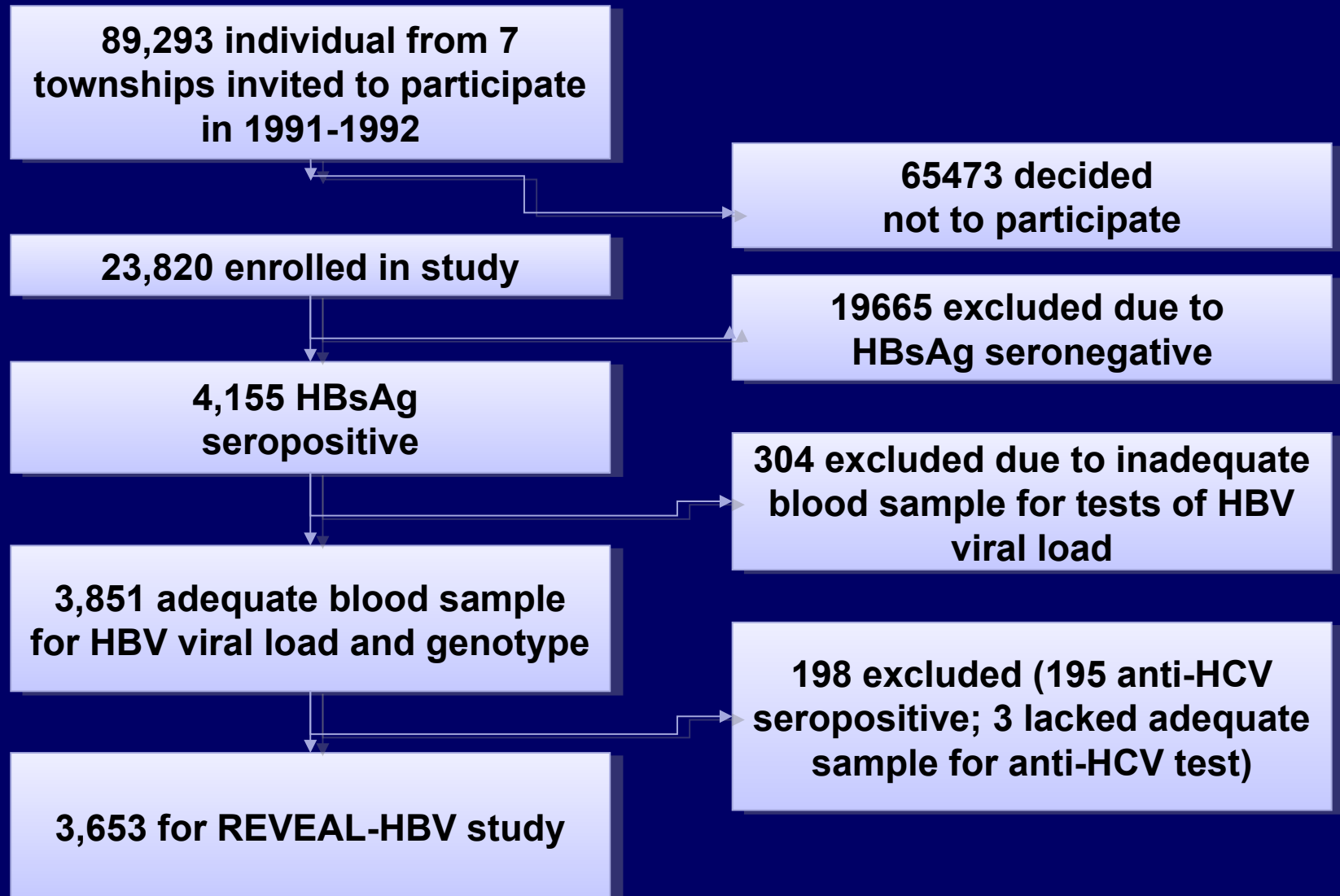
**REVEAL-HBV** = Risk Evaluation of Viral Load Elevation and Associated Liver Disease/Cancer-Hepatitis B Virus

**SEARCH-B** = Study of E Antigen seroClearance of Hepatitis B

**ERADICATE-B** = Elucidation of Risk fActors for Disease Control or Advancement in Taiwanese Hepatitis B Carriers



# Flow of REVEAL-HBV cohort

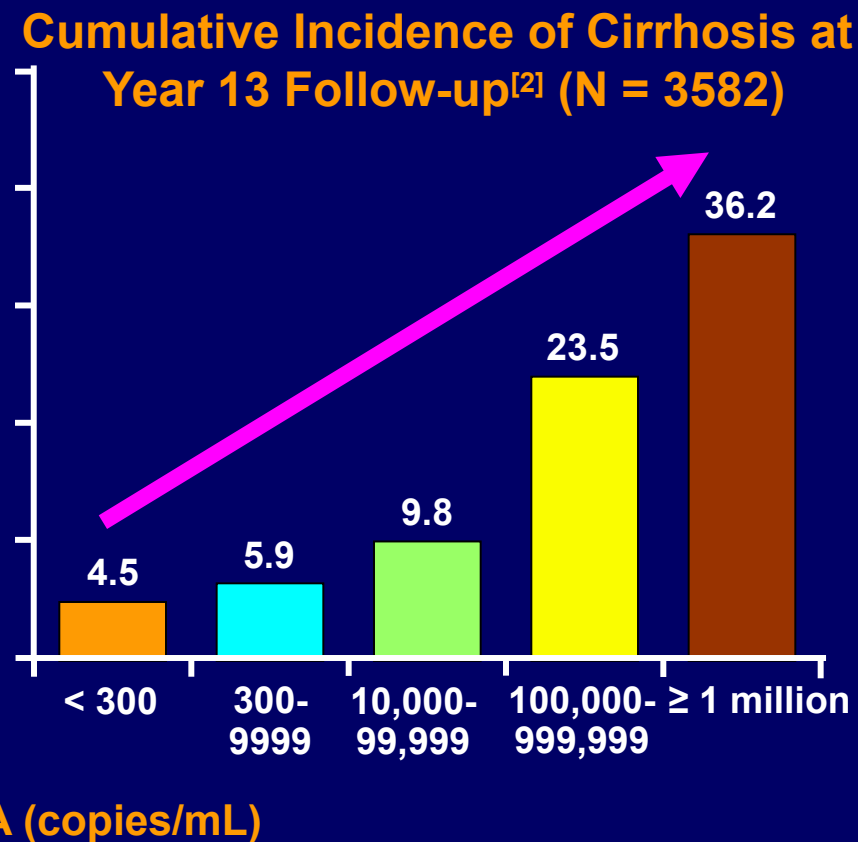
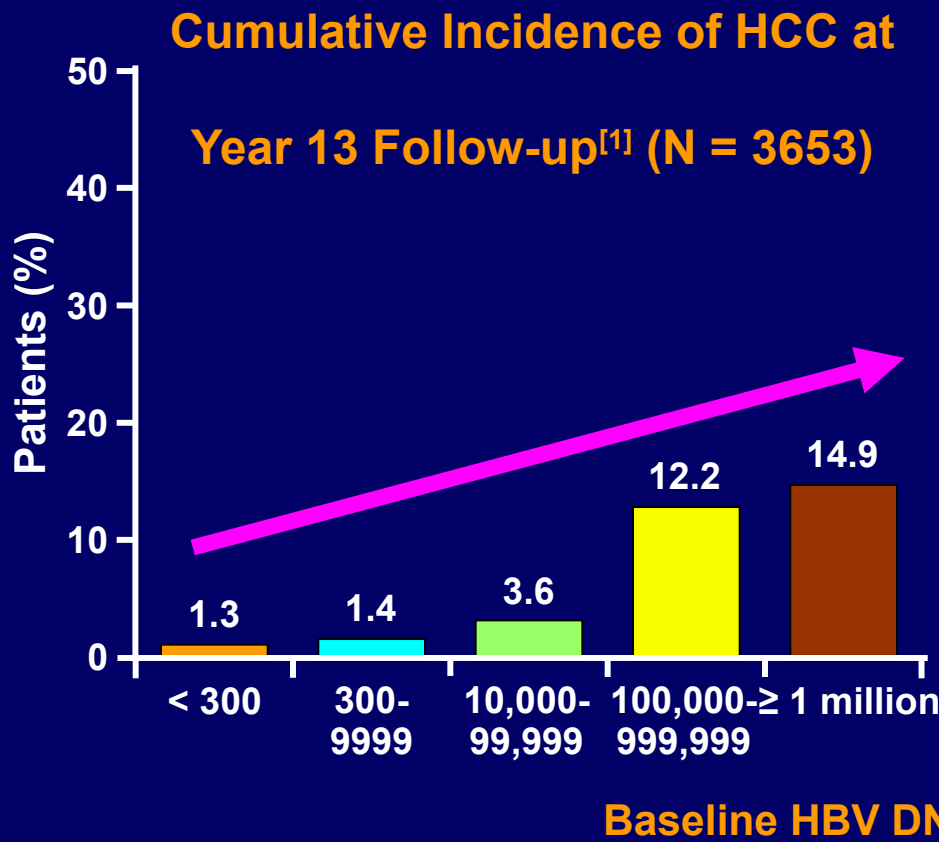


1. Chen CJ, et al. JAMA. 2006;295:65-73.
2. Yang HI et al. JCO 2010;28:2437-2444



# High baseline HBV DNA associated With increased risk of HCC and cirrhosis

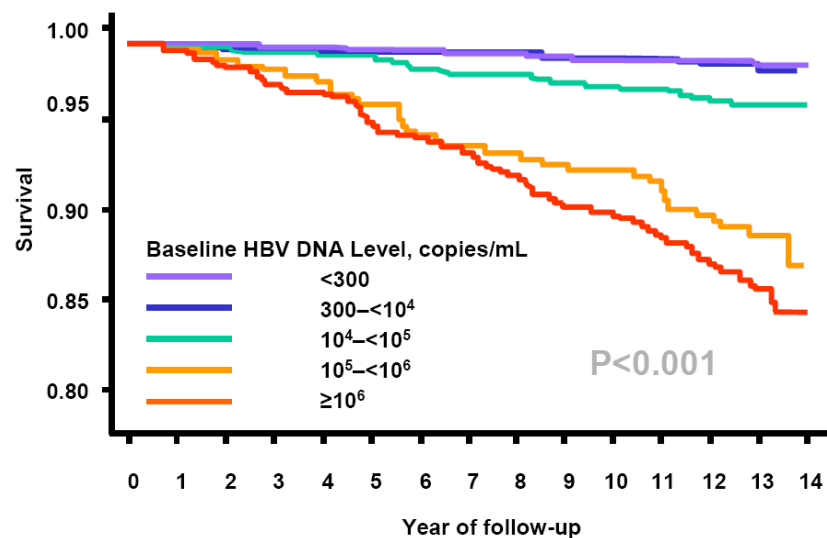
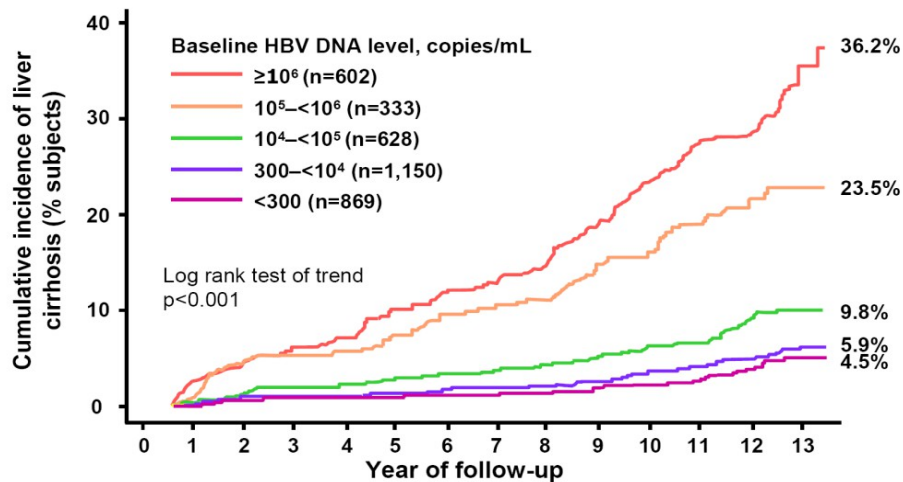
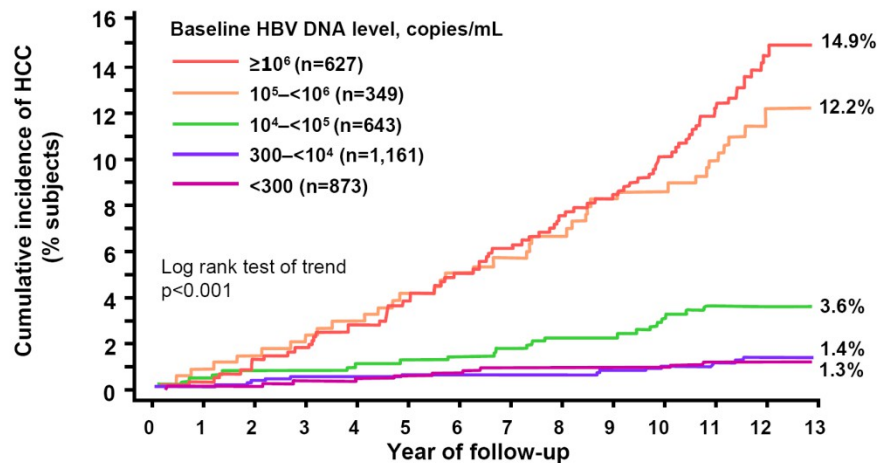
REVEAL: Long-term follow-up of untreated community-based HBsAg+ve individuals in Taiwan



1. Chen CJ, et al. JAMA. 2006;295:65-73.  
2. Iloeje UH, et al. Gastroenterology. 2006;130:678-686.



# Serum HBV DNA level and liver disease progression and survival



Chen CJ et al. JAMA 2006;295:65-73.

Iloeje UH et al. Gastroenterology 2006;130:678-686.

Iloeje UH et al. Clin Gastroenterol Hepatol 2007;5:921-931.





# ***REVEAL-HBV: summary***

- **HBV viral load is a strong risk predictor for cirrhosis and HCC independent of HBeAg status, ALT level and other risk factors**
- **Baseline serum HBV DNA level > 10,000 copies/mL may start to increase risk of cirrhosis and HCC in HBV carriers aged 30-65 years after > 10 years of follow-up**
- **Patients with persistently high HBV DNA level have the highest risk**
- **Measurements of HBV viral load may help define which HBV carriers aged 30 years or older are at high risk for cirrhosis and HCC**

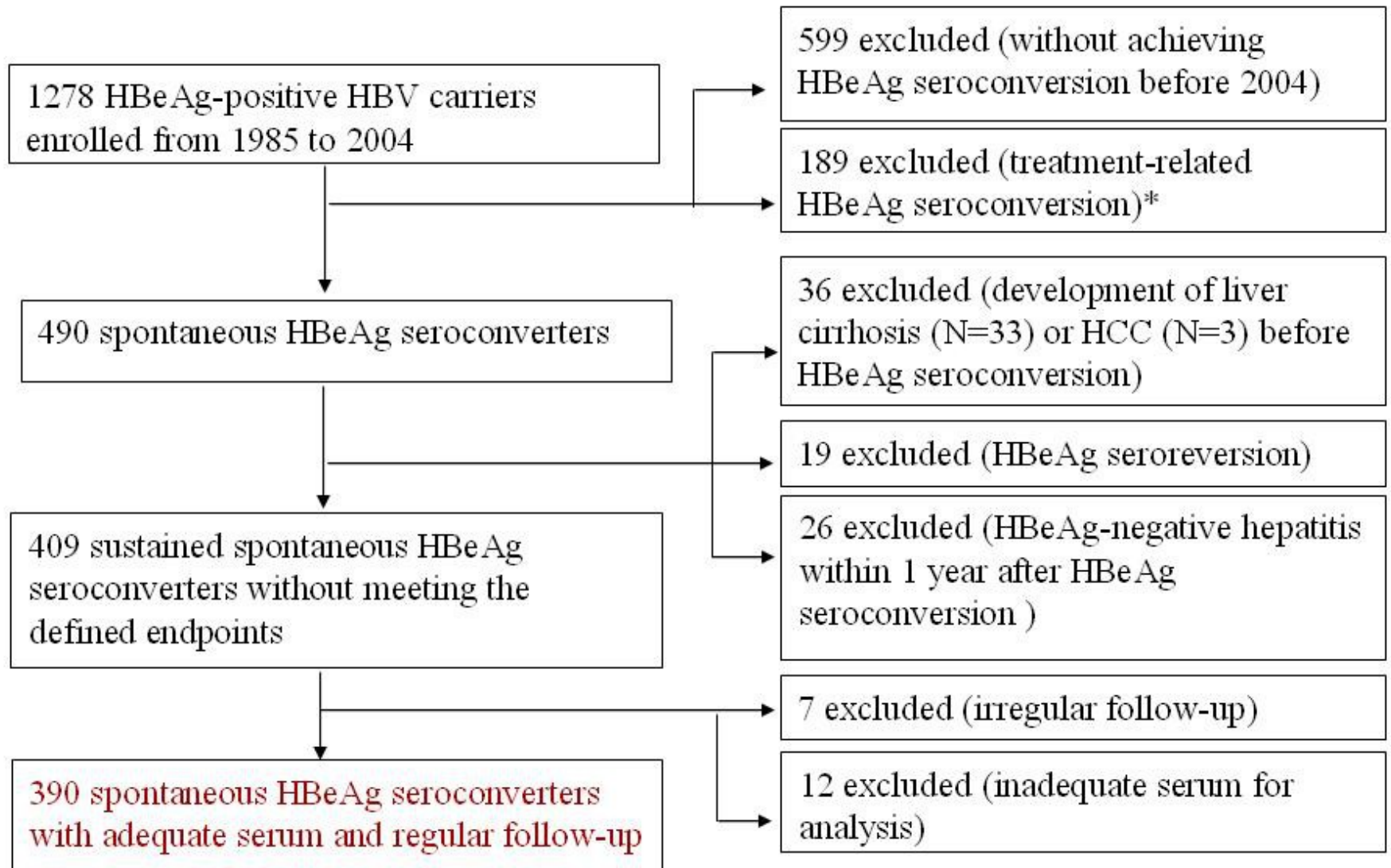


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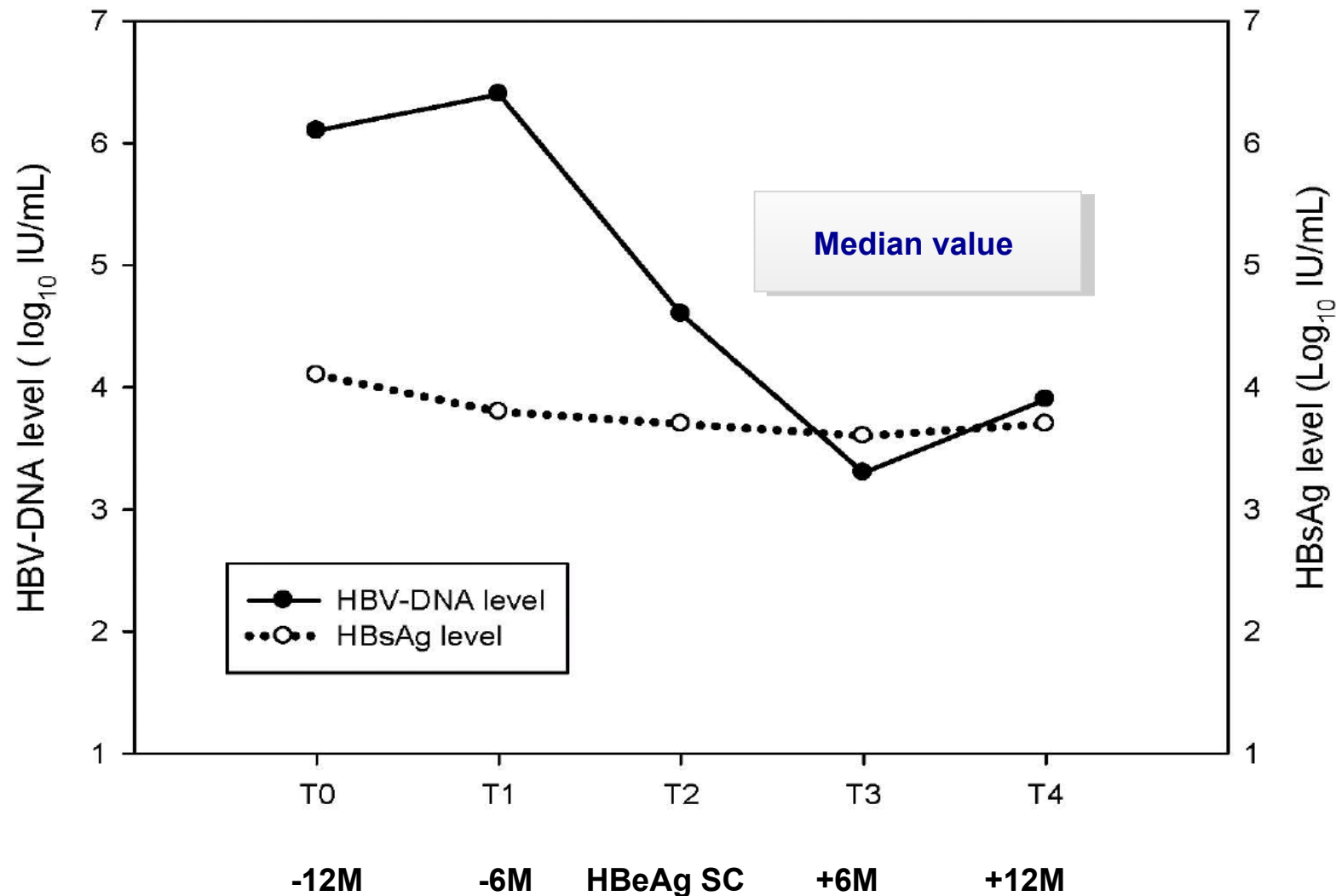


# Flow of SEARCH-B cohort

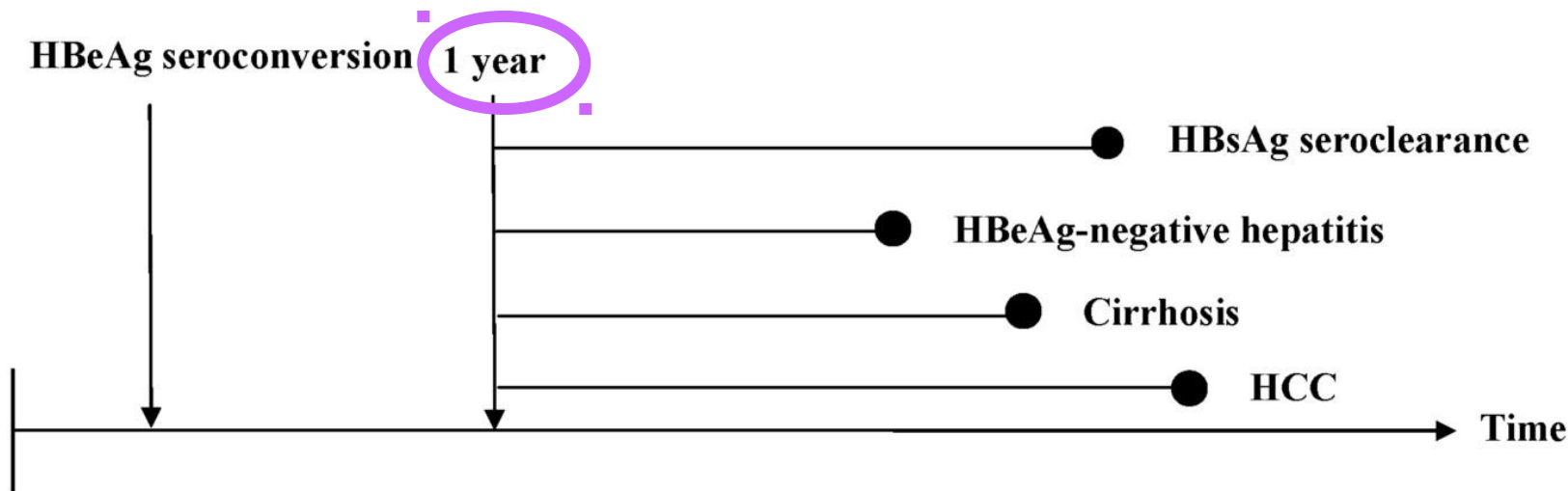




# Pilot study of viral kinetics in 42 patients



# Endpoints of follow-up



- Censored at
  - Meeting each endpoints
  - End of follow-up
  - Starting anti-viral therapy

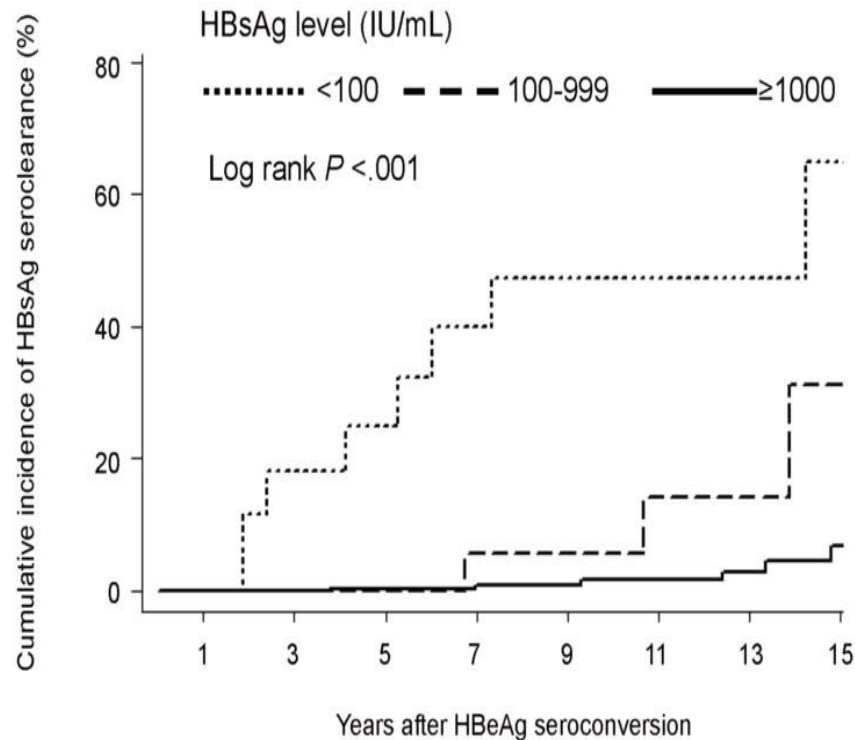
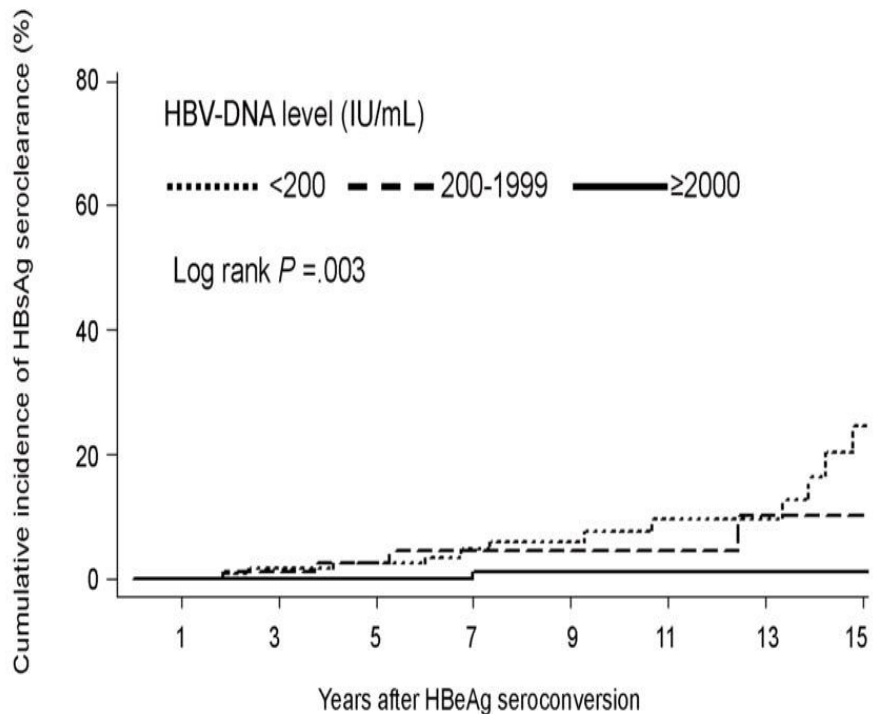


# Definition of endpoints

- **HBeAg-negative hepatitis (ENH)**
  - ALT > 80 U/L (two times the upper limit of normal)
  - HBV-DNA level >2000 IU/ml within 6 months
- **Hepatitis flare**
  - ALT elevation > 5 X ULN with a concomitant serum HBV DNA level > 2000 IU/mL
- **Cirrhosis**
  - Histologically
  - Ultrasonographic findings supplemented with clinical features
- **HCC**
  - Histology/cytology or by typical image findings in hepatic nodules > 1 cm



# Prediction of HBsAg loss: HBV DNA vs. HBsAg



Number at risk

Serum HBV-DNA level at one year post HBeAg seroconversion (IU/mL)

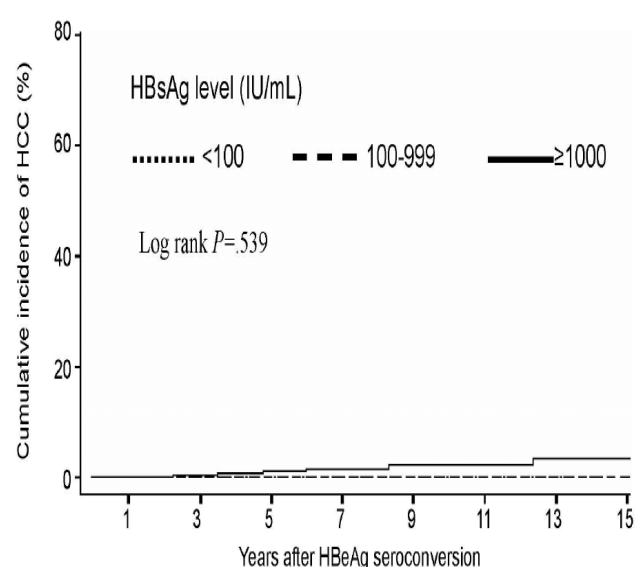
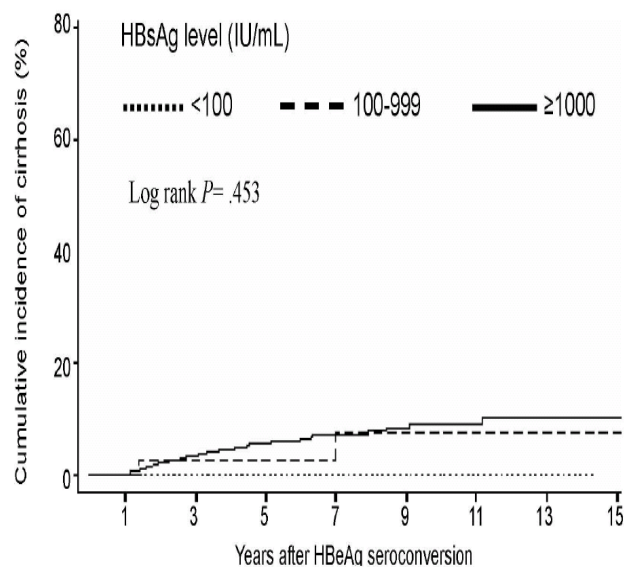
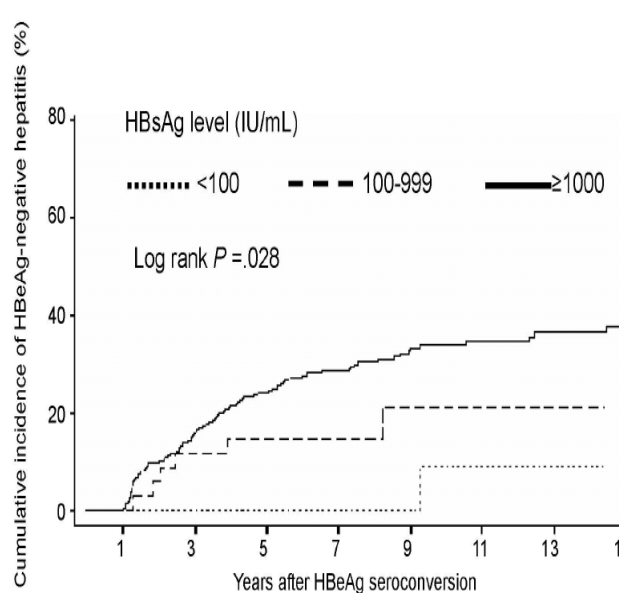
<200	139	124	108	77	63	44	29	17
200-1999	100	77	56	40	33	24	13	5
≥2000	151	134	117	86	64	51	35	19

Number at risk

Serum HBsAg level at one year post HBeAg seroconversion (IU/mL)

<100	18	15	11	8	6	6	5	3
100-999	34	33	29	17	14	10	5	3
≥1000	338	290	241	178	142	104	67	37

# Higher HBsAg level predicts incidence of ENH, but not cirrhosis, and HCC



Number at risk

Serum HBsAg level at one year post HBeAg seroconversion (IU/mL)	1	3	5	7	9	11	13	15
<100	18	15	14	12	11	8	8	8
100-999	34	30	27	17	13	7	4	4
≥1000	338	262	211	158	117	87	58	58

Number at risk

Serum HBsAg level at one year post HBeAg seroconversion (IU/mL)	1	3	5	7	9	11	13	15
<100	18	15	14	12	11	8	8	8
100-99	34	34	31	20	16	11	8	8
≥1000	338	299	258	198	147	109	74	74

Number at risk

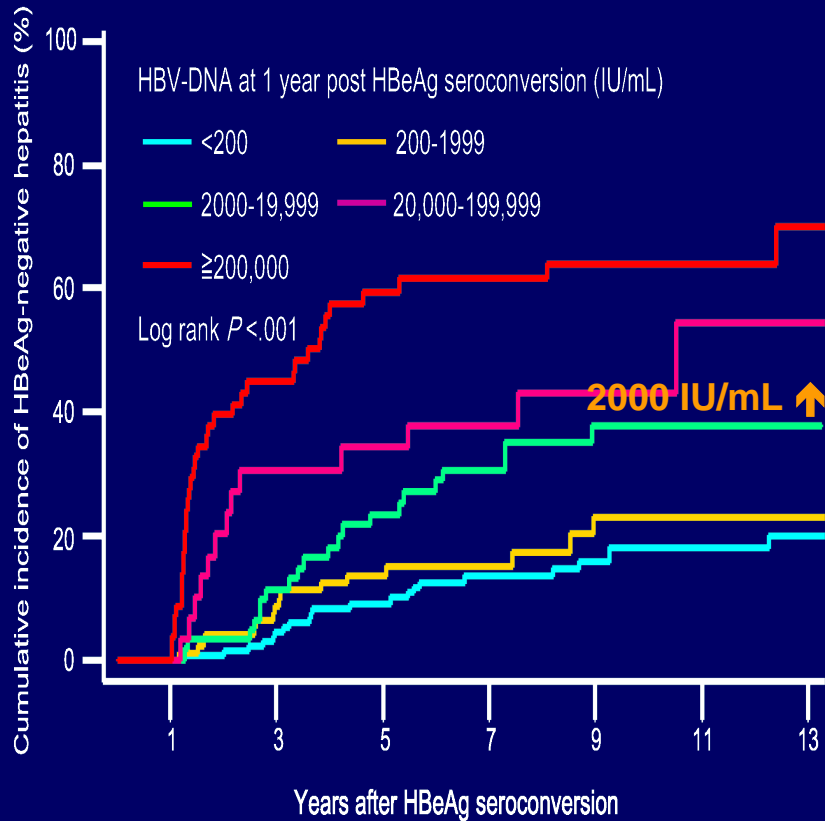
Serum HBsAg level at one year post HBeAg seroconversion (IU/mL)	1	3	5	7	9	11	13	15
<100	18	15	14	12	11	8	8	6
100-999	34	34	32	22	18	13	9	6
≥1000	338	308	268	210	158	119	81	53



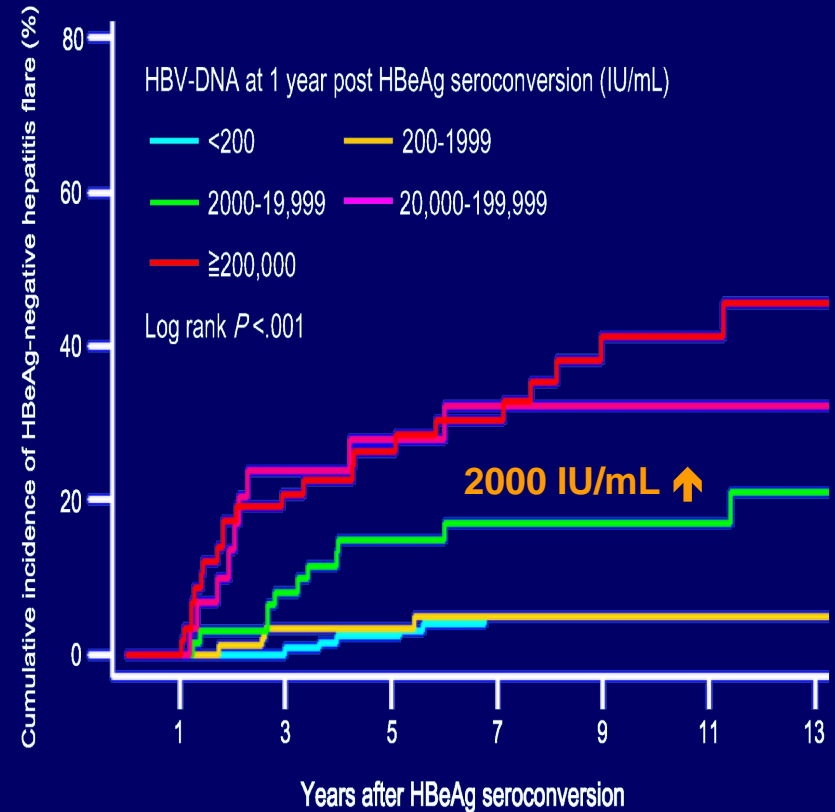


# Higher HBV DNA level predicts more ENH and hepatitis flare (SEARCH-B)

## HBeAg(-) hepatitis



## Hepatitis flare



@ HBeAg seroconversion may not always confer favorable outcomes. Serum HBV DNA levels > 2000 IU/mL at 1 year post HBeAg seroconversion correlate with increased risk of HBeAg-negative hepatitis and hepatitis flare



## ***SEARCH-B: summary***

- In spontaneous HBeAg seroconverters with HBV genotype B or C infection, a lower serum HBsAg level at early HBeAg-negative phase is associated a higher HBsAg loss rate
- **HBsAg level <100 IU/mL predicts HBsAg loss within 6 years in spontaneous HBeAg seroconverters with HBV DNA level 200 IU/mL**
- Serum HBV DNA level is better than HBsAg level in predicting disease progression in spontaneous HBeAg seroconverters

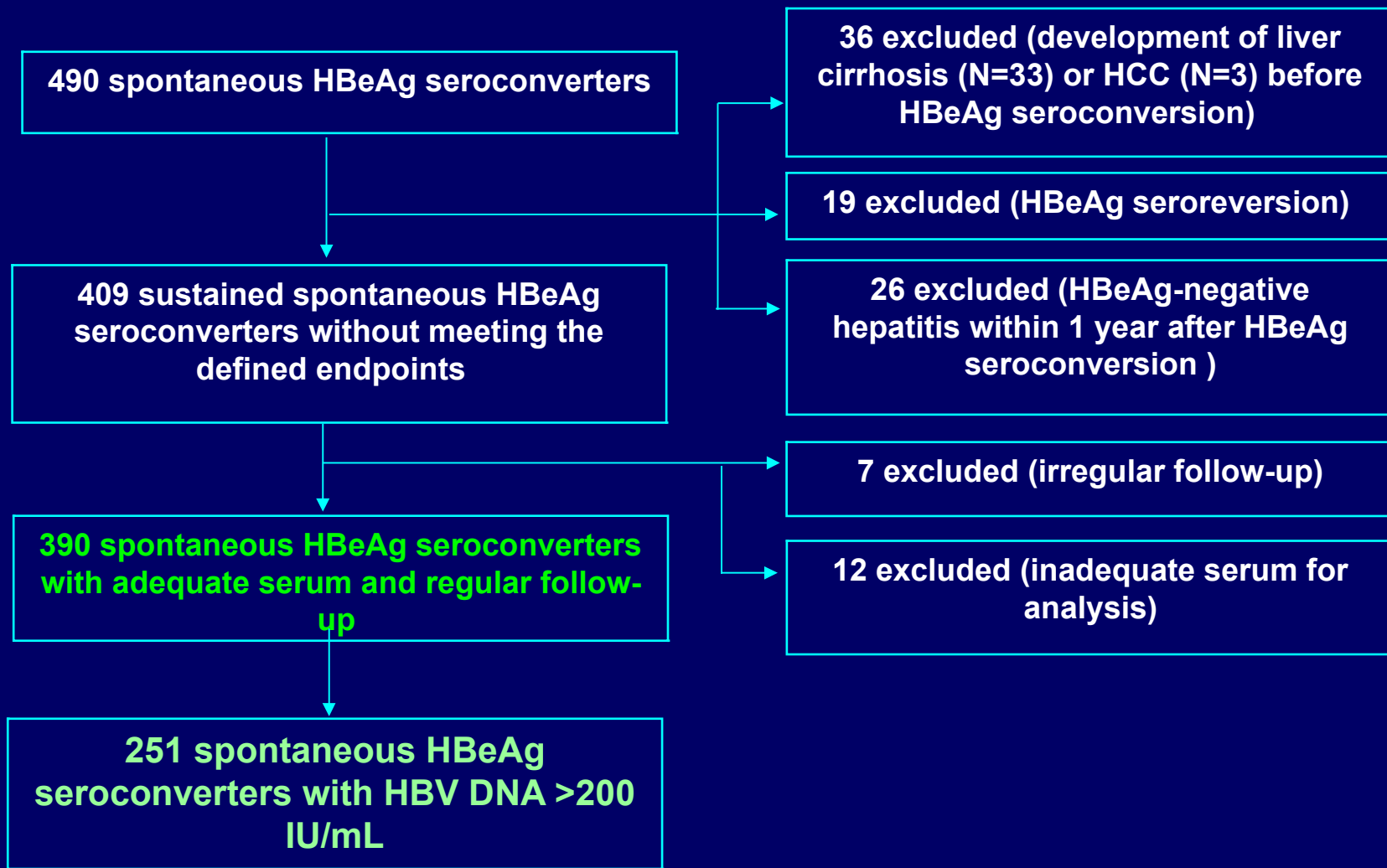


# SEARCH-B: issues remained

- **Predictive value**
  - For HBsAg loss: HBsAg level is better
  - For adverse outcomes: HBV-DNA level is better
- **Explanation**
  - HBV-DNA level, compared to HBsAg level, varies within a short period time
  - HBsAg level may be a better marker for immune control of HBV
- **Future studies in natural history**
  - **Predictive value of other biomarkers (e.g. viral variants)**
  - Cutoff HBsAg level to define true inactive carriers
  - Role of HBsAg in stratifying risk of disease progression in patients with different viral loads



# Flow of SEARCH-B subcohort qBCPm and cirrhosis risk



# Methods

- **PC and BCP variations**

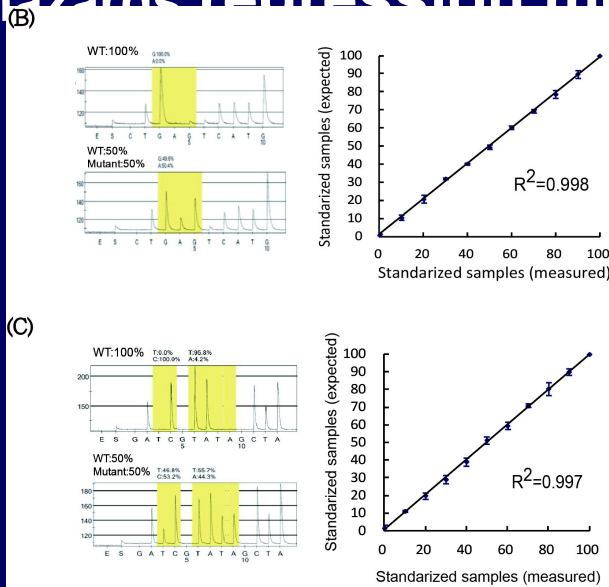
- Qualitative analysis by Taqman assay (major sequence): in VL >200 IU/mL

- Quantitative analysis by **pyrosequencing**: in VL >2000 IU/mL <sup>1</sup>

- **Statistical analysis**

- Kaplan-Meier failure estimate

- Cox proportional hazards regression models

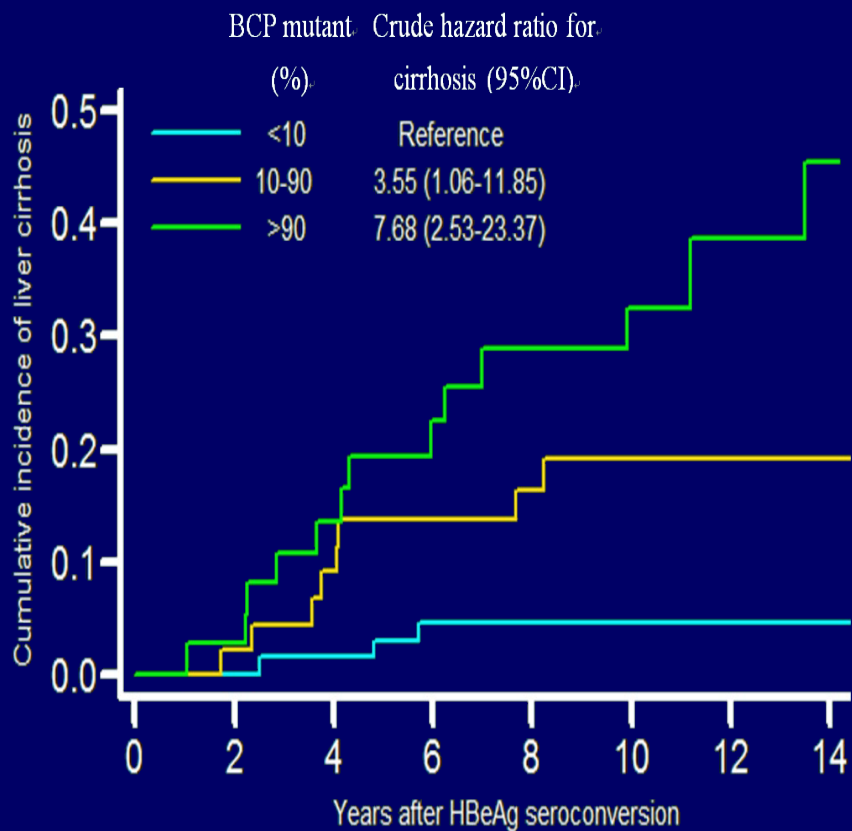


1 Yang et al. Hepatology  
2013; 57: 934-43

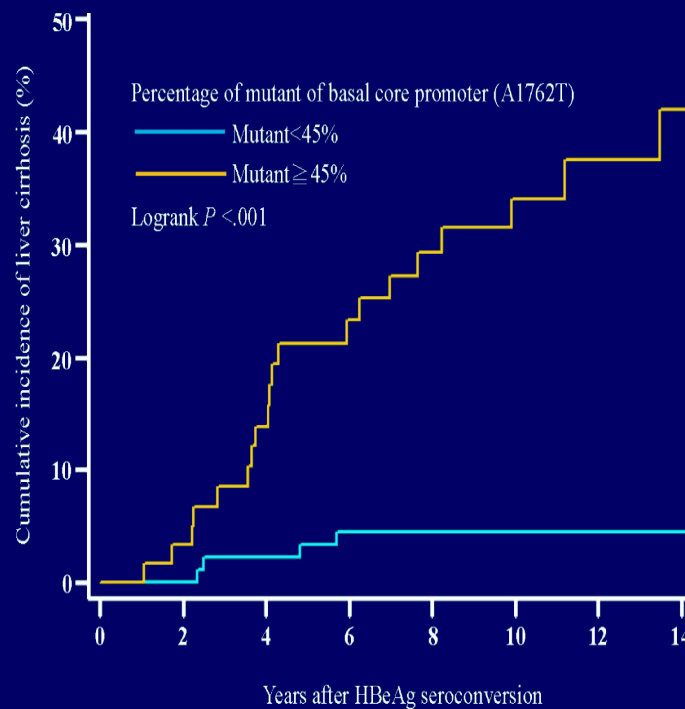


# Higher BCP mutant proportion has a higher cirrhosis risk in 151 patients with HBV DNA level > 2000 IU/mL

## Categorized by 10% & 90%



## Categorized by 45%





# ***SEARCH-B subcohort: summary***

- **PC/BCP variants are not associated with ENH**
- **A higher proportion of BCP mutant is associated with a higher risk of cirrhosis in patients with HBV DNA level > 2000 IU/mL (high viral load)**



# Outline

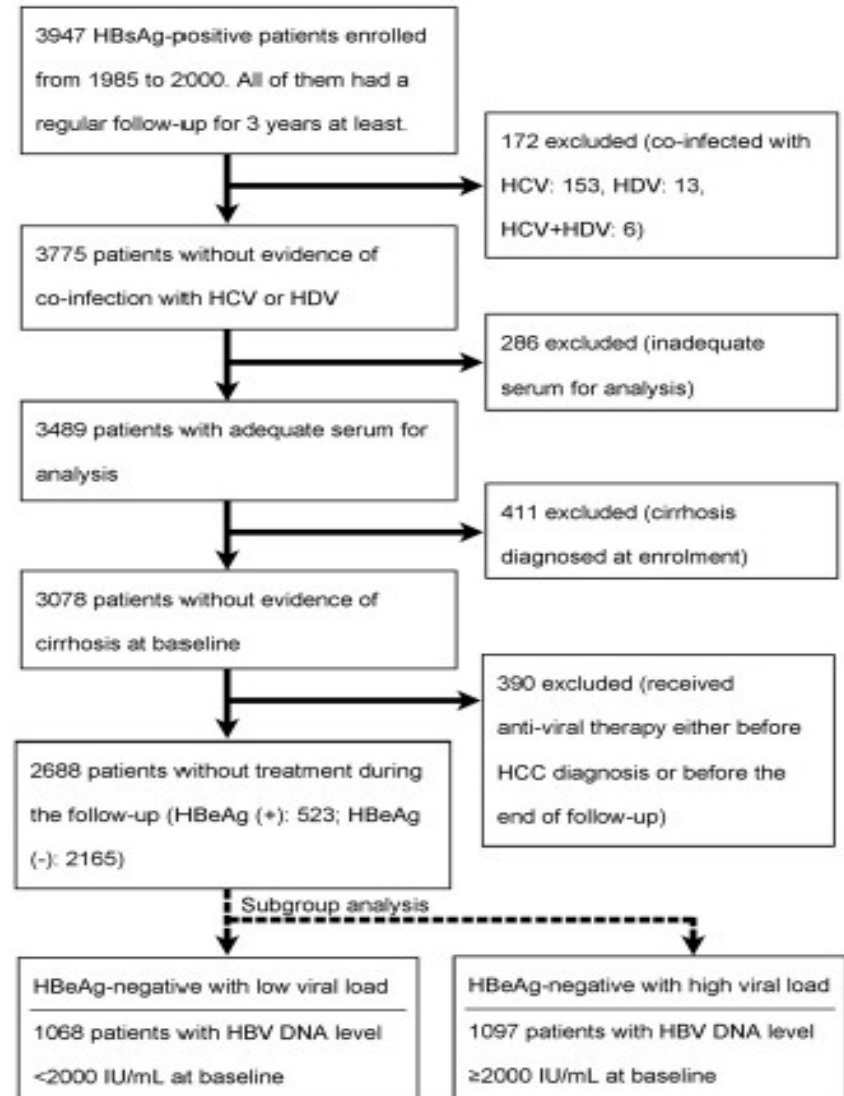
- **HBV natural history cohorts**
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# Flow of ERADICATE-B

- 2688 Taiwanese chronic hepatitis B patients followed for a mean of 14.7 years; cirrhosis excluded by USG





# ERADICATE-B Study: risk factors for higher HCC risk

Male gender

Older age

Higher ALT

Higher HBV DNA

Higher HBsAg

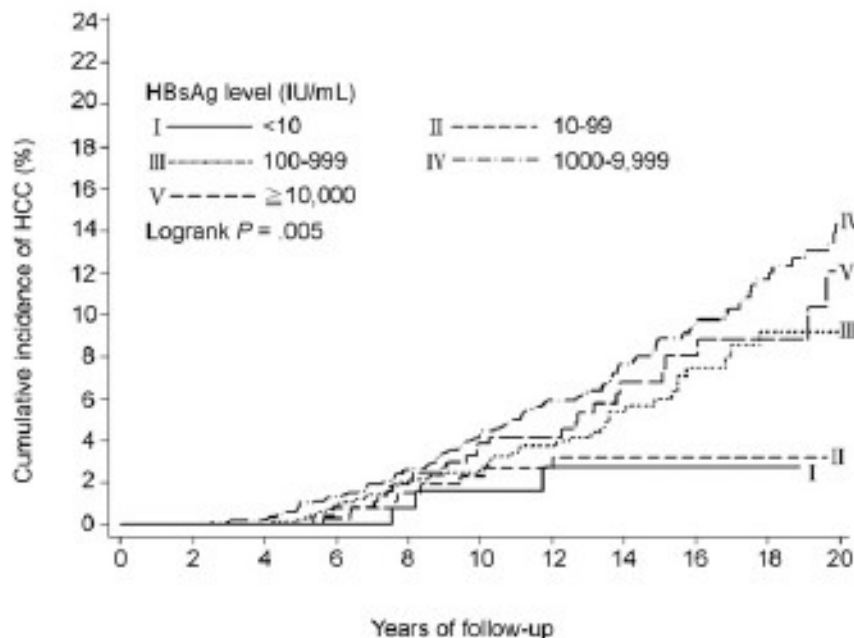
Genotype C

	Patients, n	Patient-years of follow-up	HCC, n	Annual incidence rate (per 100,000 patient-years)	Crude HR (95% CI)	P value
Sex						
Female	1054	15,440.3	37	239.6	1.0	
Male	1634	23,986.8	154	642.0	2.7 (1.9-3.8)	<.001
Age, y						
28-39	1407	21,236.5	62	292.0	1.0	
40-49	763	11,152.4	54	484.2	1.7 (1.2-2.5)	.004
50-59	369	5164.7	43	832.6	3.0 (2.1-4.5)	<.001
≥60	149	1873.5	32	1708.0	6.9 (4.5-10.6)	<.001
Serum ALT level, U/L						
<20	1051	16,611.0	27	162.5	1.0	<.001
20-39	854	11,908.6	49	411.5	2.8 (1.8-4.5)	
≥40	783	10,907.6	115	1054.3	7.2 (4.7-511.0)	<.001
HBeAg status						
Negative	2165	31,588.6	127	402.0	1.0	
Positive	523	7838.6	64	816.5	2.0 (1.5-2.7)	<.001
Serum HBV DNA level, IU/mL						
<200	438	6454.6	12	185.9	1.0	
200-1999	649	9780.3	17	173.8	0.9 (0.4-1.9)	.824
2000-19,999	555	8141.4	30	368.5	2.0 (1.0-3.9)	.044
20,000-199,999	292	4223.6	32	757.6	4.1 (2.1-8.0)	<.001
≥200,000	754	10,827.1	100	923.6	5.1 (2.9-9.2)	<.001
Serum HBsAg level, IU/mL						
<10	129	1735.8	3	172.8	1.0	
10-99	268	3916.0	8	204.3	1.1 (0.3-4.2)	.881
100-999	703	10,269.6	43	418.7	2.3 (0.7-7.3)	.171
1000-9999	1215	18,077.3	108	597.4	3.2 (1.0-10.0)	.048
≥10,000	373	5428.5	29	534.2	2.9 (0.9-9.5)	.080
HBV genotype <sup>a</sup>						
B	1308	19,154.7	93	485.5	1.0	
C	312	4327.1	69	1594.6	3.4 (2.5-4.6)	<.001

# ERADICATE-B: HCC according to baseline HBsAg level

- In overall assessment, HBsAg level was not a significant risk factor for HCC
- However, in patients with lower HBV DNA levels, HBsAg level was a significant factor for HCC risk

## Clinical utility of HBsAg level in patients with low HBV DNA



Number at risk

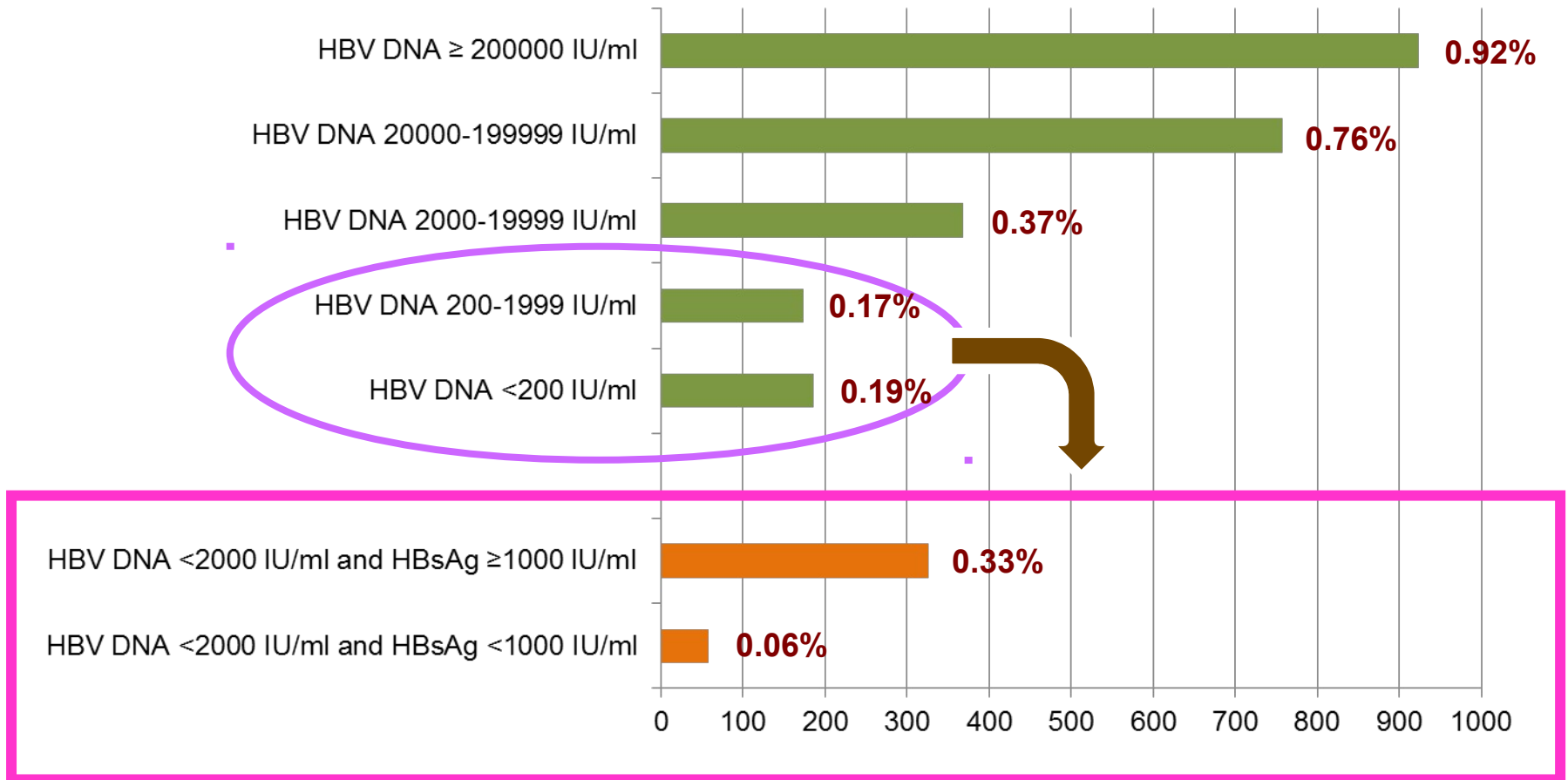
Serum HBsAg level at baseline (IU/mL)

<10	129	129	129	129	126	113	85	56	21	9	7
10-99	268	268	268	265	262	248	192	128	76	54	37
100-999	703	703	703	697	684	631	484	353	220	135	92
1000-9999	1215	1215	1212	1198	1175	1080	868	603	400	281	196
≥10000	373	373	373	372	363	329	263	184	119	74	50

# HBsAg level is an important risk factor in patients with low HBV DNA level (<2000 IU/mL)

## ERADICATE-B (2688 HBV carriers)

Risk of HCC (per 100,000 person-year)

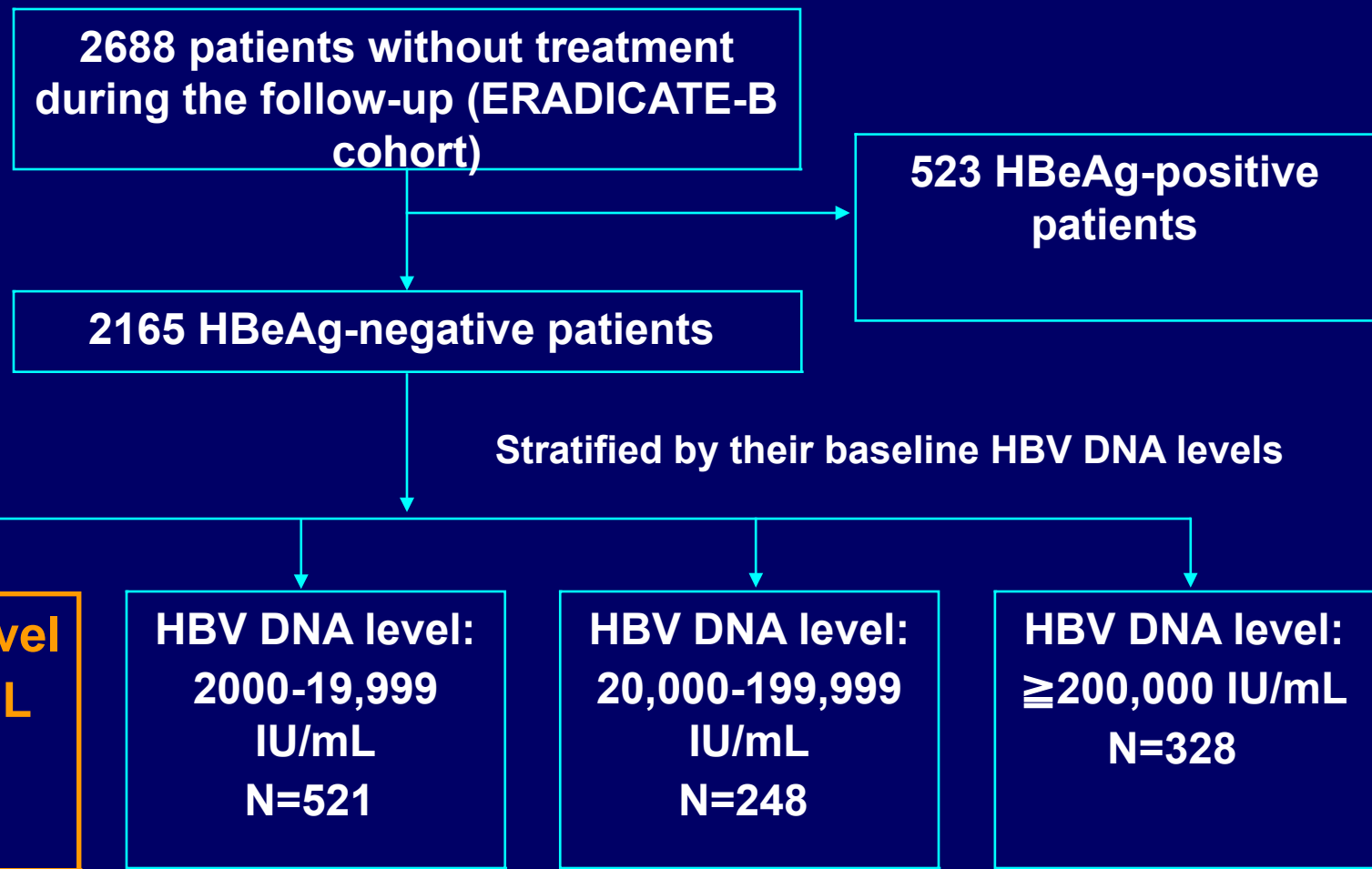


\*Start antiviral therapy at annual HCC risk of 0.3%

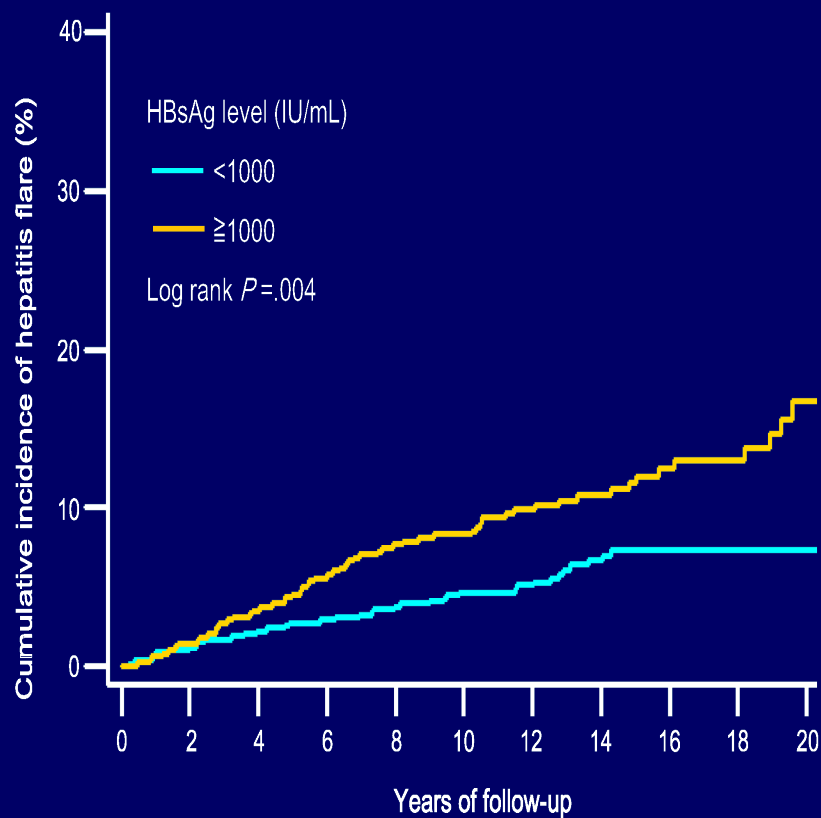


# **ERADICATE-B subcohort:**

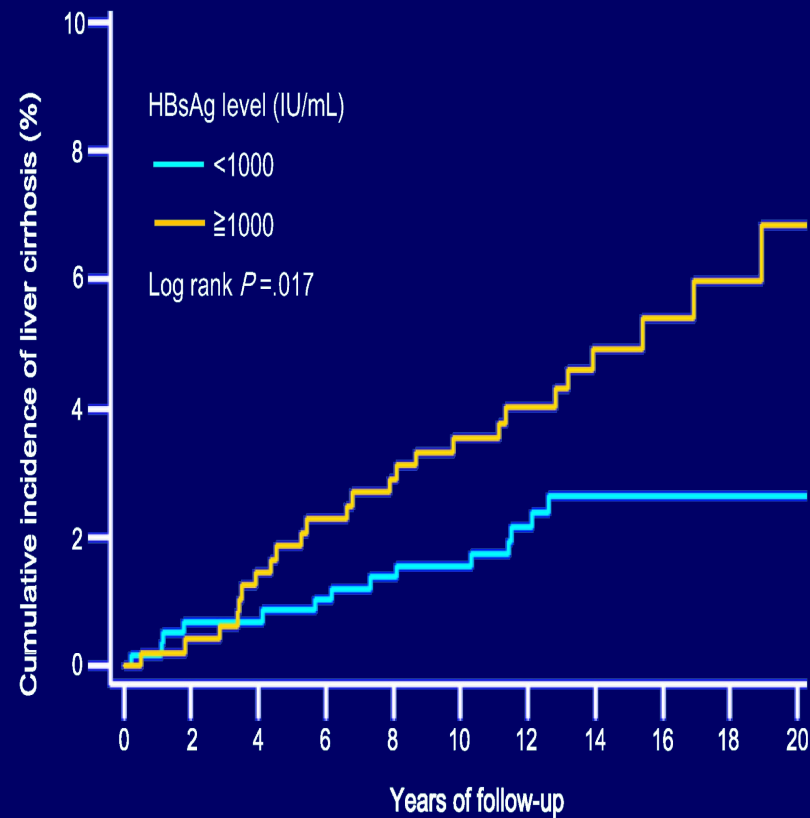
## **Low Viremia (LV) cohort**



# HBsAg level > 1000 IU/mL predicts hepatitis flare and cirrhosis

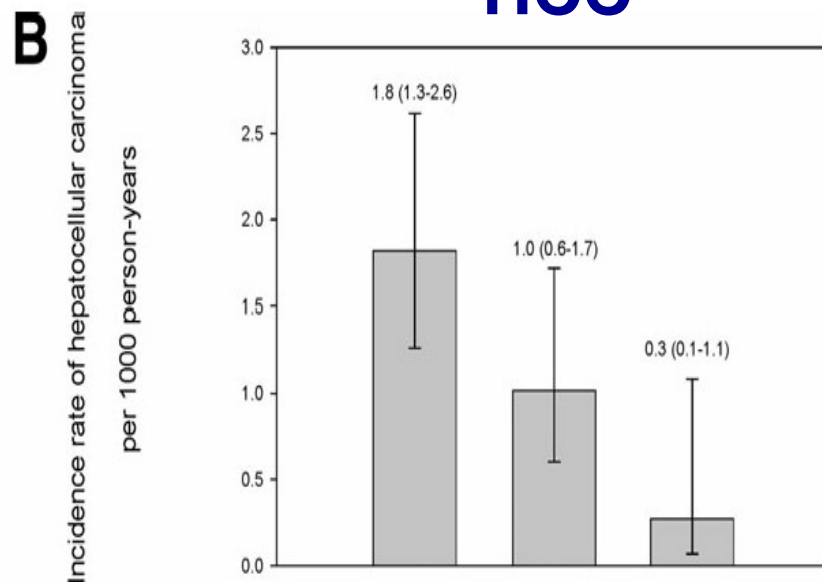
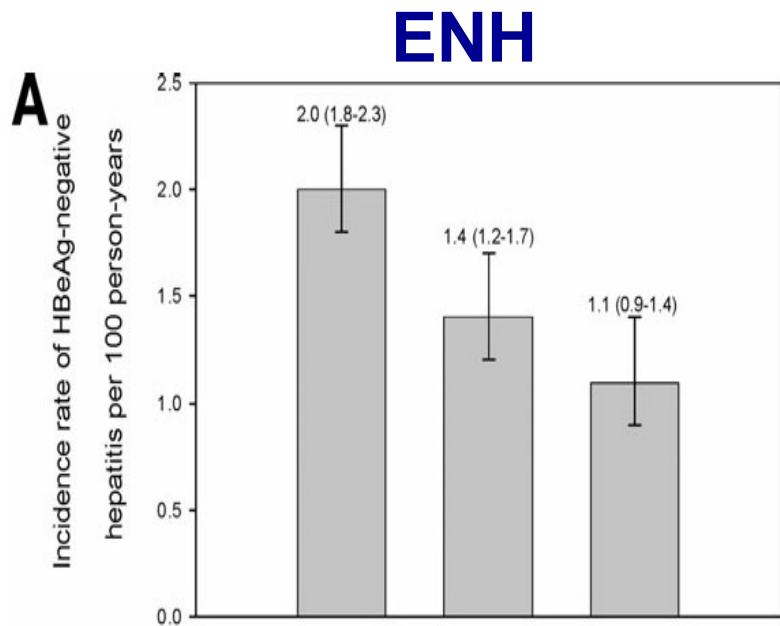


## Hepatitis flare



## Cirrhosis

# Incidence rates of ENH and HCC in different clinical settings of 1,068 patients with HBV DNA level <2,000 IU/mL



	Patient number	1068	910	495
HBV DNA	<2000 IU/mL	●	●	●
ALT	<40 U/L		●	●
HBsAg	<1000 IU/mL			●

	Patient number	1068	910	495
HBV DNA	<2000 IU/mL	●	●	●
ALT	<40 U/L		●	●
HBsAg	<1000 IU/mL			●



# Algorithm to categorize disease progression in Asian HBV carriers

Patients

Risk level

Follow-up Interval or management

HBeAg-positive HBV carriers and HBeAg-negative HBV carriers with more than one high viral risk factor from Table 1

High

3 months or start treatment

HBeAg-negative HBV carriers with HBV-DNA < 2000 IU/mL

Abnormal

Intermediate

3-6 months

ALT level

≥1000 IU/mL

Low

6-12 months

Normal

HBsAg level

< 1000 IU/mL

Minimal

12 months

Modified from Tseng et al. *Hepatology* 2013





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- HBV natural history cohorts
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# REACH-B risk score

## Development

Community-based  
REVEAL-HBV cohort

23820 cohort members  
recruited in Taiwan

4155 HBsAg  
seropositive

3851 tested serum HBV  
DNA on enrollment  
sample (REVEAL-HBV  
cohort)

3653 anti-HCV-  
seronegative subjects

3584 free of liver  
cirrhosis at study entry  
(131 developed HCC  
during follow-up)

## Validation

Hospital-based  
composite international  
cohort

CUHK  
cohort

426  
patients  
(46 HCC  
cases)

Yonsei  
U cohort

259  
patients  
(25 HCC  
cases)

UHK  
cohort

820  
patients  
(40 HCC  
cases)

Risk scores and  
predicted HCC  
risk for external  
validation



1505 CHB patients for  
validation (111  
developed HCC during  
follow-up)



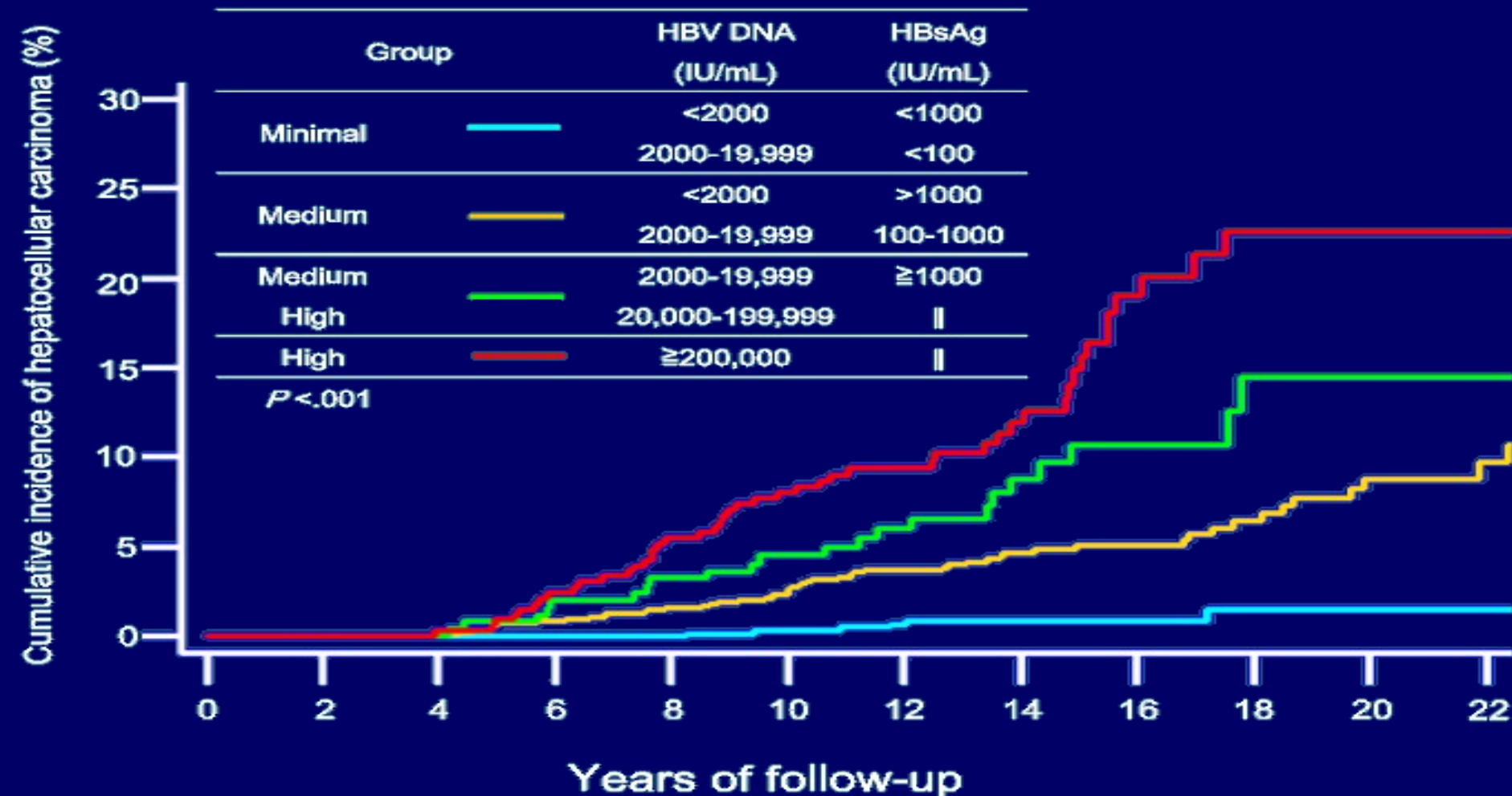
**\*Start antiviral therapy at annual HCC risk of 0.3%**



**Can incorporation of HBsAg levels  
improve risk model calculations?**



# Reclassification of HCC risk in 2165 HBeAg(-) patients





# Ongoing works on HCC risk calculator

## Development

Community-based  
REVEAL-HBV cohort

3584 HBsAg-seropositive, anti-HCV-seronegative, free of liver cirrhosis at study entry (208 developed HCC during follow-up)



Model derivation

Two model / score:

- REACH-B + qHBsAg (REACH-B IIa)
- REACH-B + qHBsAg – HBV DNA level (REACH-B IIb)

Model validation



3114 CHB patients for validation (237 developed HCC during follow-up)

## Validation

Hospital-based  
composite international  
cohort

CUHK  
cohort

426  
patients  
(46 HCC  
cases)

ERADICATE-B  
cohort

2688 patients  
(191 HCC  
cases)

\* All subjects were free of antiviral therapy during follow-up



# Comparison of various versions of REACH-B models/scores

	REACH-B	REACH-B IIa	REACH-B IIb
<b>Risk parameters</b>	Basic predictors+ HBV DNA	Basic predictors+ HBV DNA+ qHBsAg	Basic predictors+ qHBsAg
<b>Discriminatory capability</b>	Worst	Best	Good
<b>Cost</b>	Fairly expensive	Priciest	Cheapest
<b>Potential usage</b>	Should be replaced by new version tools	Used by hepatologists for management of CHB patients	First-line risk prediction tool for GP; community surveys; countries with limited resources



# Predicting Hepatitis B Virus (HBV) Surface Antigen Seroclearance in HBV e Antigen–Negative Patients With Chronic Hepatitis B: External Validation of a Scoring System

Jessica Liu,<sup>1,a</sup> Tai-Chung Tseng,<sup>2,9,a</sup> Hwai-I Yang,<sup>1,10,11</sup> Mei-Hsuan Lee,<sup>3</sup> Richard Batrla-Utermann,<sup>13</sup> Chin-Lan Jen,<sup>1</sup> Sheng-Nan Lu,<sup>12</sup> Li-Yu Wang,<sup>4</sup> San-Lin You,<sup>1</sup> Pei-Jer Chen,<sup>5,7</sup> Chien-Jen Chen,<sup>1,8</sup> and Jia-Horng Kao<sup>5,6,7</sup>

<sup>1</sup>Genomics Research Center, Academia Sinica, <sup>2</sup>Division of Gastroenterology, Department of Internal Medicine, Taipei Tzuchi Hospital, The Buddhist Tzuchi Medical Foundation, <sup>3</sup>Institute of Clinical Medicine, National Yang Ming University, <sup>4</sup>MacKay College of Medicine, <sup>5</sup>Division of Gastroenterology and Hepatology, Department of Internal Medicine, <sup>6</sup>Hepatitis Research Center, <sup>7</sup>Graduate Institute of Clinical Medicine, National Taiwan University College of Medicine, <sup>8</sup>Graduate Institute of Epidemiology and Preventative Medicine, College of Public Health, National Taiwan University, Taipei, <sup>9</sup>School of Medicine, Tzu Chi University, Hualien, <sup>10</sup>Molecular and Genomic Epidemiology Center, China Medical University Hospital Taichung, <sup>11</sup>Graduate Institute of Clinical Medical Science, China Medical University, Taichung, and <sup>12</sup>Department of Gastroenterology, Chang-Gung Memorial Hospital, Kaohsiung, Taiwan; and <sup>13</sup>Roche Diagnostics, Basel, Switzerland



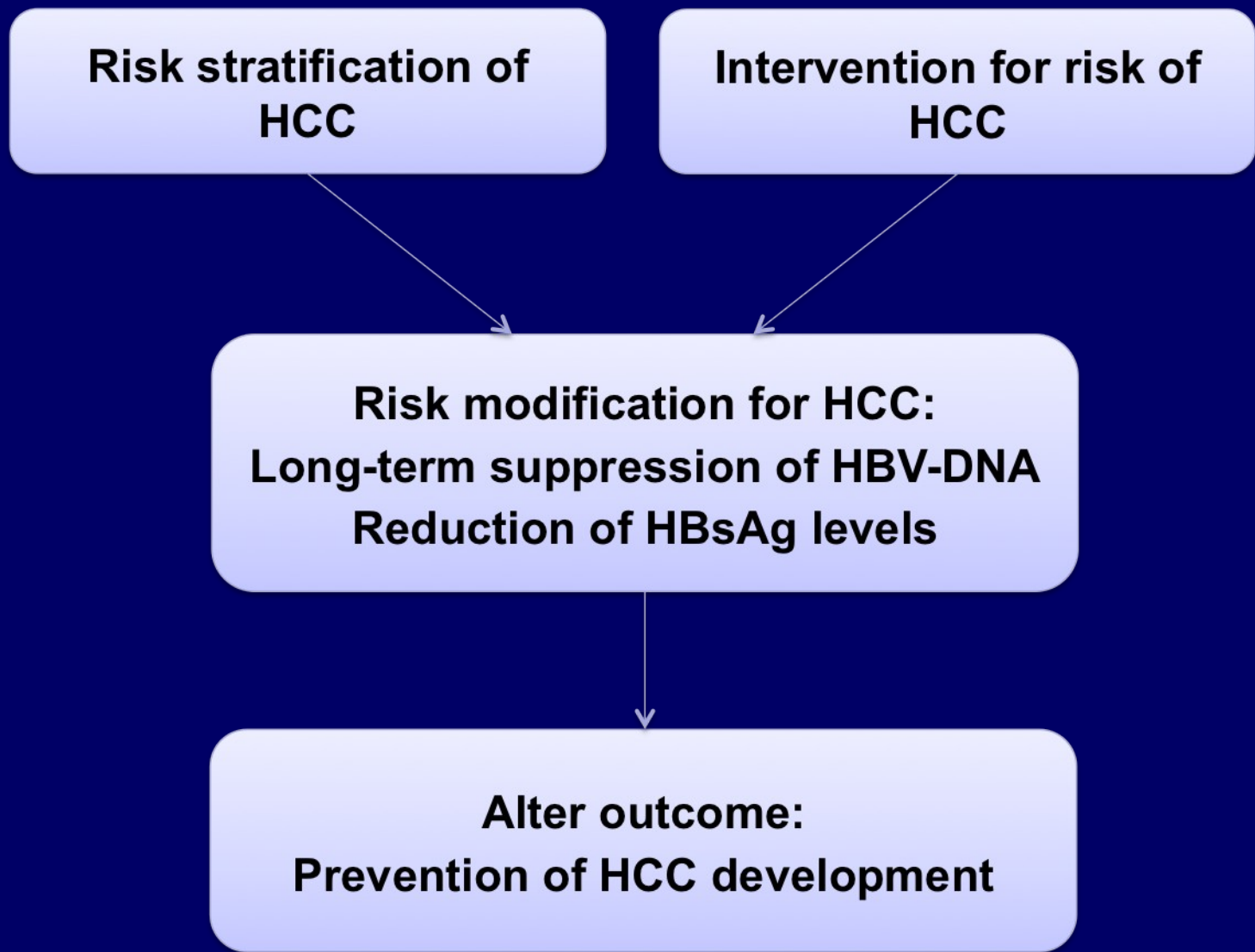


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- HBV natural history cohorts
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  - SEARCH-B
  - ERADICATE-B
- Risk calculator update
- **Conclusions**



# Assessment and modification of risk factors for HCC





# Conclusions:

## What have we learned from HBV clinical cohorts?

- CHB is a complex disease with various clinical outcomes
- HBV natural history cohorts help resolve HBV factors affecting liver disease remission or progression
- Integrating qHBsAg levels into risk calculators can aid classification of patients whose disease will or will not progress
- Risk modification by antiviral treatment is mandatory and feasible