

IA Main Paper Analysis Datasets and Variable Descriptions

Datasets

Two analysis datasets were used for the final analysis.

1. **all_IA** (a wide dataset that has all the outcomes and covariates from baseline, week 192, and week 240, and all survival outcomes).

This dataset is used for all outcome tables including the survival analysis.

Contents of this dataset:

- a. Variables with extensions `_S`, `_B`, `_192`, and `_240` refer to the time points last screening, baseline, week 192, and week 240 respectively.
- b. The following variables represent the outcomes:

Just add a `_192` or `_240` for the respective timepoints

```
sAg_loss           ="HBsAg loss (Y/N) (Central+Local)"
sAg_loss_c         ="HBsAg loss (Y/N) (Central)"
sAg_serocon        ="HBsAg seroconversion (Y/N) (Central+Local)"
sAg_serocon_c      ="HBsAg seroconversion (Y/N) (Central)"
eAg_serocon        ="HBeAg seroconversion (Y/N) (Central+Local)"
eAg_serocon_c      ="HBeAg seroconversion (Y/N) (Central)"
ALT_normal         ="ALT normalization-1 (M<=30, F<=20 U/L) (Y/N)"
ALT_normal2        ="ALT normalization-2 (M<=38, F<=25 U/L) (Y/N)"
DNAc1000           ="HBV DNA <1000 IU/mL (Y/N) (Central)"
DNAc20             ="HBV DNA <20 IU/mL-LLOQ (Y/N) (Central)"
DNA1000            ="HBV DNA <1000 IU/mL (Y/N) (Central+Local)"
DNA20              ="HBV DNA <20 IU/mL-LLOQ (Y/N) (Central+Local)"
```

Some other outcomes specifically defined at weeks 192 and 240:

```
eLoss192="HBeAg loss at week 192";
chg_s_192="Change in qHBsAg from Baseline (log10 IU/mL)";
chg_logs_192="Change in qHBsAg from Baseline (IU/mL)";
chg_e_192="Change in qHBeAg from Baseline (log10 IU/mL)";
chg_log_e_192="Change in qHBeAg from Baseline (IU/mL)";
altDNA_192="HBV DNA <1000 IU/mL and ALT normalization-2 (M<=30, F<=20 U/L)";
altDNA2_192="HBV DNA <1000 IU/mL and ALT normalization-2 (M<=38, F<=25 U/L)";
```

```
eLoss240="HBeAg loss at week 240";
chg_s_240="Change in qHBsAg from Baseline (log10 IU/mL)";
chg_logs_240="Change in qHBsAg from Baseline (IU/mL)";
chg_e_240="Change in qHBeAg from Baseline (log10 IU/mL)";
chg_log_e_240="Change in qHBeAg from Baseline (IU/mL)";
altDNA_240="HBV DNA <1000 IU/mL and ALT normalization-2 (M<=30, F<=20 U/L)";
altDNA2_240="HBV DNA <1000 IU/mL and ALT normalization-2 (M<=38, F<=25 U/L)";
sQuant_resp_240="At least 1 log decline in qHBsAg: Week 240";
```

Survival outcomes:

```
Event_sloss="Primary Endpoint: HBsAg Loss"
Event_sloss_date="Date of HBsAg Loss or last HBsAg evaluation"
Event_sloss_time="Time to HBsAg Loss or last HBsAg evaluation (weeks)"
```

Event_eloss="Secondary Endpoint: HBeAg Loss"
 Event_eloss_date="Date of HBeAg Loss or last HBeAg evaluation"
 Event_slloss_time="Time to HBeAg Loss or last HBeAg evaluation (weeks)"

Event_ALTn="Secondary Endpoint: ALT normalization"
 Event_ALTn_date="Date of ALT normalization or last ALT evaluation"
 Event_ALTn_time="Time to ALT normalization or last ALT evaluation (weeks)"

Event_DNA20="Secondary Endpoint: DNA<20"
 Event_DNA20_date="Date of DNA <20"
 Event_DNA20_time="Time to DNA<20 (weeks)"

Event_ALTDNA="Secondary Endpoint: DNA< 1000 and ALT normalization"
 Event_ALTDNA_date="Date of DNA< 1000 and ALT normalization"
 Event_ALTDNA_time="Time to DNA< 1000 and ALT normalization (weeks)"

2. IA_long (a longitudinal dataset)

Main contents of IA_long dataset:

week	"Timepoint (numeric)"
week_b1	"Weeks since baseline"
sAg_loss	"HBsAg loss (Y/N) (Central+Local)"
sAg_loss_c	"HBsAg loss (Y/N) (Central)"
sAg_serokon	"HBsAg seroconversion (Y/N) (Central+Local)"
sAg_serokon_c	"HBsAg seroconversion (Y/N) (Central)"
eAg_loss	"HBeAg loss (Y/N) (Central+Local)"
eAg_loss_c	"HBeAg loss (Y/N) (Central)"
eAg_serokon	"HBeAg seroconversion (Y/N) (Central+Local)"
eAg_serokon_c	"HBeAg seroconversion (Y/N) (Central)"
ALT_normal	"ALT normalization-1 (M<=30, F<=20 U/L) (Y/N)"
ALT_normal2	"ALT normalization-2 (M<=38, F<=25 U/L) (Y/N)"
DNAc1000	"HBV DNA <1000 IU/mL (Y/N) (Central)"
DNAc20	"HBV DNA <20 IU/mL-LLOQ (Y/N) (Central)"
DNA1000	"HBV DNA <1000 IU/mL (Y/N) (Central+Local)"
DNA20	"HBV DNA <20 IU/mL-LLOQ (Y/N) (Central+Local)"

Note that even though the variables eAg_loss and eAg_loss_c are defined as "loss" here, they actually mean whether eAg result is negative or not. When combined with baseline HBeAg positivity, this would result in "loss" outcome as defined in the wide dataset above.

Errata for Main IA Paper:

1. Table 1: in the “qHBsAg (log₁₀IU/mL), median (IQR)” row, the number 4.9 should be 4.2
2. Table 4: Last four rows relating to quantitative HBsAg and HBsAg changes will actually be as follows:

Change in qHBsAg from baseline (log₁₀ IU/mL)	N=91	N=96		N=86	N=91	
Mean (STD)	-0.83 (1.33)	-0.79 (1.18)	0.83	-1.08 (1.51)	-0.94 (1.38)	0.53
Change in qHBeAg from baseline (log₁₀ IU/mL)**	N=46	N=51		N=43	N=48	
Mean (STD)	-2.52 (1.31)	-2.25 (1.36)	0.32	-2.50 (1.40)	-2.49 (1.22)	0.98

3. Caption of Figure 4 should read: The correct caption should be: Change in qHBsAg over time in HBeAg positive and HBeAg negative participants, by treatment group. **Data presented are median and 25th and 75th percentiles.** The decline in qHBsAg occurred earlier with combination therapy than TDF alone but was not statistically different at week 240. The mean (SD) change in qHBsAg was less in those who were initially HBeAg negative (20.43 [SD = 0.69] log IU/mL) than in those who were HBeAg positive (21.16 [SD= 1.51]), with no significant difference by treatment group (P = 0.59). HBeAg, hepatitis B e antigen; TDF, tenofovir disoproxil fumarate.
4. Throughout the manuscript, the rate of HBsAg loss in combination group at weeks 192 and 240 will be 5.2% (as shown in Figure 3) instead of 5.3%. Note that both numbers are correct. If actual date of visit is used to calculate time since randomization, as reflected in Figure 3, the rate is 5.2%; However, if the time is taken as the visit week (e.g., week 240) then the rate is 5.3%.