# STATISTICAL ANALYSIS PLAN

A PHASE 2a, RANDOMIZED DOUBLE-BLIND PLACEBO-CONTROLLED STUDY OF ORAL FXR MODULATOR EYP001a COMBINED WITH NUCLEOS(T)IDE ANALOGUES (NA) IN VIROLOGICALLY SUPPRESSED CHRONIC HEPATITIS B PATIENTS TO IMPROVE FUNCTIONAL CURE RATES

**PROTOCOL NO.:** EYP001-201

**PRODUCT CODE:** EYP001a

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**SAP APPROVAL**

By my signature, I confirm that this SAP has been reviewed by ENYO Pharma SA and has been approved for use on the EYP001-201 study:

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**List of Abbreviations**

| Abbreviation | Description |
|---|---|
| AE | Adverse Event |
| Anti-HBe | Antibody to Hepatitis B e antigen |
| Anti-HBs | Antibody to Hepatitis B surface antigen |
| ATC | Anatomical Therapeutic Class |
| BA | Bile Acid |
| BMI | Body Mass Index |
| BP | Blood Pressure |
| CHB | Chronic Hepatitis B |
| CS | Clinically Significant |
| CSR | Clinical Study Report |
| CTU | Clinical Trial Unit |
| DBP | Diastolic blood pressure |
| DNA | Deoxyribonucleic Acid |
| ECG | 12-Lead Electrocardiogram |
| eCRF | Electronic Case Report Form |
| EoS | End of Study |
| ET | Early Termination |
| ETV | Entecavir |
| FDA | Food and Drug Administration |
| FGF19 | Fibroblast Growth Factor |
| FU | Follow Up |
| FXR | Farnesoid X Receptor |
| GCP | Good Clinical Practice |
| HBcrAg | Hepatitis B core-related antigen |
| HBeAg | Hepatitis B Surface e-Antigen |
| HBsAg | Hepatitis B Surface Antigen |
| HBV | Hepatitis B virus |
| HCV | Hepatitis C virus |
| HIV | Human Immunodeficiency Virus |
| IA 1 | Interim Analysis 1 |
| IA 2 | Interim Analysis 2 |
| ICH | International Council for Harmonization |
| IEC | Independent Ethics Committee |
| IRB | Institutional Review Board |
| IP | Investigational Product |
| ITT | Intent-to-Treat |
| IWRS | Interactive Web Response System |
| LLOQ | Lower Limit Of Quantification |
| LS | Least Square |
| MedDRA | Medical Dictionary for Regulatory Activities |
| mITT | Modified Intention-To-Treat |
| NA | Nucleos(t)ide analogues |
| N/A | Not Applicable |
| NCS | Not Clinically Significant |
| NK | Not Known |
| PD | Pharmacodynamic |
| pgRNA | Pg/Precore Ribonucleic Acid |
| PK | Pharmacokinetic |

| | |
|---|---|
| PP | Per Protocol |
| PT | Preferred Term |
| QD | Once Daily |
| SAE | Serious Adverse Event |
| SAP | Statistical Analysis Plan |
| SBP | Systolic blood pressure |
| SD | Standard Deviation |
| S.I. | International System of Units |
| SOC | Standard of Care |
| $SOC^2$ | System Organ Class |
| SOP | Standard Operating Procedure |
| TD | Target Detected |
| TDF | Tenofovir Disoproxil Fumarate |
| TEAE | Treatment Emergent Adverse Event |
| TFL | Tables, Figures and Listings |
| TND | Target not detected |
| VAS | Visual Analog Scale |
| VCTE | Vibration Controlled Transient Elastography |
| WHO-DD | World Health Organization Drug Dictionary |

# 1. INTRODUCTION

The following Statistical Analysis Plan (SAP) provides the outline for the statistical analysis of the data collected from the EYP001-201 study (protocol version 3.0 dated 22 January 2020).

The planned analyses identified in this SAP may be included in clinical study reports (CSRs), regulatory submissions, or future manuscripts. Also, post hoc exploratory analyses not necessarily identified in this SAP may be performed to further examine study data. Any post hoc, or unplanned, exploratory analyses performed will be clearly identified as such in the final CSR.

# 2. PROJECT OVERVIEW

## 2.1 Study Design

This is a prospective, multi-centre, international randomized, double-blind, placebo controlled, Phase 2a experimental study of oral FXR modulator EYP001a/placebo combined with Nucleos(t)ide analogues (NA) in virologically suppressed CHB patients to improve functional cure rates.

In total 49 eligible patients will be enrolled and randomized at approximately 14 study sites in 4 countries. Patients will be randomized prior to study drug (EYP001a or placebo and NA) administration on Day 1 in the ratio of 3:1 into 2 arms:

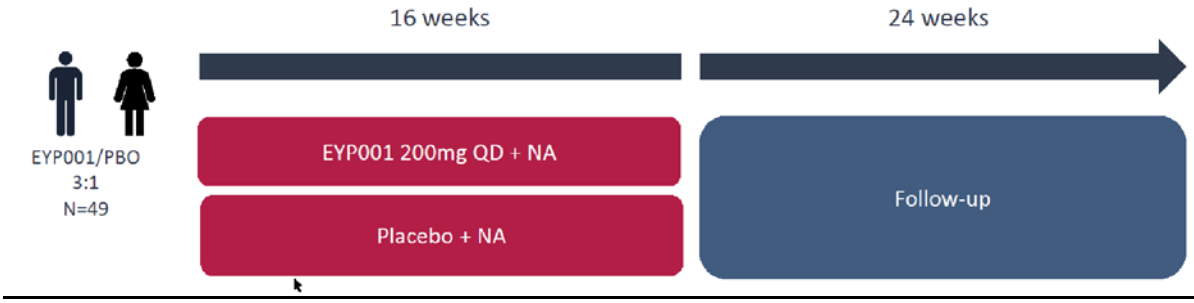
- Experimental Arm: EYP001a 200 mg once daily (QD) + NA daily (37 patients)
- Control Arm: Placebo + NA daily (12 patients)

Patients will also be stratified per HBeAg status, based on medical history HBeAg value or established during screening, to obtain a balanced randomization to both study arms.

The maximum total engagement duration for eligible patients in this study is up to 370 days: 90 days screening, 112 days (16 weeks) experimental treatment period and 168 days (24 weeks) follow-up on NA standard of care therapy (SOC) only.

Patients enrolled in the study will be assessed as outpatients. Patient screening will occur no more than 90 days prior to the Day 1 visit. Eligible patients will undergo further assessments on Day 1 to qualify for study drug administration on Day 1.

**Figure 1: Study Design**




## 2.2 Objectives

### 2.2.1 Primary objective

The primary objective of this study is:

- To determine the effect of EYP001a on top of NA (standard of care (SOC) therapy) on Hepatitis B Surface Antigen (HBsAg) plasma levels.

### 2.2.2 Secondary objective(s)

The secondary objectives of this study are:

- To establish the effect of EYP001a on top of NA on HBsAg responder rate at the end of the 16-week EYP001a treatment and at 24-week of follow-up (Week 40).
- To establish the effect of EYP001a on top of NA on HBsAg loss rate at the end of the 16-week EYP001a treatment and at 24-week of follow-up (Week 40).
- To establish the Hepatitis B virus (HBV) virologic failure rate (breakthrough) during the 24-weeks follow-up period after stopping EYP001a with ongoing NA.
- To determine HBV viral response, HBV Pg/Precore Ribonucleic Acid (pgRNA), Hepatitis B core-related antigen (HBcrAg) and Hepatitis B Surface e-Antigen (HBeAg), Antibody to Hepatitis B e

antigen (Anti-HBe) and Antibody to Hepatitis B surface antigen (Anti-HBs) at the end of the 16-week EYP001a treatment and Week 40 of follow-up.

- To explore the safety profile of EYP001a treatment in combination with NA.
- To determine the plasma concentration of EYP001a and pharmacodynamic (PD) markers (plasma C4 (7α-hydroxy-4-cholesten-3-one)), fibroblast growth factor (FGF) 19 and BAs.

## 2.3 Endpoints

### 2.3.1 Primary endpoint(s)

- Efficacy assessed as HBsAg decline ($\Delta \log_{10}$) from Day 1 to Week 16 of treatment.

### 2.3.2 Secondary endpoints(s)

Efficacy will be assessed as follows:

- HBsAg responder rate (decrease from baseline $\geq 1.0$ on the $\log_{10}$ scale) at Week 16 of treatment and Weeks 20, 28 and 40 of follow up.
- HBsAg responder rate (decrease from baseline $\geq 0.5$ on the $\log_{10}$ scale) at Weeks 12 and 16 of treatment and Weeks 20, 28 and 40 of follow up.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ/TND) at Week 16 of treatment and Weeks 20, 28 and 40 of follow-up.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ/TD) at Week 16 of treatment and Weeks 20, 28 and 40 of follow-up.
- HBsAg loss rate (Proportion of results that are Target Not Detected versus Target Detected) at Week 16 of treatment and Weeks 20, 28 and 40 of follow-up.
- Relapse rate HBsAg (% patients who became negative [HBsAg < LLOQ], then increased with HBsAg > LLOQ) at Week 16 of treatment period and Weeks 20, 28 and 40 during follow-up period.
- Virologic failure rate (breakthrough) of Hepatitis B virus Deoxyribonucleic Acid (HBV-DNA) (% patients with a confirmed quantifiable HBV DNA increase of $\geq 1\log_{10}$ HBV DNA copies/mL above LLOQ) assessed at Week 16 of treatment period and Weeks 20, 28 and 40 during follow-up period.
- % patients with HBV DNA < Lower Limit of Quantification (LLOQ/TND) at baseline, Week 4, 8, 12 and 16 of treatment and Weeks 20, 28 and 40 of follow-up
- % patients with HBV DNA < Lower Limit of Quantification (LLOQ/TD) at baseline, Week 4, 8, 12 and 16 of treatment and Weeks 20, 28 and 40 of follow-up
- HBV-pgRNA decline ($\Delta \log_{10}$) from Day 1 to Weeks 4, 8, 12, 16 of treatment period and Week 40 of maintenance period.
- HBcrAg decline ($\Delta \log_{10}$) from Day 1 to Weeks 4, 8, 12, 16 of treatment period and Week 40 of maintenance period.
- HBeAg quantification for HBeAg pos patients and changes at Week 16 of treatment and Week 40 of follow-up.
- Fibroscan Vibration Controlled Transient Elastography (VCTE) change from screening value to Weeks 16 and 40 or Early Termination (ET) value.

Safety and Tolerability will be assessed as:

- Treatment-emergent adverse events (TEAEs) (including Serious Adverse Event (SAEs))
- All-cause mortality

- Clinical laboratory tests
- Pruritus assessment (VAS and Q5D)
- Vital signs (blood pressure, heart rate, respiratory rate, and temperature)
- Concomitant medications
- Physical examinations
- 12-lead Electrocardiogram (ECG).

Pharmacokinetics (PK) assessed will be as:

- Plasma concentration of EYP001a or any relevant active metabolites (as identified in an ongoing phase 1 study).

PD biomarkers will be assessed as:

- Plasma C4 (7α-hydroxy-4-cholesten-3-one)
- FGF19
- Plasma primary and secondary BAs.

### 2.4 Sample Size

The primary endpoint is HBsAg reduction. Improvement of 1.0 on a $\log_{10}$ scale at 16 weeks is considered to be clinically meaningful. The expected accrual rate is 2 to 4 patients per week but does not affect the sample size calculation. Note that the accrual rate will not affect sample size calculations. All assumptions are given in Table 1.

**Table 1 Assumptions for primary endpoint**

| | |
|---|---|
| **Primary Endpoint** | HBsAg reduction vs baseline on a $\log_{10}$ scale ("Chg") |
| **Null hypothesis** | H0: $Chg_{exp} - Chg_{ctrl} = 0$ |
| **Alternative hypothesis** | Ha: $Chg_{exp} - Chg_{ctrl} = -1.0$ |
| **SD of change vs baseline in experimental arm** | 1.08 |
| **SD of change vs baseline in control arm** | 1.08 |
| **Drop-out** | 10% over total study duration |
| **Randomization ratio** | 3:1 for experimental:control (i.e. nE/nC=3) |
| **Power** | 80% |
| **Type I error rate (1-sided)** | 0.05 |

Chg: Change vs baseline; Ctrl: Control arm; Exp: Experimental arm; H0: Null Hypothesis; Ha: Alternative Hypothesis; SD: Standard Deviation

Patients who have dropped out, will be assumed to have a zero-difference vs baseline for conservativeness. To take this into account, the assumed effect of -1.0 on a $\log_{10}$ scale, will be multiplied by 0.9, resulting in an assumed effect of -0.9. Using these assumptions, based on a test, 49 patients will need to be enrolled. Calculations are based on a t-test.

Note that the final analysis will be done, using a general linear model for repeated measures. Using this type of model, a better power is expected, thus sample size calculations can be considered conservative.

To calculate the power to detect a difference in HBsAg loss rate, we assumed a proportion of 0.5% in the placebo arm, and of 10%in the experimental arm. A trial including 49 patients results in a power of about 55% for this endpoint (using an un-pooled estimate of the variance), using a one-sided α of 0.05.

## 2.5 Randomization

Sequential screening numbers will be assigned to patients at the time of informed consent signing. As they are enrolled into the study and after eligibility on Day -3 at the earliest and prior to dosing on Day 1 at the latest, patients will be assigned to a unique randomization number which are randomly assigned to treatment according to the specified randomization scheme.

The randomization schedule will be computer-generated before the start of the study.

An Interactive Web Response System (IWRS) will be employed to manage patient and treatment assignments.

Patients will be randomized prior to study drug (EYP001a or placebo and NA) administration on Day 1 in the ratio of approximately 3:1 (37:12) into 2 arms:

- Experimental Arm: EYP001a 200 mg QD + NA daily (37 patients)
- Control Arm: Placebo + NA daily (12 patients)

The ratio will be controlled through block randomization.

Patients will also be stratified per HBeAg status, based on medical history HBeAg value or established during screening, to obtain a balanced randomization to both study arms.

# 3. STATISTICAL CONSIDERATIONS

Data will be handled and processed per the sponsor's representative (Novotech) Standard Operating Procedures (SOPs), which are written based on the principles of good clinical practice (GCP).

## 3.1 General Considerations

All data collected on the electronic case report form (eCRF) will be presented in the data listings and will be listed and sorted by treatment arm, participant number and visit, where applicable. All descriptive summaries will be presented by treatment group and nominal visit/time point (where applicable).

Unless otherwise stated, the following methods will be applied:

- Continuous variables: Descriptive statistics will include the number of non-missing values (n), arithmetic mean, standard deviation (SD), median, minimum and maximum values.

  The minimum and maximum values will be displayed to the same decimal precision as the source data, the arithmetic mean, SD and median values will be displayed to one more decimal than the source data for the specific variable.

  95% Confidence Intervals (CIs), mean differences (among treatments and from baseline) and least-square (LS-Means) values will be displayed to one more decimal than the source data for a specific variable. P-values will be displayed to 3 decimal places.

  The appropriate precision for derived variables will be determined based on the precision of the data on which the derivations are based, and statistics will be presented in accordance with the above-mentioned rules.

- Figures based on continuous summary data:
  - X-axis will represent the linear scheduled time expressed as -Day x for screening values and +Day y on treatment values
  - Y-axis will represent the Mean (+/-SD) and be presented as box-plots (median interquartile) parameter value (unit).

- Categorical variables: Descriptive statistics will include counts and percentages per category. The denominator in all percentage calculations will be the number of participants in the relevant analysis population with non-missing data, unless specifically stated otherwise. Percentages will be displayed to one decimal place. Proportions will be displayed to 3 decimal places.

  95% Confidence Intervals (CIs), difference in proportions, odds ratio's and other categorical parameters will be displayed to one decimal place for percentages. Proportions will be displayed to 3 decimal places. P-values will be displayed to 3 decimal places.

- Repeat/unscheduled assessments: Only values collected at scheduled study visits/time points will be presented in summary tables. If a repeat assessment was performed, the result from the original assessment will be presented as the result at the specific visit/time point. All collected data will be included in the data listings.

- Assessment windows: All assessments will be included in the data listings and no visit windows will be applied to exclude assessments that were performed outside of the protocol specified procedure windows.

- Result display convention: Results will be center aligned in all summary tables and listings. Participant identifiers visit and parameter labels may be left-aligned if required.

- Date and time display conventions: The following display conventions will be applied in all outputs where dates and/or times are displayed:

  Date only: YYYY-MM-DD

  Date and time: YYYY-MM-DD HH:MM

If only partial information is available, unknown components of the date or time will be presented as 'NK' (not known), i.e., '2016-NK-NK'. Times will be reported in military time.

- End of Study (EoS) vs Early Termination (ET)

For any analyses based on safety data, efficacy and PD data, EOS and ET assessment will be summarized separately.

### 3.2 Key Definitions

The following definitions will be used:

- Baseline: The baseline value is defined as the last available valid (quantifiable continuous or categorical value), non-missing observation for each participant prior to first study drug administration. Repeat and unscheduled assessments will be included in the derivation of the baseline values.

  For HBsAg, ALT, AST, ALP, and total Bilirubin (TBL), the baseline value is defined as the average of screening and day 1 pre-dose.

  For HBeAg, the Baseline value is value taken at screening visit.

- Change from Baseline: The change from baseline value is defined as the difference between the result collected/derived at a post-baseline visit/time point and the baseline value.

  The change from baseline value at each post-baseline visit/time point will be calculated for all continuous parameters using the following formula:

  Change from Baseline Value = Result at Visit/Time Point – Baseline Value

  The change from baseline value will only be calculated if the specific post-baseline visit/time point result and the baseline value for the parameter are both available and will be treated as missing otherwise.

- Percent Change from baseline: The percent change from baseline at each post-baseline visit/time point will be calculated for all continuous parameters using the following formula:

  % Change from Baseline = 100 X [(Post-Dose Visit Value – Baseline) / Baseline]

- Study day: The study day of an event is defined as the relative day of the event starting with the date of the first study drug administration (reference date) as Day 1 (there will be no Day 0).

  The study day of events occurring before the first study drug administration will be calculated as:

  Study Day = (Date of Event - Date of First Study Drug Administration)

  For events occurring on or after Day 1, study day will be calculated as:

  Study Day = (Date of Event - Date of First Study Drug Administration) + 1

  Study days will only be calculated for events with complete dates and will be undefined for events that are 'Ongoing' at the end of the study.

  Relative days compared to an alternative reference point will be calculated similarly, but the alternative starting reference start date will be used instead of the date of the first study drug dosing.

  Please note that for this study, first study drug dosing is considered to occur on Day 1.

- Breakthrough: Quantifiable HBV DNA increase of $\geq 1$ $\log_{10}$ HBV DNA copies/mL above LLOQ.

- Lower limit of quantification (LLOQ): HBV DNA results i.e HBsAg < LLOQ will be reported as either <LLOQ/Detected (i.e. LLOQ/TD) or <LLOQ/Target Not Detected (i.e. LLOQ/TND), both are considered LLOQ. HBsAg loss rates will be further subdivided accordingly.

- HBsAg decline: Change from Baseline in HBsAg on the $\log_{10}$ scale. Negative values indicate a decline.
- HBsAg loss: Patients with HBsAg < LLOQ/TND.
- HBsAg responder A: A decrease from baseline ≥ 1.0 on the log10 scale, i.e. a change from baseline of ≤ -1.0. HBsAg results <LLOQ/Target Not Detected will be reported as 0.015 [log10(0.015) = -1.852 and HBsAg < LLOQ/Target Detected will be reported as midpoint between LLOQ/Target Not Detected and LLOQ/Target Detected, i.e. 0.04IU/mL = log10 (0.04)= -1.4. Also, HBsAg above LLOQ will be reported as the raw data is reported.
- HBsAg responder B: A decrease from baseline ≥ 0.5 on the log10 scale, i.e. a change from baseline of ≤ -0.5. HBsAg results <LLOQ/Target Not Detected will be reported as 0.015 [log10(0.015) = -1.852 and HBsAg < LLOQ/Target Detected will be reported as midpoint between LLOQ/Target Not Detected and LLOQ/Target Detected, i.e. 0.04IU/mL = log10 (0.04)= -1.4. Also, HBsAg above LLOQ will be reported as the raw data is reported.
- HBsAg Relapse Rate: Patients who became negative (HBsAg<LLOQ), then increased with HBsAg > LLOQ. HBsAg results <LLOQ/Target Not Detected will be reported as 0.015 [$\log_{10}$(0.015) = -1.852 and HBsAg < LLOQ/Target Detected will be reported as midpoint between LLOQ/Target Not Detected and LLOQ/Target Detected, i.e. 0.04IU/mL = $\log_{10}$(0.04)= -1.4. Also, HBsAg above LLOQ will be reported as the raw data is reported.
- Virologic failure: Patients with a confirmed quantifiable HBV DNA increase of ≥ 1$\log_{10}$ HBV DNA copies/mL above LLOQ. HBV DNA results < LLOQ/Target Not Detected will be reported as 10 [$\log_{10}$(10) = 1) and HBV DNA < LLOQ/Detected will be reported as midpoint between LLOQ/Target Not Detected, i.e. 20IU/mL = $\log_{10}$(20)= 1.3. Also, HBV DNA above LLOQ will be reported as the raw data is reported.
- HBV-pgRNA decline: Change from Baseline in HBV-pgRNA on the $\log_{10}$ scale. Negative values indicate a decline.
- HBcrAg decline: Change from Baseline in HBcrAg on the $\log_{10}$ scale. Negative values indicate a decline.
- Prior Medications: Prior medications are defined as any medication where the use was stopped prior to the first administration of the study medication.
- Concomitant Medications: Concomitant medications are defined as any medication (other than the study drug) that was used at least once after the first administration of the study drug. Medications that were stopped on the same date as the first study drug administration will be defined as concomitant medications. If a clear determination cannot be made (partial medication end dates) the medication will be classified as concomitant
- Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.

### 3.3 Inferential Analyses

Descriptive statistics will be used to summarize the safety and PK data. No formal hypothesis testing is planned. All efficacy analyses (unless otherwise specified) will be performed at a one-sided 5% level of significance.

- HBsAg decline (Δ $\log_{10}$) from Day 1 to Week 16 of treatment (primary)
  - Hypothesis:

    $H_{01}$: Adjusted Mean for experimental arm at Week xx minus Adjusted Mean for control arm at Week xx = 0, where xx = 2, 4, 6, 8, 10, 12, 14, and 16

    $H_{11}$: Adjusted Mean for experimental arm at Week xx minus Adjusted Mean for control arm at Week xx = -1, where xx = 2, 4, 6, 8, 10, 12, 14, and 16.

- Time Points: Change from baseline until to Week 16 of treatment.
- A general linear model for repeated measures will be used to assess HBsAg decline (Δ log10), using the stratification factors as independent variables in the model (HBeAg pos [yes, no]). Baseline HBsAg level will be included as a covariate. The analysis will be based on a one-sided test at a 5% level of significance. Degrees of freedom calculation will be based on the Kenward-Roger method. The unstructured covariance matrix structure to model the within-patient errors will be selected initially. If the unstructured covariance structure leads to non-convergence, covariance matrix structure will be selected through the maximum likelihood method. The final model will then we rerun by using the reduced maximum likelihood method.

  The following covariates will be included for this model:

  i. Baseline HBsAg level
  ii. HBeAg positive [yes, no]
  iii. Treatment Group
  iv. Study visit
  v. Interaction between treatment group and study visit

- The least-squares mean change from baseline, along with corresponding 95% CI and SE for treatment arms and experimental arm versus control arm at the one-sided 0.05 level will be provided for Week 2, 4, 6, 8 , 10 , 12, 14 and 16 for the ITT population (with Multiple imputation). This will be repeated for ITT (with no imputation), mITT (with Multiple imputation), mITT (with no imputation), PP set (with Multiple imputation) and PP set (no imputation).
- If applicable, this model will be re-analyzed with the genotype covariate as "sensitivity analysis".

- Liver Fibrosis and inflammation change from baseline from Day 1 to Week 16 of treatment
  - Hypothesis:

    $H_0$: Adjusted Mean for experimental arm at Week xx minus Adjusted Mean for control arm at Week xx = 0, where xx = 4, 8, 12 and 16

    $H_1$: Adjusted Mean for experimental arm at Week xx minus Adjusted Mean for control arm at Week xx ≠ 0, where xx = 4, 8, 12 and 16.
  - Time Points: Change from baseline until to Week 16 of treatment.
  - A general linear model for repeated measures will be used to assess Liver Fibrosis and inflammation parameters including ALT, AST, AST/ALT ratio, high sensitivity C-reactive protein, interleukin 6, tumour necrosis factor alpha, procollagen type III N terminal peptide (Pro C3), tissue inhibitor of metalloproteinases-1, using the stratification factors as independent variables in the model (HBeAg pos [yes, no]). Baseline Liver Fibrosis and inflammation parameters value will be included as a covariate. The analysis will be based on a two-sided test at a 5% level of significance. Degrees of freedom calculation will be based on the Kenward-Roger method. The unstructured covariance matrix structure will be selected initially. If the unstructured covariance structure leads to non-convergence, covariance matrix structure will be selected through the maximum likelihood method. The final model will then we rerun by using the reduced maximum likelihood method.

    The following covariates will be included for this model:

    i. Baseline liver fibrosis and inflammation parameters value
    ii. HBeAg positive [yes, no]
    iii. Treatment Group

iv. Study visit

v. Interaction between treatment group and study visit

- The least-squares mean change from baseline, along with corresponding 95% CI and SE for treatment arms and experimental arm versus control arm at the two-sided 0.05 level will be provided for Week 4, 8, 12 and 16 for the Safety Set.
- If applicable, this model will be re-analyzed with the genotype covariate as "sensitivity analysis".

- HBsAg responder rate (decrease from baseline ≥ 1.0 on the $log_{10}$ scale) at Week 16 of treatment and Weeks 40 of follow up. (secondary)
  - Hypothesis: $H_0$: Treatment is not associated with endpoint

    $H_A$: Treatment is associated with endpoint
  - Time Points: Week 16 and Week 40.
  - The Pearson Chi-squared test will be used to compare the differences in proportions between the treatment groups at Week 16 and Week 40. At Week 16 and Week 40, this endpoint will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure (see section 3.4 for more detail). The analysis will be based on a one-sided test at a 5% level of significance.
- HBsAg responder rate (decrease from baseline ≥ 0.5 on the $log_{10}$ scale) at 16 of treatment and Weeks 40 of follow up.
  - Hypothesis: $H_0$: Treatment is not associated with endpoint

    $H_A$: Treatment is associated with endpoint
  - Time Points: Week 16 and Week40.
  - The Pearson Chi-squared test will be used to compare the differences in proportions between the treatment groups at Week 16 and Week 40. At Week 16 and Week 40, this endpoint will consider multiplicity considering multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure (see section 3.4 for more detail). The analysis will be based on a one-sided test at a 5% level of significance.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ)/TND) at Week 16 of treatment and Week 40 of follow-up.
  - Hypothesis: $H_0$: Treatment is not associated with endpoint

    $H_A$: Treatment is associated with endpoint
  - Time Points: Week 16 and Week40.
  - The Pearson Chi-squared test will be used to compare the differences in proportions between the treatment groups at Week 16, and Week 40. At Week 16 and Week 40, this endpoint will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure (see section 3.4 for more detail). The analysis will be based on a one-sided test at a 5% level of significance.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ)/TD) at Week 16 of treatment and Week 40 of follow-up.
  - Hypothesis: $H_0$: Treatment is not associated with endpoint

    $H_A$: Treatment is associated with endpoint
  - Time Points: Week 16 and Week 40.

- The Pearson Chi-squared test will be used to compare the differences in proportions between the treatment groups at Week 16, and Week 40. At Week 16 and Week 40, this endpoint will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure (see section 3.4 for more detail). The analysis will be based on a one-sided test at a 5% level of significance.

### 3.4 Multiple Comparisons and Multiplicity Adjustments.

For the analysis of secondary endpoints during the final analysis, multiplicity will be considered by using a combination of a hierarchical fixed test procedure and a Hochberg procedure.

Only if the primary endpoint is significant at 16 weeks, the key secondary endpoints "HBsAg loss rate (<LLOQ/TND and <LLOQ/TD)" and "HBsAg responder rates (B and A see section 3.2)" will be tested at the same one-sided α level of 0.05, using a Hochberg procedure at Week 16. This procedure goes as follows: the p-values will be ordered from small to large $p(1) \leq p(2) \leq (p3) \leq (p4)$. The largest p-value p(4) will then be compared to $\alpha=0.05$. If significant, then all hypotheses will be rejected. If not, the next largest p-value p(3) is compared to $\alpha/2=0.025$. If significant, then these hypotheses corresponding to p(1) , p(2) and (p3) are rejected. If not, the next largest p-value p(2) is compared to $\alpha/3=0.017$. If significant, then both hypotheses corresponding to p(1) and p(2) are rejected. If not, the smallest p-value is compared to $\alpha/4=0.0125$. If significant, then only the hypothesis corresponding to the smallest p-value is rejected.

At 40 weeks, the key secondary endpoints HBsAg responder rates (B and A) and HBsAg loss rate will be tested a one-sided α level of 0.05, using a Hochberg procedure.

To calculate the power to detect a difference in HBsAg loss rate, we assumed a proportion of 0.5% in the placebo arm, and of 10% in the experimental arm. A trial including 49 patients results in a power of about 55% for this endpoint (using an un-pooled estimate of the variance), using a one-sided α of 0.05.

### 3.5 Handling of Missing Data

For the classification of Treatment emergent adverse event (TEAE) and Concomitant medication, the following will be applied in the following order:

a. If all dates/times (start and stop) missing, the event/medication will automatically be classified as a TEAE/Concomitant medication.

b. For AEs with a missing start date/time, if the event end date/time is prior to first study drug administration, the event will not be classified as a TEAE.

c. If only the AE start year/ medication end year is present and is the same or is after the first study drug administration year unit, the event/medication will be classified as a TEAE/Concomitant medication.

d. If the AE start month and year/medication end month and year are present and are the same or after the first study drug administration month and year units, the event/medication will classified as a TEAE/Concomitant medication.

For the efficacy analysis of values that are below the LLOQ, the following imputations will be made for continuous data analyses:

- HBsAg LLOQ/TND values will be set to 0.015[$\log_{10}(0.015) = -1.852$]
- HBsAg LLOQ/TD values will be set to the midpoint between LLOQ/TND and LLOQ/TD.
- HBV DNA LLOQ/TND values will be set to 10 ($\log_{10}(10) = 1$).
- HBV DNA LLOQ/TD (< 1.30 log IU/mL) values will be set to the midpoint of LLOQ/TND (the midpoint = 1.15)
- HBV DNA = "insufficient sample" will be set to missing.
- HBcrAg LLOQ/TND values will be set to 30 ($\log_{10}(30) = 1.5$).

- HBcrAg LLOQ/TD (<3.0 log U/mL) values will be set to 2.25 (log U/mL)
- HBcrAg = "insufficient sample" will be set to missing.
- HBV-pgRNA = "insufficient sample" will be set to missing.
- HBV-pgRNA LLOQ/TND values will be set to 100 ($\log_{10}(100) = 2$).
- HBV-pgRNA values = "<4.04" will be set to 3.02 log C/mL
- HBV-pgRNA LLOQ/TD values will be set to the midpoint of LLOQ/TND (the midpoint = 3.02 log C/mL)

For the handling of missing primary efficacy data (excluding LLOQ/TND and LLOQ/TD), missing primary efficacy data (HBsAg) will be imputed using multiple imputation process (MI SAS procedure) with MAR pattern. For completeness, analysis will be repeated under the scenario of no imputation.

The Multiple imputation will be performed as follows:

- Missing data will be imputed using multiple imputation technique with Markov chain Monte Carlo method assuming MAR and multivariate normality.
- This is carried out by using the SAS procedure PROC MI with the MCMC option, the seed number will be 20201113. The number of burn-in iterations will be 200, which is the default value. Nevertheless, if diagnosis plots show that the convergence has not yet occurred, this will be adjusted.
- Imputation will be repeated N=1000 times. The $\log_{10}$(HBsAg) will then be calculated for each of the data set.
  **SAS Code:**

```
Proc mi data=new nimpute = 1000 out= mi_mvn seed= 20201113;
  mcmc nbiter =200 plots=trace ;
  By Treatment;
  Var Baseline log10(HBsAg);
Run;
```

- The difference in HBsAg (Δ log10) from Day 1 to Week 16 between treatment and placebo will be analysed using a general linear model for repeated measures for each imputation.
  **SAS Code:**

```
Proc mixed data= mi_mvn ;
 By _imputation_;
 Class ID TRT VISIT  HBeAg;
 Model CHG = Baseline  HBeAg TRT VISIT TRT*VISIT /
 SOLUTION CL;
DDFM=KenwardRoger;
 Repeated VISIT /SUBJECT = ID TYPE = UN ;
Lsmeans TRT*VISIT / DIFF CL;
Run;
```

- The parameter estimates obtained from the above are then combined and reported using SAS - Proc mianalyze procedure.

Conversion of categorical values

In some instances, continuous variables are expressed as a range (i.e. < 10). In such cases, values may be converted to the range boundary (upper or lower limit as applicable). As an example, a value of <10 may be converted to 10. Such substitutions will be clearly documented in the footnotes of relevant outputs.

There will be no imputations or substitution made for missing safety data points.

### 3.6 Coding of Events and Medications

Medical history and AE verbatim terms will be coded using the Medical Dictionary for Regulatory Activities (MedDRA) using the latest version available at the time of study commencement. Terms will be coded to the full MedDRA hierarchy, but the system organ class (SOC) and preferred terms (PT) will be of primary interest for the analysis.

Prior and concomitant medications will be coded using the World Health Organization Drug Dictionary using the latest version available at the time of study commencement. Medications will be mapped to the full WHO-DD Anatomical Therapeutic Chemical (ATC) class hierarchy, but PTs will be of primary interest in this analysis.

### 3.7 Treatment Groups/Treatment Sequence

TFLs will be presented by treatment arms, and for all study patients in the given analysis set, where applicable.

The following order will be used for all summary outputs (with the treatment arm displayed, as applicable to the output):

- EYP001a 200 mg QD + NA daily (N=37)
- EYP001a 200 mg QD + NA daily HBeAg+ (N=xx)
- EYP001a 200 mg QD + NA daily HBeAg- (N=xx)
- Placebo + NA daily (N=12)
- Placebo HBeAg+ (N=xx)
- Placebo HBeAg- (N=xx)
- All HBeAg+ (N=xx)
- All HBeAg- (N=xx)
- All Study Patients (N=49)

The following treatment group labels will be used for all by-participant listings:

- EYP001a 200 mg QD + NA daily HBeAg+
- EYP001a 200 mg QD + NA daily HBeAg-
- Placebo HBeAg+
- Placebo HBeAg-

# 4. ANALYSIS SETS

In this study 5 analysis populations are defined: Intention-To-Treat (ITT) Analysis Set, Modified Intention-To-Treat (mITT) Analysis Set, Safety Analysis Set (SAS), PK Analysis Set, the PD Analysis Set and the Per Protocol (PP) Analysis Set.

Furthermore, any additional exploratory analysis not identified in the SAP will be identified in the final CSR as exploratory post hoc analyses, including analyses for additional study populations or subgroups of interest.

## 4.1 Population Descriptions

### 4.1.1 Intention-To-Treat (ITT) Analysis Set

The ITT set will include all randomized patients, irrespective of whether a patient receives any study drug. This set will be based on randomized treatment. The ITT set will be used for the baseline, demographic summaries and efficacy summaries.

### 4.1.2 Modified Intention-To-Teat (mITT) Analysis Set

The mITT set will include all randomized patients, who received any amount of study drug, have a measurable baseline HBsAg assessment and a 16-week post baseline efficacy assessment. This set will be based on randomized treatment. The mITT set will be used for efficacy analyses.

### 4.1.3 Safety Analysis Set (SAS)

The Safety analyses set will be defined as all patients who receive at least one confirmed dose of the study drug and will be based on actual treatment received. The SAS will be used for all safety and tolerability analyses.

### 4.1.4 Pharmacokinetic (PK) Analysis Set (will be done by Calvagone)

The PK set will consist of all patients who received any study drug administration and that have sufficient and interpretable EYP001a concentrations data. Protocol violations and individual patient profiles will be assessed on a case-by-case basis to determine if the patient, or specific concentration values, should be excluded from the PK set.

### 4.1.5 Pharmacodynamic (PD) Analysis Set

All patients included in the SAS with a measurable baseline PD assessment and at least one measurable post baseline PD assessment, will be included in the PD set.

### 4.1.6 Per Protocol (PP) Analysis Set

The PP set is defined as the set of patients who meet the mITT set requirements and were not associated with a major protocol violation. This set will be identified before the start of the final analysis and will be used to support the analysis conducted for the primary efficacy endpoint. Patients will be analyzed based on the actual treatment received and patients with the study drug compliance of <50% will be excluded.

# 5. PARTICIPANT DISPOSITION AND ANALYSIS POPULATIONS

Participant disposition and analysis population analysis will be based on the ITT population. Participant disposition and analysis populations will be summarized descriptively as described in section 3.1 (categorical descriptive analysis).

## 5.1.1 Participant Disposition

Participant disposition will include the number of participants who completed the study as planned, participants withdrawn from the study, as well as the primary reason for early termination. Participant disposition will be summarized descriptively.

A listing of patient disposition with study discontinuation and treatment discontinuation will be presented. Whether a patient had any ongoing AEs, the date of last dose (EYP001a/Placebo and NA), reason for treatment discontinuation (if applicable), date of last contact (or date of death) and date of withdrawal of consent (if applicable) will be included.

Screening failures and reason for screening failure, will be noted in the listing of eligibility criteria. All withdrawals from the study, taking place on or after study drug administration, will be fully documented in the body of the clinical study report (CSR).

## 5.1.2 Analysis Populations

The number of participants included in each study populations will be summarized descriptively.

In addition, the inclusion of each participant into/from each of the defined analysis populations will be presented in the by-participant data listings.

## 6. PROTOCOL DEVIATIONS

Protocol deviations will be presented for each participant in the by-participant data listings for the enrolled set. All data will be listed by treatment group.

Prior to database lock, all protocol deviations will be reviewed by medical monitors and assigned a status of Important if qualifying as such.

Protocol deviations and important protocol deviations will be categorized as noted in the Protocol Deviation Management Plan Version 1.0 dated 2020-01-13.

# 7. DEMOGRAPHIC AND BASELINE INFORMATION

Demographic and baseline information analysis will be based on the ITT population. Summary tables may be repeated for the mITT, Safety and PP analysis sets if different from the ITT analysis set. Demographic and baseline information will be summarized descriptively as described in section 3.1.

## 7.1 Demographics

The following demographic parameters will be analyzed:

Continuous descriptive analysis:

- Age (years)
- Height (cm)
- Weight (kg)
- BMI ($kg/m^2$)
- Audit-C overall score

Categorical descriptive analysis:

- Sex
- Childbearing Potential
- Race
- Ethnicity
- HBV Genotype
- HBeAg Status (Positive/Negative)

## 7.2 Medical history

Medical / Surgical history will be coded using MedDRA® currently in effect at Novotech at the time of database lock. and will be presented in the by-participant data listings.

## 7.3 Viral Serology

Hepatitis D virus (anti-HDV), antibody to HIV (anti-HIV), antibody to HCV (anti-HCV), quantitative HBsAg, anti-HBs, Anti-HBe, a PCR-based quantitative HCV viral load (for positive HCV antibody-test results only), will be presented in the by-participant data listings.

The viral serology result will be summarized at baseline visit by treatment group.

## 7.4 Drugs of Abuse

Drugs of abuse results will be presented in the by-participant data listings.

## 8. TREATMENT EXPOSURE AND COMPLIANCE

EYP001a/Placebo administration information (study drug administered (Yes/No), reason for non-administration date and time of administration, reason for dose adjustment and adjusted dose administered will be listed by treatment group. Patient fasting listed will also be noted.

For NA, treatment administered, reason not administered, date and time of administration, dose taken per protocol (Yes/No), reason for dose adjustment and adjusted dose administered will be listed by treatment group. NA switching during the screening period will also be listed.

Missed doses and reason for missed doses along with corresponding AEs will be listed as well.

EYP001a/Placebo and NA accountability will be listed by treatment group. The following fields will be included: number of 200mg tablets dispensed, date dispensed, number of 200mg tablets used, date returned, doses missed (Yes/No), patient compliant (Yes/No), if no reason not compliant and the percentage of treatment compliance.

Treatment Compliance is defined as:

$$\left(\frac{\text{Total Drug Administered}}{\text{Expected Drug Administered}}\right) * 100$$

The total drug administered is defined as:

(Number of 200mg Tablets Used + Number of NA Tablets Used during treatment period)

The expected drug administered is defined as:

The expected drug administered for EYP001a/Placebo + The expected drug administered for NA during treatment period

- The expected drug administered for EYP001a/Placebo is defined as:

Number of treatment days for EYP001a/Placebo × daily dosage (= 1 tablet), where the number of treatment days for EYP001a/Placebo will be calculated as:

Number of treatment Day = (Date of treatment visit 1 - Date of last treatment visit) +1 during treatment period.

- The expected drug administered for NA is defined as:

Number of treatment days for NA × daily dosage (= 1 tablet), where the number of treatment days for NA will be calculated as:

Number of treatment Day = (Date of treatment visit 1 - Date of last treatment visit) +1 during treatment period.

Treatment compliance (including count and percentage with <50% compliance, >=50% and =< 80%, and > 80% compliance) will be summarized descriptively as described in section 3.1(categorical descriptive analysis) under Safety analysis set.

## 9. PRIOR AND CONCOMITANT MEDICATIONS

Concomitant medications will be summarized by Anatomical Therapeutic Chemical (ATC) class Level 3 and PT as noted in section 3.1 (categorical descriptive analysis) using Safety analysis set. Participant who used the same medication on multiple occasions will only be counted once in the specific category (PT). PTs will be sorted alphabetically. In addition to the summaries by the coded terms, the number of participants who used at least one concomitant medication during the study will be presented.

Prior and concomitant medications will be presented in the by-participant data listings using Safety analysis set.

## 10. PHARMACOKINETICS

The PK analysis falls outside the scope of this SAP.

## 11. PHARMACODYNAMICS

All pharmacodynamic analysis will be based on the PD analysis Set.

The following PD endpoints will be analyzed:

- Plasma C4 (7α-hydroxy-4-cholesten-3-one)
- FGF19
- Plasma primary and secondary BAs (optional)

PD endpoints will be summarized descriptively as described in section 3.1 (continuous descriptive analysis).

## 12. EFFICACY

All Efficacy analyses will be based on the ITT analysis set unless otherwise specified.

The following Efficacy endpoints will be analyzed:

- HBsAg decline ($\Delta \log_{10}$) from Baseline (screen and Day 1 average) to Week 16 of treatment.
- HBsAg responder rate (decrease from baseline $\geq 1.0$ on the $\log_{10}$ scale) at Week 16 of treatment and Weeks 20, 28 and 40 of follow up.
- HBsAg responder rate (decrease from baseline $\geq 0.5$ on the $\log_{10}$ scale) at Weeks 12 and 16 of treatment and Weeks 20, 28 and 40 of follow up.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ)/TND) at Week 16 of treatment and Weeks 20, 28 and 40 of follow-up.
- HBsAg loss rate (Proportion of results that are Target Not Detected versus Target Detected) at Week 16 of treatment and Weeks 20, 28 and 40 of follow-up.
- Relapse rate HBsAg (% patients who became negative [HBsAg < LLOQ], then increased with HBsAg > LLOQ) at Week 16 of treatment period and Weeks 20, 28 and 40 during follow-up period.
- Virologic failure rate (breakthrough) of Hepatitis B virus Deoxyribonucleic Acid (HBV-DNA) (% patients with a confirmed quantifiable HBV DNA increase of $\geq 1\log_{10}$ HBV DNA copies/mL above LLOQ) assessed at Week 16 of treatment period and Weeks 20, 28 and 40 during follow-up period.
- HBV-pgRNA decline ($\Delta \log_{10}$) from Day 1 to Weeks 4, 8, 12, 16 of treatment period and Week 40 of maintenance period.
- HBcrAg decline ($\Delta \log_{10}$) from Day 1 to Weeks 4, 8, 12, 16 of treatment period and Week 40 of maintenance period.
- HBeAg quantification for HBeAg pos patients and changes at Week 16 of treatment and Week 40 of follow-up.
- Fibroscan Vibration Controlled Transient Elastography (VCTE) change from screening value to Weeks 16 and 40 or Early Termination (ET) value.
- Anti-HBs: Percent of subjects detectable (reactive) for Anti-HBs at baseline, Week 16 of treatment and Week40 of follow-up
- Anti-HBe: Percent of subjects detectable (reactive) for Anti-HBe at baseline, Week 16 of treatment and Week40 of follow-up

Efficacy endpoints at each scheduled visit will be summarized descriptively as described in section 3.1 (categorical descriptive analysis). All HBV response marker data collected at scheduled and unscheduled visits will be included in the listings.

For HBsAg, and HBV DNA, box plots for actual value and change from baseline value over time by treatment group, by HBeAg (positive and negative) and by A Genotype (yes and no) will be generated separately. Also, series plots for individual actual value over time and in change from baseline by HBeAg and by A genotype will be generated separately.

Furthermore, HBsAg, HBV-pgRNA, HBcrAg, HBeAg quantification for HBeAg pos patients and Fibroscan Vibration Controlled Transient Elastography (VCTE) at each scheduled visit and change from baseline values will be summarized descriptively as described in section 3.1 (continuous descriptive analysis). Counts (%) of number participants with Anti-HBs and Anti-HBe results at baseline, week 16 and week40 will also be presented (categorical descriptive analysis).

### 12.1 Inferential Analyses

The following endpoints will be analyzed as described in sections 3.3:

- HBsAg decline ($\Delta \log_{10}$) from Day 1 to Week 16 of treatment
- HBsAg responder rate (decrease from baseline $\geq 1.0$ on the $\log_{10}$ scale) at Week 16 of treatment and Week 40 of follow up. (secondary)
- HBsAg responder rate (decrease from baseline $\geq 0.5$ on the $\log_{10}$ scale) at Weeks 16 of treatment and Week 40 of follow up.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ)/TND) at Week 16 of treatment and Week 40 of follow-up.
- HBsAg loss rate (% patients with HBsAg < Lower Limit of Quantification (LLOQ)/TD) at Week 16 of treatment and Week 40 of follow-up.

### 12.2 Other Analyses

ENYO is developing a mathematical computational HBV disease model. The results from EYP001-201 will serve as clinical data for the calibration of in silico HBV patients simulating the effect of combinational treatments that will eventually support designing later trials. With its different sub-models (HBV replication and excretion, BAs metabolism, cholesterol metabolism, immune system, fibrosis, blood virus related changes, and EYP001a, ETV and PEG-IFNα2a drug models) the disease model of chronic HBV infection will be used to predict quantitative efficacy on relevant endpoints (DNA HBV in blood, HBsAg) in a representative virtual population. The computational model is a system of ordinary differential equations (ODEs) which integrates more than 300 biological variables and more than 1000 parameters. It will be used to explore the effect of combinations of different treatments regimens including EYP001a, ETV and PEG-IFNα2a. Iterations of the validated model will serve for the exploration of alternative arms in future trials and in the EYP001-203 study (conducted in parallel EYP001-201, with treatment naive or virologically non-suppressed patients treated with EYP001a combined with NA and peg-IFN), by simulating different doses and treatment regimens. Disease model simulations will support future explorations of development strategies, with the upcoming EYP001a pivotal study designs.

This analysis is reported in a separate analysis plan (reference : Validation protocol HBV EYP001 modeling and simulation project) falls outside the scope of the SAP.

## 13. SAFETY

Safety endpoints will be analyzed using the Safety population. Safety endpoints will be summarized descriptively as described in section 3.1.

### 13.1 Adverse Events

All AEs including will be coded using MedDRA. All AE summaries will be restricted to TEAEs only. Summary tables will include the number of participants (%) experiencing an event and the number of events. Participants will be counted only once for each SOC and PT level (categorical descriptive analysis).

AE and SAE will be analysed taking into account any identified subject with Sars-Cov2 infection during and post-pandemic measures phases. Such an analysis will be operated through the independent Data Monitoring Committee (DMC).

The TEAE summaries will include:

- Overall summary of TEAEs.
    - Number of TEAEs
    - Number of TEAEs with Severity ≥ Grade 3 Severe
    - Number of Serious TEAEs
    - Number of Study Drug Related TEAEs (Drug Related: A Possibly, Probably or Definitely related TEAE)
    - Number of Entecavir (ETV) Related TEAEs (Drug Related: A Possibly, Probably or Definitely related TEAE)
    - Number of Tenofovir Disoproxil Fumarate (TDF) Related TEAEs (Drug Related: A Possibly, Probably or Definitely related TEAE)
    - Number of TEAEs leading to study drug withdrawal
- TEAE summary by SOC and PT.
- TEAE summary of serious events by SOC and PT.
- TEAE summary by SOC, PT and Severity.
- TEAE summary by SOC, PT and relationship to study drug.
- TEAE summary by SOC, PT and relationship to ETV.
- TEAE summary by SOC, PT and relationship to TD.
- TEAE summary of events leading to the study drug discontinuation by SOC and PT.

All AEs will be listed and will include verbatim term, PT, SOC, treatment, causality to study drug, ETV and TDF, severity, seriousness, outcome, and action taken with regards to the study drug and AE. Separate listings will be created for SAEs and events leading to study drug withdrawal.

### 13.2 Safety Laboratory Assessments

Blood and urine samples will be collected at the time points specified in the Schedule of Events (refer to the Protocol) to conduct hematology, chemistry, coagulation, lipid and metabolic profile and urinalysis (including microscopic examinations) analyses.

The following tests will be performed within each of the specified test panels:

Hematology:

- Red blood cell count
- White blood cell count

- Haemoglobin
- Haematocrit
- Partial automated differentiation
    - Thrombocytes (% and Abs)
    - Lymphocytes (% and Abs)
    - Monocytes (% and Abs),
    - Eosinophils (% and Abs),
    - Basophils (% and Abs),
    - Neutrophils (% and Abs)
    - Platelets (% and Abs).

Coagulation:

- Prothrombin Time (s)
- INR
- Activated Partial Thromboplastin Time
- Fibrinogen

Serum Chemistry:

- Albumin
- ALP
- ALT
- Amylase
- Apo A1
- AST
- AST/ALT ratio
- Bilirubin conjugated (direct bilirubin)
- BUN
- Calcium
- Creatine Kinase
- Creatinine phosphokinase (CPK)
- Creatinine
- C-Reactive Protein-hs
- Estimation of glomerular filtration rate
- GGT
- Glucose
- Insulin
- Lactate dihydrogenase
- Potassium

- Sodium
- Total Bilirubin (if >ULN, add conjugated bilirubin)
- Total Protein
- Uric Acid

Lipid Metabolic Profile

- Cholesterol
- Branched-chain amino acid concentrations as liver function test, (analyze done by Labcorp)
- Haemoglobin A1c,
- Homeostatic model assessment for insulin resistance (morning fasting glucose and insulin),
- Lipoprotein insulin resistance index by nuclear magnetic resonance based on serum cholesterol (analyze done by Labcorp),
- HDL-C (analyze done by Labcorp),
- LDL-C (analyze done by Labcorp),
- Triglycerides (analyze done by Labcorp),
- Apolipoprotein B,
- Small dense LDL (analyze done by Labcorp),

Urinalysis (Dipstick) & Microscopic Urinalysis:

- Blood
- Bilirubin
- Glucose
- Ketones
- Leukocytes
- Haemoglobin
- pH
- Protein
- Specific Gravity
- Urobilinogen
- Microscopic Examinations (abnormalities on any of the following 3 dipstick results: leukocyte esterase, blood, or nitrite, and if judged clinically significant by the Investigator)

Immunochemistry

- T4 (free)
- T3 (free)
- TSH
- FSH
- AFP
- IL-6ha
- TNF-alpha hs

All laboratory data collected at scheduled and unscheduled visits will be included in the listings, but only results collected as scheduled visits will be included in the summary tables.

Results for individual parameters may be reported in different units depending on the analyzing laboratory. If required, the results (and the corresponding normal range cut-off values) for individual parameters may be converted to International System of Units (S.I.) units to summarize the data.

For all the parameters where a unit value has been reported, the parameter names that will be used in the outputs will comprise of the test name and the unit of measure, for example, 'Albumin (g/L)'. For the urinalysis parameters, the parameter name will be the reported test name only. Parameters will be sorted alphabetically within tables and listings.

For all parameters where a normal range limit value was reported, the normal range will be derived based on the available lower and upper limit values and any reported mathematical symbols. If both a lower and upper limit value is available, the normal range will be presented as '(Lower, Upper)'.

The reported results for each parameter with a defined normal range will be classified ('Low', 'Normal', 'High') in relation to the defined normal range limits. If a result is equal to the normal range cut-off value, the result will be considered 'Normal'.

The hematology, coagulation, chemistry and lipid and metabolic profile results tables will present summary statistics for each laboratory parameter within the specific test panel. For each parameter, summaries will be presented for the baseline and each scheduled post-baseline visit. In addition, summaries will be presented for the change from baseline values(and % change from baseline for the lipid and metabolic profile results) at each scheduled post-baseline visit (continuous descriptive analysis).

The decimal precision to which the summaries for each parameter will be based on the maximum number of decimals to which the reported result or the normal range limits are presented to in the raw data. The results and normal ranges will be displayed to the same decimal precision in the listings.

Additionally, counts (%) of number participants with values out of normal range at each scheduled time point will also be presented along with shift tables that will represent the changes in normal range categories across post-baseline time points (categorical descriptive analysis).

For ALT, AST, Total Bilirubin, and GGT tests, individual (for each participant) actual and change from baseline values over time will be displayed graphically and box plots over time by treatment group will be generated as well. A summary of maximum CTCAE Grades for post treatment assessments will be produced. Also, the HBV DNA versus ALT and AST at each visit will be displayed graphically.

For Lipid parameters-total cholesterol, LDL-C, HDL-C and triglycerides, individual (for each participant) actual values over time will be displayed graphically.

The urinalysis table will present counts and percentages of normal, abnormal clinically significant and clinically significant for the reported results at baseline and each post-baseline visit for all parameters (categorical descriptive analysis).

### 13.3 Vital Signs

The following vital signs measurements will be taken at the time points specified in the Schedule of Events (refer to the Protocol):

- Heart Rate (beats/min);
- Systolic blood pressure (SBP) (mmHg)
- Diastolic blood pressure (DBP) (mmHg)
- Respiratory rate (breaths/min)
- Temperature (ºC)

All vital signs data collected at scheduled and unscheduled visits will be included in the listings, but only results collected as scheduled visits will be included in the summary tables.

The parameter names that will be used in the outputs will comprise of the test name and the unit of measure, for example, 'Systolic Blood Pressure (mmHg)'. Parameters will be sorted in the order that the measurements were collected in on the Vital Signs eCRF page within the tables and listings.

Vital signs measurements will present summary statistics for the results at the baseline and each scheduled post-baseline visit for each of the parameters. In addition, summaries will be presented for the change from baseline values at each scheduled post-baseline visit (continuous descriptive analysis).

In the summaries for each parameter one more decimal place will be added to the maximum number for the results reported in the eCRF for decimal precision. For example: 2 decimals reported in the eCRF will be reported as 3 decimals for precision.

In addition, parameters with clinically significant findings will be noted in the listings.

### 13.4 12-Lead Electrocardiogram (ECG)

The following ECG measurements will be taken at the time points specified in the Schedule of Events (refer to the Protocol):

- Heart Rate (beats/min)
- PR Interval (msec)
- RR Interval (msec)
- QT Interval (msec)
- QTc Interval (msec)
- QRS Duration (msec)
- Overall Investigator Finding

All ECG data collected at scheduled and unscheduled visits will be included in the listings, but only results collected as scheduled visits will be included in the summary tables.

The parameter names that will be used in the outputs will comprise of the test name and the unit of measure, for example, 'Ventricular Rate (beats/min)'. Parameters will be sorted in the order that the measurements were collected in on the ECG eCRF page within the tables and listings.

ECG measurements will present summary statistics for the results at the baseline and each scheduled post-baseline visit for each of the parameters. In addition, summaries will be presented for the change from baseline values at each scheduled post-baseline visit (continuous descriptive analysis).

The decimal precision for each parameter will be based on the maximum number of decimals to which the results were reported on the eCRF.

The summary of overall interpretation findings table will present counts and percentages for the reported results at baseline and each post-baseline visit/time point. Result categories will be ordered as 'Normal', 'Abnormal Not Clinically Significant (NCS)', 'Abnormal Clinically Significant (CS)' and 'Not Evaluable' (categorical descriptive analysis).

The listings of ECG measurements will include all the information collected data. In addition, the observations that are used as the baseline record (value) for each parameter will be flagged, and the change from baseline values at each post-baseline visit will be presented. For clinically significant assessments, cardiologist confirmation (Yes/No) and additional comments will be listed.

### 13.5 Pruritus Assessment

Pruritus will be assessed using a visual analog scale (VAS) and a 5-D (degree, duration direction, disability, and distribution) itch scale at each study visit after screening.

The 5-D Pruritus Scale is a multidimensional measure that quantifies pruritus. The scale consists of five domains: duration (1 item), degree (1 item), direction (1 item), disability (4 items), and distribution (16

locations of itch). All items of the first four domains were measured on a five-point Likert scale. A total score of 4 indicates 'no Pruritus' and 35 indicates 'most sever Pruritus'.

The scores of each of the five domains are achieved separately and then summed together to obtain a total 5-D score. 5-D scores can potentially range between 4 (no pruritus) and 35 (most severe pruritus.)

Single-item domain scores (duration, degree, and direction) are equal to the value indicated below the response choice (range 1-5). The score for the disability domain is achieved by taking the highest score on any of the four items. For the distribution domain, the number of affected body parts is tallied (potential sum 0-16) and the sum is sorted into five scoring bins:

- sum of 0-2 = 1
- sum of 3-5 = 2
- sum of 6-10 = 3
- sum of 11-13 = 4
- sum of 14-16 = 5.

The total score including change from baseline to each post baseline will be summarized. Domain and total scores along with changes from baseline will be listed.

In addition, the Pruritus visual analog scale result will be listed and summarized per time point by treatment group.

### 13.6 Physical Examinations

By-participant data listings will be created for all complete physical examination and symptom directed assessments and all time points.

### 13.7 Liver Fibrosis and inflammation Assessment

The following Liver fibrosis and inflammation assessments will be taken at the time points specified in the Schedule of Events (refer to the protocol):

- ALT
- AST
- AST/ALT ratio
- High sensitivity C-reactive protein
- Interleukin 6
- Tumour necrosis factor alpha
- Procollagen type III N terminal peptide (Pro C3)
- Tissue inhibitor of metalloproteinases-1
- ELF score (HA, TIMP-2, PIIINP)

All liver fibrosis and inflammation data collected at scheduled and unscheduled visits will be included in the listings, but only results collected as scheduled visits will be included in the summary tables.

Liver fibrosis and inflammation assessments will present summary statistics for the results at the baseline and each scheduled post-baseline visit for each of the parameters. In addition, summaries will be presented for the change from baseline values at each scheduled post-baseline visit (continuous descriptive analysis).

#### 13.7.1 Inferential Analyses

The following endpoint will be analyzed as described in sections 3.3:

- Liver Fibrosis and inflammation change from baseline from Day 1 to Week 16 of treatment

### 13.8 Liver Imaging

Liver imaging assessment will be listed for all time points.

The assessment of liver imaging table will present counts and percentages for the reported results at screening and Week 40 of follow up. Result categories will be ordered as 'Normal', 'Abnormal Not Clinically Significant (NCS)' and 'Abnormal Clinically Significant (CS)' (categorical descriptive analysis).

### 13.9 Pregnancy Test Results

All information related to pregnancy testing (urine and serum based) will be presented in the by-participant data listings.

## 14. IMMUNOGENICITY

No Immunogenicity analysis is planned for this study.

## 15. CHANGES TO THE PLANNED ANALYSIS

Safety review will be performed when 20 patients have reached w8 (expected by 1st March 2021 with data cut-off point defined to be 5th March 2021, replacing when 50% (n=25) patients reach week 8.

Sponsor decided on February 17th, 2021 to suspend further enrollments (after approx. 25 randomizations).

A request to deviate from the protocol has been initiated and executed by the sponsor and will be documented here. The changes to the planned analysis from the protocol are described in the following table:

| Protocol | Key Changes |
|---|---|
| Based on the protocol section 11.3.3.1, for the primary efficacy endpoints (HBsAg decline), imputing missing data at 16 weeks as zero difference versus baseline | ▪ Missing primary efficacy data (HBsAg) will be imputed using multiple imputation process (MI SAS procedure) with MAR pattern. |
| Not in the protocol | ▪ Inferential Analyses for liver Fibrosis and inflammation change from baseline from Day 1 to Week 16 of treatment<br>▪ To summarize the Maximum CTCAE for ALT, AST, BILI and GGT for Post Treatment Assessments using CTCAE to do the toxicity grading. |
| Not in the protocol - The primary efficacy variables | ▪ Additional primary efficacy variable:<br>▪ Anti-HBs<br>▪ Anti-HBe. |
| Based on the protocol section 11.3.3.1, for the primary efficacy endpoints (HBsAg decline), A Genotype [yes, no] needs to be included in the general linear model | ▪ A Genotype variable will be removed from the general linear model because the CRAs went back and cross checked there is no available historical genotype available in the medical history source other than what is currently in the EDC and also for most of the patients, there is no virus available in the samples to genotype. |

# 16. INTERIM AND FINAL ANALYSIS

## 16.1 Interim Analysis (DSMC Review meeting)

An unscheduled DSMC review meeting of all available unblinded preliminary safety study data will be conducted when any stopping rules (Protocol Section 4.6) are met in two or more patients. All stopping rules will be listed by treatment group.

Two DSMC Review meeting are scheduled:

1. DSMC Safety Review Meeting on all available unblinded preliminary safety study data:

   Safety assessment when 40.8% (n=20 out of 49) patients reach week 8 resulting in a decision on continuation of the study based on safety (Go/No go decision); enrolment would remain ongoing during this review.

2. DSMC Safety Review and Futility Analysis Meeting on all available unblinded preliminary virology, safety, PK and PD study data:

   Safety and futility when 50% patients (n=25) reached week 12, resulting in a decision on continuation of the study (Go/No go decision) based on safety and evidence of a benefit of EYP001 (HBsAg, other secondary viral markers); enrolment is ongoing during this review.

The DSMC review meeting will be performed on all available primary and secondary endpoints according to the DSMC charter, which describes the overall guidelines, composition, roles, and responsibilities of the independent DSMC for the EYP001-201 study, including the selection of DSMC members, timing of meetings, methods of providing information to and from the DSMC, frequency and format of meetings, data analysis recommendations, and DSMC relationships with other parties participating in the conduct of this study.

The futility assessment will be performed to determine if EYP001 has no benefit at a point when 50% of patients have reached 12 weeks of dosing. The futility assessment will be performed by the DSMC according to the following rules:

- A treatment effect of -1.0 on a log10 scale of HBsAg for the primary endpoint at 16 weeks, and a common standard deviation of 1.08 was assumed and the treatment effect would be -0.5 after 12 weeks of treatment, with common standard deviation of 0.7 Using a one-sided alpha of 0.05 and 80% power (beta = 0.20), a group sequential design, incorporating a futility and efficacy O'Brien-Fleming analysis when 50% of patients have reached 12 weeks of treatment, needs inclusion of 49 patients.
- Table 2 gives the probability of stopping early under the null and alternative hypothesis, at the time of the interim analysis.

  The probability of stopping correctly for futility is 40%. The probability of stopping wrongly for futility is only 3.5%.

**Table 2 Probability of different decisions at the DSMC Safety Review and Futility Analysis Meeting**

| Under H0 | | Under Ha | |
|---|---|---|---|
| Efficacy | Futility | Efficacy | Futility |
| 0.001 | 0.4 | 0.073 | 0.035 |

H0: Null Hypothesis; Ha: Alternative Hypothesis

- The efficacy boundary is crossed when the 12-week p-value is less than 0.001, or the difference is less than -0.971 on a log scale. The futility boundary is crossed when the 12-week p-value is higher than 0.603, or the difference is more than 0.085 on a log scale.

The stopping of the study for futility will be considered by the DSMC by applying these rules. The study will not stop for efficacy at Week 12 DSMC Safety Review and Futility Analysis Meeting even if

efficacy boundary is crossed. The criteria are not binding and DSMC can overrule after overall consideration.

Data will be summarized and presented by treatment group and time point in summary tables. Descriptive statistics including number of patients (N), means, standard deviations, medians, and minimum and maximum values will be presented for continuous variables. Counts and percentages will be presented for categorical variables. In addition, by- patient listing for all safety and efficacy data will be presented.

Note that all DMSC review meeting will be descriptive, except 2nd scheduled DSMC safety and futility review meeting containing mentioned futility testing.

Based on the protocol clarification letter #13, the first interim analysis as described in the current EYP001-201 Study Protocol v3.0 dated 29th January 2020 corresponds to the first planned DSMC meeting and is performed on all available preliminary safety study data at the time of database snapshot (20 patients reach week 8, expected by 1st March 2021 with data cut-off point defined to be 5th March 2021,). Safety data only will be evaluated, based upon the review of the individual values (clinical significant abnormalities), descriptive statistics (summary tables, graphics) and if needed,). The term "first interim analysis" should be replaced by "DSMC Safety Review Meeting". The "second interim analysis" corresponds to the second planned DSMC meeting covering safety review and futility analysis and is performed on all available virology, safety, PK and PD study data at the time of database snapshot when 25 patients have reached w12 (expected by 16th March 2021 with data cut-off point defined to be 15th May 20201 Safety and futility will be evaluated, based upon the review of the individual values (clinical significant abnormalities), descriptive statistics (summary tables, graphics) and on statistical analysis (futility analysis as described in section 11.5 of the study protocol). The term "second interim analysis" should be replaced by an interim analysis corresponding to "DSMC Safety and Futility Review Meeting"

There will be an additional database lock performed on all patient visits to Week 16 / Visit 9 for all randomised patients. All patients will be unblinded following database lock. Novotech Biostatistician will convert the datasets to CDISC format. Novotech data management will provide ENYO with raw data and Biostatistician will provide ENYO with CDISC converted datasets.

### 16.2 Final Analysis (End of Study)

The final analysis will be conducted after all participants have completed the study (at the end of the study), the clinical database has been hard locked, the analysis populations have been approved and the study has been unblinded.

The final analysis will be based on the final version of the SAP. Any deviations from the planned analysis will be documented in the CSR.

## 17. SOFTWARE

- SAS® Version 9.2 or higher (SAS Institute, Cary, North Carolina, USA).

## 18. TABLES

| Table Number | Table Title | Population | DSMC Safety | DSMC Safety and Futility |
|---|---|---|---|---|
| | | | | |
| **14.1** | **Demographics and Other Baseline Characteristics** | | | |
| 14.1.1 | Summary of Participant Enrolment and Disposition | ITT | X | X |
| 14.1.2.1 | Summary of Demographics and Baseline Characteristics | ITT | | |
| 14.1.2.2 | Summary of Demographics and Baseline Characteristics | mITT | | |
| 14.1.2.3 | Summary of Demographics and Baseline Characteristics | Safety | X | X |
| 14.1.2.4 | Summary of Demographics and Baseline Characteristics | PP | | |
| 14.1.3.1 | Summary of Viral Serology at Screening | ITT | | |
| 14.1.3.2 | Summary of Viral Serology at Screening | mITT | | |
| 14.1.3.3 | Summary of Viral Serology at Screening | Safety | | |
| 14.1.3.4 | Summary of Viral Serology at Screening | PP | | |
| 14.1.4 | Summary of Treatment Compliance | Safety | X | X |
| **14.2** | **Efficacy** | | | |
| 14.2.1.1.1 | Summary of HBsAg by A Genotype – Imputation | ITT | | X |
| 14.2.1.1.2 | Summary of HBsAg by A Genotype – No imputation | ITT | | X |
| 14.2.1.2.1 | Summary of HBsAg by A Genotype – Imputation | mITT | | |
| 14.2.1.2.2 | Summary of HBsAg by A Genotype – No Imputation | mITT | | |

| | | | | |
|---|---|---|---|---|
| 14.2.1.3.1 | Summary of HBsAg by A Genotype - Imputation | PP | | |
| 14.2.1.3.2 | Summary of HBsAg by A Genotype – No Imputation | PP | | |
| 14.2.2.1.1 | Analysis of HBsAg: Baseline to Week 16 – Imputation | ITT | | X |
| 14.2.2.1.2 | Analysis of HBsAg: Baseline to Week 16 – No Imputation | ITT | | X |
| 14.2.2.2.1 | Analysis of HBsAg: Baseline to Week 16 - Imputation | mITT | | |
| 14.2.2.2.2 | Analysis of HBsAg: Baseline to Week 16 – No Imputation | mITT | | |
| 14.2.2.3.1 | Analysis of HBsAg: Baseline to Week 16 – Imputation | PP | | |
| 14.2.2.3.2 | Analysis of HBsAg: Baseline to Week 16 – No Imputation | PP | | |
| 14.2.3.1 | Summary and Analysis of HBsAg Loss Rate A | ITT | | X |
| 14.2.3.2 | Summary and Analysis of HBsAg Loss Rate B | ITT | | X |
| 14.2.4.1 | Summary and Analysis of HBsAg Responder Rate A | ITT | | X |
| 14.2.4.2 | Summary and Analysis of HBsAg Responder Rate B | ITT | | X |
| 14.2.5 | Summary of HBsAg Relapse Rate | ITT | | |
| 14.2.6 | Summary of Virologic Failure Rate of HBV DNA | ITT | | X |
| 14.2.7 | Summary of HBV-pgRNA | ITT | | X |
| 14.2.8 | Summary of HBcrAg | ITT | | X |
| 14.2.9 | Summary of HBeAg | ITT (HBeAg+ patients) | | X |
| 14.2.10 | Summary of Fibroscan VCTE | ITT | | X |
| 14.2.11 | Summary of HBsAg Loss Rate (Target not detected vs. Target detected) | ITT | | |

| | | | | |
|---|---|---|---|---|
| 14.2.12 | Summary of Anti-HBs | ITT | | |
| 14.2.13 | Summary of Anti-HBe | ITT | | |
| 14.2.14 | Summary of PD Markers | PD | | |
| **14.3** | **Safety** | | | |
| 14.3.1 | Summary of Concomitant Medication | Safety | X | X |
| **14.3.3** | **Adverse Events** | | | |
| 14.3.3.1 | Summary of Overall Treatment Emergent Adverse Events | Safety | X | X |
| 14.3.3.2 | Summary of Treatment Emergent Adverse Events by SOC and PT | Safety | X | X |
| 14.3.3.3 | Summary of Serious Treatment-Emergent Adverse Events by SOC and PT | Safety | X | X |
| 14.3.3.4.1 | Summary of Treatment-Emergent Adverse Events by Relationship to Study Drug by SOC and PT | Safety | X | X |
| 14.3.3.4.2 | Summary of Treatment-Emergent Adverse Events by Relationship to ETV by SOC and PT | Safety | | |
| 14.3.3.4.3 | Summary of Treatment-Emergent Adverse Events by Relationship to TD by SOC and PT | Safety | | |
| 14.3.3.5 | Summary of Treatment-Emergent Adverse Events by SOC, PT and Severity | Safety | X | X |
| 14.3.3.6 | Summary of Treatment Emergent Adverse Events Leading to Study Drug Discontinuation by SOC and PT | Safety | X | X |
| **14.3.4** | **Laboratory Parameters** | | | |
| 14.3.4.1.1 | Summary of Hematology & Coagulation | Safety | X | X |
| 14.3.4.1.2 | Summary of Hematology & Coagulation Shifts from Baseline | Safety | | |
| 14.3.4.2.1 | Summary of Serum Chemistry | Safety | X | X |

| | | | | |
|---|---|---|---|---|
| 14.3.4.2.2 | Summary of Serum Chemistry Shifts from Baseline | Safety | | |
| 14.3.4.3.1 | Summary of Lipid Metabolic Profile | Safety | X | X |
| 14.3.4.3.2 | Summary of Lipid Metabolic Profile Shifts from Baseline (Low, Normal, High) | Safety | | |
| 14.3.4.3 | Summary of Urinalysis | Safety | X | X |
| 14.3.4.4 | Summary of Maximum CTCAE for ALT, AST, BILI and GGT for Post Treatment Assessments | Safety | | X |
| **14.3.5** | **Other Safety** | | | |
| 14.3.5.1 | Summary of Vital Signs | Safety | X | X |
| 14.3.5.2.1 | Summary of 12-Lead ECG | Safety | X | X |
| 14.3.5.2.2 | Summary of 12-Lead ECG Interpretation | Safety | X | X |
| 14.3.5.3 | Summary of Pruritus Assessment - 5-D Pruritus Scale | Safety | | |
| 14.3.5.4 | Summary of Pruritus Assessment - Visual Analogue Scale | Safety | X | X |
| 14.3.5.5 | Summary of Liver Fibrosis and Inflammation Assessment | Safety | | |
| 14.3.5.6 | Analysis of Liver Fibrosis and Inflammation Assessment: Baseline to Week 16 | Safety | | X |
| 14.3.5.7 | Summary of Liver Imaging | Safety | X | X |

## 19. LISTINGS

| Listing Number | Listing Title | Population | DSMC Safety | DSMC Safety and Futility |
|---|---|---|---|---|
| | | | | |
| **16.2.1** | **Subject Disposition** | | | |
| 16.2.1.1 | Analysis Populations | ITT | | X |
| 16.2.1.2 | Participant Disposition | ITT | | X |
| **16.2.2** | **Protocol Deviations** | | | |
| 16.2.2.1 | Protocol Deviations | ITT | | X |
| **16.2.4** | **Demographic and Other Baseline Data** | | | |
| 16.2.4.1 | Demographics and Baseline Characteristics | ITT | | X |
| 16.2.4.2 | Medical History | ITT | | X |
| 16.2.4.3 | Drugs of Abuse Screen | ITT | | X |
| 16.2.4.4 | AUDIT - Interview Version | ITT | | X |
| 16.2.4.5 | Serology | ITT | | X |
| 16.2.4.6 | Eligibility Criteria | All Screened Patients | | X |
| **16.2.5** | **Treatment Administration** | | | |
| 16.2.5.1 | Subject Randomization | ITT | | |
| 16.2.5.2 | Treatment Exposure | ITT | | X |
| 16.2.5.3 | Study Drug Accountability | ITT | | |

| | | | | |
|---|---|---|---|---|
| 16.2.5.4 | Missed Dose | ITT | | X |
| **16.2.6** | **Efficacy/PK/PD** | | | |
| 16.2.6.1 | HBsAg (IU/mL) | ITT | | X |
| 16.2.6.2 | HBV DNA (Log IU/mL) | ITT | | X |
| 16.2.6.3 | HBV-pgRNA (Log IU/mL) | ITT | | X |
| 16.2.6.4 | HBcrAg (Log IU/mL) | ITT | | X |
| 16.2.6.5 | HBeAg (PEI U/mL) | ITT | | |
| 16.2.6.6 | Anti-HBs | ITT | | |
| 16.2.6.7 | Anti-HBe | ITT | | |
| 16.2.6.8 | Fibroscan VCTE | ITT | | X |
| 16.2.6.9 | PD Markers | ITT | | |
| **16.2.7** | **Adverse Events** | | | |
| 16.2.7.1 | Adverse Events | Safety | X | X |
| 16.2.7.2 | Serious Adverse Events | Safety | X | X |
| 16.2.7.3 | Adverse Events Leading to Study Drug Withdrawal | Safety | X | X |
| **16.2.8** | **Laboratory Parameters** | | | |
| 16.2.8.1.1 | Hematology & Coagulation | Safety | X | X |
| 16.2.8.1.2 | Abnormal Haematology & Coagulation | Safety | | |
| 16.2.8.2.1 | Serum Chemistry | Safety | X | X |
| 16.2.8.2.2 | Abnormal Serum Chemistry | Safety | | |

| | | | | |
|---|---|---|---|---|
| 16.2.8.3.1 | Lipid and Metabolic Profile | Safety | X | X |
| 16.2.8.3.2 | Abnormal Lipid and Metabolic Profile | Safety | | |
| 16.2.8.4.1 | Urinalysis | Safety | X | X |
| 16.2.8.4.2 | Urine Microscopy | Safety | | |
| **16.2.9** | **Other Safety** | | | |
| 16.2.9.1 | Vital Signs | Safety | X | X |
| 16.2.9.2 | 12-Lead ECG | Safety | X | X |
| 16.2.9.3 | Physical Examination | Safety | X | X |
| 16.2.9.4 | Liver Fibrosis and inflammation Assessment | Safety | | |
| 16.2.9.5 | Liver Imaging | Safety | | |
| 16.2.9.6 | Pregnancy Test Results | Safety | X | X |
| 16.2.9.7 | Pruritus Assessments – 5-D Pruritus Scale | Safety | | |
| 16.2.9.8 | Pruritus Assessments – Visual Analogue Scale | Safety | X | X |
| 16.2.9.9 | Stopping Rules | Safety | X | X |
| **16.2.10** | **Prior & Concomitant Medication** | | | |
| 16.2.10.1 | Prior Medication | ITT | X | X |
| 16.2.10.2 | Concomitant Medication | ITT | X | X |
| | | | | |

## 20. FIGURES

| Figure Number | Figure Title | Population | DSMC Safety | DSMC Safety and Futility |
|---|---|---|---|---|
| | | | | |
| **14.2** | **Efficacy/PK/PD** | | | |
| 14.2.12.1 | Series Plot of Mean Actual Value over Time for PD Markers | PD | | |
| 14.2.12.2 | Series Plot of Mean Change from Baseline over Time for PD Markers | PD | | |
| 14.2.12.3 | Series Plot of Mean % Change from Baseline over Time for PD Markers | PD | | |
| 14.2.12.4.1 | Boxplot of HBsAg (IU/mL) over Time by Treatment | Safety | | |
| 14.2.12.4.2 | Boxplot of HBsAg (IU/mL) over Time by HBeAg | Safety | | |
| 14.2.12.4.3 | Boxplot of HBsAg (IU/mL) over Time by A Genotype | Safety | | |
| 14.2.12.5.1 | Boxplot of HBsAg (IU/mL) Change from Baseline by Treatment | Safety | | X |
| 14.2.12.5.2 | Boxplot of HBsAg (IU/mL) Change from Baseline by HBeAg | Safety | | |
| 14.2.12.5.3 | Boxplot of HBsAg (IU/mL) Change from Baseline by A Genotype | Safety | | |
| 14.2.12.6.1 | Boxplot of HBV DNA (Log IU/mL) over Time by Treatment | Safety | | X |
| 14.2.12.6.2 | Boxplot of HBV DNA (Log IU/mL) over Time by HBeAg | Safety | | |
| 14.2.12.6.3 | Boxplot of HBV DNA (Log IU/mL) over Time by A Genotype | Safety | | |
| 14.2.12.7.1 | Boxplot of HBV DNA (Log IU/mL) Change from Baseline by Treatment | Safety | | |
| 14.2.12.7.2 | Boxplot of HBV DNA (Log IU/mL) Change from Baseline by HBeAg | Safety | | |
| 14.2.12.7.3 | Boxplot of HBV DNA (Log IU/mL) Change from Baseline by A Genotype | Safety | | |

| | | | | |
|---|---|---|---|---|
| 14.2.12.8.1 | Series Plot of Individual Actual Value over Time for HBsAg (IU/mL) by HBeAg | Safety | | X |
| 14.2.12.8.2 | Series Plot of Individual Actual Value over Time for HBsAg (IU/mL) by A Genotype | Safety | | |
| 14.2.12.9.1 | Series Plot of Individual Change from Baseline Value for HBsAg (IU/mL) by HBeAg | Safety | | |
| 14.2.12.9.2 | Series Plot of Individual Change from Baseline Value for HBsAg (IU/mL) by A Genotype | Safety | | |
| 14.2.12.10.1 | Series Plot of Individual Actual Value over Time for HBV DNA (Log IU/mL) by HBeAg | Safety | | |
| 14.2.12.10.2 | Series Plot of Individual Actual Value over Time for HBV DNA (Log IU/mL) by A Genotype | Safety | | |
| 14.2.12.11.1 | Series Plot of Individual Change from Baseline Value for HBV DNA (Log IU/mL) by HBeAg | Safety | | |
| 14.2.12.11.2 | Series Plot of Individual Change from Baseline Value for HBV DNA (Log IU/mL) by A Genotype | Safety | | |
| **14.3** | **Laboratory Parameters** | | | |
| 14.3.4.2.3 | Individual ALT over Time | Safety | X | X |
| 14.3.4.2.4 | Individual ALT Change from Baseline | Safety | | |
| 14.3.4.2.5 | Boxplot of ALT over Time by Treatment | Safety | X | X |
| 14.3.4.2.6 | Individual AST over Time | Safety | X | X |
| 14.3.4.2.7 | Individual AST Change from Baseline | Safety | | |
| 14.3.4.2.8 | Boxplot of AST over Time by Treatment | Safety | X | X |
| 14.3.4.2.9 | Individual ALP over Time | Safety | X | X |

| | | | | |
|---|---|---|---|---|
| 14.3.4.2.10 | Individual ALP Change from Baseline | Safety | | |
| 14.3.4.2.11 | Boxplot of ALP over Time by Treatment | Safety | | |
| 14.3.4.2.12 | Individual GGT over Time | Safety | | |
| 14.3.4.2.13 | Individual GGT Change from Baseline | Safety | | |
| 14.3.4.2.14 | Boxplot of GGT over Time by Treatment | Safety | | |
| 14.3.4.2.15 | Individual Total Bilirubin over Time | Safety | X | X |
| 14.3.4.2.16 | Individual Total Bilirubin Change from Baseline | Safety | | |
| 14.3.4.2.17 | Boxplot of Total Bilirubin over Time by Treatment | Safety | | |
| 14.3.4.2.18 | Individual Lipid Parameters over Time | Safety | | X |
| 14.3.4.2.19 | Individual HBV DNA versus ALT at each visit | Safety | | X |
| 14.3.4.2.20 | Individual HBV DNA versus AST at each visit | Safety | | X |

## 21. REFERENCES

1) Clinical Study Protocol Version 3.0 dated 22 January 2020.
2) EYP001-201 Protocol Clarification Letter #13 dated 27 January 2021.
3) EYP001-201 Protocol Clarification Letter #11 dated 08 January 2021.

**Mock Tables**

## Table of Contents

# GENERAL COMMENTS

- Where a count is 0, the percentage will not be shown (e.g. 0(0.0%) will be displayed as 0)
- Unless otherwise states, parameters will be listed in alphabetical order.
- The minimum and maximum values will be presented to the same number of decimal places as recorded in the electronic Case Report Form (eCRF)
- Mean, SD, and Median will be presented to one more decimal place than the raw data
- Percentages will be rounded to one decimal place, with the denominator being the number of subjects in the relevant population with non-missing data, unless otherwise specified
- Change from Baseline:
  Change from Baseline will be calculated as:
  Change from Baseline = post baseline value – baseline value
- Unscheduled visits will be excluded from summary tables but included in all by-participant listings.
- **Names and order of Treatment Groups for Table Summaries**
  - Group 1 = EYP001a 200 mg QD + NA daily
  - Group 2 = EYP001a 200 mg QD + NA daily HBeAg+
  - Group 3 = EYP001a 200 mg QD + NA daily HBeAg-
  - Group 4 = Placebo + NA daily
  - Group 5 = Placebo HBeAg+
  - Group 6 = Placebo HBeAg-
  - Group 7 = All HBeAg+
  - Group 8 = All HBeAg-
  - Group 9 = All Study Patients

- **Treatment Display by Page**

Page 1, 3, 5, etc.

| EYP001a 200 mg QD + NA daily (N=xx) | = EYP001a 200 mg QD + NA daily HBeAg+ (N=xx) | = EYP001a 200 mg QD + NA daily HBeAg- (N=xx) | Placebo + NA daily (N=xx) |
|---|---|---|---|

Page 2, 4, 6, etc.

| Placebo HBeAg+ (N=xx) | Placebo HBeAg- (N=xx) | All HBeAg+ (N=xx) | All HBeAg- (N=xx) | All Study Patients (N=xx) |
|---|---|---|---|---|

Section 14.3.1 and Section 14.3.3.x

Page 1, 3, 5, etc.

| Group 1 (N=xx) n (%) m | Group 2 (N=xx) n (%) m | Group 3 (N=xx) n (%) m | Group 4 (N=xx) n (%) m |
|---|---|---|---|

Page 2, 4, 6, etc.

| Group 5 (N=xx) n (%) m | Group 6 (N=xx) n (%) m | Group 7 (N=xx) n (%) m | Group 8 (N=xx) n (%) m | Group 9 (N=xx) n (%) m |
|---|---|---|---|---|

- **Names and order of Treatment Groups for Listings**
  - EYP001a 200 mg QD + NA daily HBeAg+
  - EYP001a 200 mg QD + NA daily HBeAg-
  - Placebo HBeAg+
  - Placebo HBeAg-
- **Names of visits**
  - Screening (Listing only)
  - Baseline (Table only)
  - Visit 1 = Day 1
  - Visit 2 = Week 2
  - Visit 3 = Week 4
  - Visit 4 = Week 6
  - Visit 5 = Week 8
  - Visit 6 = Week 10
  - Visit 7 = Week 12
  - Visit 8 = Week 14
  - Visit 9 = Week 16
  - Visit 10 = Week 20 (Follow-up Visit 1)
  - Visit 11 = Week 28 (Follow-up Visit 2)
  - Visit 12 = Week 40 (EOS)
  - Early Termination
  - Unscheduled (Listing only)

- Column widths and text-wrapping may be altered in final output in order to best present the data.
- Footnotes may be added/amended if required.

Table 14.1.1 Summary of Participant Enrolment and Disposition (ITT Set)

| | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|
| Intention-to-Treat Set | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Modified Intention-To-Teat Set | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Safety Analysis Set | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Pharmacodynamic Analysis Set | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Per Protocol Analysis Set | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Number of Participants who Completed the Study | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Number of Participants who did not Complete the Study | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Primary Reason for Non-Completion | | | |
| Adverse Event | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Death | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Protocol Violation | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Withdrawal by Subject | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Lack of Efficacy | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Study Terminated by Sponsor | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Non-compliance with Study Drug | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Lost to Follow Up | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Screen Failure | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Other | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.1.1, 16.2.1.2
Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT Set in each treatment group (N).

Table 14.1.2.x Summary of Demographics and Baseline Characteristics (ITT Set)

| Parameter | Statistic | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|
| Age (years) at Screening | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | x.x | x.x | x.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |
| Sex n(%) | Female | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Male | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Childbearing Potential n(%)* | Yes | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | No | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Race n (%) | American Indian or Alaskan Native | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Asian | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Black or African American | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Native Hawaiian or Other Pacific Islander | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | White | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Other | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Unknown | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Not Reported | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Ethnicity n(%) | Hispanic or Latino | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Not Hispanic or Latino | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Not Reported | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Unknown | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.4.1
SD: Standard Deviation. Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT set in each treatment group (N).
*For childbearing potential, percentages are based on the number of female participants.

Table 14.1.2.x Summary of Demographics and Baseline Characteristics (*ITT set*)

| Parameter | Statistic | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|
| Weight (kg) at Screening | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |
| Height (cm) at Screening | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |
| Body Mass Index($kg/m^2$) at Screening | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |
| HBeAg Status | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.4.1

SD: Standard Deviation. Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT Set in each treatment group (N).
*For childbearing potential, percentages are based on the number of female participants.

Table 14.1.2.x Summary of Demographics and Baseline Characteristics (ITT set)

| Parameter | Statistic | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|
| HBV Genotype | A | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | B | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | C | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | D | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | E | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | F | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | G | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | H | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | I | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | J | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Audit-C overall score | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |

Source Listing: 16.2.4.1

SD: Standard Deviation. Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT Set in each treatment group (N).
*For childbearing potential, percentages are based on the number of female participants.

Programming note:
- Repeat for table 14.1.2.2 (mITT Set), table 14.1.2.3 (Safety Set) and table 14.1.2.4 (PP Set)

Table 14.1.3.x Summary of Viral Serology at Screening (ITT set)

| Parameter | Category | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|
| Hepatitis D virus (anti-HDV) | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Antibody to HIV (anti-HIV) | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Antibody to HCV (anti-HCV), | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| PCR-based Quantitative HCV Viral Load * | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Anti-HBs | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Anti-HBe | n | xx | xx | xx |
| | Positive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Negative | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.4.5

SD: Standard Deviation. Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT Set in each treatment group (N).
*For PCR-based Quantitative HCV Viral Load, percentages are based on the number of anti-HCV positive participants.

Table 14.1.3.x Summary of Viral Serology at Screening (ITT set)

| Parameter | Category | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|
| Quantitative HBsAg Level | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |
| Second Quantitative HBsAg Level | n | xx | xx | xx |
| | Mean | xx.x | xx.x | xx.x |
| | SD | xx.x | xx.x | xx.x |
| | Median | xx.x | xx.x | xx.x |
| | Minimum | xx | xx | xx |
| | Maximum | xx | xx | xx |

Source Listing: 16.2.4.5

SD: Standard Deviation. Percentages are calculated (the denominator used for the calculation) based on the number of participants in the ITT Set in each treatment group (N).
*For PCR-based Quantitative HCV Viral Load, percentages are based on the number of anti-HCV positive participants.

Programming note:
- Repeat for table 14.1.3.2 (mITT Set), table 14.1.3.3 (Safety Set) and table 14.1.3.4 (PP Set)

Table 14.1.4 Summary of Treatment Compliance (Safety set)

| Category | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|
| n | xx | xx | xx |
| < 50% Compliance | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| >= 50% and =< 80% Compliance | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| > 80% Compliance | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.5.2, 16.2.5.3

Table 14.2.1.1.x Summary of HBsAg by A Genotype (ITT Set)

Genotype: A

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.1

SD: Standard Deviation. N/A = Not Applicable.
[1] Baseline is defined as the average of screening and day 1 pre-dose.

Programming Note:
- Repeat for Genotype: Non A
- Repeat for table 14.2.1.1.2 (ITT set with no imputation), 14.2.1.2.1 (mITT with imputation), ), 14.2.1.2.2 (mITT with no imputation) , 14.2.1.3.1 (PP set with imputation) and 14.2.1.3.2 (PP set with no imputation) .

Table 14.2.2.x Analysis of HBsAg: Baseline to Week 16 (ITT Set)

| | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
|---|---|---|
| Week 2 | | |
| n | XX | XX |
| Mean change from baseline | XX | XX |
| LS Mean change from baseline | XX | XX |
| 95% CI on LS mean change from baseline | XX,XX | XX,XX |
| SE on LS mean change from baseline | xx.xx | xx.xx |
| p-value | .xxx | .xxx |
| Difference in change from baseline at Week 10 | | |
| N | XX | |
| Mean | XX | |
| LS Mean | XX,XX | |
| 95% on LS Mean | XX,XX | |
| SE on LS Mean | xx.xx | |
| p-value | .xxx | |
| <Repeat for Week 4,6,8,10,12,14,16> | | |

Source Listing: 16.2.6.1
LS mean is derived from a general linear model for repeated measures. The covariates are treatment groups, visit, baseline HBsAG, A Genotype, HBeAg positive and the interaction term of treatment group*visit.
Covariance structure is XXX.
CI = Confidence Interval. SE = Standard Error.

Programming Note:
- Repeat for table 14.2.2.1.2 (ITT set with no imputation), 14.2.2.2.1 (mITT with imputation), ), 14.2.2.2.2 (mITT with no imputation) , 14.2.2.3.1 (PP set with imputation) and 14.2.2.3.2 (PP set with no imputation) .

-The SAS code used to implement this analysis is given below:

```
PROC MIXED DATA=dataset;
  CLASS  ID TRT VISIT HBeAg;
  MODEL CHG = Baseline HBeAg TRT VISIT TRT*VISIT / SOLUTION CL;
  DDFM=KenwardRoger;
  REPEATED VISIT /SUBJECT = ID TYPE = UN ;
  LSMEANS TRT*VISIT / DIFF CL;
  RUN;
```

Table 14.2.3.1 Summary and Analysis of HBsAg Loss Rate A (ITT Set)

| Visit | Category | Statistics | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
|---|---|---|---|---|
| Week 16 | | n | xx | xx |
| | HBsAg Loss | n (%) [1] | xx (xx.x %) | xx (xx.x %) |
| | | p-value | 0.XXX | |
| <Repeat for Week 40> | | | | |

Source Listing: 16.2.6.1
p-value is based on the Person Chi-squared Test.
HBsAg Loss is defined as HBsAg value < LLOQ/TND.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Programming Note:
- Only present Week 16 and Week 40 will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure to adjust p-value.

Table 14.2.3.2 Summary and Analysis of HBsAg Loss Rate B (ITT Set)

| Visit | Category | Statistics | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
|---|---|---|---|---|
| Week 16 | | n | xx | xx |
| | HBsAg Loss | n (%) [1] | xx (xx.x %) | xx (xx.x %) |
| | | p-value | 0.XXX | |
| <Repeat for Week 40> | | | | |

Source Listing: 16.2.6.1
p-value is based on the Person Chi-squared Test.
HBsAg Loss is defined as HBsAg value < LLOQ/TD.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Programming Note:
- Only present Week 16 and Week 40 will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure to adjust p-value.

Table 14.2.4.1 Summary and Analysis of HBsAg Responder Rate A (ITT Set)

| | | | Decrease from Baseline ≥ 1.0 on the log10 Scale | |
|---|---|---|---|---|
| Visit | Category | Statistics | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
| Week 16 | | n | | |
| | HBsAg Responder | n (%) [1] | | |
| | | p-value | | |
| Week 40 | | n | xx | xx |
| | | n (%) [1] | xx (xx.x %) | xx (xx.x %) |
| | | p-value | 0.XXX | |

Source Listing: 16.2.6.1

p-value is based on the Person Chi-squared Test.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Programming Note:
- Only to present Week 16 and Week 40 will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure to adjust p-value.

Table 14.2.4.2 Summary and Analysis of HBsAg Responder Rate B (ITT Set)

| | | | Decrease from Baseline ≥ 0.5 on the log10 Scale | |
|---|---|---|---|---|
| Visit | Category | Statistics | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
| Week 16 | | n | xx | xx |
| | HBsAg Responder | n (%) [1] | xx (xx.x %) | xx (xx.x %) |
| | | p-value | 0.XXX | |
| Week 40 | | n | xx | xx |
| | | n (%) [1] | xx (xx.x %) | xx (xx.x %) |
| | | p-value | 0.XXX | |

Source Listing: 16.2.6.1

p-value is based on the Person Chi-squared Test.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Programming Note:
- Only to present Week 16 and Week 40 will consider multiplicity by a combination of a hierarchical fixed test procedure and a Hochberg procedure to adjust p-value.

Table 14.2.5 Summary of HBsAg Relapse Rate (ITT Set)

| Visit | Category | Statistics | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|---|
| Week 16 | | n | xx | xx | xx |
| | HBsAg Relapse | n (%) [1] | xx (xx.x %) | xx (xx.x %) | xx (xx.x %) |
| <Repeat for Week 20, 28, 40> | | n | xx | xx | xx |
| | HBsAg Relapse | n (%) [1] | xx (xx.x %) | xx (xx.x %) | xx (xx.x %) |

Source Listing: 16.2.6.1

HBsAg Relapse is defined as patients who became negative [HBsAg < LLOQ], then increased with HBsAg > LLOQ.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Table 14.2.6 Summary of Virologic Failure Rate of HBV DNA (ITT Set)

| Visit | Category | Statistics | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|---|
| Week 16 | | n | xx | xx | xx |
| | Virologic Failure Rate | n (%) [1] | xx (xx.x %) | xx (xx.x %) | xx (xx.x %) |
| <Repeat for Week 20, 28, 40> | | n | xx | xx | xx |
| | Virologic Failure Rate | n (%) [1] | xx (xx.x %) | xx (xx.x %) | xx (xx.x %) |

Source Listing: 16.2.6.2

Virologic Failure Rate of HBV DNA is defined as patients with a confirmed quantifiable HBV DNA increase of ≥ 1log10 HBV DNA copies/mL above LLOQ.
[1] Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Table 14.2.7 Summary of HBV-pgRNA (ITT Set)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.3

SD: Standard Deviation. N/A = Not Applicable.
[1] Baseline is defined as the last valid, non-missing assessment prior to first study drug administration.

Table 14.2.8 Summary of HBcrAg (ITT Set)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.4

SD: Standard Deviation. N/A = Not Applicable.
[1] Baseline is defined as the last valid, non-missing assessment prior to first study drug administration.

Table 14.2.9 Summary of HBeAg (ITT Set and HBeAg Positive Patients)

| | Group 2 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 16 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week 40 | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.5

SD: Standard Deviation. N/A = Not Applicable.
[1] Baseline is defined as the HBeAg value at screening visit..

Programming Note:
This table is only for ITT set and HBeAg Positive Patients so that the treatment groups will be presented as below:
Group 2 = EYP001a 200 mg QD + NA daily HBeAg+
Group 5 = Placebo HBeAg+
Group 7 = All HBeAg+
Group 9 = All Study Patients (HBeAg + only)

Table 14.2.10 Summary of Fibroscan VCTE (ITT Set)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 16 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week 40 | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.8

SD: Standard Deviation. N/A = Not Applicable.
[1] Baseline is defined as the last valid, non-missing assessment prior to first study drug administration.

Table 14.2.11 Summary of HBsAg Loss Rate (Target not detected vs. Target detected) (ITT Set)

| Visit | Result | Statistics | Group 1 (N=xx) | etc. | Group x (N=xx) |
|---|---|---|---|---|---|
| Week 16 | | n | xx | xx | xx |
| | TND | n (%) | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | TD | n (%) | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 20 | | n | xx | xx | xx |
| | TND | n (%) | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | TD | n (%) | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| <Repeat for Week 28, 40> | | | | | |

Source Listing: 16.2.6.1

TND = Target Not Detected. TD = Target Detected.
Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Table 14.2.12 Summary of Anti-HBs (ITT Set)

| Visit | Category | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline[1] | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 16 | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 40 | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.6.6

Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Table 14.2.13 Summary of Anti-HBe (ITT Set)

| Visit | Category | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline[1] | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 16 | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 40 | n | xx | xx | xx |
| | Non-Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Indeterminate | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Reactive | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |

Source Listing: 16.2.6.7

Number of subjects at each visit (Visit n) will be used as the denominator for the calculation of all percentages.

Table 14.2.14 Summary of PD Markers (PD Set)

Parameters: Plasma C4 (7α-hydroxy-4-cholesten-3-one)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source Listing: 16.2.6.9

SD: Standard Deviation.
[1] Baseline is defined as the last valid, non-missing assessment prior to first study drug administration.

Table 14.3.1 Summary of Concomitant Medications (Safety Set)

| Anatomical Therapeutic Class (ATC) [Level 3]<br>Preferred Term (PT) | Group 1<br>(N=xx)<br>n (%) m | etc. | Group x<br>(N=xx)<br>n (%) m |
|---|---|---|---|
| Subjects with at least one Concomitant Medication | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| ATC 1 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| PT 1 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| PT 2 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| …. | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| ATC 2 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| PT 1 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| PT 2 | xx (xx.x%) x | xx (xx.x%) x | xx (xx.x%) x |
| …… | | | |

Source: Listing 16.2.10.2

Concomitant medications are defined as any medication (other than the study drug) that was used at least once after the first administration of the study drug. If a participant has multiple occurrences of a concomitant medication, the participant is presented only once in the participant count (n) column for a given ATC and PT. Occurrences are counted each time in the mentions/occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

World Health Organization-Drug Dictionary (WHO-DD) Version xx, YYYY

Table 14.3.3.1 Summary of Overall Treatment Emergent Adverse Events (*Safety Set*)

| | Group 1 (N=xx) n (%) m | etc. | Group x (N=xx) n (%) m |
|---|---|---|---|
| Number of Participants Reporting at least: | | | |
| One TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One Serious TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One TEAE with Common Terminology Criteria for Adverse Events (CTCAE) Toxicity ≥ Grade 3 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One Study Drug Related TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One Entecavir (ETV) Related TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One Tenofovir Disoproxil Fumarate (TDF) Related TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| One TEAE Leading to Discontinuation of Study Drug | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.
Treatment Related TEAE is defined as any TEAE reported as being “Possibly”, “Probably” or “Definitely” to Study Drug/EV/TDF.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.2 Summary of Treatment Emergent Adverse Events by System Organ Class and Preferred Term (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |
| SOC2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT3 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT4 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| …. | | | |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication. If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.3 Summary of Serious Treatment Emergent Adverse Events by System Organ Class and Preferred Term (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one Serious TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |
| SOC2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT3 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT4 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| …. | | | |

Source: Listing 16.2.7.2

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication. If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.4.1 Summary of Treatment Emergent Adverse Events by Relationship to Study Drug by System Organ Class, Preferred Term (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one TEAE related to study drug | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.4.2 Summary of Treatment Emergent Adverse Events by Relationship to ETV by System Organ Class, Preferred Term (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one TEAE related to ETV | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.4.3 Summary of Treatment Emergent Adverse Events by Relationship to TD by System Organ Class, Preferred Term (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one TEAE related to TD | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Definitely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Probably Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Possibly Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unlikely Related | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Unrelated | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.5 Summary of Treatment Emergent Adverse Events by System Organ Class, Preferred Term and Severity (Safety Set)

| | Group 1 (N=xx) n (%) m | | Group x (N=xx) n (%) m |
|---|---|---|---|
| | | etc. | |
| Participants with at least one TEAE | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Mild | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Moderate | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Severe | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Life-threatening | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Fatal | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Mild | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Moderate | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Severe | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Life-threatening | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Fatal | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Mild | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Moderate | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Severe | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Life-threatening | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| Fatal | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |

Source: Listing 16.2.7.1

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.3.6 Summary of Treatment Emergent Adverse Events Leading to Stud Drug Discontinuation by System Organ Class and Preferred Term
(Safety Set)

| | Group 1 (N=xx) n (%) m | etc. | Group x (N=xx) n (%) m |
|---|---|---|---|
| Participants with at least one TEAE Leading to Discontinuation of Study Drug | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| SOC1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| ….. | | | |
| SOC2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT1 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT2 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT3 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| PT4 | xx (xx.x%) xx | xx (xx.x%) xx | xx (xx.x%) xx |
| …. | | | |

Source: Listing 16.2.7.3

Treatment Emergent Adverse Events (TEAEs) are defined as adverse events that occurred following the first administration of study medication.
If a participant has multiple occurrences of a TEAE, the participant is presented only once in the Participant count (n) column for a given System Organ Class and Preferred Term. Occurrences are counted each time in the mentions/Occurrence (m) column.

Percentages are calculated (the denominator used for the calculation) based on the number of participants in the safety set in each treatment group (N).

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Table 14.3.4.1.1 Summary of Hematology and Coagulation (Safety Set)

Parameter: Basophils (unit)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit<br>Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.8.1.1
[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.4.1.2 Summary of Hematology and Coagulation Shifts from Baseline (Safety Set)

Parameter: Hemoglobin (unit)

| Baseline [1] | Visit | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline | Week 2 | | | |
| Low | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.8.1.1
[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Table 14.3.4.2.1 Summary of Serum Chemistry (Safety Set)

Parameter: Basophils (unit)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.8.2.1

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
For ALT, AST, ALP, and total Bilirubin (TBL), the baseline value is defined as the average of screening and day 1 pre-dose.
N/A = Not Applicable. SD = Standard Deviation.

Programming Note:
- For ALT, AST, ALP, and total Bilirubin (TBL), the baseline value is defined as the average of screening and day 1 pre-dose.

Table 14.3.4.2.2 Summary of Serum Chemistry Shifts from Baseline (*Safety Set*)

Parameter: Basophils (unit)

| Baseline [1] | Visit | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline | Week 2 | | | |
| Low | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.8.2.1
[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Table 14.3.4.3.1 Summary of Lipid Metabolic Profile (Safety Set)

Parameter: HDL-C (unit)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.8.3.1

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
For ALT, AST, ALP, and total Bilirubin (TBL), the baseline value is defined as the average of screening and day 1 pre-dose.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.4.3.2 Summary of Serum Chemistry Shifts from Baseline (*Safety Set*)

Parameter: HDL-C (unit)

| Baseline [1] | Visit | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline | Week 2 | | | |
| Low | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Low | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Normal | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Low | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| High | Hight | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.8.3.1

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Table 14.3.4.3 Summary of Urinalysis (*Safety Set*)

Parameter: Glucose (unit)

| Visit | Category | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Baseline[1] | n | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week xx | n | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.8.4.1

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Table 14.3.4.4 Summary of Maximum CTCAE for ALT, AST, BILI and GGT for Post Treatment Assessments (*Safety Set*)

| Parameters/ grade | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|
| Number of subjects with any CTCAE | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| ALT | | | |
| No CTCAE (Grade 0) | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Grade 1 | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Grade 2 | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Grade 3 | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Grade 4 | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Grade 5 | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| < repeat for AST, BILI and GGT > | | | |
| Etc. | | | |

Source: Listing 16.2.8.2.1

This table is based on maximum grading using CTCAE version 5.0
BILI = Total Bilirubin; GGT= Gamma Glutamyl Transferase; ALT =Alanine Aminotransferase; AST = Aspartate Aminotransferase

Table 14.3.5.1 Summary of Vital Signs (*Safety Set*)

Parameter: Heart rate (beats/min)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit<br>Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 2 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.9.1

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.5.2.1 Summary of 12-Lead ECG (Safety Set)

Parameter: Heart Rate (bpm)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week xx | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.9.2

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.5.2.2 Summary of 12-Lead ECG Interpretation (Safety Set)

Parameter: Overall ECG Interpretation

| Visit | Category | Group 1 (N=XXX) | Group 2 (N=XXX) | Group 3 (N=XXX) |
|---|---|---|---|---|
| Baseline[1] | n | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Not Evaluable | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week xx | N | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Not Evaluable | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.9.2

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Table 14.3.5.3 Summary of Pruritus Assessment - 5-D Pruritus Scale (Safety Set)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit<br>Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week xx | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.9.7

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.5.4 Summary of Pruritus Assessment - Visual Analogue Scale (Safety Set)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit<br>Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week xx | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.9.8

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Table 14.3.5.5 Summary of Liver Fibrosis and Inflammation Assessment (Safety Set)

Parameter: ALT (unit)

| | Group 1 (N=XXX) | | etc. | | Group x (N=XXX) | |
|---|---|---|---|---|---|---|
| Visit Statistics | Actual Value | Change from Baseline | Actual Value | Change from Baseline | Actual Value | Change from Baseline |
| Baseline [1] | | | | | | |
| N | XX | N/A | XX | N/A | XX | N/A |
| Mean | XX | N/A | XX | N/A | XX | N/A |
| SD | XX | N/A | XX | N/A | XX | N/A |
| Median | XX | N/A | XX | N/A | XX | N/A |
| Minimum | XX | N/A | XX | N/A | XX | N/A |
| Maximum | XX | N/A | XX | N/A | XX | N/A |
| Week 4 | | | | | | |
| N | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |
| Week xx | | | | | | |
| n | XX | XX | XX | XX | XX | XX |
| Mean | XX | XX | XX | XX | XX | XX |
| SD | XX | XX | XX | XX | XX | XX |
| Median | XX | XX | XX | XX | XX | XX |
| Minimum | XX | XX | XX | XX | XX | XX |
| Maximum | XX | XX | XX | XX | XX | XX |

Source: Listing 16.2.9.4

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. SD = Standard Deviation.

Programming Note:
- These parameter (ALT, AST, AST/ALT ratio, high sensitivity C-reactive protein, interleukin 6, tumour necrosis factor alpha, procollagen type III N terminal peptide (Pro C3), tissue inhibitor of metalloproteinases-1) will be included.
For ALT and AST, the baseline value is defined as the average of screening and day 1 pre-dose

Table 14.3.5.6 Analysis of Liver Fibrosis and Inflammation Assessment: Baseline to Week 16 (Safety Set)

Parameter: AST (unit)

| | EYP001a 200 mg QD + NA daily (N=XXX) | Placebo + NA daily (N=XXX) |
|---|---|---|
| Week 4 | | |
| n | XX | XX |
| Mean change from baseline | XX | XX |
| LS Mean change from baseline | XX | XX |
| 95% CI on LS mean change from baseline | XX,XX | XX,XX |
| SE on LS mean change from baseline | xx.xx | xx.xx |
| Difference in change from baseline at Week 4 | | |
| N | XX | |
| Mean | XX | |
| LS Mean | XX,XX | |
| 95% on LS Mean | XX,XX | |
| SE on LS Mean | xx.xx | |

<Repeat for Week 8,12,16>

Source Listing: 16.2.9.4

LS mean is derived from a general linear model for repeated measures. The covariates are treatment groups, visit, baseline value of liver fibrosis and inflammation assessment, A Genotype, HBeAg positive and the interaction term of treatment group*visit.
Covariance structure is XXX.
CI = Confidence Interval. SE = Standard Error.

Programming note:

The SAS code used to implement this analysis is given below:

```
PROC MIXED DATA=dataset;
  CLASS  ID TRT VISIT HBeAg;
  MODEL CHG = Baseline HBeAg TRT VISIT TRT*VISIT / SOLUTION CL;
  DDFM=KenwardRoger;
  REPEATED VISIT /SUBJECT = ID TYPE = UN ;
  LSMEANS TRT*VISIT / DIFF CL;
  RUN;
```

Table 14.3.5.7 Summary of Liver Imaging (*Safety Set*)

Parameter: Glucose (unit)

| Visit | Category | Group 1 (N=XXX) | etc. | Group x (N=XXX) |
|---|---|---|---|---|
| Screening | n | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Week 40 | n | xx | xx | xx |
| | Normal | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Not Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| | Abnormal, Clinically Significant | xx (xx.x%) | xx (xx.x%) | xx (xx.x%) |
| Etc. | Etc. | | | |

Source: Listing 16.2.9.5

Number of participants at each visit (n) will be used as the denominator for the calculation of all percentages.

Listing 16.2.1.1 Analysis Populations (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Intention-to-Treat Set | Modified Intention-to-Treat Set | Safety Set | Pharmacodynamic Set | Per Protocol Set | Reason for Exclusion |
|---|---|---|---|---|---|---|
| XXX | Yes | Yes | Yes | Yes | Yes | |
| XXX | Yes | Yes | Yes | Yes | Yes | |
| XXX | Yes | Yes | Yes | Yes | Yes | |
| XXX | Yes | Yes | No | Yes | No | xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx |
| …. | | | | | | |

Listing 16.2.1.2 Participant Disposition (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| | Informed Consent | | | | | |
|---|---|---|---|---|---|---|
| Subject ID | Date (YYYY-MM-DD) | Date for the storage and use of blood samples (YYYY-MM-DD) | Did the Participant Complete the Study? | Study Completion/ Early Termination Date (YYYY-MM-DD) | Primary Reason for Non-completion | Date for Consent Withdrawal (YYYY-MM-DD) |
| XXX | YYYY-MM-DD | YYYY-MM-DD | Yes | YYYY-MM-DD | | |
| XXX | YYYY-MM-DD | YYYY-MM-DD | Yes | YYYY-MM-DD | | |
| XXX | YYYY-MM-DD | YYYY-MM-DD | No | YYYY-MM-DD | Withdrawal by Subject | YYYY-MM-DD |
| XXX | YYYY-MM-DD | YYYY-MM-DD | Yes | YYYY-MM-DD | | |
| …. | | | | | | |

Listing 16.2.2.1 Protocol Deviation (*ITT Set*)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Date of Deviation (YYYY-MM-DD) | Type of Deviation | Deviation Description | Important Deviation |
|---|---|---|---|---|
| XXX | YYYY-MM-DD | YYYYYYYYYYYYYYY | XXXXXXXXXXXXX | No |
| XXX | YYYY-MM-DD | YYYYYYYYYYYYYYY | XXXXXXXXXXXXX | No |
| …. | | | | |

Listing 16.2.4.1 Demographics and Baseline Characteristics (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Date of Informed Consent (YYYY-MM-DD) | Date of Birth (YYYY-MM-DD) | Age at Informed Consent (years) | Sex | Childbearing Potential | Reason not of Childbearing Potential | Race | Ethnicity | Height (cm) | Weight (kg) | Body Mass Index (kg/m$^2$) | Audit-C overall score | HBV Genotype | HBeAg Status |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| XXX | YYYY-MM-DD | YYYY-MM-DD | xx | Female | No | Other - xxxxx | Asian | xxxxx | xxx | xx.x | xx.x | 3 | A | Positive |
| XXX | YYYY-MM-DD | YYYY-MM-DD | xx | Male | N/A | | White | xxxxx | xxx | xx.x | xx.x | 3 | B | Negative |
| …. | | | | | | | | | | | | | | |

N/A = Not Applicable.

Listing 16.2.4.2 Medical History (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | MH Id | Medical History Term/ System Organ Class /Preferred Term | Start Date (YYYY-MM-DD) | End Date (YYYY-MM-DD) |
|---|---|---|---|---|
| XXX | xx | XXXXXXXXXX/ YYYYYYYYY/ ZZZZZZZZZ | YYYY-MM-DD | YYYY-MM-DD |
| | xx | XXXXXXXXXX/ YYYYYYYYY/ ZZZZZZZZZ | YYYY-MM-DD | Ongoing |
| ….. | | | | |

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Listing 16.2.4.3 Drugs of Abuse Screen (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Test Performed / No-Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Any Positive Result | Tests Positive |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | Yes | Amphetamines |
| ……. | | | | | Barbiturates |
| | | | | | …. |
| | Treatment Visit 1 | Yes | YYYY-MM-DD/ HH:MM | No | |
| XXX | Screening | No - XXXXXX | | | |
| ….. | …. | | | | |

Listing 16.2.4.4 AUDIT – Interview Version (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Interview Performed Administered/ No - Reason | Test Date (YYYY-MM-DD) | Questions | Result |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD | How often do you have a drink containing alcohol? | Never |
| | | | | How many drinks containing alcohol do you have on a typical day when you are drinking? | 1 or 2 |
| | | | | How often do you have six or more drinks on one occasion? | Less than monthly |
| | | | | How often during the last year have you found that you were not able to stop drinking once you had started? | Less than monthly |
| | | | | How often during the last year have you failed to do what was normally expected from you because of drinking? | Daily or almost daily |
| | | | | How often during the last year have you needed a first drink in the morning to get yourself going after a heavy drinking session? | Never |
| | | | | How often during the last year have you had a feeling of guilt or remorse after drinking | Never |
| | | | | How often during the last year have you been unable to remember what happened the night before because you had been drinking | Never |
| | | | | Have you or someone else been injured as a result of your drinking | Never |
| | | | | Has a relative or friend or a doctor or another health worker been concerned about your drinking or suggested you cut down | Never |
| | | | | AUDIT Overall Score | 6 |
| | Day 1 | No - xxxxxxx | | How often do you have a drink containing alcohol? | N/A |
| | | | | Etc. | |
| XXX | Screening | Yes | YYYY-MM-DD | How often do you have a drink containing alcohol? | |
| ….. | ….. | | | Etc. | |

Programming Note:
- Patients with AUDIT-C scores 3 points at screening will receive the full AUDIT and will be excluded if they score 8 points on the full AUDIT. Patients with AUDIT C scores <3 points will not receive the full AUDIT.

Listing 16.2.4.5 Serology (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Test Name | Result |
|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | Hepatitis D Antibody (Anti-HDV) | Negative |
| | | | HIV-1 Antibody/HIV-2 Antibody (Anti-HIV) | Negative |
| | | | Hepatitis B Antibody (Anti-HBsAg) | Negative |
| | | | hepatitis B e-antibody (Anti-HBe) | Negative |
| | | | Quantitative HBsAg | xx |
| | | | Hepatitis C Antibody (Anti-HCV) | Positive |
| ….. | | | PCR-based quantitative HCV viral load | Negative |

Programming Note:
- When Anti-HCV is Positive, a PCR-based quantitative HCV viral load assessment will be performed.

Listing 16.2.4.6 Eligibility Criteria (All Screened Patients)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Participant Eligible | Category Failed (Inclusion/ Exclusion) | Inclusion/ Exclusion Criterion not met |
|---|---|---|---|---|
| XXX | Screening | No | Inclusion and Exclusion | Exclusion: xx, xx; Inclusion xx, xx |
| | Day 1 | Yes | | |
| …. | …. | | | |

Listing 16.2.5.1 Participant Randomization (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Randomization Date/Time (YYYY-MM-DD/ HH:MM) | Randomization Number | Randomized Treatment Received |
|---|---|---|---|
| XXX | YYYY-MM-DD/ HH:MM | XXX | EYP001a 200 mg QD + NA daily |
| XXX | YYYY-MM-DD/ HH:MM | XXX | EYP001a 200 mg QD + NA daily |
| XXX | YYYY-MM-DD/ HH:MM | XXX | EYP001a 200 mg QD + NA daily |
| …. | | | |

Listing 16.2.5.2 Treatment Exposure (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Study Drug Administered/ No - Reason | Date/Time of Administration (YYYY-MM-DD/ HH:MM) | Did the subject take 200mg as per protocol? / No - Reason | Fasting? | NA Administered (Treatment)/ No - Reason | Date/Time of Administration for NA (YYYY-MM-DD/ HH:MM) | Did the subject take NA as per protocol? / No - Reason |
|---|---|---|---|---|---|---|---|---|
| XXX | Day 1 | Yes | YYYY-MM-DD/ HH:MM | Yes | No | Yes (TD) | YYYY-MM-DD/ HH:MM | Yes |
| | Week 2 | Yes | YYYY-MM-DD/ HH:MM | No - xxxxx | No | Yes (ETV) | YYYY-MM-DD/ HH:MM | No - xxxx |
| | Etc. | | | | | | | |
| XXX | Day 1 | No - xxxxxxxx | | | | | | |
| ... | | | | | | | | |

NA = Nucleos(T)ide Analogue. TD = Tenofovir Disopropil. ETV = Entecavir

Listing 16.2.5.3 Study Drug Accountability (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Drug Accountability (EYP001a/Placebo)

| Subject ID | Visit | Number of 200mg Tablets Used | Date of Return (YYYY-MM-DD) | Number of 200mg Tablets Dispensed | Date of Dispense (YYYY-MM-DD) | Dose Missed | Was the subject compliant with EYP001a/Placebo Dosing? | reason for non-compliance |
|---|---|---|---|---|---|---|---|---|
| XXX | Day 1 | xx | YYYY-MM-DD | xx | YYYY-MM-DD | No | Yes | |
| | Week 4 | xx | YYYY-MM-DD | Xx | YYYY-MM-DD | No | Yes | |
| | Etc. | | | | | | | |
| XXX | Day 1 | No - xxxxxxxx | | | | | | |
| ... | | | | | | | | |

Drug Accountability (NA)

| Subject ID | Visit | Number of Tablets Used | Date of Return (YYYY-MM-DD) | Drug | Number of Tablets Dispensed | Date of Dispense (YYYY-MM-DD) | Dose Missed | Was the subject compliant with NA Dosing? | reason for non-compliance |
|---|---|---|---|---|---|---|---|---|---|
| XXX | Day 1 | xx | YYYY-MM-DD | ETV | xx | YYYY-MM-DD | Yes | No | Xxxx,yyy,zzz |
| | Week 4 | xx | YYYY-MM-DD | ETV | Xx | YYYY-MM-DD | No | Yes | |
| | Etc. | | | | | | | | |
| XXX | Day 1 | No - xxxxxxxx | | | | | | | |
| ... | | | | | | | | | |

NA = Nucleos(T)ide Analogue. TDF = Tenofovir Disopropil. ETV = Entecavir

Programming note:
- in the reason for non-compliance, to present all that apply and separated by a ","

Listing 16.2.5.4 Missed Dose (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Date of Missed EYP001a/Placebo Dose (YYYY-MM-DD) | Reason for missed EYP001a/Placebo dose | Date of Missed NA Dose (YYYY-MM-DD) | Reason for missed NA dose |
|---|---|---|---|---|
| XXX | YYYY-MM-DD | Patient Forgot | | Patient Forgot |
| | YYYY-MM-DD | AE- xxxxxxx | | Other - xxxxx |
| XXX | | | | |
| ... | | | | |

NA = Nucleos(T)ide Analogue.

Listing 16.2.6.1 HBsAg (IU/mL) (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | $log_{10}$ | |
|---|---|---|---|---|---|---|
| | | | | | Actual Value | Change from Baseline [1] |
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | N/A |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | N/A |
| | Week 2 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| | Week 4 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| | Etc. | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| etc. | etc. | | | | | |

[1] Baseline is defined as the average of screening and Day 1 pre-dose.
N/A = Not Applicable. EOS = End of Study.

Listing 16.2.6.2 HBV DNA (Log IU/mL) (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Week 2 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Week 4 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Etc. | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| etc. | etc. | | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. EOS = End of Study.

Listing 16.2.6.3 HBV-pgRNA (Log IU/mL) (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Week 2 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Week 4 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Etc. | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| etc. | etc. | | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. EOS = End of Study.

Listing 16.2.6.4 HBcrAg (Log IU/mL) (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | N/A |
| | Week 2 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Week 4 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| | Etc. | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x |
| etc. | etc. | | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. EOS = End of Study.

Listing 16.2.6.5 HBeAg (PEI U/ml) (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | $log_{10}$ Actual Value | $log_{10}$ Change from Baseline [1] |
|---|---|---|---|---|---|---|
| XXX | Screening [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | N/A |
| | Day 1 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | N/A |
| | Week 16 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| | Week 40 (EOS) | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| | | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | xx.x |
| etc. | etc. | | | | | |

[1] Baseline is defined as HBeAg value at screening visit.
EOS = End of Study.

Listing 16.2.6.6 Anti-HBs (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value |
|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Week 16 | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Week 40 (EOS) | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| etc. | etc. | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.

Listing 16.2.6.7 Anti-HBe (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was HBV Response Marker Sample Collected / No - Reason | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value |
|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Week 16 | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | Week 40 (EOS) | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| | | Yes | YYYY-MM-DD/ HH:MM | xx.x |
| etc. | etc. | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.

Listing 16.2.6.8 Fibroscan VCTE (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Fibroscan VCTE Performed/ No - Reason | Assessment Date/ Time (YYYY-MM-DD/ HH:MM) | Liver stiffness measure (LSM) result (kpa) | Change from Baseline [1] | Date and Time of Last Solid Meal (YYYY-MM-DD/ HH:MM) |
|---|---|---|---|---|---|---|
| XXX | Screening [1] | Yes | YYYY-MM-DD/ HH:MM | xx.x | | YYYY-MM-DD/ HH:MM |
| | Week 16 | Yes | YYYY-MM-DD/ HH:MM | xx.x | xx.x | YYYY-MM-DD/ HH:MM |
| | Week 40 (EOS) | No - XXXXXX | YYYY-MM-DD/ HH:MM | xx.x | xx.x | YYYY-MM-DD/ HH:MM |
| etc. | etc. | | | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable.EOS = End of Study.

Listing 16.2.6.9 PD Markers (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: FGF-19 (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | Comments |
|---|---|---|---|---|---|
| XXX | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | xxxxxxxx |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | |
| | Week 8 | YYYY-MM-DD/ HH:MM | xx | xx | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
Lower Limit of Quantitation is xx.xx (unit)
N/A = Not Applicable. LLOQ = Lower Limit of Quantitation.

Listing 16.2.7.1 Adverse Events (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | AE No. | Adverse Event Verbatim/ System Organ Class/ Preferred Term | Start Date/Time End Date/Time (YYYY-MM-DD/ HH:MM) | SAE | TEAE | Severity | Relationship to Study Drug/ETV/TD | Action Taken for AE | Concomitant Medication | Action Taken for Study treatment | Outcome |
|---|---|---|---|---|---|---|---|---|---|---|---|
| XXX | xx | XXXXXXXXXXXXXXXXXX<br>ZZZZZZZZZZZZZZZZZZ<br>YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM<br>YYYY-MM-DD/ HH:MM | Yes | Yes | Mild | Related/Unlikely/Possibly Related | Medication required | XXXXXX | Dose Not Changed | Recovered/ Resolved |
| XXX | xx | XXXXXXXXXXXXXXXXXX<br>ZZZZZZZZZZZZZZZZZZ<br>YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM<br>Ongoing | Yes | No | Moderate | Related/Unlikely/Possibly Related | None | | N/A | Recovering / Resolving |

….

SAE = Serious Adverse Event. TEAE = A treatment-emergent adverse event. ETV = Entecavir. TD = Tenofovir Disoproxil.

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Listing 16.2.7.2 Serious Adverse Events (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Adverse Event Verbatim/ System Organ Class/ Preferred Term | Start Date/Time End Date/Time (YYYY-MM-DD/ HH:MM) | SAE | SAE Criteria | TEAE | Severity | Relationship to Study Drug/ETV/TD | Action Taken for AE | Concomitant Medication | Action Taken for Study treatment | Outcome |
|---|---|---|---|---|---|---|---|---|---|---|---|
| XXX | XXXXXXXXXXXXXXXXXX ZZZZZZZZZZZZZZZZZZ YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM YYYY-MM-DD/ HH:MM | Yes | Life Threatening | Yes | Mild | Related/Unlikely/Possibly Related | Medication required | XXXXXX | Dose Not Changed | Recovered/ Resolved |
| XXX | XXXXXXXXXXXXXXXXXX ZZZZZZZZZZZZZZZZZZ YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM Ongoing | Yes | Congenital Anomaly or Birth Defect | No | Moderate | Related/Unlikely/Possibly Related | None | | N/A | Recovering / Resolving |
| …. | | | | | | | | | | | |

SAE = Serious Adverse Event. TEAE = A treatment-emergent adverse event. ETV = Entecavir. TD = Tenofovir Disoproxil.

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Listing 16.2.7.3 Adverse Events Leading to Study Drug Withdrawal (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Adverse Event Verbatim/ System Organ Class/ Preferred Term | Start Date/Time End Date/Time (YYYY-MM-DD/ HH:MM) | SAE | TEAE | Severity | Relationship to Study Drug/ETV/TD | Action Taken for AE | Concomitant Medication | Action Taken for Study treatment | Outcome |
|---|---|---|---|---|---|---|---|---|---|---|
| XXX | XXXXXXXXXXXXXXXXXX<br>ZZZZZZZZZZZZZZZZZZ<br>YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM<br>YYYY-MM-DD/ HH:MM | Yes | Yes | Mild | Related/Unlikely/Possibly Related | Medication required | XXXXXX | Dose Not Changed | Recovered/ Resolved |
| XXX | XXXXXXXXXXXXXXXXXX<br>ZZZZZZZZZZZZZZZZZZ<br>YYYYYYYYYYYYYYYYYY | YYYY-MM-DD/ HH:MM<br>Ongoing | Yes | No | Moderate | Related/Unlikely/Possibly Related | None | | N/A | Recovering / Resolving |

….

SAE = Serious Adverse Event. TEAE = A treatment-emergent adverse event. ETV = Entecavir. TD = Tenofovir Disoproxil.

Medical Dictionary for Regulatory Activities (MedDRA) Version xx.x

Programming Note:
- Select action taken for EYO001a/Placebo = “Drug Withdrawn”.

Listing 16.2.8.1.1 Hematology and Coagulation (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Hemoglobin (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xx | N/A | | | |
| | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | H | | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.1.2 Abnormal Hematology and Coagulation (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Hemoglobin (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|
| XXX | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | L | NCS | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | H | CS | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | H | NCS | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.2.1 Serum Chemistry (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Sodium (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xx | N/A | | | |
| | Day 1 | YYYY-MM-DD/ HH:MM | xx | N/A | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | H | | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Programming note:
For AST, ALT, total BILI and GGT, to present the CTCAE Grade with High /Low Flag. For example, H – CTCAE Grade 1

Listing 16.2.8.2.2 Abnormal Serum Chemistry (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Sodium (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline[1] | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|
| XXX | Day 1 1 | YYYY-MM-DD/ HH:MM | xx | N/A | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | L | | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | H | | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | L | | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | L | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.3.1 Lipid and Metabolic Profile (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Serum Cholesterol (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | Fasting | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xx | N/A | Yes | | | |
| | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | No | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | No | | | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | No | H | | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | No | | | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | No | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.3.2 Abnormal Lipid and Metabolic Profile (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Serum Cholesterol (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline [1] | Fasting | High/Low Flag | Clinically Significant | Comments |
|---|---|---|---|---|---|---|---|---|
| XXX | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | No | H | NCS | xxxxxxxx |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | xx | No | H | NCS | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | No | H | NCS | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | No | L | NCS | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | No | L | NCS | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.4.1 Urinalysis (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Glucose (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Clinically Significant |
|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| | Day 1[1] | YYYY-MM-DD/ HH:MM | xxxxxxx | NCS |
| | Week 4 | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| | Week 8 | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| …. | Etc. | YYYY-MM-DD/ HH:MM | xxxxxxx | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.8.4.2 Urine Microscopy (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Parameter (unit)

| Subject ID | Visit | Collection Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Clinically Significant |
|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| | Day 1 | YYYY-MM-DD/ HH:MM | xxxxxxx | NCS |
| | Week 4 | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| | Etc. | YYYY-MM-DD/ HH:MM | xxxxxxx | |
| …. | | | | |

CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.9.1 Vital Signs (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Heart Rate (bpm)

| Subject ID | Visit | Assessment Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline[1] | Clinically Significant |
|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xx | N/A | |
| | Day 1 [1] | YYYY-MM-DD/ HH:MM | xx | N/A | NCS |
| | Week 2 | YYYY-MM-DD/ HH:MM | xx | N/A | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | |
| | Week 6 | YYYY-MM-DD/ HH:MM | xx | xx | |
| | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | |

….

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant.

Listing 16.2.9.2 12-Lead ECG (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: Heart Rate (beats/min)

| Subject ID | Visit | Assessment Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline[1] | Abnormal Description | confirmed by a cardiologist | Comments |
|---|---|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD/ HH:MM | xx | N/A | | | |
| | Day 1 | YYYY-MM-DD/ HH:MM | xx | N/A | | | |
| | Week 4 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| | Week 8 | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| | Etc. | YYYY-MM-DD/ HH:MM | xx | xx | | | |
| …. | | | | | | | |

[1] Baseline is defined as the last available, valid, non-missing observation prior to first study drug administration.
N/A = Not Applicable. CS = Clinically Significant, NCS = Not Clinically Significant. WCS = Worst Case Scenario.

Programming Note:
-
- In addition, the ECG finding will be included as a separate parameter. And “Abnormal Description” and “Was the clinically significant abnormality confirmed by a cardiologist” will be specified if the result is abnormal.

Listing 16.2.9.3 Physical Examination (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Assessment Date (YYYY-MM-DD) | Body System | Result | Description of Abnormality |
|---|---|---|---|---|---|
| XXX | Screening | YYYY-MM-DD | General Appearance | Normal | |
| | | | EYES/EARS/NOSE/THROAT | Normal | |
| | | | HEAD AND NECK | Normal | |
| | | | … | Normal | |
| | | | EXTREMITIES | Normal | |
| | | | Other - XXXXXXXX | Normal | |
| | Day 1 | YYYY-MM-DD | Symptom Directed Physical Examination | Normal | |
| | | | … | Normal | |
| … | Etc. | | | | |

CS = Clinically Significant, NCS = Not Clinically Significant.

Programming Note:
- A complete physical examination will be performed at screening. Brief, symptom-directed physical examinations will be performed on all other study visits.

Listing 16.2.9.4 Liver Fibrosis and Inflammation Assessment (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Parameter: XXXX (unit)

| Subject ID | Visit | Assessment Sample Collected/ No - Reason | Assessment Date/ Time (YYYY-MM-DD/ HH:MM) | Actual Value | Change from Baseline[1] |
|---|---|---|---|---|---|
| XXX | Day 1 [1] | Yes | YYYY-MM-DD/ HH:MM | xx | N/A |
| | Week 4 | No - xxxxxxxxxxxx | YYYY-MM-DD/ HH:MM | xx | xx |
| | Week 8 | Yes | YYYY-MM-DD/ HH:MM | xx | xx |
| | Etc. | Yes | YYYY-MM-DD/ HH:MM | xx | xx |
| XXX | Day 1 | Yes | YYYY-MM-DD/ HH:MM | xx | N/A |
| ….. | ….. | | | | |

N/A = Not Applicable.

Programming Note:
- These parameter (ALT, AST, AST/ALT ratio, high sensitivity C-reactive protein, interleukin 6, tumour necrosis factor alpha, procollagen type III N terminal peptide (Pro C3), tissue inhibitor of metalloproteinases-1) will be included.

Listing 16.2.9.5 Liver Imaging (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was liver imaging done? / No - Reason | Method | Assessment Date/ Time (YYYY-MM-DD/ HH:MM) | Result | Abnormal Description | Risk factor |
|---|---|---|---|---|---|---|---|
| XXX | Screening | Yes | CT | YYYY-MM-DD/ HH:MM | Normal | | Xxxx,yyyy,zzzz |
| | Week 40 (EOS) | No – xxxxxxxx | | | | | |
| XXX | Screening | Yes | US | YYYY-MM-DD/ HH:MM | Abnormal NCS | xxxxxxx | |
| ….. | ….. | | | | | | |

N/A = Not Applicable. CT = Computed Tomography. US = Ultrasonography. MRI = Magnetic Resonance Imaging.
CS = Clinically Significant. NCS = Not Clinically Significant.

Programming Note:
- in the risk factor, to present all that apply and separated by a ","

Listing 16.2.9.6 Pregnancy Test Results (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Was Test Performed – Reason Not Performed | Collection Date/Time (YYYY-MM-DD/ HH:MM) | Type | Result |
|---|---|---|---|---|---|
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | Serum | Negative |
| | Day 1 | Yes | YYYY-MM-DD/ HH:MM | Urine | Negative |
| | Week 4 | No - xxxx | | | |
| | Etc. | | | | |
| XXX | Screening | Yes | YYYY-MM-DD/ HH:MM | Serum | Negative |
| | Etc. | | | | |

Programming Note:
- A serum hCG test will be performed at Screening and EOS/ET Visits in WOCBP only. Urine hCG tests will be performed at all other visits

Listing 16.2.9.7 Pruritus Assessment – 5-D Pruritus Scale (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

Domains: Duration

| Subject ID | Visit | Assessment Assessed – Reason no Performed | Assessment Date (YYYY-MM-DD) | Actual Value | Change from Baseline [1] |
|---|---|---|---|---|---|
| XXX | Day 1 [1] | Yes | YYYY-MM-DD | xx | N/A |
| | Week 2 | Yes | YYYY-MM-DD | xx | xx |
| | Week 4 | No - xxxxx | YYYY-MM-DD | xx | xx |
| | Etc. | | | | |
| …. | | | | | |

N/A = Not Applicable.

Programming Note:
- repeated for 5 domains – Duration, Degree, Direction, disability and distribution and total score.
- Single-item domain scores (duration, degree, and direction) are equal to the value indicated below the response choice (range 1-5).
- The score for the disability domain is achieved by taking the highest score on any of the four items.
- For the distribution domain, the number of affected body parts is tallied (potential sum 0-16) and the sum is sorted into five scoring bins:

sum of 0-2 = 1
sum of 3-5 = 2
sum of 6-10 = 3
sum of 11-13 = 4
sum of 14-16 = 5.

Listing 16.2.9.8 Pruritus Assessment – Visual Analogue Scale (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Assessment Assessed – Reason no Performed | Assessment Date (YYYY-MM-DD) | Actual Value | Change from Baseline[1] |
|---|---|---|---|---|---|
| XXX | Day 1 [1] | Yes | YYYY-MM-DD | xx | N/A |
| | Week 2 | No - xxxxxxxxxxx | | | |
| | Week 4 | Yes | YYYY-MM-DD | xx | xx |
| | Week 6 | Yes | YYYY-MM-DD | xx | xx |
| | Etc. | Yes | YYYY-MM-DD | xx | xx |
| XXX | Day 1 | Yes | YYYY-MM-DD | xx | N/A |
| ….. | ….. | | | | |

N/A = Not Applicable.

Listing 16.2.9.9 Stopping Rule (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | Visit | Participant Met any of the following stopping rules | Stopping Rules Met |
|---|---|---|---|
| XXX | Day 1 | Yes | Stopping rules: 01, 02,xx |
| | Week 2 | Yes | Stopping rules: 05, 06, 08 |
| …. | …. | | |

Listing 16.2.10.1 Prior Medication (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | CM Id | Concomitant Medication Therapy/ Anatomical Therapeutic Class (ATC) [Level 3]/ Preferred Term (PT) | Indication | Start Date (YYYY-MM-DD) End Date (YYYY-MM-DD) | Dose | Unit | Frequency | Route | Reason for Use |
|---|---|---|---|---|---|---|---|---|---|
| XXX | xx | XXXXXXXXXXXXXXXXXXXXX/ ZZZZZZZZZZZZZZZZZZZZZ/ YYYYYYYYYYYYYYYYYYYYY | zzzzzzzz | YYYY-MM-DD/ YYYY-MM-DD | XX | Unit | YYYYYY | ZZZZZ | xxx |
| | xx | XXXXXXXXXXXXXXXXXXXXX/ ZZZZZZZZZZZZZZZZZZZZZ/ YYYYYYYYYYYYYYYYYYYYY | zzzzzzzz | YYYY-MM-DD/ YYYY-MM-DD | XX | Unit | YYYYYY | ZZZZZ | xxx |
| … | | … | | | | | | | |

Prior medications are defined as any medication where the use was stopped prior to the first administration of the study medication.

World Health Organization-Drug Dictionary (WHO-DD) Version xx, YYYY

Listing 16.2.10.2 Concomitant Medication (ITT Set)

Group 1: EYP001a 200 mg QD + NA daily

| Subject ID | CM Id | Concomitant Medication Therapy/ Anatomical Therapeutic Class (ATC) [Level 3]/ Preferred Term (PT) | Indication | Start Date (YYYY-MM-DD) End Date (YYYY-MM-DD) | Dose | Unit | Frequency | Route | Reason for Use |
|---|---|---|---|---|---|---|---|---|---|
| XXX | xx | XXXXXXXXXXXXXXXXXXXXX/ ZZZZZZZZZZZZZZZZZZZZZ/ YYYYYYYYYYYYYYYYYYYY | zzzzzzzz | YYYY-MM-DD/ YYYY-MM-DD | XX | Unit | YYYYYY | ZZZZZ | xxx |
| | xx | XXXXXXXXXXXXXXXXXXXXX/ ZZZZZZZZZZZZZZZZZZZZZ/ YYYYYYYYYYYYYYYYYYYY | zzzzzzzz | YYYY-MM-DD/ YYYY-MM-DD | XX | Unit | YYYYYY | ZZZZZ | xxx |
| … | | … | | | | | | | |

Concomitant medications are defined as any medication (other than the study drug) that was used at least once after the first administration of the study drug.

World Health Organization-Drug Dictionary (WHO-DD) Version xx, YYYY

Figure 14.2.12.1 Series Plot of Mean Actual Value over Time for PD Markers (PD Set)

Parameter: FGF-19 (unit)

Source Table 14.2.12

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the mean of PD markers (unit)
All treatments will be represented on a single page. Each treatment group will be presented as a distinct line type.

Figure 14.2.12.2 Series Plot of Mean Actual Value over Time for PD Markers (PD Set)

Parameter: FGF-19 (unit)

Source Table 14.2.12

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the mean of PD markers (unit)
All treatments will be represented on a single page. Each treatment group will be presented as a distinct line type.
For baseline visit, the mean of CFB will set to zero.

Figure 14.2.12.3 Series Plot of Mean % Change from Baseline over Time for PD Markers (PD Set)

Parameter: FGF-19 (unit)

Source Table 14.2.12

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the mean % change from baseline for each PD marker (unit)
All treatments will be represented on a single page. Each treatment group will be presented as a distinct line type.
For baseline visit, the mean %of CFB will set to zero.

Figure 14.2.12.4.1 Boxplot of HBsAg (IU/mL) over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page.

Figure 14.2.12.4.2 Boxplot of HBsAg (IU/mL) over Time by HBeAg (Safety Set)

HBeAg: Positive

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per HBeAg status (positive and negative) will be represented on a single page.

Figure 14.2.12.4.3 Boxplot of HBsAg (IU/mL) over Time by A Genotype (Safety Set)

A Genotype: Yes

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per A genotype (Yes /No) will be represented on a single page.

Figure 14.2.12.5.1 Boxplot of HBsAg (IU/mL) Change from Baseline by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL) change from baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page.

Figure 14.2.12.5.2 Boxplot of HBsAg (IU/mL) Change from Baseline by HBeAg (Safety Set)

HBeAg: Positive

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL) change from baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per HBeAg status (positive and negative) will be represented on a single page.

Figure 14.2.12.5.3 Boxplot of HBsAg (IU/mL) Change from Baseline by A Genotype (Safety Set)

A Genotype: Yes

Source Table: 14.2.1.3.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBsAg (IU/mL) Change from Baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per A genotype (Yes /No) will be represented on a single page.

Figure 14.2.12.6.1 Boxplot of HBV DNA (Log IU/mL) over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBV DNA (Log IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page.

Figure 14.2.12.6.2 Boxplot of HBV DNA (Log IU/mL) over Time by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBV DNA (Log IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per HBeAg status (positive and negative) will be represented on a single page.

Figure 14.2.12.6.3 Boxplot of HBV DNA (Log IU/mL) over Time by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent HBV DNA (Log IU/mL)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per A genotype (Yes /No) will be represented on a single page.

Figure 14.2.12.7.1 Boxplot of HBV DNA (Log IU/mL) Change from Baseline by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBV DNA (Log IU/mL) change from baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page.

Figure 14.2.12.7.2 Boxplot of HBV DNA (Log IU/mL) Change from Baseline by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBV DNA (Log IU/mL) change from baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per HBeAg status (positive and negative) will be represented on a single page.

Figure 14.2.12.7.3 Boxplot of HBV DNA (Log IU/mL) Change from Baseline by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the HBV DNA (Log IU/mL) Change from Baseline
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per A genotype (Yes /No) will be represented on a single page.

Figure 14.2.12.8.1 Series Plot of Individual Actual Value over Time for HBsAg (IU/mL) by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.1

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBsAg (IU/mL)
All participants per HBeAg status (positive or negative) (one page for HBeAg status) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.8.2 Series Plot of Individual Actual Value over Time for HBsAg (IU/mL) by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.1

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBsAg (IU/mL)
All participants per A Genotype (Yes/No) (one page for A Genotype) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.9.1 Series Plot of Individual Change from Baseline Value for HBsAg (IU/mL) by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.1

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBsAg (IU/mL) Change from baseline
All participants per HBeAg status (positive or negative) (one page for HBeAg status) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.9.2 Series Plot of Individual Change from Baseline Value for HBsAg (IU/mL) by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.1

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBsAg (IU/mL) Change from baseline
All participants per A Genotype (Yes/No) (one page for A Genotype) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.10.1 Series Plot of Individual Actual Value over Time for HBV DNA (Log IU/mL) by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBV DNA (Log IU/mL)
All participants per HBeAg status (positive or negative) (one page for HBeAg status) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.10.2 Series Plot of Individual Actual Value over Time for HBV DNA (Log IU/mL) by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBV DNA (Log IU/mL)
All participants per A Genotype (Yes/No) (one page for A Genotype) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.11.1 Series Plot of Individual Change from Baseline Value for HBV DNA (Log IU/mL) by HBeAg (Safety Set)

HBeAg: Positive

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBV DNA (Log IU/mL) Change from baseline
All participants per HBeAg status (positive or negative) (one page for HBeAg status) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.2.12.11.2 Series Plot of Individual Change from Baseline Value for HBV DNA (Log IU/mL) by A Genotype (Safety Set)

A Genotype: Yes

Source Listing: 16.2.6.2

Programming Note:
The x-axis will represent the actual study time in days.
The y-axis will represent the HBV DNA (Log IU/mL) Change from baseline
All participants per A Genotype (Yes/No) (one page for A Genotype) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.3 Individual ALT over Time (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the ALT (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.4 Individual ALT Change from Baseline (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the ALT (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.5 Boxplot of ALT over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.3.4.2.1

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the ALT (unit)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.6 Individual AST over Time (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the AST (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.7 Individual AST Change from Baseline (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the AST (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.8 Boxplot of AST over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.3.4.2.1

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the AST (unit)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.9 Individual ALP over Time (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the ALP (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.10 Individual ALP Change from Baseline (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the ALP (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.11 Boxplot of ALP over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.3.4.2.1

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the ALP (unit)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.12 Individual GGT over Time (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the GGT (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.13 Individual GGT Change from Baseline (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the GGT (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.14 Boxplot of GGT over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.3.4.2.1

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the GGT (unit)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.15 Individual Total Bilirubin over Time (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the Total Bilirubin (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.16 Individual Total Bilirubin Change from Baseline (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the Total Bilirubin (unit)
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.17 Boxplot of Total Bilirubin over Time by Treatment (Safety Set)

Group 1: EYP001a 200 mg QD + NA daily

Source Table: 14.3.4.2.1

Programming Note:
The x-axis will represent the scheduled study time in days.
The y-axis will represent the Total Bilirubin (unit)
Box Plot will show first quartile, median, third quartile, minimum and maximum.
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.18 Individual Lipid Parameters over Time (Safety Set)

Parameter: total cholesterol
Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the scheduled and unscheduled study time in days.
The y-axis will represent the lipid parameters (unit) accordingly
All participants per treatment group (one page for each treatment group) will be represented on a single page. Each subject will be presented as a distinct line type.

Figure 14.3.4.2.19 Individual HBV DNA versus ALT at Each Visit (Safety Set)

Visit: Screening
Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the HBV DNA (unit).
The y-axis will represent the ALT (unit)
All participants per treatment group per scheduled visit will be represented on a single page. Each subject will be presented as a distinct line type.
Only include the scheduled visits with both HBV DNA and ALT values.

Figure 14.3.4.2.20 Individual HBV DNA versus AST at Each Visit (Safety Set)

Visit: Screening
Group 1: EYP001a 200 mg QD + NA daily

Source Listing: 16.2.8.2.1

Programming Note:
The x-axis will represent the HBV DNA (unit).
The y-axis will represent the AST (unit)
All participants per treatment group per scheduled visit will be represented on a single page. Each subject will be presented as a distinct line type.
Only include the scheduled visits with both HBV DNA and AST values.