CLINICAL RESEARCH IN INFECTIOUS DISEASES

STATISTICAL ANALYSIS PLAN
for
DMID Protocol: 22-0004

Study Title:
Phase 2 Clinical Trial to Optimize Immune Coverage of SARS-CoV-2 Existing and Emerging Variants

COVID-19 VAriant Immunologic Landscape Trial (COVAIL)

NCT05289037

Version 1.0

DATE: 10OCT2023

RESTRICTED

STUDY TITLE

Protocol Number Code:	**DMID Protocol: 22-0004**
Development Phase:	Phase 2
Products:	Moderna [mRNA-1273, mRNA-1273.351, mRNA-1273.529, mRNA-1273.617.2] Pfizer [BNT162b2 (wildtype), BNT162b2 (B.1.351, Beta), BNT162b2 (B1.1.529, Omicron), BNT162b2 bivalent (wildtype and Omicron BA.1) and BNT162b2 bivalent (wildtype and Omicron BA.4/BA.5)] Sanofi [CoV2 preS dTM-AS03 [D614] (prototype), CoV2 preS dTM-AS03 [B.1.351] (Beta), and CoV2 preS dTM-AS03 [D614 + B.1.351] (prototype + Beta)]
Form/Route:	Injection
Indication Studied:	COVID-19
Sponsor:	Division of Microbiology and Infectious Diseases National Institute of Allergy and Infectious Diseases National Institutes of Health
Clinical Trial Initiation Date:	30MAR2022
Clinical Trial Completion Date:	Ongoing
Date of the Analysis Plan:	10 October 2023
Version Number:	1.0

This study was performed in compliance with Good Clinical Practice.

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LIST OF ABBREVIATIONS

AE	Adverse Event
CI	Confidence Interval
CRF	Case Report Form
DMID	Division of Microbiology and Infectious Diseases
DSMB	Data and Safety Monitoring Board
EDC	Electronic Data Capture
ECLIA	Electrochemiluminescence Immunoassay
GMT	Geometric Mean Titer
FRNT	Focus Reduction Neutralization Assay
GMFD	Geometric Mean Fold Drop
GMFR	Geometric Mean Fold Rise
GMR	Geometric Mean Ratio
ICH	International Conference on Harmonisation
IRB	Institutional Review Board
ITT	Intention to Treat
LLOD	Lower Limit of Detection
MedDRA	Medical Dictionary for Regulatory Activities
mITT	Modified Intention to Treat
N	Number (typically refers to subjects)
NIH	National Institutes of Health
PI	Principal Investigator
PP	Per Protocol
PsVNA	Pseudovirus Neutralization Assay
PT	Preferred Term
SAE	Serious Adverse Event
SD	Standard Deviation
SDCC	Statistical and Data Coordinating Center
SMC	Safety Monitoring Committee
SOC	System Organ Class

List of Abbreviations *(continued)*

SOP	Standard Operating Procedures
WHO	World Health Organization

1. PREFACE

The Statistical Analysis Plan (SAP) for "Phase 2 Clinical Trial to Optimize Immune Coverage of SARS-CoV-2 Existing and Emerging Variants" (DMID Protocol 22-0004) describes and expands upon the statistical information presented in the protocol.

This document describes all planned analyses and provides reasons and justifications for these analyses. It also includes sample tables, listings, and figures planned for the final analyses. Regarding the final analyses and Clinical Study Report (CSR), this SAP follows the International Conference on Harmonisation of Technical Requirements for Registration of Pharmaceuticals for Human Use (ICH) Guidelines, as indicated in Topic E3 (Structure and Content of Clinical Study Reports), and more generally is consistent with Topic E8 (General Considerations for Clinical Trials) and Topic E9 (Statistical Principles for Clinical Trials). The structure and content of the SAP provides sufficient detail to meet the requirements identified by the FDA and ICH, while all work planned and reported for this SAP will follow internationally accepted guidelines published by the American Statistical Association and the Royal Statistical Society for statistical practice.

This document contains four sections: (1) a review of the study design, (2) general statistical considerations, (3) comprehensive statistical analysis methods for immunogenicity and safety outcomes, and (4) a list of proposed tables and figures. Within the table, figure, and listing mock-ups (Appendix 1, Appendix 2, and Appendix 3), references to CSR sections are included. Any deviation from this SAP will be described and justified in protocol amendments and/or in the CSR, as appropriate. The reader of this SAP is encouraged to also review the study protocol for details on conduct of the study and the operational aspects of clinical assessments.

2. INTRODUCTION

The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) was first detected in Wuhan, Hubei Province, China in December 2019. The corresponding illness designation, coronavirus disease 2019 (COVID-19), was declared as a pandemic respiratory illness in March 2020 [1]. As of 18 August 2022, it has infected close to 600 million people worldwide and resulted in more than 6 million deaths, including close to 1 million in the United States [1, 2].

Six Phase 3 efficacy trials of SARS-CoV-2 vaccine constructs were conducted and are in long-term follow-up in the U.S. The ModernaTX, Inc mRNA-1273 and Pfizer/BioNTech BNT162b2 mRNA platforms encode for the full-length spike (S) protein of SARS-CoV-2, modified to introduce 2 proline residues to stabilize the S protein (S-2P) in a prefusion conformation, derived from the Wuhan-Hu-1 strain (prototype) [3]. The Janssen Pharmaceutical/Johnson & Johnson COVID-19 Vaccine (Ad26.COV.2) is composed of recombinant, replication-incompetent human adenovirus type 26, encoding a prefusion-stabilized SARS-CoV-2 spike antigen [4]. Studies of the Pfizer and Moderna mRNA vaccines demonstrated high efficacy against all symptomatic and severe disease and received Emergency Use Authorization (EUA) on December 12 and 18, 2020, respectively and full FDA approval on August 23, 2021 and January 31, 2022. Similarly, Janssen Pharmaceuticals reported 66% vaccine efficacy with a single dose and high-level protection against severe disease and death. FDA EUA was issued on February 26, 2021. Novavax's NVX-CoV2373, a recombinant nanoparticle vaccine containing the full-length spike protein received FDA EUA on July 13, 2022[5]. AstraZeneca/Oxford's ChAdOx-2, a recombinant, replication-incompetent chimpanzee adenovirus vector that expresses the spike protein, and Sanofi/GSK's adjuvanted recombinant spike protein vaccine are currently not licensed [6, 7]. Despite widespread vaccine distribution and availability, and high coverage among adults in the United States (87.4% of the US population ≥ 18 years of age have received at least one dose) [8], ongoing waves of the pandemic continue to cause significant disease burden, notable for increasing incidence of breakthrough infections in fully vaccinated individuals. Studies have suggested that vaccine protection against symptomatic SARS-CoV-2 infection wanes over time though protection against severe COVID-19 outcomes remains relatively intact [9, 10, 11, 12]. However, the evolution of variant strains may favor immune escape or reinfection among previously infected or vaccinated individuals. A variant first identified in late 2020 (B.1.351), is associated with increased transmission, higher viral burden, and possibly increased mortality in infected persons [13]. Another variant identified in December 2020 (B.1.617.2) is associated with increased transmission, higher risk of severe disease and hospitalization than the ancestral strain [14]. B.1.617.2 was the dominant strain worldwide before being replaced by B.1.1.529 in November 2021 which is characterized by a replication advantage, higher re-infection rates and evasion of humoral immunity mediated by more than 30 mutations in the spike protein [15].

Recent data suggest that a booster dose given as either a third dose for most vaccines (mRNA, protein and ChAdOx-2) or a second dose for Janssen improved vaccine effectiveness against new variants in the short term [16, 17, 18]. Data on immunogenicity with booster doses of BNT162b2, mRNA-1273, and AD26.COV2.S demonstrated higher antibody titers to D614G after either homologous and heterologous prime-boost combinations [19]. The result is better neutralizing activity against B.1.351, B.1.617.2 and B.1.1.529 [20, 21, 22]. In an open label phase 2 study of participants who received a single 50 mcg booster dose of mRNA-1273 ≥ 6 months after a primary series, a 13-fold rise in antibody titers against D614G were noted from pre-boost levels as well as a 17-fold rise in in titers against the B.1.617.2 variant [20]. In another study, participants boosted with 50 mcg of mRNA-1273 demonstrated ID_{50} GMTs against the omicron variant 20 times higher than those described 1 month after the second vaccination of the primary series; these titers were 2.9 times lower than titers for the D614G variant [21].

The Sanofi/GSK adjuvanted recombinant prefusion spike protein vaccine (CoV2 preS dTM-AS03 [D614]) was developed from an established, platform used for influenza vaccines. A phase 2 study showed the safety and immunogenicity of a two-dose primary series of CoV2 preS dTM-AS03 [D614] in adults who were SARS-CoV-2 naïve and those who were previously infected [23]. The dose-finding results informed selection of the adjuvanted formulation with 10 mcg antigen as primary dose and the adjuvanted formulation with 5 mcg antigen as boost dose for further evaluation. Neutralizing antibody titers were higher in non-naïve participants after one dose than in naïve participants after two doses. In addition, 5 mcg booster dose increased neutralizing antibody titers when used as a heterologous (18-30 times) or homologous (≥ 84 times) boost compared to pre boost [24]. Interim results from an international phase 3 trial showed 57.9% (95% confidence interval 26.5% to 76.7%) efficacy of the two-dose primary series against any symptomatic disease and 75% efficacy against moderate or severe COVID-19 with an acceptable safety and reactogenicity profile [24].

FDA EUA was subsequently issued for a booster 30 ug dose of Pfizer BNT162b2 on September 24, 2021, 50 ug booster dose of Moderna mRNA-1273 on October 21, 2021, and a 5×10^{10} viral particles booster dose of J&J AD26.COV2 on October 21, 2021. This was recommended for adults 18 years of age and older who received a FDA authorized and CDC recommended primary booster series with an mRNA vaccine at least 5 months prior or a primary series with AD26.COV2 at least 2 months prior. The Sanofi/GSK vaccine is currently undergoing regulatory review for approval of their vaccine candidate for the prevention of COVID-19.

Published reports have also provided some early evidence for the safety and immunogenicity of a fourth dose of an mRNA vaccine. An open-label study of healthcare workers in Israel suggests that a fourth dose was well-tolerated and restored neutralizing antibody titers for variants to levels similar to those after a third dose [25]. Notably, this study did not include older adults, and rates of infection with B.1.1.529 (omicron) were similar for the control and Pfizer or Moderna 4th dose groups. In a retrospective study conducted by the Israeli Ministry of Health, of 1,138,681 adults aged 60 to 100 years of age, a fourth dose of mRNA was associated with 2 times lower rate of confirmed infection 12 or more days after vaccination compared to those who had only received 3 doses and the rate of severe illness was lower by a factor of 4.3 [26]. However, the added protection of an additional booster shot is small in absolute terms since less than 0.1% mortality was noted after a 3rd dose. Additionally, a separate study of adults age 60 or older suggests that vaccine effectiveness of a fourth dose against infection wanes quickly declining from a peak of 64% to 29% within 2 months though effectiveness of >73% was maintained against severe disease [27].

On March 29, 2022, the FDA authorized an additional booster dose of an mRNA vaccine for adults 50 years of age or older, or for those with immunocompromising conditions (12 years and older with immunocompromising conditions could receive a second booster with the Pfizer vaccine and 18 years and older could receive a second booster with the Moderna vaccine). Subsequent to this authorization, the CDC updated vaccination guidance to permit an additional booster dose for these groups in recognition of the increased and ongoing risk for severe disease in these populations.

The emergence of variant strains has raised concerns about the breadth and duration of immunity and protection achieved by the current vaccines. Studies of vaccine immunogenicity for early variants of concern demonstrated those vaccinated to prototype vaccine may have reduced neutralizing activity to the variants [28]. For variants like B.1.351, pivotal studies testing both viral vector and adjuvanted protein technologies had lower efficacy in regions where B.1.351 was known to be circulating [29, 30]. Moreover, sera from individuals vaccinated with mRNA-based vaccines had a 6-to-9-fold reduction in neutralizing activity against a B.1.351-matched pseudovirion relative to a Wuhan-matched pseudovirion [10, 11]. Similarly, sera from

individuals vaccinated with mRNA-1273 had an 8-fold reduction in neutralizing activity against the B.1.617.2 variant compared to titers against the D614G variant [21].

Studies have also demonstrated 6.7 fold reduction in neutralizing activity for Pfizer BNT162b2 against B.1.351 with two doses of Pfizer BNT162b2 [31]. Additionally, in one assessment of sera obtained from individuals vaccinated with Pfizer BNT162b2, obtained one month after the second dose, a 25 fold reduction in neutralizing antibody geometric mean titers against B.1.1.529 was noted compared to the wild-type virus [32]. Neutralizing activity has been shown to be partially restored by vaccination with a third dose of Pfizer BNT162b2. However, even with three doses, neutralizing activity was 4 times lower against B.1.1.529 and 3 times lower against B.1.351 compared to B.1.617.2 and 7-8 times lower compared to wild-type virus [33]. Thus, additional vaccinations, higher doses or variant specific vaccines may improve protection against current and emerging variants of concern.

Vaccine manufacturers have performed some trials of candidate variant vaccines. For example, a phase 2a open label clinical trial to examine the immunological benefit of boosting subjects previously vaccinated 6 months prior with mRNA-1273 with mRNA-1273.351, a B.1.351 strain-specific mRNA construct (50 mcg), or mRNA-1273.211 (50 mcg) showed 61.6 and 33.7 times higher titers against B.1.351 compared to titers from participants one month after the second dose of the primary series, with similar titers against B.1.617.2 [22]. Similar findings were seen from a study of a boost with a bivalent mRNA-1273.213 vaccine (a 1:1 mix of beta and delta variant mRNA) [21].

Similarly, several BNT162b2-based variant vaccines that target these variants are also being developed including BNT162b2 (B.1.617.2), BNT162b2 (B.1.351) and BNT162b2 (B.1.1.529). In addition, Sanofi has developed a SARS-CoV2 prefusion Spike delta TM with AS03 adjuvant (CoV2 preS dTM-AS03 [B.1.351]) monovalent vaccine and a SARS-CoV2 prefusion Spike delta TM with AS03 adjuvant bivalent vaccine (D614/B.1.351 (CoV2 preS dTM-AS03 [D614 + B.1.351]). In a nonhuman primate model, these vaccines used as boosters induced cross-neutralizing antibodies against variants of concern including Delta and Omicron [34].

However, current efforts are directed towards modifying the existing vaccines to include the current circulating Omicron variant, though this may not be the circulating variant during the next wave of COVID-19. It is therefore important to look beyond Omicron, and understand the immunologic landscape and how we can use prototype and variant vaccines alone or in combination to address emerging variants.

For seasonal influenza viruses, the antigenic, viral genetic and epidemiological data guide annual updates of the seasonal influenza virus vaccines. Antigenic cartography is a visualization tool aimed at understanding the relationship among SARS-CoV-2 variants of concern (VOCs) in terms of their ability to induce cross-neutralizing antibodies. A recent study using the antigenic mapping approach showed that Omicron represents the first widely circulating new major SARS-CoV-2 variant [35]. Though the dimensions of the cartography, representing new VOCs that could circulate in the future, remain largely unknown, a better understanding of diverse immune landscape induced by vaccination and natural infection could lead, along with vaccine modification, to more durable and broadly protective immunity. The update in vaccine formulations proposed in this study will still rely on similar platforms, route of administration and dosing, though will include an update of immunogens with VOCs alone or in combination that could result in broadly cross reactive serological and cellular immune responses especially in groups with high risk for mortality (e.g., older adults).

This phase 2 clinical trial will evaluate the safety and immunogenicity of additional doses of vaccine to expand and optimize immune coverage of the existing and emerging antigenic space. Utilizing several prototype and variant specific COVID-19 vaccines based on mRNA and other approved platforms, we propose to evaluate innate, cellular, and humoral immune responses elicited from different vaccine

candidates. As part of an adaptive design, we anticipate adding groups with other variant-lineage spike proteins and other vaccine platforms, subject to availability.

2.1. Purpose of the Analyses

These analyses will assess the immunogenicity and safety of additional doses of prototype and variant (alone or in combination) vaccine candidates in previously vaccinated participants with or without prior SARS-CoV-2 infection, and will evaluate innate, cellular, and humoral immune responses to inform on how to shift the immune response to cover new variants as they emerge.

Data may be disseminated to public health officials and partners as needed and included in publications and presentations to inform the global scientific community. Early analyses will include safety and immunogenicity as described in Protocol v5.0 Sections 9.4.6.1, 9.4.6.2, and 9.4.6.3. Further, the protocol team will review data periodically to confirm no halting criteria have been met as described in Protocol v5.0 Section 7.1.1.

3. STUDY OBJECTIVES AND ENDPOINTS

Table 1: Objectives and Endpoints (Outcome Measures)

OBJECTIVES	ENDPOINTS (OUTCOME MEASURES)
Primary	
• To evaluate humoral immune responses of candidate SARS-CoV-2 variant vaccines	• Response rate and magnitude of SARS-CoV-2-specific antibody binding and neutralization titers in serum samples as assessed via a range of assays at all timepoints
Secondary	
• To evaluate the safety of candidate SARS-CoV-2 variant vaccines	• Local and systemic solicited Adverse Events for 7 days following each vaccine dose • Unsolicited Adverse Events from Dose 1 to 28 days following each vaccine dose • SAEs, MAAEs, NOCMCs, AESIs, and AEs leading to withdrawal from the study from Dose 1 to 12 months after the last vaccine dose
Exploratory	
• To assess, in at least a subset of samples, the B cell immune response of candidate SARS-CoV-2 variant vaccines	• Magnitude, phenotype, and percentage of SARS-CoV-2-specific B cells, as measured by flow cytometry and targeted B cell subset analysis at selected time points post-vaccination
• To assess, in at least a subset of samples, the SARS-CoV-2 spike protein-specific T cell responses of candidate SARS-CoV-2 variant vaccines	• Magnitude, phenotype, and percentage of cytokine-producing S protein T cells as measured by flow cytometry at selected time points post-vaccination.
• To assess, in at least a subset of samples, the magnitude, phenotype, and percentage of innate immune cells with candidate SARS-CoV-2 variant vaccines	• Magnitude, phenotype, and percentage of innate immune cells as measured by flow cytometry at D1 and 14 days after each vaccination
• To assess, in at least a subset of samples, the function potential of SARS-CoV-2 specific antibodies to mediate Fc-effector functions	• Characterization of antigen-specific antibody by a) subclass, b) isotype, c) ability to interact with Fc receptors, d) innate immune

OBJECTIVES	ENDPOINTS (OUTCOME MEASURES)
across candidate SARS-CoV-2 variant vaccines	receptors, e) lectin-like molecules, and f) lectins at different times post-vaccination • Functional Fc effector assessments which may include quantification of antigen-specific antibody-mediated NK cell activation (ADCC-NK) levels, antibody-dependent cellular phagocytosis (ADCP) levels, antibody-dependent complement deposition (ADCD) and/or antibody-dependent neutrophil activation/phagocytosis levels at different times post-vaccination
• To evaluate breakthrough SARS-CoV-2 infection by sequencing strains for variant spike lineage and assessing anti-nucleocapsid serology	• Sequence analysis on breakthrough NAAT-confirmed SARS-CoV-2 strains at any time post-vaccination • Anti-nucleocapsid immunoassay at different times post-vaccination

3.1. Study Definitions and Derived Variables

For calculations using the baseline value, the value obtained pre-fourth vaccination (Day 1) will be used.

If a value falls below the lower limit of detection for the immunogenicity assay, the value will be replaced by one-half the lower limit of detection in analyses.

Subjects infected at baseline will be defined as by either self-report or positive for N-antibody.

Major protocol deviations will be defined by the sponsor.

Unless otherwise noted Omicron refers to B.1.1.529/BA.1.

4. INVESTIGATIONAL PLAN

4.1. Overall Study Design and Plan

This is a Phase 2 randomized, adaptive, open label, non-placebo controlled multi-site, multi-stage clinical trial in individuals, 18 years of age and older, who are in stable state of health, have received a complete authorized/approved vaccine series (primary series + booster either with homologous or heterologous vaccine products) and meet all other eligibility criteria.

Approximately 1500 subjects will be enrolled at up to 30 clinical research sites. At enrollment, subjects will be stratified by i) age (18-64 and ≥ 65 years of age) (however arms 16 and 17 or stage 4 will only enroll participants between the ages of 18-49 years) and ii) confirmed prior SARS-CoV-2 infection, and randomly assigned to one of several study arms of variant vaccines. The study will target the enrollment of approximately 45% older adults (≥ 65 years of age) for stages 1, 2, and 3. Additionally, the study will target to enroll approximately 20% of participants with a history of confirmed SARS-CoV-2 infection. It is estimated that another 10-30% will have undiagnosed prior infection. Taken together, we anticipate about 40% of the total enrolled participants will have prior infection. The study team will decide, based on latest epidemiology, if enrollment of participants in any particular groups are slowed in order to ensure good representation of previously infected and not previously infected.

The adaptive design of this study will include additional arms, an increase in sample size, or additional vaccine doses or different dosing and provide rapid information about the immunogenicity and the safety of candidate SARS-CoV-2 variant vaccines to inform near term public health policy. This trial will provide proof of concept on how variant vaccines could shift the immune response to become more specific to the VOCs' antigens or broaden the antigenic landscape for emergent variants.

Screening can occur up to 28 days prior to the first dose of study product or on Day 1 prior to administration of Dose 1. Safety will be assessed during the study and blood will be drawn for immunogenicity assays at enrollment and in-person follow-up visits. Swabs will be self-collected or collected by staff at unscheduled illness visits to evaluate breakthrough SARS-CoV-2 infection (symptomatic infection or asymptomatic infection with a positive SARS-CoV-2 test outside the study). A summary of the four currently planned stages can be found in Table 2.

4.2. Discussion of Study Design, Including the Choice of Control Groups

This phase 2 study is an open-label study, without administration of a placebo formulation. An open-label study will facilitate the need for rapid review and dissemination of study data for public health reasons. Safety findings are not expected to be dissimilar from Phase 1/2/3 studies conducted for similar vaccine constructs. Randomization will improve comparisons between different arms. Each stage will contain an arm with a monovalent prototype vaccine (except for stage 4).

Selected arms will assess 2 study doses of vaccine candidates to assess if 2 doses provide a more durable and specific response to variant viruses.

An interval of 4 months was chosen since a recent study performed by the investigators showed that an interval of 3 months between primary series and boost had acceptable safety and immunogenicity responses [19].

4.3. Selection of Study Population

All participants will have received a complete (primary and booster) US approved/authorized vaccine series. The US population has received either homologous primary series and boost (i.e. Moderna mRNA-1273 for 1st dose, second dose, and booster), or heterologous boosters, and some were infected with SARS-CoV-2 either prior to or after vaccination. This trial will enroll this immunologically diverse population, to ensure any findings are applicable to the larger population.

Based on CDC data about use of primary vaccine or boost (https://covid.cdc.gov/covid data-tracker/#vaccinations_vacc-total-admin-rate-total), it is estimated that of people in the US that have received a primary vaccine series and booster:

- 50% will have received Pfizer primary series and Pfizer boost,
- 37% will have received Moderna primary series and Moderna boost,
- 4% will have received Pfizer primary series and Moderna boost,
- 3% will have received Moderna primary series and Pfizer boost,
- 1% will have received Janssen primary series and Janssen boost,
- 2% will have received Janssen primary series and Moderna boost,
- 2% will have received Janssen primary series and Pfizer boost.

Additionally, approximately 20% of the US population has been infected with SARS-CoV-2, likely higher with asymptomatic infections [36].

It is anticipated the enrollment into this trial will be similar to these proportions.

Subject Inclusion and Exclusion Criteria must be confirmed by a study clinician, licensed to make medical diagnoses and listed on the Form FDA 1572. No exemptions are granted on Subject Inclusion or Exclusion Criteria in DMID-sponsored studies.

Inclusion Criteria

Participants must meet all the following criteria to be eligible to participate in this study:

1. Individuals ≥ 18 years of age at the time of consent (18-49 years for stage 4).
2. Confirmed receipt of a complete primary and booster COVID-19 vaccine series, either homologous or heterologous, with an FDA authorized/approved vaccine at least 16 weeks prior to study vaccine dose 1
3. Willing and able to comply with all scheduled visits, vaccination plan, laboratory tests and other study procedures
4. Determined by medical history, targeted physical examination and clinical judgement of the investigator to be in stable state of health

   Note: Participants with pre-existing stable chronic medical conditions defined as condition not requiring significant change in therapy or hospitalization for worsening disease within 4 weeks form enrollment, can be included at the discretion of the investigator.

Exclusion Criteria

Participants meeting any of the following criteria will be excluded from participation in this study:

1. Confirmed SARS-CoV-2 infection < 16 weeks prior to any study vaccine dose
2. Pregnant and breastfeeding participants
3. Prior administration of an investigational coronavirus vaccine at any time or SARS-CoV-2 immunoglobulin, monoclonal antibody or plasma antibody therapy in the preceding 3 months

   Note: Subjects that participated in clinical trials of products that are now FDA approved/authorized are allowed to participate.
4. Current/planned simultaneous patriation in another interventional study or receipt of any investigational study product within 28 days prior to vaccine study dose(s)
5. A history of anaphylaxis, urticaria, or other significant adverse reaction requiring medical intervention after receipt of a vaccine, polyethylene glycol (PEG), or nanolipid particles.
6. A history of myocarditis or pericarditis at any time prior to enrollment (for subjects in stages 1, 2 and 4).
7. Received or plans to receive a vaccine within 28 days prior to or after any dose of study vaccine.

   Note: Receipt of seasonal influenza vaccine is allowed at any time
8. Bleeding disorder diagnosed by a healthcare provider (e.g., factor deficiency, coagulopathy, or platelet disorder requiring special precautions) or bleeding difficulties with intramuscular injections or blood draws.
9. Current or previous diagnosis of an immunocompromising condition or other immunosuppressive condition.
10. Advanced liver or kidney diseases.
11. Advanced (CD4 count < 200) and/or untreated HIV, untreated Hepatitis B or untreated Hepatitis C.
12. Received oral, intramuscular or intravenous systemic immunosuppressants, or immune-modifying drugs for >14 days in total within 6 months prior to any study vaccine dose (for corticosteroids ≥ 20 mg/day of prednisone equivalent).

    Note: Topical medications are allowed.
13. Received immunoglobulin or blood-derived products, within 3 months prior any study vaccine dose.
14. Received chemotherapy, immunotherapy or radiation therapy within 6 months prior to any study vaccine dose.
15. Study personnel or an immediate family member or household member of study personnel.
16. Is acutely ill or febrile 72 hours prior to or at vaccine dosing (fever defined as ≥ 38.0°C/100.4°F). Participants meeting this criterion may be rescheduled within the relevant window periods.

    Note: Afebrile participants with minor illnesses can be enrolled at the discretion of the Investigator, as long as the illness is not suggestive of COVID-19.
17. Plan to receive a COVID-19 booster vaccine outside of the study within the next 180 days. (for subjects in Stage 4 only)

Exclusion of Specific Populations

The effects of SARS-CoV-2 vaccines on the developing fetus are not known, though there are data to suggest that mRNA vaccines are safe. Pregnant subjects will not be eligible for the trial as the immune responses to vaccines can be different than non-pregnant subjects. Children will not be included in this trial as presently there are limited safety data in adults for the variant strains.

4.4. Treatments

4.4.1. Treatments Administered

Seventeen treatment arms administer various combinations of COVID-19 vaccines (Table 2).

4.4.2. Identity of Investigational Product(s)

Products: mRNA-1273 (Prototype), mRNA-1273.351 (Beta), mRNA-1273.617.2 (Delta), and mRNA-1273.529 (Omicron)

mRNA-1273 (0.2 mg/mL) is an LNP dispersion containing an mRNA that encodes for the pre-fusion stabilized S protein of the Wuhan-Hu-1 strain of SARS-CoV-2. mRNA-1273 consists of an mRNA Drug Substance that is manufactured into LNPs composed of the proprietary ionizable lipid, SM-102, and 3 commercially available lipids, cholesterol, 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC), and PEG2000 DMG.

mRNA-1273.351 (0.1 mg/mL) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the B.1.351 (Beta) variant SARS-CoV-2 strain.

mRNA-1273.617.2 (0.2 mg/mL) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the B.1.617.2 (Delta) variant SARS-CoV-2 strain.

mRNA-1273.529 (0.2 mg/mL) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the B.1.1.529 (Omicron) variant SARS-CoV-2 strain.

BNT162b2 (wildtype), BNT162b2 (B.1.351, Beta), BNT162b2 (B1.1.529, Omicron), BNT162b2 bivalent (wildtype and Omicron BA.1) and BNT162b2 bivalent (wildtype and Omicron BA.4/BA.5)

BNT162b2 (500 mcg/mL for stage 2) is a preservative-free, sterile dispersion of RNA formulated in LNP in aqueous cryoprotectant buffer. mRNA encodes for the pre fusion stabilized S protein of the ancestral strain of SARS-CoV-2.

BNT162b2 (B.1.351) (500 mcg/mL for stage 2) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the B.1.351 (Beta) variant SARS-CoV-2 strain.

BNT162b2 (B.1.1.529)(500 mcg/mL for stage 2) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the B.1.1.529 (Omicron) variant SARS-CoV-2 strain.

BNT162b2 bivalent (wildtype and Omicron BA.1 100mcg/mL for stage 4) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the Omicron BA.1 variant SARS-CoV-2 strain and the ancestral strain of SARS-CoV-2..

BNT162b2 bivalent (wildtype and Omicron BA.4/BA.5 100mcg/mL for stage 4) is formulated in the same way but contains mRNA that encodes for the prefusion stabilized S protein of the Omicron BA.4/BA.5 variant SARS-CoV-2 strain and the ancestral strain of SARS-CoV-2.

CoV2 preS dTM-AS03 [D614] (prototype), CoV2 preS dTM-AS03 [B.1.351] (Beta), and CoV2 preS dTM-AS03 [D614 + B.1.351] (prototype + Beta)

CoV2 preS dTM-AS03 [D614] (Recombinant COVID-19 Vaccine 20 mcg/mL + AS03) is a liquid formulation made of recombinant protein placed in a formulation buffer and to be mixed with equal volumes of AS03 adjuvant (supplied separately) at the study site before administration. The antigen solution contains the Spike protein sequence of the ancestral strain of SARS-CoV-2. AS03 is an adjuvant system containing α-tocopherol and squalene in an oil/water emulsion. For this formulation, the antigen and AS03 vials are not packaged in a carton box together but are supplied as individual vials.

CoV2 preS dTM-AS03 [B.1.351] (Recombinant COVID-19 Vaccine B1.351 20 mcg/mL+ AS03) is formulated in the same way but contains the Spike protein sequence of the B.1.351 (Beta) variant SARS-CoV-2 strain. Both antigen and AS03 vials are packaged in a carton box.

CoV2 preS dTM-AS03 [D614 + B.1.351] (Recombinant COVID-19 Bivalent Vaccine 10/10 mcg/mL + AS03) is formulated in the same way but contains the Spike protein sequences of the ancestral and B.1.351 (Beta) variant SARS-CoV-2 strains. Both antigen and AS03 vials are packaged in a carton box.

Diluent: 0.9% NaCl for injection, USP

The USP grade 0.9% NaCl or normal saline for injection is a sterile, nonpyrogenic, isotonicsolution; each mL contains NaCl 9 mg. It contains no bacteriostatic agent, antimicrobial agent,preservatives, or added buffer and is supplied only in single-dose containers. This product should be used to dilute the vaccine to the desired concentration.

4.4.3. Method of Assigning Subjects to Treatment Groups (Randomization)

Subjects will be randomized to study intervention in an equal allocation ratio within each stage. The study will be open label and study sites will administer product to a subject according to which study arm the subject has been assigned. Sites will be asked to recruit for all arms within a stage.

4.4.4. Selection of Doses in the Study

The dosages of mRNA vaccines selected are those authorized for booster doses under EUA, and previously shown in prior studies to elicit good immune responses with no major safety concerns.

In an open label study of participants in the Moderna Phase 3 clinical trial who received a single 50 mcg booster dose of mRNA-1273 ≥ 6 months after a primary series, a 13 fold rise in antibody titers against D614G was noted from pre-boost levels as well as a 17-fold rise in in titers against the B.1.617.2 variant [20]. This is now the CDC recommended dose for booster vaccinations with the Moderna mRNA-1273 product in immunocompetent adults, to be given at least 5 months from the last inoculation in the primary series [37]. Similarly, in a recent study, boosting with a 50 mcg total antigen dose of a bivalent mRNA-1273.213 vaccine (a 1:1 mix of beta and delta variant mRNA) produced only modestly lower antibody titers than using a 100 mcg booster dose [21]. A separate study evaluating safety and immunogenicity of multiple boost strategies suggests that a heterologous boost strategy generates antibody and neutralizing responses and that 100 mcg of mRNA-1273 (the authorized dose at the time) is likely higher than needed for a booster dose after primary mRNA series [38]. In addition, surveillance data indicate that following an mRNA boost, local and systemic reactions are less common and myocarditis is rarely reported, suggesting that the currently authorized doses are safe [39]. These findings support the evaluation of mRNA-1273, mRNA-1273.351, mRNA-1273.617.2 and mRNA-1273.529 at total dosages of 50 mcg per vaccination.

For BNT162b2, the dose is the same for primary or booster doses in adults. In an open-label clinical study, immunogenicity and safety of a fourth dose of either 30 mcg of BNT162b2 (Pfizer–BioNTech) or 50 mcg of mRNA-1273 (Moderna) administered 4 months after the third dose was assessed in 154 and 120 health care workers, respectively [25]. After the fourth dose, both messenger RNA (mRNA) vaccines increased neutralizing antibody titers to D614G, B.1.617.2 and B.1.1.529 by a factor of 9 to 10 and were slightly higher than those achieved after the third dose [25]. There were no significant adverse events with only mild system and local reactogenicity reported which was comparable with previous doses of mRNA vaccines. The bivalent booster of BNT162b2 was authorized by the FDA based on pre-clinical data (Omicron BA.4/BA.5 + prototype) [40].

For CoV2 preS dTM-AS03 vaccines, none are currently approved. The dose used for booster vaccination is as established in the phase 2 trial and is the adjuvanted formulation with 5 mcg for any variant vaccine candidate in stage 3 [24]. That booster dose increased neutralizing antibody titers when used as a heterologous (18-30 times) or homologous (≥ 84 times) boost [24]. However, no data exist on CoV2 preS dTM-AS03 vaccines as a second boost after primary series with mRNA or adenoviral vectored vaccines.

4.4.5. Selection and Timing of Dose for Each Subject

Subjects will be randomly assigned to a study intervention. Subjects assigned to the arm receiving 2 doses will receive dose 2 eight weeks after dose 1.

4.4.6. Blinding

This study is unblinded.

4.4.7. Prior and Concomitant Therapy

Concomitant medications include prescription medications and vaccinations taken within 28 days of screening or Day 1. Topical, ophthalmic and OTC medications, herbal supplements and vitamins will not be collected. This information is asked to assess eligibility. Only COVID-19 vaccination received at any time in the past will be captured in the trial database. After enrollment, immunosuppressant drugs, COVID-19 vaccines received outside of the study as well as COVID-19 related treatment and prophylaxis should be reported at any time during study participation and captured in the trial database. At each study visit, if there are new SAEs, concomitant medications should be recorded on the appropriate DCF and not included in the database unless these are immunosuppressant drugs, COVID-19 vaccines received outside of the study or COVID-19 related treatment and prophylaxis.

4.4.8. Treatment Compliance

Subjects in all treatment arms except for treatment arm 3 will receive a single dose of study product administered in the clinic. Subjects in treatment arm 3 will receive 2 total doses (Days 1 and 57) of study product administered in the clinic.

4.5. Immunogenicity and Safety Variables

Immunogenicity

Humoral Immunogenicity Assays:

The following humoral immunogenicity assays may be performed:

- IgG ELISA or Multiplex MSD antibody binding assays to SARS-CoV-2 proteins (may include nucleocapsid protein, and multiple variant Receptor Binding Domains (RBD) and variant spike proteins).
- Neutralization assays using SARS-CoV-2 variant specific S-pseudotyped viruses.
- Neutralization assays using different strains of live SARS-CoV-2.
- Characterization of antigen-specific antibody by a) subclass, b) isotype, c) ability to interact with Fc receptors, d) innate immune receptors, e) lectin-like molecules and f) lectins at different times post-vaccination.
- Functional Fc effector assays which may include quantification of antigen specific antibody-mediated NK cell activation (ADCC-NK) levels, antibody-dependent cellular phagocytosis (ADCP) activity, Antibody-dependent complement deposition (ADCD) and/or Antibody-dependent neutrophil activation/phagocytosis activity.

Cellular Immunology Assays:

This trial may also investigate innate, B and T cell immune responses using multiparametric flow cytometry. Refer to the protocol-specific immune monitoring plan for details.

Safety

All safety endpoints for this trial are obtained by reporting of adverse events.

- New symptoms will be queried with broad open-ended questions at the Day 8 telephone call and by specifically asking about symptoms of chest pain, shortness of breath or palpitations that may represent myocarditis and/or pericarditis.
- Data on new medical conditions, doctors' office visits (outside of routine care), emergency room visits, and hospitalizations will be collected.
- Memory Aid: All subjects will complete a Memory Aid from the time of each vaccination through 7 days after each vaccination. Subjects will be asked to confirm completion of the Memory Aid and will be queried on the presence of any grade 3 symptoms. Based on the information provided, subjects may be asked to return to the clinic for evaluation. Fourteen days after each vaccination, Memory Aids are reviewed thoroughly with the subject and confirmed data recorded in the CRF.

As these vaccines are similar to licensed vaccines, there are no laboratory assessments for safety that will be done for this trial.

Adverse Events

AE means any untoward medical occurrence associated with the use of an intervention in humans, whether or not considered intervention-related [21 CFR 312.32 (a)]. An AE can therefore be any unfavorable and unintended sign, symptom or disease temporally associated with the use of medicinal (investigational) product.

Any medical condition that is present at the time that the subject is screened will be considered as baseline and not reported as an AE. However, if the severity of any pre-existing medical condition increases, it should be recorded as an AE.

AEs can be further divided into solicited AEs and unsolicited AEs. Solicited AEs are those that are described in the package insert as local or systemic reactogenicity occurring in the first 7 days after vaccination. Unsolicited AEs are those events that the subject reports occurring without being queried about the specific event.

AEs will be assessed for severity and relationship to study intervention. Reporting of all AEs, solicited and unsolicited, will occur during the period from study product administration on Day 1 through 28 days after each vaccination. After 28 days post last vaccination through the end of study, only SAEs, Protocol Specified AESIs, MAAEs, NOCMCs, and AEs leading to withdrawal from the study will be reported.

All AEs, solicited and unsolicited, will be captured on the appropriate DCF. Solicited AEs will be regarded as related to the study product and will not require separate entry into the AE log. Information to be collected for unsolicited AEs includes event description, date of onset, assessment of severity, relationship to study product and alternate etiology (assessed only by those with the training and authority to make a diagnosis and listed on the Form FDA 1572 as the participating site PI or appropriate sub-investigator), date of resolution, seriousness, and outcome. AEs occurring during the study-collection and reporting period will be documented appropriately regardless of relationship.

AEs will be followed to resolution or stabilization.

Solicited Adverse Events

Solicited AEs are anticipated local and systemic AEs for which consistent collection of information is desired. Study clinicians will follow and collect resolution information for any reactogenicity symptoms that are not resolved within 7 days.

Solicited AEs (i.e., reactogenicity) will be collected using a memory aid and confirmed data recorded on the appropriate DCF from the time of each vaccination through 7 days post each vaccination.

For this study, solicited AEs will be:

- Injection site Pain
- Injection site Erythema
- Injection site Edema/Induration
- Headache
- Fatigue
- Myalgia
- Arthralgia
- Nausea
- Fever
- Chills

Unsolicited Adverse Events

All AEs spontaneously reported by the subject and/or in response to an open question from study staff or revealed by observation, physical examination or other diagnostic procedures must be recorded on the appropriate DCF.

Unsolicited AEs of all severities will be reported from the time of study product administration through 28 days post each vaccination.

After 28 days post last vaccination through the end of study, only SAEs, AESIs, NOCMCs, MAAEs, and AEs leading to withdrawal from the study will be reported.

Serious Adverse Events

An SAE is defined in 21 CFR 312.32 as follows: "An AE or suspected adverse reaction is considered serious if, in the view of either the participating site PI or appropriate sub-investigator or the sponsor, it results in any of the following outcomes:

- Death,
- a life-threatening AE,
- inpatient hospitalization or prolongation of existing hospitalization,
- a persistent or significant incapacity or substantial disruption of the ability to conduct normal life functions,
- or a congenital anomaly/birth defect.

Important medical events that may not result in death, be life-threatening, or require hospitalization may be considered serious when, based upon appropriate medical judgment, they may jeopardize the patient or subject and may require medical or surgical intervention to prevent one of the outcomes listed in this definition. Examples of such medical events include allergic bronchospasm requiring intensive treatment in an emergency room or at home, blood dyscrasias or convulsions that do not result in inpatient hospitalization, or the development of drug dependency or drug abuse."

"Life-threatening" refers to an AE that at occurrence represents an immediate risk of death to a subject. An event that may cause death if it occurs in a more severe form is not considered life-threatening. Similarly, a hospital admission for an elective procedure is not considered an SAE.

All SAEs, as with any AE, will be assessed for severity and relationship to study intervention.

All SAEs will be recorded on the appropriate SAE DCF.

All SAEs will be followed through resolution or stabilization by a study clinician, licensed to make medical diagnoses and listed on the Form FDA 1572 as the participating site PI or appropriate sub-investigator.

All SAEs will be reviewed and evaluated by DMID and will be sent to the DSMB (for periodic review unless related) and IRB/IEC as needed.

Adverse Events of Special Interest (AESIs)

AESIs represent any events for which additional data (besides the standard AE data) are desired. An adverse event of special interest (serious or nonserious) is one of scientific and medical concern specific to the sponsor's product or program, for which ongoing monitoring and rapid communication by the investigator to the sponsor is required. Such an event may require further investigation in order to characterize and understand it. Depending on the nature of the event, rapid communication by the trial sponsor to other parties (e.g., regulators) may also be required. These may be at the request of the regulatory agency, industry partner or DMID, and driven by a regulatory requirement, or known or potential risk from the product or class.

Protocol Specified AESIs are listed in Appendix A of the protocol. In addition, for stage 3, AESIs will also include a list of pIMD.

Potential immune-mediated diseases (pIMDs)

pIMDs are a subset of AESIs that include autoimmune diseases and other inflammatory and/or neurologic disorders of interest which may or may not have an autoimmune etiology. AESIs that need to be recorded and reported as pIMDs for Stage 3 participants are listed in Appendix A of the protocol.

However, the investigator will exercise their medical and scientific judgement in deciding whether other diseases have an autoimmune origin (that is pathophysiology involving systemic or organspecific pathogenic autoantibodies) and should also be recorded as a pIMD.

When there is enough evidence to make any of the diagnoses mentioned in Appendix A of the protocol, the AESI must be reported as a pIMD. Symptoms, signs or conditions which might (or might not) represent the above diagnoses, should be recorded and reported as AEs but not as pIMDs until the final or definitive diagnosis has been determined, and alternative diagnoses have been eliminated or shown to be less likely.

New Onset of Chronic Medical Conditions (NOCMCs)

NOCMCs are defined as any new ICD diagnosis (per current International Statistical Classification of Diseases and Related Health Problems) that is applied to the subject during the course of the study, after receipt of the study agent, that is expected to continue for at least 3 months and requires continued health care intervention.

Medically Attended Adverse Events (MAAEs)

MAAEs are defined as a hospitalization < 24 hours, emergency room visit or an otherwise unscheduled visit to or from medical personnel for any reason; and considered related or possibly related to study product.

Time Period and Frequency for Event Assessment and Follow-Up

For this study:

- Solicited Adverse Events will be collected for 7 days following each vaccine dose.
- Unsolicited AEs will be collected until 28 days after each vaccination.
- AESIs, NOCMCs, MAAEs, SAEs, and AEs leading to withdrawal from the study will be collected from Day 1 through the end of the study.

SARS-CoV-2 infection

Confirmed SARS-CoV-2 infection at any time during the study defined as a positive RT-PCR test performed by the site or using a non-site testing method (RT-PCT or antigen test), will be documented. While this event would occur on study, it is not typical AE and therefore captured as an exploratory efficacy assessment.

5. SAMPLE SIZE CONSIDERATIONS

Sample Size Calculations for the Safety Endpoints

Rare AEs are not demonstrable in a clinical study of this size; however, the probabilities of observing one or more AEs given various true event rates are presented in Table 5. With the assumption that all enrolled subjects will likely complete immunizations and safety visits in this relatively short study duration, the following statistical considerations apply. With approximately 100 subjects there is a greater than 99.9% chance of observing at least one AE of probability 10%. With approximately 50 subjects, there is a 99.5% chance of observing at least one AE of probability 10%. With approximately 25 subjects, there is a 92.8% chance of observing at least one AE of probability 10%. Finally, with approximately 15 subjects, there is a 79.4% chance of observing at least one AE of probability 10%. Therefore, if no AEs of a given type occur in a group (or strata/subgroup), we can be relatively confident that they will occur in fewer than 10% of people if the vaccine is implemented.

Sample Size Calculations for the Immunogenicity Endpoints

The primary objective of this study is to evaluate the magnitude and durability of SARS-CoV-2 specific antibody titers in serum samples. This objective is descriptive in nature and will be accomplished by estimating 95% confidence intervals (CI) for the geometric mean titer (GMT) at each timepoint when samples are collected.

The precision with which the GMT can be estimated from observed data depends on the standard deviation (SD) of the measurements, on the logarithmic scale, and the sample size. Table 6 displays two-sided 95% confidence intervals for the GMT for several values of the observed antibody titer.

6. GENERAL STATISTICAL CONSIDERATIONS

6.1. General Principles

Unless otherwise noted, continuous variables will be summarized using the following descriptive statistics: n (non-missing sample size), mean, standard deviation, median, maximum, and minimum. The frequency and percentages (based on the non-missing sample size) of observed levels will be reported for all categorical measures. In general, all data will be listed, sorted by vaccine arm and subject, and when appropriate by visit number within subject. Summary tables will be structured with a column for each variant and will be annotated with the total population size relevant to that table/cohort, including any missing observations.

6.2. Timing of Analyses

Interim analyses will occur as needed. Statistical analyses of immunogenicity endpoints, by vaccine arm, may be performed when subjects have completed key immunogenicity visits.

6.3. Analysis Populations

A tabular listing of all subjects, visits, and observations excluded from the immunogenicity analysis will be provided in the CSR (Listing 5).

6.3.1. Modified Intention-to-Treat (mITT) Population

The modified intention-to-treat (mITT) population includes all subjects who received at least one dose of vaccine and contributed both pre- and at least one post-vaccination venous blood sample for immunogenicity testing for which valid results were reported.

6.3.2. Per Protocol Population

In the final analysis, protocol deviations will be reviewed to determine which protocol deviations may affect the analysis. The per protocol (PP) population will then be defined. The PP population will, at minimum, exclude the following from the mITT Population:

- Data from all available visits for subjects found to be ineligible at baseline.
- Data from all visits subsequent to the protocol deviations that are considered to affect the science.
- Data from any visit that occurs substantially out of window.

6.3.3. Safety Population

The safety analysis population includes all enrolled subjects who received at least one dose of study vaccine. This population will be summarized according to the actual study vaccine received, not necessarily the vaccine to which a subject was randomized.

6.4. Covariates and Subgroups

Subgroup analyses, by age group and infection status, will be completed. Analyses for each subgroup will include descriptive summaries and confidence intervals but no formal hypothesis testing, following recommendations for subgroup analyses that may inflate false positive conclusion rates and lack statistical power. Additional exploratory subgroup analyses may be performed as required.

6.5. Missing Data

There are no imputations planned for missing data.

For immunogenicity assays, any values below the lower limit of detection will be imputed as one-half of the lower limit of detection for analysis purposes. Any such imputations will be noted in the corresponding analysis.

6.6. Interim Analyses and Data Monitoring

Cumulative safety information, study status, and primary endpoint results may be published, presented at a public forum, or presented as summaries aggregated by vaccination group at the discretion of the sponsor while the study is ongoing. None of the interim analyses will include any formal statistical hypothesis testing; therefore, p-value adjustment will not be made to any analyses.

6.7. Multicenter Studies

Data will be pooled across all clinical sites. Center effects are not anticipated because the sites are using standardized procedures for vaccination and assessment of solicited and unsolicited adverse events, and the study relies on central laboratories for the assessment of immunogenicity endpoints.

6.8. Multiple Comparisons/Multiplicity

No hypothesis testing will be conducted, therefore, there are no p-value adjustments planned for multiple comparisons. Confidence intervals may be adjusted as appropriate.

7. STUDY SUBJECTS

7.1. Disposition of Subjects

Table 11 will present a summary of the reasons that subjects were screened but not enrolled.

The composition of analysis populations, including reasons for subject exclusion, by vaccination arm, is presented in Table 10.

The disposition of subjects in the study will be tabulated by vaccination group (Table 9). The table shows the total number of subjects screened, enrolled, receiving at least 1 dose, receiving 2 doses (if applicable), discontinued dosing or terminated from study follow-up and the number completing the study.

A flowchart showing the disposition of study subjects, adapted from the Consort Statement [41] will be included (Figure 1). This figure will present the number of subjects screened, enrolled, lost to follow-up, and analyzed, by vaccination arm.

A listing of subjects who discontinued dosing or terminated from study follow-up and the reason will be included in Listing 1.

7.2. Protocol Deviations

A summary of subject-specific protocol deviations will be presented by the reason for the deviation, the deviation category, and vaccination group for all subjects (Table 7) as well as similar summaries for major subject-specific protocol deviations that may affect analyses (Table 8). All subject-specific protocol deviations and non-subject specific protocol deviations will be included in Appendix 3 as data listings (Listing 2 and Listing 3, respectively).

8. IMMUNOGENICITY EVALUATION

8.1. Primary Immunogenicity Analyses

Descriptive summaries of immunogenicity data will be presented for the mITT population. If there are protocol deviations which may affect the analysis, an analysis of the per-protocol (PP) population may also be performed.

The results of three immunological assays will be analyzed. The 10-plex (ECLIA) assay is a fit-for-purpose assay that reports antibody concentrations as arbitrary units (AU) interpolated from ECL signal of internal standards or reports as area under the curve (AUC) and is used to assess antibody binding for variants of concern. The results of the 10-plex ECLIA assay will be summarized for each group at each timepoint by the geometric mean (GM), geometric mean fold rise (GMFR) from baseline (Day 1), geometric mean ratio (GMR) against D614G, and geometric mean fold drop (GMFD) from Day 29 (and Day 85 for 2 dose group) along with corresponding 95% confidence intervals (CIs). GMFR is defined as the ratio of the result at a timepoint divided by the result at Day 1. GMR is defined as the ratio of the result for a variant of concern to D614G (e.g. Beta to D614G). GMFD is defined as the ratio of the result at Day 29 (or day 85) divided by the result at a timepoint following day Day 29 (or Day 85). Seropositive rate is the proportion of subjects with a result above the lower limit of detection. The lower limit of detection will be annotated in the tables and figures where applicable. Summaries of the 10-plex ECLIA results are shown starting with Table 15 and ending with Table 122. Graphical displays will include geometric mean over time (starting with Figure 2 and ending with Figure 109), and distribution of responses over time (starting with Table 326 and ending with Table 433).

The SARS-CoV-2 pseudovirus neutralization assay (PsVNA) and focus reduction neutralization test (FRNT) will be run using serial dilutions against available variants (*e.g.* Beta, Delta, Omicron). From these assays, ID_{50}, which estimates the amount of antibodies required for a neutralization rate of 50%, will be reported. Neutralization titers will be summarized by the GM, GMFR, GMR, GMFD, and seropositive rate with corresponding 95% CIs, for each group at each timepoint. The summaries of PsVNA results are shown starting with Table 123 and ending with Table 230, and the summaries of FRNT results are shown starting with Table 231 and ending with Table 338. Graphical displays for PsVNA and FRNT will include geometric mean over time (starting with Figure 110 and ending with Figure 325) and distributions of responses over time (starting with Figure 434 and ending with Figure 649).

The immunogenicity timepoints for single-dose arms are Study Days 1, 15, 29, 91, 181, 271, and 366. The timepoints for the two-dose arm are Study Days 1, 15, 29, 57, 71, 85, 147, 237, 327, and 422. CIs for GM, GMFR, GMR, and GMFD will be calculated using the Student's t-distribution and CIs for seropositive rates will be calculated using the Clopper-Pearson binomial method. If additional immunological assays are determined to be necessary, then the results will be summarized in a similar manner to that of the assays described above.

The ELISA SARS-CoV-2 Nucleoprotein IgG (N-Protein) assay will be used to test for antibodies to the N-protein as an indicator of previous COVID-19 infection during the course of the study. This assay will return a result of negative or positive for previous COVID-19 infection. The result may be used in subgroup analyses.

For the pseudovirus neutralization assay, an ANCOVA model will be implemented to obtain estimates of the treatment group effect adjusted for prior infection status (determined by the N-Protein assay or self-report), $\log_{10}$ of baseline antibody titers, and age group. A $\log_{10}$ transformation will be applied to the dependent variable, which will be antibody titers, to obtain the treatment effect estimates as ratios of each treatment

group relative to the prototype treatment arm. The ANCOVA model will be applied to all immunogenicity study time points in single dose arms. Estimates and 95% CIs will be reported for the treatment group effects, and a Bonferroni adjustment will be applied to adjust the CIs for the number of treatment group comparisons. The model will be estimated for the mITT population as well as the subsample of the mITT population of subjects who do not have a history of COVID-19 infection, as determined by the N-Protein assay or self report. When the model is applied to the sample of uninfected subjects, prior infection status will not be included as a covariate (Table 339, Table 340, Table 341, and Table 342).

Correlations between the results from samples tested at different labs (e.g. PsVNA) may be calculated to evaluate the consistency of results across testing facilities.

Individual immunogenicity responses are shown in Listing 8.

8.2. Secondary Immunogenicity Analyses

See Section 9 for safety analyses which are the secondary endpoints of this study.

8.3. Exploratory Immunogenicity/Efficacy Analyses

8.3.1. T-cells

The magnitude, phenotype and percentage of cytokine expressing S protein specific T cells will be summarized at selected timepoints by vaccination group. Mean percentages of CD4 and CD8 T cells expressing cytokines and proportions of responders with 95% CI, along with median, minimum, and maximum, will be presented by peptide pool stimulation (starting with Table 343 and ending with Table 414). Distributions of T cell percentages will be graphically displayed (starting with Figure 650 and ending with Figure 757).

Individual T-cell responses are shown in Listing 9.

8.3.2. B-cells

Antigen-specific memory B cells were defined as CD3, CD8, CD14, CD16, and CD56 negative, but CD19, CD20, CD27, IgG or IgA (both on the same color) positive, and positive for one or more of WT or SA RBD, NTD (both variants on a single color) or S-2P. Longitudinal timepoints from each study participant were analyzed as a unit to mitigate batch effects and allow internal normalization to each individual's baseline sample. Median percentages of antigen specific B-cells along with min, max, median fold rise, and min and max of fold rise will be presented by probe (starting with Table 415 and ending with Table 450). Distributions of B cell percentages will be graphically displayed (starting with Figure 758 and ending with Figure 1009.

Individual B-cell responses are shown in Listing 10.

8.3.3. Breakthrough Infections

Confirmed SARS-CoV-2 infection at any time during the study, defined as a positive RT-PCR test performed by the site or using a non-site testing method (RT-PCR or antigen test) or N-antibody positive at a visit, will be documented as an exploratory efficacy assessment. Kaplan-Meier curves and 95% confidence intervals of infection free survival will be calculated (starting with Figure 1010 and ending with Figure 1018). Time to infection restricted mean survival time analyses will also be reported (starting with Table 451 and ending with Table 459).

8.3.4. Sequencing Results of Breakthrough Infections

The Simon and Bakel labs at the Icahn School of Medicine at Mount Sinai will analyze nasopharyngeal swab specimens collected from participants who experienced a SARS-CoV-2 breakthrough infection. The analysis aims to provide data on SARS-CoV-2 copy numbers and SARS-CoV-2 genotype/lineage.

The SARS-CoV-2 breakthrough positive nasopharyngeal specimens will be provided either as a dry swab or resuspended in viral transport media (both specimen types cryo-preserved at –80C). Biospecimen will be accessioned and processed according to the SOPs developed in collaboration with Dr. Greninger [42]. Briefly, each specimen undergoesRNA extraction, Reverse Transcriptase quantitative real time PCR (RT qPCR) and cDNA synthesis, whole-genome amplification followed by library preparation and next generation Illumina sequencing if the amount of SARS-CoV-2 passes the minimum requirements (e.g., less than threshold cycle 32). SARS-CoV-2 genomes will be assembled and subjected to quality control using the lab's custom vRAPID pipeline [43]. Genomes with at least 95% coverage and 100X depth across all regions will be considered complete. Genotypic analysis and clade/lineage assignment of complete genomes will be performed using the Nextclade CLI (v2.13.1), pangolin (v2.4) and pangoLEARN (v1.19) pipelines. Samples will be traced to their ancestral lineage assignments by obtaining the first letter and first numerical character of the lineage aliases provided by Nextclade.

A summary of variant PANGO calls are provided starting at Table 460 and ending at Table 468. A visual summary is provided starting at Figure 1019 and ending at Figure 1024.

Individual sequencing results are shown in Listing 11.

Further details on the analyses of exploratory endpoints will be described in an addendum to the Statistical Analysis Plan.

9. SAFETY EVALUATION

Summaries and analysis of safety data will be presented for the Safety Analysis Population.

Solicited non serious AEs will be collected from the time of each vaccination until 7 days after. Solicited AEs will be summarized by severity for each day post each vaccination and as the maximum severity over all 8 days. Additionally, solicited AEs will be analyzed using standard techniques, such as 95% CIs (using the Clopper-Pearson method), to summarize the proportion of subjects reporting each symptom, any application site symptom, and any systemic symptom.

Unsolicited non-serious AEs will be collected from the time of first vaccination through 28 days after each vaccination. Unsolicited AEs will be coded by MedDRA for preferred term and system organ class (SOC). SAEs, MAAEs, NOCMCs, AESIs, and AEs leading to withdrawal from the study will be collected from the time of first vaccination through 12 months after the last vaccine dose. The numbers of SAEs, MAAEs, NOCMCS, AESIs, and AEs leading to withdrawal from the study will be reported by detailed listings showing the event description, MedDRA preferred term and SOC, relevant dates (vaccinations and AEs), severity, relatedness, and outcome for each event. Non-serious unsolicited AEs will be summarized as number and percentage of subjects reporting at least one event in each MedDRA preferred term and SOC, cross tabulated by severity and relationship to study product. Additionally, the proportion of subjects and 95% CIs of AEs in aggregate and by MedDRA categories will be computed.

9.1. Demographic and Other Baseline Characteristics

Summaries of age, sex, ethnicity, race, time from first booster, time since covid infection, time since 1st booster or covid infection, and prior infection status (by self-report, N-Protein, either) will be presented by vaccination group (Table 12 and Table 13). Ethnicity is categorized as Hispanic or LatinX, or not Hispanic and not LatinX. In accordance with NIH reporting policy, subjects may self-designate as belonging to more than one race or may refuse to identify a race, the latter reflected in the CRF as "No" to each racial option.

Individual subject listings (Appendix 3) will be presented for all demographics (Listing 6).

9.1.1. Prior and Concurrent Medical Conditions

All current illnesses and past pre-existing medical conditions will be MedDRA® coded using MedDRA dictionary version 23.0 or higher.

Summaries of subjects' pre-existing medical conditions will be presented by vaccination group (Table 14).

Individual subject listings will be presented for all medical conditions (Listing 7).

9.1.2. Prior and Concomitant Medications

Summaries of medications that were started prior to dosing and continuing at the time of dosing will be presented by WHO Drug Terms 2 and 3 and treatment group (Table 486).

Individual subject listings will be presented for all concomitant medications (Listing 17).

9.2. Measurements of Treatment Compliance

All subjects are to receive one or two doses of study product administered in the clinic. The number of subjects receiving each dose will be summarized as part of the subject disposition table (Table 9).

9.3. Adverse Events

When calculating the incidence of adverse events (i.e., on a per subject basis), each subject will only be counted once and any repetitions of adverse events within a subject will be ignored; the denominator will be the total population size. All adverse events reported will be included in the summaries and analyses.

9.3.1. Solicited Events and Symptoms

Systemic solicited adverse events were collected pre-vaccination, and systemic and local solicited adverse events were collected 30 minutes post-vaccination and then daily for 7 days after each vaccination and graded on a scale of 0 (absent), 1 (mild), 2 (moderate) and 3 (severe). Systemic events include fatigue, headache, myalgia, and fever. Local events include pain at injection site, erythema, and induration.

The proportion of subjects reporting at least one solicited adverse event will be summarized for each solicited adverse event, any systemic symptom, any local symptom, and any symptoms. The 95% CI will be calculated using the Clopper-Pearson method (Table 470, Table 471, Table 472, Figure 1025, and Figure 1026).

For each systemic and local event, any systemic event, any local event, and any solicited event, the maximum severity over 7 days after each vaccination will be summarized for the Safety population. The number and percentage of subjects reporting each event will be summarized by the maximum severity and treatment group, separately for each vaccination and over all vaccinations. For each event the denominator is the number of subjects with non-missing data for the specific event (Table 471, Table 472, Figure 1025, and Figure 1026).

The number of subjects reporting a solicited adverse event will be summarized for each day post vaccination for each vaccination and for all vaccinations combined both in a summary table (Table 473, Table 474, Table 475, Table 476, Table 477, Table 478) and graphically in a bar chart (Figure 1027 and Figure 1028).

The mean, standard deviation, median, minimum, and maximum duration of solicited events will be summarized (Table 479). Day of solicited symptom onset will be summarized graphically (Figure 1029, Figure 1030, Figure 1031, Figure 1032)

Solicited adverse events by subject will be presented in Listing 9 and Listing 10, and graphically starting with Figure 1033 and ending with Figure 1044.

9.3.2. Unsolicited Adverse Events

Unsolicited AEs will be collected until 28 days after each vaccination. The proportion of subjects reporting at least one unsolicited adverse event will be summarized by MedDRA system organ class and preferred term for each vaccination and over all vaccinations. Denominators for percentages are the number of subjects who received the vaccination being summarized.

Adverse events by subject will be presented in Listing 14.

The following summaries for unsolicited adverse events will be presented by MedDRA system organ class, preferred term, vaccination, and treatment group:

- Summary of severity and relationship to study product (Table 480, Table 481, and Table 482);
- Subject listing of non-serious adverse events of moderate or greater severity (Table 484);
- Bar charts of incidence and frequency of adverse events by severity and MedDRA system organ class (Figure 1045 and Figure 1046).

9.4. Deaths, Serious Adverse Events and other Significant Adverse Events

The following listings will be presented including Subject ID, Age (years) Adverse Event Description, Adverse Event Onset Date/End Date, Last Dose Received/Days Post Dose, Reason Reported as an SAE, Relationship to Treatment, Alternate Etiology if not Related, Outcome, and Duration of Event (days):

- Deaths and Serious Adverse Events (Table 483);
- Adverse Events of Special Interest (Table 485);
- New Onset Chronic Medical Conditions and Medically Attended Adverse Events (Table 485).

9.5. Pregnancies

For any subjects in the Safety population who became pregnant during the study, every attempt was made to follow these subjects to completion of pregnancy to document the outcome, including information regarding any complications with pregnancy and/or delivery. In addition, a listing of pregnancies and outcomes will be presented (Listing 18, Listing 19, Listing 20, Listing 21, and Listing 22).

9.6. Clinical Laboratory Evaluations

Not applicable.

9.7. Vital Signs and Physical Evaluations

Vital sign measurements included systolic blood pressure, diastolic blood pressure and oral temperature. Vital signs were assessed at screening visit and Day 1 (Listing 15).

Physical Examinations performed at screening visit and Day 1 (Listing 16).

There are no planned vital sign measurements or physical examinations for follow-up visits. No tabulations will be made.

9.8. Concomitant Medications

Concomitant medications will be coded to the Anatomical Therapeutic Classification using the WHO Drug Dictionary. The use of prior and concomitant medications taken during the study will be recorded on the CRFs. A by-subject listing of concomitant medication use will be presented (Listing 17). The use of concomitant medications during the study will be summarized by ATC1, ATC2 code and treatment group for the Safety population (Table 486).

9.9. Other Safety Measures

Not applicable.

10. PHARMACOKINETICS

Not applicable.

11. IMMUNOGENICITY

See Section 8.

12. OTHER ANALYSES

Not applicable.

13. REPORTING CONVENTIONS

The mean, standard deviation, and other statistics will be reported to 1 decimal place greater than the original data. The minimum and maximum will use the same number of decimal places as the original data. Proportions will be presented as 2 decimal places; values greater than zero but <0.01 will be presented as "<0.01". Percentages will be reported to the nearest whole number; values greater than zero but < 1% will be presented as "<1"; values greater than 99% but less than 100% will be reported as >99%. Estimated parameters, not on the same scale as raw observations (e.g. regression coefficients) will be reported to 3 significant figures.

14. TECHNICAL DETAILS

SAS version 9.4 and R 3.6.2 or above will be used to generate all tables, figures, and listings.

15. SUMMARY OF CHANGES IN THE CONDUCT OF THE STUDY OR PLANNED ANALYSES

ANCOVA models were added to compare vaccination groups to prototype.

An analysis of breakthrough infections was also added that includes Kaplan-Meier Curves and restricted mean survival time.

An analysis of geometric mean fold drop was added.

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17. LISTING OF TABLES, FIGURES, AND LISTINGS

Table, figure, and listing shells are presented in Appendices 1, 2, and 3. Note, shells are shown only for stage 1 as examples. Tables, figures and listings will be presented for each stage in the CSRs.

APPENDICES

APPENDIX 1. TABLE MOCK-UPS

LIST OF TABLES

9.1 Overall Study Design and Plan Description

Table 2: Study Design

	Arms	Vaccine Platform	Sample Size	Vaccine Candidate	Interval (weeks)*	Timing of First Dose	Timing of Second Dose
		Moderna mRNA-1273	100	Prototype	≥16	D1	NA
			100	Beta + Omicron	≥16	D1	NA
			100	Beta + Omicron	≥16	D1	D57
			100	Delta + Omicron	≥16	D1	NA
			100	Omicron	≥16	D1	NA
			100	Omicron + Prototype	≥16	D1	NA
		Pfizer/ BioNTech BNT162b2	50	Wildtype (Prototype)	≥16	D1	NA
			50	Beta + Omicron	≥16	D1	NA
			50	Omicron	≥16	D1	NA
			50	Beta	≥16	D1	NA
			50	Beta + Wildtype	≥16	D1	NA
			50	Omicron + Wildtype	≥16	D1	NA
		Sanofi CoV2 preS dTM-AS03	50	Prototype	≥16	D1	NA
			50	Beta	≥16	D1	NA
			50	Beta+ Prototype	≥16	D1	NA
		Pfizer/ BioNTech BNT162b2 bivalent	100	Omicron BA.1 + Wildtype (Prototype)	≥16	D1	NA
			100	Omicron BA.4/BA.5 + Wildtype (Prototype)	≥16	D1	NA

Two age strata:

- 18-64 years
- ≥ 65 years (~45% in ≥ 65 years).

^For arms 16 and 17 or stage 4, only participants between the ages of 18 to 49 years will be enrolled.

Two infection strata:

- Confirmed prior SARS-CoV-2 infection (~20%)
- No known history of prior infection.

*interval (in weeks) since last exposure to SARS-CoV-2 infection or vaccination

9.5.1 Immunogenicity and Safety Measurements Assessed and Flow Chart

Table 3: Schedule of Study Procedures - Single Dose

Study Day	**D-28 to D-1**	**1**	**4**	**8[b]**	**15**	**29**	**91**	**181**	**271**	**366**	**Illness/ Unscheduled Visit[k,m]**	**Early Termination Visit**
Visit Number	**00[a]**	**1**	**1A**	**2**	**3**	**4**	**5**	**6**	**7**	**8**		
Window (+/-)		**0**	**1**	**1**	**2**	**2**	**7[m]**	**14[m]**	**14[m]**	**28[m]**		
Informed Consent[a]	X											
Eligibility Criteria	X											
Medical History	X											
Vaccination		X										
Concomitant Meds	X	X	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]
Interim History		X	X	X	X	X	X	X	X	X	X	X
Physical Exam[c] - Targeted	X	X									(X)	
Vital Signs[c]	X	X									(X)	
Height/Weight (BMI)[a]	X											
Urine β-HCG[d]	X	X										
Memory Aid[e]		X	X	X								
Solicited AEs		X	X	X								
Unsolicited AEs		X	X	X	X	X						
MAAEs, SAEs, NOCMCs, AEs leading to withdrawal from the study and AESIs		X	X	X	X	X	X	X	X	X	X	X
Nasal swab for PCR & Sequencing[f]											(X)	
Assays												
Serum for Serological Immunogenicity Assays[g] and Biomarker Testing[l]		34[l]	4[l]		34	34	34	34	34	34	4[l]-34[m]	34
PBMC Cellular Assays & Plasma[g,h] *(select sites only)*		64-70			64-70		64-70	64-70	64-70		64-70[m]	64-70
Daily Volume (mL)[g,i]		98-104	4		98-104	34	98-104	98-104	98-104	34	4-104	98-104

Cumulative Volume (mL) over 56 day-period[g,i]		98-104	102-108		200-212	234-246	132-138	98-104	98-104	132-138		
Total Cumulative Volume (mL)[g,i]		98-104	102-108		200-212	234-246	332-350	430-454	528-558	562-592		

[a] Optional screening visit – informed consent and screening activities can be a separate visit or combined with Day 1.
[b] Telephone visit
[c] Vital signs and targeted physical exam will be performed on screening and before vaccination otherwise, only as clinically indicated or based on interim medical history.
[d] For subjects of childbearing potential, a urine pregnancy will be performed at screening. If enrollment occurs on a separate day, a repeat urine pregnancy test will be done within 24 hours of study vaccine administration and negative results confirmed prior to dosing.
[e] The memory aid will be distributed at the Day 1 visit, queried for completion at the Day 8 telephone call and reviewed during an interview with the subject at the D15 visit and confirmed data recorded on the DCF.
[f]Collect nasal swab for PCR (1-2). Swabs can be self-collected and visit done by phone. Sequencing will be performed on all Illness visit-confirmed SARS-CoV-2 specimens.
[g] Inability (e.g., failure of venipuncture) to collect all baseline samples on Day 1 will not exclude the subject from further participation in this study as long as a minimum of baseline blood volume is collected (refer to the MOP for the protocol defined minimum number of required aliquots). Blood volume for PBMC varies depending on the type of tubes used for blood collection (refer to the MOP).
[h] Selected sites will perform PBMC separation on selected subjects (refer to MOP for more guidance).
[i] Blood volumes for early termination visit are not included in the blood volume totals.
[j] After vaccination on Day 1, immunosuppressant drugs, COVID-19 related prophylaxis and therapies as well as vaccines will be recorded. For any SAE occurring at any time during the study, all medications will be recorded.
[k] If an unscheduled visit is performed to evaluate an adverse event, vital signs and targeted physical exam will be performed, as indicated. If, in the judgement of the site investigator, the event, occurring within 4 weeks after vaccination, is a case of suspected myocarditis and/or pericarditis, the site will coordinate an appropriate diagnostic workup to make a determination of probable or confirmed myocarditis and/or pericarditis which may include, but is not limited to, an ECG, cardiac troponin testing and referral to a cardiologist (directly, or through the emergency department or primary care clinic). The suspected myocarditis and/or pericarditis case should be reported to the DMID Medical Monitor within 24 hours of site awareness.
[l]Serum for biomarker testing will be collected on Day 4 and stored for potential biomarker testing at a central laboratory and compared to testing of an aliquot from serum obtained on Day 1. If an unscheduled visit is related to a concern for myocarditis and/or pericarditis within 4 weeks after vaccination, a 4 mL SST will be collected and stored for potential biomarker testing at a central laboratory.
[m]If a participant is planning to receive a COVID-19 booster outside the study, an unscheduled visit will be performed where safety and immunogenicity (collection of sera, plasma and PBMC) assessments will be performed. However, if that planned visit falls within twice the window for an upcoming visit (e.g +/- 14 days for D 91, +/-28 days for D 181 and D 271, +/- 56 days for D 366) then it will occur and be documented as out of window for the planned upcoming scheduled visit (refer to MOP for more guidance).

Table 4: Schedule of Study Procedures - 2 Doses

Study Day	**D-28 to D-1**	**1**	**4**	**8[b]**	**15**	**29**	**57**	**60**	**64[b]**	**71**	**85**	**147**	**237**	**327**	**422**	**Illness/ Unscheduled Visit[k,m]**	**Early Termination Visit**
Visit Number	**00[a]**	**1**	**1A**	**2**	**3**	**4**	**5**	**5A**	**6**	**7**	**8**	**9**	**10**	**11**	**12**		
Window (+/-)		**0**	**1**	**1**	**2**	**2**	**3**	**1**	**1**	**2**	**2**	**7[m]**	**14[m]**	**14[m]**	**28[m]**		
Informed Consent[a]	X																
Eligibility Criteria	X						X										
Medical History	X						X										
Vaccination		X					X										
Concomitant Meds	X	X	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]	X[j]
Interim History		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Physical Exam[c] – Targeted	X	X					X									(X)	
Vital Signs[c]	X	X					X									(X)	
Height/Weight (BMI)[a]	X																
Urine β-HCG[d]	X	X					X										
Memory Aid[e]		X	X	X			X	X	X								
Solicited AEs		X	X	X			X	X	X								
Unsolicited AEs		X	X	X	X	X	X	X	X	X	X						
MAAEs, SAEs, NOCMCs, AEs leading to withdrawal from the study and AESIs		X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
Nasal swab for PCR & Sequencing[f]																(X)	
Assays																	
Serum for Serological Immunogenicity		34[l]	4[l]		34	34	34[l]	4[l]		34	34	34	34	34	34	4[l]-34[m]	34

Study Day	**D-28 to D-1**	**1**	**4**	**8[b]**	**15**	**29**	**57**	**60**	**64[b]**	**71**	**85**	**147**	**237**	**327**	**422**	**Illness/ Unscheduled Visit[k,m]**	**Early Termination Visit**
Visit Number	**00[a]**	**1**	**1A**	**2**	**3**	**4**	**5**	**5A**	**6**	**7**	**8**	**9**	**10**	**11**	**12**		
Window (+/-)		**0**	**1**	**1**	**2**	**2**	**3**	**1**	**1**	**2**	**2**	**7[m]**	**14[m]**	**14[m]**	**28[m]**		
Assays[g] and Biomarker Testing[l]																	
PBMC Cellular Assays & Plasma[g,h] *(select sites only)*		64-70			64-70		64-70			64-70		64-70	64-70	64-70		64-70[m]	64-70
Daily Volume (mL)[g,i]		98-104	4		98-104	34	98-104	4		98-104	34	98-104	98-104	98-104	34	4-104	98-104
Cumulative Volume (mL) over 56 day-period[g,i]		98-104	102-108		200-212	234-246	332-350	238-250		336-354	268-280	132-138	98-104	98-104	132-138		
Total Cumulative Volume (mL)[g,i]		98-104	102-108		200-212	234-246	332-350	336-354		434-458	468-492	566-596	664-700	762-804	796-838		

[a] Optional screening visit – informed consent and screening activities can be a separate visit or combined with Day 1.
[b] Telephone visit
[c] Vital signs and targeted physical exam will be performed on screening and before vaccination otherwise, only as clinically indicated or based on interim medical history.
[d] For subjects of childbearing potential, a urine pregnancy test will be performed at screening. If enrollment occurs on a separate day as screening, a repeat urine pregnancy test will be done within 24 hours of first study vaccine administration and repeated on day 57 prior to second study vaccine administration. Negative results must be confirmed prior to each dosing.
[e] The memory aid will be distributed at the Day 1 and Day 57 visits, queried for completion at the Day 8 and Day 64 telephone calls and reviewed during an interview with the subject at the D15 and Day 71 visits and confirmed data recorded on the DCF.
[f] Collect nasal swab for PCR (1-2). Swabs can be self-collected and visit done by phone. Sequencing will be performed on all Illness visit-confirmed SARS-CoV-2 specimens.
[g] Inability (e.g., failure of venipuncture) to collect all baseline samples on Day 1 will not exclude the subject from further participation in this study as long as a minimum of baseline blood volume is collected (refer to the MOP for the protocol defined minimum number of required aliquots). Blood volume for PBMC varies depending on the type of tubes used for the blood collection (refer to the MOP).
[h] Selected sites will perform PBMC separation on selected subjects (refer to MOP for more guidance).
[i] Blood volumes for early termination visit are not included in the blood volume totals.
[j] After vaccination on Day 1, immunosuppressant drugs, COVID-19 related prophylaxis and therapies as well as vaccines will be recorded. For any SAE occurring at any time during the study, all medications will be recorded.

[k] If an unscheduled visit is performed to evaluate an adverse event, vital signs and targeted physical exam will be performed, as indicated. If, in the judgement of the site investigator, the event, occurring within 4 weeks after each vaccination, is a case of suspected myocarditis and/or pericarditis, the site will coordinate an appropriate diagnostic workup to make a determination of probable or confirmed myocarditis and/or pericarditis which may include, but is not limited to, an ECG, cardiac troponin testing and referral to a cardiologist (directly, or through the emergency department or primary care clinic). The suspected myocarditis and/or pericarditis case should be reported to the DMID Medical Monitor within 24 hours of site awareness.

[l]Serum for biomarker testing will be collected on Days 4 and 60 and stored for potential biomarker testing at a central laboratory and compared to testing of an aliquot of serum obtained on Days 1 and 57, respectively. If an unscheduled visit is related to a concern for myocarditis and/or pericarditis within 4 weeks after vaccination, a 4 mL SST will be collected and stored for potential biomarker testing at a central laboratory.

[m]If a participant is planning to receive a COVID-19 booster outside the study, an unscheduled visit will be performed where safety and immunogenicity (collection of sera, plasma and PBMC) assessments will be performed. However, if that planned visit falls within twice the window for an upcoming visit (e.g +/- 14 days for D 147, +/-28 days for D 237 and D 327, +/- 56 days for D 422) then it will occur and be documented as out of window for the planned upcoming scheduled visit (refer to MOP for more guidance).

Note Windows for subsequent visits should be based off the preceding vaccination visit.
If intercurrent SARS- CoV-2 infection occurs between the first and prior to the planned second study dose or if a COVID-19 vaccine is given outside the study between the first and prior to the planned second study dose, no second vaccination will be given. Participants who do not receive a second dose will revert to the schedule of activities for single dose participants.

9.7.1 Sample Size

Table 5: Probability of observing one or more Adverse Events for various event rates in one vaccine group (or strata)

N	"True" Event Rate	Probability of Observing ≥ 1 events (%)	N	"True" Event Rate	Probability of Observing ≥ 1 events (%)
100	0.1%	9.5	50	0.1%	4.9
	0.5%	39.4		0.5%	22.2
	1.0%	63.4		1.0%	39.5
	2.0%	86.7		2.0%	63.6
	3.0%	95.2		3.0%	78.2
	4.0%	98.3		4.0%	87
	5.0%	99.4		5.0%	92.3
	10.0%	>99.9		10.0%	99.5
	15.0%	>99.9		15.0%	>99.9
	20.0%	>99.9		20.0%	>99.9
	30.0%	>99.9		30.0%	>99.9
25	0.1%	2.5	15	0.1%	1.5
	0.5%	11.8		0.5%	7.2
	1.0%	22.2		1.0%	14
	2.0%	39.7		2.0%	26.1
	3.0%	53.3		3.0%	36.7
	4.0%	64.0		4.0%	45.8
	5.0%	72.3		5.0%	53.7
	10.0%	92.8		10.0%	79.4
	15.0%	98.3		15.0%	91.3
	20.0%	99.6		20.0%	96.5
	30.0%	>99.9		30.0%	99.5

Table 6: Two-sided 95% confidence intervals based on observing a particular average $\log_e$-antibody titer in subjects' vaccine groups and potential strata sizes

Observed average $\log_e$ antibody titer	SD of $\log_e$ antibody titer	95% confidence interval of GMT in vaccine groups and strata			
		N = 100	N = 50	N = 25	N = 15
$\log_e$ (5)	0.5	(4.5, 5.5)	(4.3, 5.8)	(4.1, 6.1)	(3.8, 6.6)
$\log_e$ (20)		(18.1, 22.1)	(17.4, 23.1)	(16.3, 24.6)	(15.2, 26.4)
$\log_e$ (50)		(45.3, 55.2)	(43.4, 57.6)	(40.7, 61.5)	(37.9, 66)
$\log_e$ (100)		(90.6, 110.4)	(86.8, 115.3)	(81.4, 122.9)	(75.8, 131.9)

Observed average $\log_e$ antibody titer	SD of $\log_e$ antibody titer	95% confidence interval of GMT in vaccine groups and strata			
		N = 100	N = 50	N = 25	N = 15
$\log_e$ (250)		(226.4, 276.1)	(216.9, 288.2)	(203.4, 307.3)	(189.5, 329.8)
$\log_e$ (500)		(452.8, 552.1)	(433.8, 576.3)	(406.8, 614.6)	(379.1, 659.5)
$\log_e$ (1000)		(905.6, 1104.3)	(867.5, 1152.7)	(813.5, 1229.2)	(758.1, 1319)
$\log_e$ (5)	1.0	(4.1, 6.1)	(3.8, 6.6)	(3.3, 7.6)	(2.9, 8.7)
$\log_e$ (20)		(16.4, 24.4)	(15.1, 26.6)	(13.2, 30.2)	(11.5, 34.8)
$\log_e$ (50)		(41, 61)	(37.6, 66.4)	(33.1, 75.6)	(28.7, 87)
$\log_e$ (100)		(82, 121.9)	(75.3, 132.9)	(66.2, 151.1)	(57.5, 174)
$\log_e$ (250)		(205, 304.9)	(188.2, 332.2)	(165.5, 377.8)	(143.7, 435)
$\log_e$ (500)		(410, 609.7)	(376.3, 664.3)	(330.9, 755.5)	(287.4, 869.9)
$\log_e$ (1000)		(820, 1219.5)	(752.6, 1328.7)	(661.8, 1511)	(574.8, 1739.8)

10.2 Protocol Deviations

Table 7: Distribution of Protocol Deviations by Category, Type, and Treatment Group

[Implementation Note: Only display deviations that have occurred in at least one treatment group.]

Category	Deviation Type	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) [two doses] (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
		No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.
Eligibility/enrollment	Any type														
	Did not meet inclusion criterion	x	x	x	x	x	x	x	x	x	x	x	x	x	x
	Met exclusion criterion														
	ICF not signed prior to study procedures														
	Other														
Treatment administration schedule	Any type														
	Out of window visit														
	Missed visit/visit not conducted														
	Missed treatment administration														
	Delayed treatment administration														
	Other														
Follow-up visit schedule	Any type														
	Out of window visit														
	Missed visit/visit not conducted														
	Other														
Protocol procedure/assessment	Any type														
	Incorrect version of ICF signed														
	Blood not collected														
	COVID-19 test swab not collected														
	Other specimen not collected														

Category	Deviation Type	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) [two doses] (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
		No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.	No. of Subj	No. of Dev.
	Too few aliquots obtained														
	Specimen result not obtained														
	Required procedure not conducted														
	Required procedure done incorrectly														
	Study product temperature excursion														
	Specimen temperature excursion														
	Other														
Treatment administration	Any type														
	Required procedure done incorrectly														
	Study product temperature excursion														
	Other														
Note: N=Number of subjects in the Safety Population.															

Table with similar format:

Table 8: Distribution of Major Protocol Deviations by Category, Type, and Treatment Group

12.2.2 Displays of Adverse Events

The toxicity grading scales in the FDA "Toxicity Grading Scale for Healthy Adult and Adolescent Volunteers Enrolled in Preventive Vaccine Clinical Trials" will be used.

12.4.1 Individual Laboratory Measurements and Abnormal Laboratory Values

Not applicable.

14.1 Description of Study Subjects

14.1.1 Disposition of Subjects

Table 9: Subject Disposition by Treatment Group

Subject Disposition	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Screened	--	--	--	--	--	--	--	--	--	--	--	--	x	--
Enrolled/Randomized	x	100	x	100	x	100	x	100	x	100	x	100	x	100
Received First Vaccination	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
Received Second Vaccination	NA	NA	x	xx	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Completed Final Blood Draw														
Completed Follow-up[a]														
Completed Per Protocol[b]														

Note: N=Number of subjects enrolled in the study.

[a] Refer to Listing 2 for reasons subjects discontinued or terminated early.

[b] Refer to Listing 5 for reasons subjects are excluded from the Analysis populations.

Table 10: Analysis Populations by Treatment Group

Analysis Populations	Reason Subjects Excluded	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
		n	%	n	%	n	%	n	%	n	%	n	%	%	n
mITT Population	Any Reason	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
	[Reason 1, for example: Did not meet eligibility criteria]														
	[Reason 2]														
	[Reason 3]														
	[Reason 4]														
Per Protocol Population	Any Reason														
	[Reason 1]														
	[Reason 2]														
Safety Population	Any Reason														
	[Reason 1]														
	[Reason 2]														
Note: N=Number of subjects enrolled in the study.															

Table 11: Ineligibility Summary of Screen Failures

[Implementation Note: See section 4.3 for inclusion and exclusion criteria.]

Inclusion/Exclusion Category	Inclusion/Exclusion Criterion	n[a]	%[b]
Inclusion and Exclusion	Number of subjects failing any eligibility criterion	x	100
Inclusion	Any inclusion criterion	x	xx
	[inclusion criterion 1]	x	xx
	[inclusion criterion 2]	x	xx
	[inclusion criterion 3]	x	xx
Exclusion	Any exclusion criterion	x	xx
	[exclusion criterion 1]	x	xx
	[exclusion criterion 2]	x	xx
	[exclusion criterion 3]	x	xx

[a] More than one criterion may be marked per subject.
[b] Denominator for percentages is the total number of screen failures.

14.1.2 Demographic Data by Study Group

Table 12: Summary of Categorical Demographic and Baseline Characteristics by Treatment Group, All Enrolled Subjects

Variable	Characteristic	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
		n	%	n	%	n	%	n	%	n	%	n	%	n	%
Sex	Male	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
	Female														
Ethnicity	Not Hispanic or LatinX	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
	Hispanic or LatinX														
	Not Reported														
	Unknown														
Race	American Indian or Alaska Native	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
	Asian														
	Native Hawaiian or Other Pacific Islander														
	Black or African American														
	White														
	Multi-Racial														
	Unknown														
Age Group	18-64 years														
	>= 65 years														
Prior Infection (Self Report)	Yes														
	No														

Variable	Characteristic	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
		n	%	n	%	n	%	n	%	n	%	n	%	n	%
Prior Infection (Positive Nuclear Protein Antibody or Self-Report)	Yes														
	No														
SARS-COV-2 Vaccination Regimen	mRNA Primary, mRNA Boost														
	Ad26 Primary, mRNA Boost														
	Ad26 Primary, Ad26 Boost														
Note: N=Number of subjects in the Safety Population.															

Table 13: Summary of Continuous Demographic and Baseline Characteristics by Treatment Group, All Enrolled Subjects

Variable	Statistic	Prototype (N=X)	Beta (B.1.351) + Omicron (B.1.1.529) (N=X)	Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)	Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)	Omicron (B.1.1.529) (N=X)	Omicron (B.1.1.529) + Prototype (N=X)	All Subjects (N=X)
Age (Years)	Mean	xx	xx	xx	xx	xx	xx	xx
	Standard Deviation	xx	xx	xx	xx	xx	xx	xx
	Median	x	x	x	x	x	x	x
	Minimum	x	x	x	x	x	x	x
	Maximum	x	x	x	x	x	x	x
Height (cm)	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Weight (kg)	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
BMI (kg/m^2)	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Days since most recent COVID19 Vaccine	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Days since most recent self-reported COVID19 infection	n							
	Mean							
	Standard Deviation							

Variable	Statistic	Prototype (N=X)	Beta (B.1.351) + Omicron (B.1.1.529) (N=X)	Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)	Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)	Omicron (B.1.1.529) (N=X)	Omicron (B.1.1.529) + Prototype (N=X)	All Subjects (N=X)
	Median							
	Minimum							
	Maximum							
Days since most recent self-reported COVID19 infection or COVID19 Vaccination	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Note: N=Number of subjects in the Safety Population								

14.1.3 Prior and Concurrent Medical Conditions

Table 14: Summary of Subjects with Pre-Existing Medical Conditions by MedDRA System Organ Class and Treatment Group

MedDRA System Organ Class	Prototype (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (N=X)		Beta (B.1.351) + Omicron (B.1.1.529) (2 Doses) (N=X)		Delta (B.1.617.2) + Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) (N=X)		Omicron (B.1.1.529) + Prototype (N=X)		All Subjects (N=X)	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Any SOC	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
[SOC 1]														
[SOC 2]														

Note: N=Number of subjects in the Safety Population; n = Number of subjects reporting medical history within the specified SOC.
A subject is only counted once per SOC.

14.2 Immunogenicity Data

Table 15: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.5/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 91	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.5/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 181	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 271	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 366	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.5/BA.5 (N=X)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns may be added for additional variants.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Add a note to indicate the lower limit of detection for the assay used to calculate the seropositive rate.

Tables with Similar Format:

Table 16: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Overall – Per Protocol Population

Table 17: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Younger Cohort – mITT Population

Table 18: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Younger Cohort – Per Protocol Population

Table 19: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Older Cohort – mITT Population

Table 20: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Older Cohort – Per Protocol Population

Table 21: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 22: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 105: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 57	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 71	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 85	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 147	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 237	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 327	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 422	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns may be added for additional variants.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Add a note to indicate the lower limit of detection for the assay used to calculate the seropositive rate.

Tables with Similar Format:

Table 106: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall– Per Protocol Population

Table 107: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – mITT Population

Table 108: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – Per Protocol Population

Table 109: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – mITT Population

Table 110: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – Per Protocol Population

Table 111: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 112: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 123: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 91	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 181	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 271	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 366	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns included as placeholders may not be needed.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Add a note to indicate the lower limit of detection for the assay used to calculate the seropositive rate.

Tables with Similar Format:

Table 124: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Overall – Per Protocol Population

Table 125: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Younger Cohort – mITT Population

Table 126: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Younger Cohort – Per Protocol Population

Table 127: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Older Cohort – mITT Population

Table 128: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Older Cohort – Per Protocol Population

Table 129: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 130: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 211: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Omicron + Prototype, Older Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 212: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, Omicron + Prototype, Older Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 213: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 57	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 71	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 85	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 147	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 237	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 327	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 422	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns may be added for additional variants.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Add a note to indicate the lower limit of detection for the assay used to calculate the seropositive rate.

Tables with Similar Format:

Table 214: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall – Per Protocol Population

Table 215: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – mITT Population

Table 216: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – Per Protocol Population

Table 217: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – mITT Population

Table 218: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – Per Protocol Population

Table 219: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 220: Pseudovirus Neutralization Assay ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 231: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1(N=X)	BA.4/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 91	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1(N=X)	BA.4/BA.5 (N=X)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 181	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 271	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 366	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1(N=X)	BA.4/BA.5 (N=X)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns may be added for additional variants.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Tables with Similar Format:

Table 232: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Overall– Per Protocol Population

Table 233: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Younger Cohort – mITT Population

Table 234: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Younger Cohort – Per Protocol Population

Table 235: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Older Cohort – mITT Population

Table 236: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Older Cohort – Per Protocol Population

Table 237: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 238: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 239: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 240: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 241: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, Prototype, Younger Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 321: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall – mITT Population

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
Day 1	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 15	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 29	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 57	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 71	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 85	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 147	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 237	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 327	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)
Day 422	n	x	x	x	x	x	x
	GMT (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Median (Min,Max)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMR_{D614G} (95% CI)	NA	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	GMFR (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)

Time Point	Statistic	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	BA.1 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	GMFD (95% CI)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)	x.x (x.x, x.x)
	Seropositive (95% CI)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)	0.0X (0.xx,0.xx)

Note: N=Number of subjects in the mITT Population.

n=Number of subjects with results available at time point.

GM=Geometric Mean, GMR_{D614G}=Geometric Mean Ratio to D614G variant, GMFR=Geometric Mean Fold Rise, GMFD=Geometric Mean Fold Drop.

Confidence intervals of the GM, GMR, GMFR, and GMFD were calculated with the Student's t distribution on log-transformed data. Confidence intervals of the Seropositive rate were calculated with the Clopper-Pearson method.

Implementation notes:

Extra variant columns may be added for additional variants.

For tables using the PP population, update footnote to read: "Notes: N=Number of subjects in the Per Protocol population."

Add a note to indicate the lower limit of detection for the assay used to calculate the seropositive rate.

Tables with Similar Format:

Table 322: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Overall – Per Protocol Population

Table 323: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – mITT Population

Table 324: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Younger Cohort – Per Protocol Population

Table 325: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – mITT Population

Table 326: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Older Cohort – Per Protocol Population

Table 327: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 328: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 329: Focus Reduction Neutralization Test ID_{50} Summary Results by Time Point and Variant, 2 Dose Beta + Omicron, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 339: Pseudovirus Neutralization Treatment Group Effects as Ratios Relative to the Prototype Arm from ANCOVA model, Overall – mITT Population

Study Day	Treatment Group	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	B.1.1.529 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
Day 15	Beta + Omicron						
	Delta + Omicron						
	Omicron						
	Omicron + Prototype						
Day 29	Beta + Omicron						
	Delta + Omicron						
	Omicron						
	Omicron + Prototype						
Day 91	Beta + Omicron						
	Delta + Omicron						
	Omicron						
	Omicron + Prototype						
Day 181	Beta + Omicron						
	Delta + Omicron						
	Omicron						
	Omicron + Prototype						
Day 271	Beta + Omicron						
	Delta + Omicron						
	Omicron						
	Omicron + Prototype						
Day 366	Beta + Omicron						
	Delta + Omicron						
	Omicron						

Study Day	Treatment Group	D614G (N=X)	B.1.351 (N=X)	B.1.617.2 (N=X)	B.1.1.529 (N=X)	BA.2.12.1 (N=X)	BA.4/BA.5 (N=X)
	Omicron + Prototype						
Note: N=Number of subjects in the mITT Population. Effect estimates are ratios relative to the Prototype treatment group. Effect estimates and CIs are from an ANCOVA model adjusted for prior infection, $\log_{10}$ of baseline antibody titers, age group, and previous vaccination regimen. A Bonferroni adjustment is applied to the CIs.							

Tables with Similar Format:

Table 340: **Pseudovirus Neutralization Treatment Group Effects as Ratios Relative to the Prototype Arm from ANCOVA model, Overall – Per Protocol Population**

Table 341: **Pseudovirus Neutralization Treatment Group Effects as Ratios Relative to the Prototype Arm from ANCOVA model, Uninfected (by Self-Report or N-Protein) Cohort – mITT Population**

Table 342: **Pseudovirus Neutralization Treatment Group Effects as Ratios Relative to the Prototype Arm from ANCOVA model, Uninfected (by Self-Report or N-Protein) Cohort – Per Protocol Population**

Table 343: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Overall – mITT Population

[Implementation Note: Tables should include rows for median, min, max, GMFR and 95% CI of GMFR. Column order should be Peptide Pool, Cytokine and Time Point.]

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
Day 1, Pre-Booster Dose	**Beta Mutations**	**IFNγ**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 and 154	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 or 154	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 or 154/C	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 or 154/E	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 or 154/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2 or 154/T	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IL-17a	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
		IL-2	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IL-4 and 154	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IL-4 IL-5 IL-13 and 154	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		TNFα	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Beta S	**IFNγ**	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		Repeat for all cytokines							
	Conserved S1	**IFNγ**	n						
			Mean						
			95% CI[a]						
			Response Rate						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			95% CI[b]						
		IFNγ or IL-2	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		Repeat for all cytokines							
	Conserved S2	**IFNγ**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2	n						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		Repeat for all cytokines							
	Original Matched	**IFNγ**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		Repeat for all cytokines							
	Original S	**IFNγ**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2	n						
			Mean						
			95% CI[a]						
			Response Rate						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		Repeat for all cytokines							
Repeat for all study days									

Note: N=Number of Subjects.
n=Number of subjects with results available at time point.
NE=Not Estimable
[a] Confidence interval calculated based on the Student's t-distribution
[b] Exact binomial confidence interval calculated using the Clopper-Pearson methodology.

Tables with Similar Format:

Table 344: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Overall – Per Protocol Population

Table 345: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Cohort – mITT Population

Table 346: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Cohort – Per Protocol Population

Table 347: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Cohort – mITT Population

Table 348: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Cohort – Per Protocol Population

Table 361: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Overall – mITT Population

[Implementation Note: Tables should include rows for median, min, max, GMFR and 95% CI of GMFR. Column order should be Peptide Pool, Cytokine and Time Point.]

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
Day 1, Pre-Booster Dose	**Beta Mutations**	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2 and 154	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2 or 154	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2 or 154/C	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2 or 154/E	n	
			Mean	
			95% CI[a]	
			Response Rate	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			95% CI[b]	
		IFNγ or IL-2 or 154/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2 or 154/T	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IL-17a	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IL-4 and 154	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
		IL-4 IL-5 IL-13 and 154	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		TNFα	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Beta S	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Conserved S1	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
	Conserved S2	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Original Matched	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Original S	**IFNγ**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Tables with Similar Format:

Table 362: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Overall – Per Protocol Population

Table 363: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Cohort – mITT Population

Table 364: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Cohort – Per Protocol Population

Table 365: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Cohort – mITT Population

Table 366: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Cohort – Per Protocol Population

Table 367: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 368: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 369: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 370: Mean Percentages of CD4 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 379: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Overall – mITT Population

[Implementation Note: Tables should include rows for median, min, max, GMFR and 95% CI of GMFR. Column order should be Peptide Pool, Cytokine and Time Point.]

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
Day 1, Pre-Booster Dose	**Beta Mutations**	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Beta S	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Conserved S1	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Conserved S2	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Original Matched	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
	Original S	**IFNγ or IL-2**	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/CM	n						
			Mean						
			95% CI[a]						

Time Point	Peptide Pool	Cytokine	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/EM	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/N	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
		IFNγ or IL-2/TD	n						
			Mean						
			95% CI[a]						
			Response Rate						
			95% CI[b]						
Repeat for all study days									

Note: N=Number of Subjects.
n=Number of subjects with results available at time point.
NE=Not Estimable
[a] Confidence interval calculated based on the Student's t-distribution
[b] Exact binomial confidence interval calculated using the Clopper-Pearson methodology.

Tables with Similar Format:

Table 380: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Overall – Per Protocol Population

Table 381: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Cohort – mITT Population

Table 382: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Cohort – Per Protocol Population

Table 383: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Cohort – mITT Population

Table 384: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Cohort – Per Protocol Population

Table 385: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 386: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 387: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 388: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 389: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 390: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 391: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 392: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Older Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 393: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Infected (by Self-Report) Cohort – mITT Population

Table 394: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 395: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 396: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 1 Dose Groups, Younger Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 397: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Overall – mITT Population

[Implementation Note: Tables should include rows for median, min, max, GMFR and 95% CI of GMFR. Column order should be Peptide Pool, Cytokine and Time Point.]

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
Day 1, Pre-Booster Dose	**Beta Mutations**	**IFNγ or IL-2**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			Response Rate	
			95% CI[b]	
	Beta S	**IFNγ or IL-2**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			95% CI[b]	
	Conserved S1	**IFNγ or IL-2**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
	Conserved S2	**IFNγ or IL-2**	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Original Matched	**IFNγ or IL-2**	n	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
	Original S	**IFNγ or IL-2**	n	
			Mean	

Time Point	Peptide Pool	Cytokine	Statistic	2 Dose Beta + Omicron (N=X)
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/CM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/EM	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/N	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	
		IFNγ or IL-2/TD	n	
			Mean	
			95% CI[a]	
			Response Rate	
			95% CI[b]	

Tables with Similar Format:

Table 398: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Overall – Per Protocol Population

Table 399: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Cohort – mITT Population

Table 400: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Cohort – Per Protocol Population

Table 401: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Cohort – mITT Population

Table 402: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Cohort – Per Protocol Population

Table 403: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 404: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 405: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 406: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 407: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 408: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 409: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 410: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Older Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 411: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 412: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 413: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 414: Mean Percentages of CD8 T Cells Expressing Cytokines with 95% CI, 2 Dose Group, Younger Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 415: Percent of Total B-cells by timepoint and Vaccination arm, Overall – mITT Population

Probe	Time Point	Statistic	Prototype (N=X)	1 Dose Beta + Omicron (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All 1 Dose Subjects (N=X)
NTD WT_SA+	Day 1	n	xx	xx	xx	xx	xx	xx
		Median (%)	xx.x	xx.x	xx.x	xx.x	xx.x	xx.x
		Min, Max (%)	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x
	Day 15	n	xx	xx	xx	xx	xx	xx
		Median (%)	xx.x	xx.x	xx.x	xx.x	xx.x	xx.x
		Min, Max (%)	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x
		Median Fold Rise	xx.x	xx.x	xx.x	xx.x	xx.x	xx.x
		Min, Max Fold Rise	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x	xx.x, xx.x
Repeat for probes for RBD WT+, RBD WT+ SA+, S2P SA+, S2P WT+, S2P WT+ SA+, Any probe. Include all available time points.								
N=number of subjects in group. n=number of subjects with data available at visit.								

Tables with Similar Format:

Table 416: Percent of Total B-cells by timepoint and Vaccination arm, Overall – Per Protocol Population

Table 417: Percent of Total B-cells by timepoint and Vaccination arm, Older Cohort – mITT Population

Table 418: Percent of Total B-cells by timepoint and Vaccination arm, Older Cohort – Per Protocol Population

Table 419: Percent of Total B-cells by timepoint and Vaccination arm, Younger Cohort – mITT Population

Table 420: Percent of Total B-cells by timepoint and Vaccination arm, Younger Cohort – Per Protocol Population

Table 421: Percent of Total B-cells by timepoint and Vaccination arm, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 422: Percent of Total B-cells by timepoint and Vaccination arm, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 423: Percent of Total B-cells by timepoint and Vaccination arm, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 424: Percent of Total B-cells by timepoint and Vaccination arm, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 425: Percent of Total B-cells by timepoint and Vaccination arm, Older Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 426: Percent of Total B-cells by timepoint and Vaccination arm, Older Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 427: Percent of Total B-cells by timepoint and Vaccination arm, Older Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 428: Percent of Total B-cells by timepoint and Vaccination arm, Older Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 429: Percent of Total B-cells by timepoint and Vaccination arm, Younger Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 430: Percent of Total B-cells by timepoint and Vaccination arm, Younger Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 431: Percent of Total B-cells by timepoint and Vaccination arm, Younger Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 432: Percent of Total B-cells by timepoint and Vaccination arm, Younger Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 433: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Overall – mITT Population

Probe	Time Point	Statistic	2 Dose Beta + Omicron (N=X)
NTD WT_SA+	Day 1	n	xx
		Median (%)	xx.x
		Min, Max (%)	xx.x, xx.x
	Day 15	n	xx
		Median (%)	xx.x
		Min, Max (%)	xx.x, xx.x
		Median Fold Rise	xx.x
		Min, Max Fold Rise	xx.x, xx.x
Repeat for probes for RBD WT+, RBD WT+ SA+, S2P SA+, S2P WT+, S2P WT+ SA+, Any probe. Include all available time points.			
N=number of subjects in group. n=number of subjects with data available at visit.			

Tables with Similar Format:

Table 434: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Overall – Per Protocol Population

Table 435: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Cohort – mITT Population

Table 436: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Cohort – Per Protocol Population

Table 437: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Cohort – mITT Population

Table 438: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Cohort – Per Protocol Population

Table 439: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 440: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 441: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 442: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 443: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 444: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 445: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 446: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Older Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 447: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Infected (by Self-Report or N-protein) Cohort – mITT Population

Table 448: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 449: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Table 450: Percent of Total B-cells by timepoint and Vaccination arm, 2 Dose Group, Younger Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Table 451: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Overall – mITT Population

Vaccination Group	Total Number Subjects with COVID-19 Infection	Proportion Infected at Day 29 (95% CI)[b]	Proportion Infected at Day 91 (95% CI)[b,c]	Proportion Infected at Day 181 (95% CI)[b,c]	Tau[a]	Restricted Mean Infection Time (Days)	
						Estimate	95% CI
Prototype	x					x.x	x.x, x.x
1 Dose Beta+Omicron	x					x.x	x.x, x.x
2 Dose Beta+Omicron	x					x.x	x.x, x.x
Delta+Omicron	x					x.x	x.x, x.x
Omicron	x					x.x	x.x, x.x
Omicron+Prototype	x					x.x	x.x, x.x

N= Number of subjects in the specified vaccination group.
[a] Tau is the truncation time point for the Restricted Mean Survival Time analysis and is equal to the minimum of the largest observed times in each group

[b]Kaplan-Meier Estimate and 95% confidence interval.

[c]91/181 days after last vaccination.

Programming Notes:

Within a subgroup:

```
proc lifetest data=dat plots=(rmst) method=breslow rmst(cl);
by subgroup;
time infday * Censor(1);
strata trtcode /diff=all;
ods output  rmst=rmst;
run;
```

Tables with Similar Formatting:

Table 452: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Younger Cohort– mITT Population

Table 453: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Older Cohort – mITT Population

Table 454: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Infected Cohort (By Self-Report or N-protein) – mITT Population

Table 455: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Uninfected Cohort (By Self Report or N-protein) – mITT Population

Table 456: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Younger Infected Cohort (By Self-Report or N-protein)– mITT Population

Table 457: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Younger Uninfected Cohort (By Self-Report or N-protein)– mITT Population

Table 458: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Older Infected Cohort (By Self-Report or N-protein)– mITT Population

Table 459: Time to Infection Restricted Mean Survival Analysis by Vaccination Group, Older Uninfected Cohort (By Self-Report or N-protein)– mITT Population

Table 460: Number of Breakthrough Infections by PANGO Call and Treatment Group, Overall – Safety Population

[Implementation Note: Listed variants are examples only, the sequenced variants will be included in the table. Percentages are based on the number of sequenced samples available during the interval.]

Interval	Variant	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
Day 1 to Day 8 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 9 to Day 15 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 16 to Day 29 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 30 to Day 91 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)

Interval	Variant	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 92 to Day 181 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 182 to Day 271 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Day 272 to Day 366 (n=x)	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Any Time Point **(n=x)**	D614G	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Beta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	Delta	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)

Interval	Variant	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
	BA.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	BA.4/5	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
	XBB.1	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)	x (xx.x%)
Note: N=Number of subjects in Safety Population with sequencing done. n=number of subjects with reported infections and sequencing available at a given visit.								

Tables with Similar Format:

Table 461: Breakthrough Infections by PANGO Call and Treatment Group, Older Cohort – Safety Population

Table 462: Breakthrough Infections by PANGO Call and Treatment Group, Younger Cohort – Safety Population

Table 463: Breakthrough Infections by PANGO Call and Treatment Group, Infected (by Self-Report or N-protein) Cohort – Safety Population

Table 464: Breakthrough Infections by PANGO Call and Treatment Group, Uninfected (by Self-Report or N-protein) Cohort – Safety Population

Table 465: Breakthrough Infections by PANGO Call and Treatment Group, Older Infected (by Self-Report or N-protein) Cohort – Safety Population

Table 466: Breakthrough Infections by PANGO Call and Treatment Group, Older Uninfected (by Self-Report or N-protein) Cohort – Safety Population

Table 467: Breakthrough Infections by PANGO Call and Treatment Group, Younger Infected (by Self-Report) Cohort – Safety Population

Table 468: Breakthrough Infections by PANGO Call and Treatment Group, Younger Uninfected (by Self-Report or N-protein) Cohort – Safety Population

14.3 Safety Data

14.3.1 Displays of Adverse Events

Table 469: Overall Summary of Adverse Events by Treatment Group – All Subjects

Subjects[a] with		Prototype (N=X)		Beta + Omicron (N=X)		Beta + Omicron (2 Doses) (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
Category 1	**Category 2**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
At least one local solicited adverse event	NA														
At least one systemic solicited adverse event	NA														
At least one unsolicited adverse event	NA														
At least one related unsolicited adverse event	Any Grade														
	Mild (Grade 1)														
	Moderate (Grade 2)														
	Severe (Grade 3)														
At least one severe (Grade 3) unsolicited adverse event	Any relationship														
	Related														
	Unrelated														
At least one serious adverse event[b]	Any relationship														
	Related														
	Unrelated														

Subjects[a] with		Prototype (N=X)		Beta + Omicron (N=X)		Beta + Omicron (2 Doses) (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
Category 1	**Category 2**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
At least one adverse event leading to early termination[c]	NA														
At least one Adverse Event of Special Interest	NA														
At least one medically attended adverse event	NA														
At least one new onset chronic medical condition	NA														

N = Number of subjects in the Safety Population
[a]Subjects are counted once for each category regardless of the number of events.
[b]A listing of Serious Adverse Events is included in Table 483.
[c]As reported on the Adverse Event eCRF.

Table 470: Serious Adverse Events and Non-Serious Adverse Events Occurring in 5% of Subjects in Any Treatment Group by MedDRA System Organ Class and Preferred Term, and Treatment Group – Safety Population

Preferred Term	MedDRA System Organ Class	Prototype (N=X)			Beta + Omicron (N=X)			Beta + Omicron (2 Doses) (N=X)			Delta + Omicron (N=X)			Omicron (N=X)			Omicron + Prototype (N=X)			All Subjects (N=X)		
		n	%	Events	n	%	Events	n	%	Events	n	%	Events	n	%	Events	n	%	Events	n	%	Events
Serious Adverse Events																						
All	All	x	x	x	x	x	x													x	x	x
PT1	SOC1	x	x	x	x	x	x													x	x	x
Etc.	Etc.																					
Other (Non-serious) Adverse Events																						
All	All	x	x	x	x	x	x													x	x	x
PT1	SOC1	x	x	x	x	x	x													x	x	x
Etc	Etc																					

N = number of subjects in the Safety Population (number of subjects at risk).
n = number of subjects reporting event.
Events = total frequency of events reported.

14.3.1.1 Solicited Adverse Events

Table 471: Number and Percentage of Subjects Experiencing Solicited Events with 95% Confidence Intervals by Symptom, Dose, and Treatment Group – Post Dose 1

		Prototype (N=X)		Beta + Omicron (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Any Symptom	**None**												
	Mild												
	Moderate												
	Severe												
Any Systemic Symptom	**None**												
	Mild												
	Moderate												
	Severe												
Arthralgia	**None**												
	Mild												
	Moderate												
	Severe												
Fatigue	**None**												
	Mild												
	Moderate												
	Severe												
Fever[a]	**None**												
	Mild												
	Moderate												

		Prototype (N=X)		Beta + Omicron (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
	Severe												
Feverishness	**None**												
	Mild												
	Moderate												
	Severe												
Headache	**None**												
	Mild												
	Moderate												
	Severe												
Myalgia	**None**												
	Mild												
	Moderate												
	Severe												
Nausea	**None**												
	Mild												
	Moderate												
	Severe												
Any Local Symptom	**None**												
	Mild												
	Moderate												
	Severe												
Erythema/Redness	**None**												

		Prototype (N=X)		Beta + Omicron (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
	Mild												
	Moderate												
	Severe												
Erythema/Redness Measurement (mm)	**None**												
	Mild												
	Moderate												
	Severe												
Induration/Swelling	**None**												
	Mild												
	Moderate												
	Severe												
Induration/Swelling Measurement (mm)	**None**												
	Mild												
	Moderate												
	Severe												
Pain	**None**												
	Mild												
	Moderate												
	Severe												

Severity is the maximum severity reported over all solicited symptoms post dosing for each subject.
N=All subjects receiving vaccination with any solicited event data recorded in the database.

Table 472: Number and Percentage of Subjects Experiencing Solicited Events with 95% Confidence Intervals by Symptom, Dose, and Treatment Group – Two Dose Treatment Group

		Beta + Omicron (2 Doses) Post Dose 2 (N=X)		Beta + Omicron (2 Doses) Post Either Dose (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**
Any Symptom	**None**				
	Mild				
	Moderate				
	Severe				
Any Systemic Symptom	**None**				
	Mild				
	Moderate				
	Severe				
Arthralgia	**None**				
	Mild				
	Moderate				
	Severe				
Fatigue	**None**				
	Mild				
	Moderate				
	Severe				
Fever[a]	**None**				
	Mild				
	Moderate				
	Severe				

		Beta + Omicron (2 Doses) Post Dose 2 (N=X)		Beta + Omicron (2 Doses) Post Either Dose (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**
Feverishness	**None**				
	Mild				
	Moderate				
	Severe				
Headache	**None**				
	Mild				
	Moderate				
	Severe				
Myalgia	**None**				
	Mild				
	Moderate				
	Severe				
Nausea	**None**				
	Mild				
	Moderate				
	Severe				
Any Local Symptom	**None**				
	Mild				
	Moderate				
	Severe				
Erythema/Redness	**None**				
	Mild				

		Beta + Omicron (2 Doses) Post Dose 2 (N=X)		Beta + Omicron (2 Doses) Post Either Dose (N=X)	
Symptom	**Severity**	**n**	**%**	**n**	**%**
	Moderate				
	Severe				
Erythema/Redness Measurement (mm)	**None**				
	Mild				
	Moderate				
	Severe				
Induration/Swelling	**None**				
	Mild				
	Moderate				
	Severe				
Induration/Swelling Measurement (mm)	**None**				
	Mild				
	Moderate				
	Severe				
Pain	**None**				
	Mild				
	Moderate				
	Severe				

Table 473: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Prototype

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Any Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Systemic Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Arthralgia	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fatigue	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fever	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Feverishness	**None**																						
	Mild																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
	Moderate																						
	Severe																						
Headache	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Myalgia	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Nausea	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Local Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Erythema/Redness	**None**																						
	Mild																						
	Moderate																						
	Severe																						
	None																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Erythema/Redness Measurement (mm)	**Mild**																						
	Moderate																						
	Severe																						
Induration/Swelling	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Induration/Swelling Measurement (mm)	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Pain	**None**																						
	Mild																						
	Moderate																						
	Severe																						

Notes: N=Number of subjects in the Safety Population.
Severity is the maximum severity reported post dosing for each subject for each day.
[1] Day 8+ includes the maximum severity of each symptom reported on or after Day 8 (includes ongoing symptoms)
[2] Indicates how many subjects had "None", "Mild", "Moderate", or "Severe" as their maximum severity for any day. A subject may be counted in more than one of these categories.

Tables with Similar Format:

Implementation note: For any symptoms or days with missing data, add a "Not Reported" row.

Table 474: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Beta + Omicron

Table 475: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Delta + Omicron

Table 476: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Omicron

Table 477: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Omicron + Prototype

Table 478: Summary of Solicited Events by Days Post Treatment, Symptom, and Treatment Group – Beta+Omicron

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Dose 2																							
Any Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Systemic Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Arthralgia	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fatigue	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fever	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Feverishness	**None**																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
	Mild																						
	Moderate																						
	Severe																						
Headache	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Myalgia	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Nausea	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Local Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Erythema/Redness	**None**																						
	Mild																						
	Moderate																						
	Severe																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Erythema/Redness Measurement (mm)	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Induration/Swelling	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Induration/Swelling Measurement (mm)	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Pain	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Dose																							
Any Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
	None																						
	Mild																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Any Systemic Symptom	**Moderate**																						
	Severe																						
Arthralgia	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fatigue	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Fever	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Feverishness	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Headache	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Myalgia	**None**																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
	Mild																						
	Moderate																						
	Severe																						
Nausea	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Any Local Symptom	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Erythema/Redness	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Erythema/Redness Measurement (mm)	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Induration/Swelling	**None**																						
	Mild																						
	Moderate																						
	Severe																						

		Pre-Dose (N=X)		Post-Dose (N=X)		Day 1 (N=X)		Day 2 (N=X)		Day 3 (N=X)		Day 4 (N=X)		Day 5 (N=X)		Day 6 (N=X)		Day 7 (N=X)		Day 8+ [1] (N=X)		Any Post-Dose[2]	
Symptom	**Severity**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Induration/Swelling Measurement (mm)	**None**																						
	Mild																						
	Moderate																						
	Severe																						
Pain	**None**																						
	Mild																						
	Moderate																						
	Severe																						

Notes: N=Number of subjects in the Safety Population.
Severity is the maximum severity reported post dosing for each subject for each day.
[1] Day 8+ includes the maximum severity of each symptom reported on or after Day 8 (includes ongoing symptoms)
[2] Indicates how many subjects had “None”, “Mild”, “Moderate”, or “Severe” as their maximum severity for any day. A subject may be counted in more than one of these categories.

Table 479: Summary of Duration of Solicited Symptoms by Treatment Group - All Subjects

Variable	Statistic	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
Any Symptom	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Any Systemic Symptom	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Arthralgia	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Fatigue	n							

Variable	Statistic	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Fever	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Feverishness	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Headache	n							
	Mean							
	Standard Deviation							

Variable	Statistic	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
	Median							
	Minimum							
	Maximum							
Myalgia	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Nausea	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Any Local Symptom	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							

Variable	Statistic	Prototype (N=X)	Beta + Omicron (N=X)	Beta + Omicron (Second Dose) (N=X)	Delta + Omicron (N=X)	Omicron (N=X)	Omicron + Prototype (N=X)	All Subjects (N=X)
Erythema/redness	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Induration/swelling	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							
Pain	n							
	Mean							
	Standard Deviation							
	Median							
	Minimum							
	Maximum							

Notes: N=Number of subjects in the Safety Population.
n=Number of solicited adverse events.

14.3.1.2 Unsolicited Adverse Events

Table 480: All Adverse Events Cross-Classified by MedDRA System Organ Class, Severity, Relationship to Study Treatment, and Treatment Group

			Relationship to Vaccination		
Treatment Group	**MedDRA System Organ Class**	**Severity**	**Not Related (n)**	**Related (n)**	**Not Yet Determined (n)**
Prototype (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
Beta + Omicron (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
Beta + Omicron (Post Second Dose) (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
Delta + Omicron (N=X)	Any SOC	Mild			
		Moderate			

			Relationship to Vaccination		
Treatment Group	**MedDRA System Organ Class**	**Severity**	**Not Related (n)**	**Related (n)**	**Not Yet Determined (n)**
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
Omicron (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
Omicron + Prototype (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			
All Subjects (N=X)	Any SOC	Mild			
		Moderate			
		Severe			
	[Repeat for all reported SOC]	Mild			
		Moderate			
		Severe			

			Relationship to Vaccination		
Treatment Group	**MedDRA System Organ Class**	**Severity**	**Not Related (n)**	**Related (n)**	**Not Yet Determined (n)**
Notes: N=Number of subjects in the Safety Population. n=Number of events.					

Table 481: Summary of All Unsolicited Adverse Events by MedDRA System Organ Class and Preferred Term, Severity, Relationship, and Treatment Group

				Severity			Relationship to Study Vaccination		
Treatment Group	**System Organ Class (SOC)**	**Preferred Term (PT)**	**Total Events (n)**	**Mild (n)**	**Moderate (n)**	**Severe (n)**	**Not Related (n)**	**Related (n)**	**Not Yet Determined (n)**
Prototype (N=X)	Any SOC	Any PT							
	Gastrointestinal disorders	Any PT							
		Flatulence							
		Vomiting							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							
Beta + Omicron (N=X)	Any SOC	Any PT							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							
Beta + Omicron (Post Second Dose) (N=X)	Any SOC	Any PT							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							
Delta + Omicron (N=X)	Any SOC	Any PT							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							
Omicron (N=X)	Any SOC	Any PT							
		Any PT							

				Severity			Relationship to Study Vaccination		
Treatment Group	**System Organ Class (SOC)**	**Preferred Term (PT)**	**Total Events (n)**	**Mild (n)**	**Moderate (n)**	**Severe (n)**	**Not Related (n)**	**Related (n)**	**Not Yet Determined (n)**
	[Repeat for all reported SOC]	[Repeat for all reported PT]							
Omicron + Prototype (N=X)	Any SOC	Any PT							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							
All Subjects (N=X)	Any SOC	Any PT							
	[Repeat for all reported SOC]	Any PT							
		[Repeat for all reported PT]							

Notes: N=Number of subjects in the Safety Population.
n=Number of events.

Table 482: Number and Percentage of Subjects Experiencing Unsolicited Adverse Events by MedDRA® System Organ Class and Preferred Term, Severity, Relationship, and Treatment Group

					Severity						Relationship to Study Vaccination			
			Any Incidence		Mild		Moderate		Severe		Not Related		Related	
Treatment Group	MedDRA System Organ Class	MedDRA Preferred Term	n	%	n	%	n	%	n	%	n	%	n	%
Prototype (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												
Beta + Omicron (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												
Beta + Omicron (Post Second Dose) (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												
Delta + Omicron (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												
Omicron (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												

					Severity						Relationship to Study Vaccination			
			Any Incidence		Mild		Moderate		Severe		Not Related		Related	
Treatment Group	**MedDRA System Organ Class**	**MedDRA Preferred Term**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Omicron + Prototype (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												
All Subjects (N=X)	Any SOC	Any PT												
	[Repeat for all reported SOC]	Any PT												
		[Repeat for all reported PT]												

Note: N=Number of subjects in the Safety Population.
n=Number of subjects reporting event with the specified SOC.
This table presents number and percentage of subjects. A subject is only counted once per PT and is summarized according to their highest severity and closest relationship.

14.3.2 Listing of Deaths, Other Serious and Significant Adverse Events

Table 483: Listing of Serious Adverse Events

Adverse Event	Associated with Dose No.	No. of Days Post Associated Dose (Duration)	No. of Days Post Dose the Event Became Serious	Reason Reported as an SAE	Severity	Relationship to Study Treatment	If Not Related, Alternative Etiology	Action Taken with Study Treatment	Subject Discontinued Due to AE	Outcome	MedDRA System Organ Class	MedDRA Preferred Term
Subject ID: , Treatment Group: , AE Number:												
Comments:												
Subject ID: , Treatment Group: , AE Number:												
Comments:												

Table 484: Listing of Non-Serious, Unsolicited, Moderate or Severe Adverse Events

Adverse Event	Associated with Dose No.	No. of Days Post Associated Dose (Duration)	Severity	Relationship to Study Treatment	If Not Related, Alternative Etiology	Action Taken with Study Treatment	Subject Discontinued Due to AE	Outcome	MedDRA System Organ Class	MedDRA Preferred Term
Subject ID: , Treatment Group: , AE Number:										
Comments:										
Subject ID: , Treatment Group: , AE Number:										
Comments:										

Table 485: Listing of AESIs, MAAEs and NOCMCs

Subject ID	Treatment Group	Event Description	Date of Product Administration[a]	Duration of Event	Date of Onset	MedDRA® Sytem Organ Class	MAAEs	NOCMCs	AESI	Relationship[b]	Outcome

14.3.3 Narratives of Deaths, Other Serious and Significant Adverse Events

(not included in SAP, but this is a placeholder for the CSR)

14.3.4 Abnormal Laboratory Value Listings (by Subject)

Not Applicable.

14.3.5 Displays of Laboratory Results

Not Applicable.

14.3.6 Displays of Vital Signs

Not Applicable.

14.4 Summary of Concomitant Medications

Table 486: Number and Percentage of Subjects with Prior and Concurrent Medications by WHO Drug Classification and Treatment Group

WHO Drug Code Level 1, Anatomic Group	WHO Drug Code Level 2, Therapeutic Subgroup	Prototype (N=X)		Beta + Omicron (N=X)		Beta + Omicron (Second Dose) (N=X)		Delta + Omicron (N=X)		Omicron (N=X)		Omicron + Prototype (N=X)		All Subjects (N=X)	
		n	%	n	%	n	%	n	%	n	%	n	%	n	%
Any Level 1 Codes	Any Level 2 Codes	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx	x	xx
[ATC Level 1 - 1]	Any [ATC 1 – 1]														
	[ATC 2 - 1]														
	[ATC 2 - 2]														
	[ATC 2 - 3]														
[ATC Level 1 – 2]	[ATC 2 - 1]														
	[ATC 2 - 2]														
	[ATC 2 - 3]														

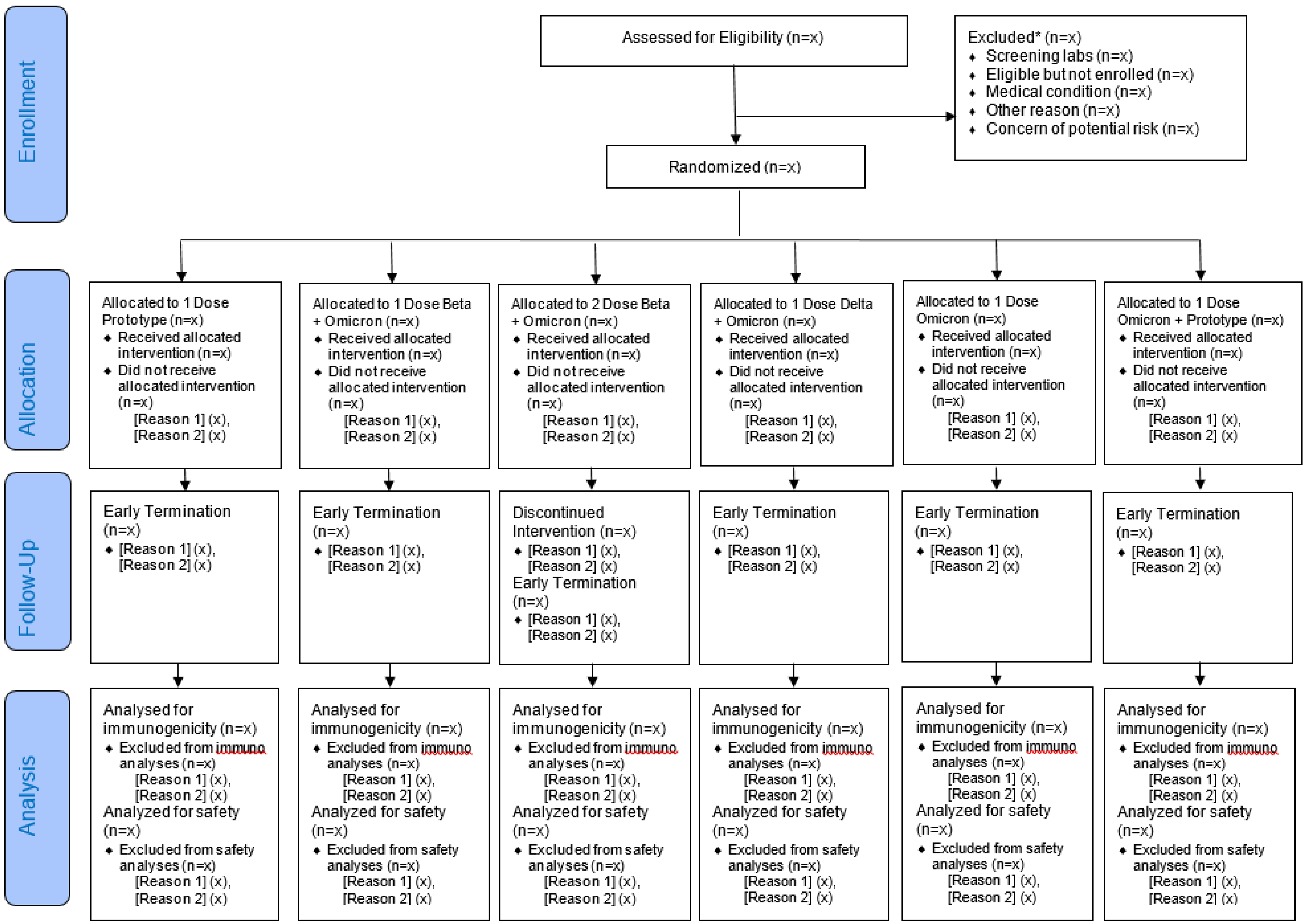
N = [define the population for this table, e.g., Number of subjects in the Safety Population].
n=Number of subjects reporting taking at least one medication in the specific WHO Drug Class.

APPENDIX 2. FIGURE MOCK-UPS

LIST OF FIGURES

10.1 Disposition of Subjects

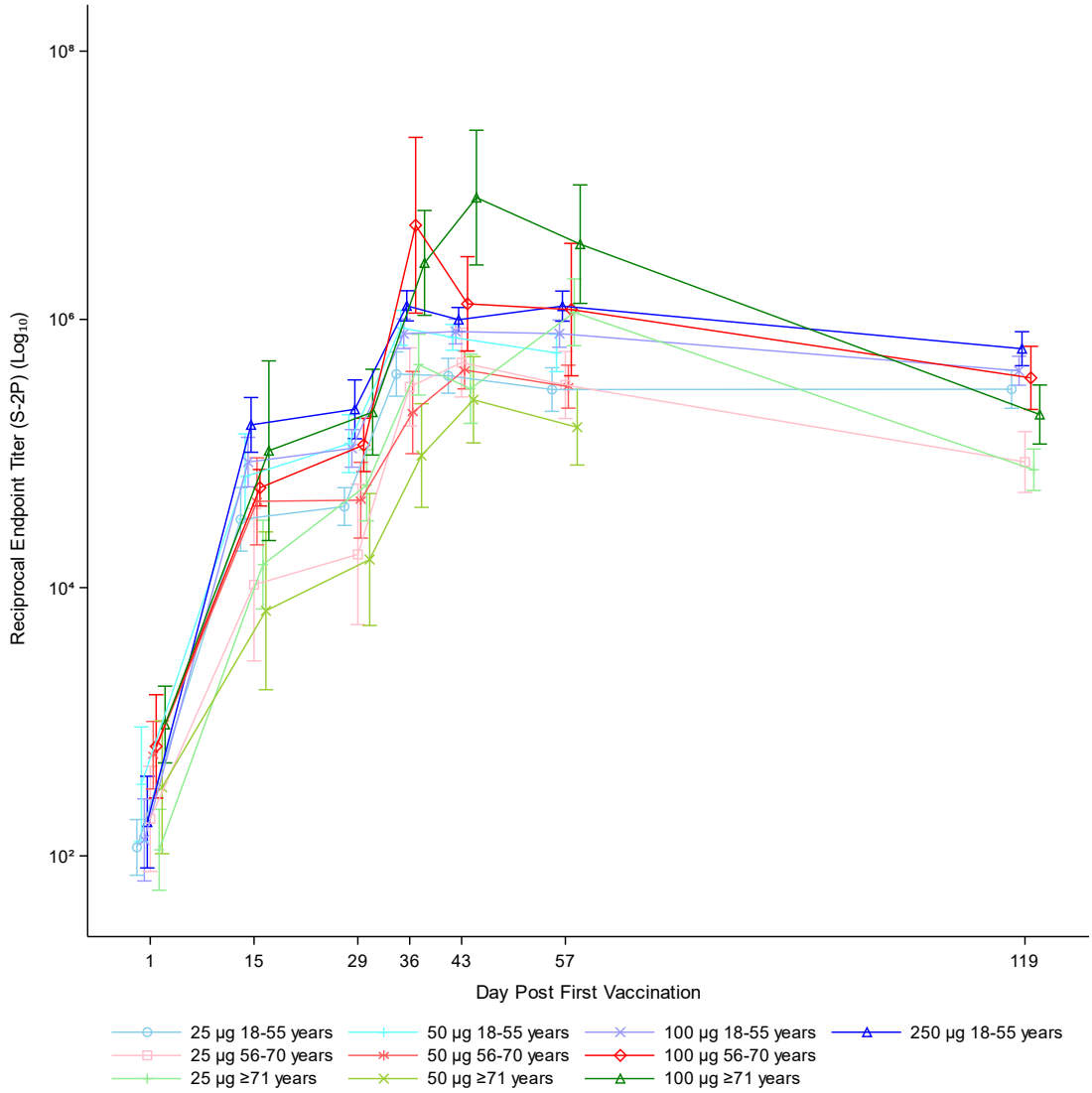
Figure 1: CONSORT Flow Diagram



14.2.2 Immunogenicity Response Figures by Measure, Treatment/Vaccination, and Time Point

Figure 2: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Overall – mITT Population

[Implementation Note: Below is an example figure. Lines will be shown for each variant. Y-axis label will say Area Under the Curve (Log_{10}).]



Figures with Similar Format:

Figure 3: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Overall – Per Protocol Population

Figure 4: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Cohort – mITT Population

Figure 5: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Cohort – Per Protocol Population

Figure 6: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Older Cohort – mITT Population

Figure 7: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Older Cohort – Per Protocol Population

Figure 8: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – mITT Population

Figure 9: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Figure 10: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Figure 11: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Figure 12: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Infected (by Self-Report or N-protein) Cohort – mITT Population

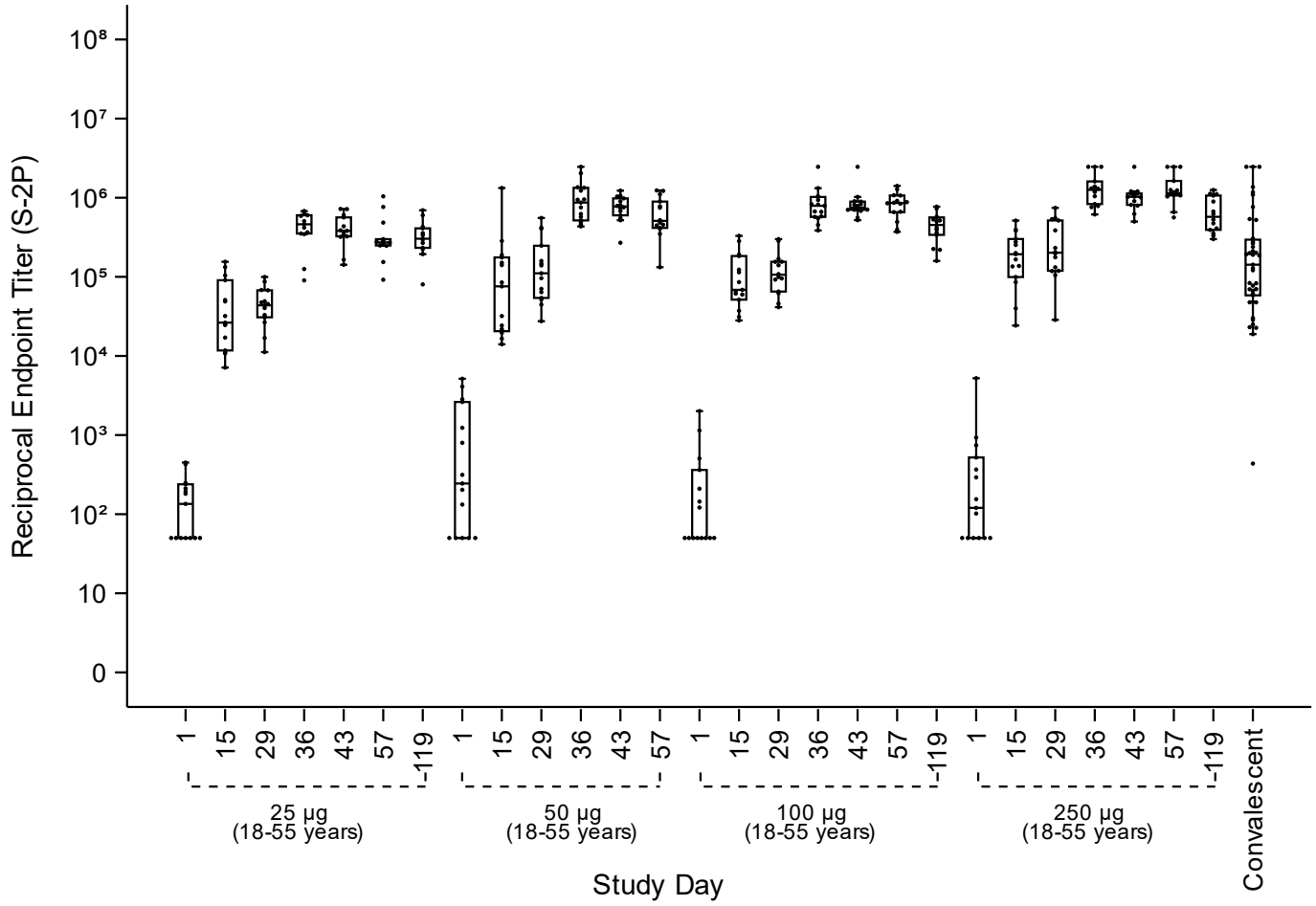
Figure 13: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Infected (by Self-Report or N-protein) Cohort – Per Protocol Population

Figure 14: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Uninfected (by Self-Report or N-protein) Cohort – mITT Population

Figure 15: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Geometric Mean by Time Point and Variant, Prototype, Younger Uninfected (by Self-Report or N-protein) Cohort – Per Protocol Population

Figure 326: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Distribution by Time Point and Variant, Prototype, Overall – mITT Population

[Implementation Note: Below is an example figure. Group boxplots by variant instead of by treatment arm as in the example figure. Y-axis label will say Area Under the Curve (Log_{10}). Include lines to connect points between each box plot over time (the lines will connect the points for a subject).]



Figures with Similar Format:

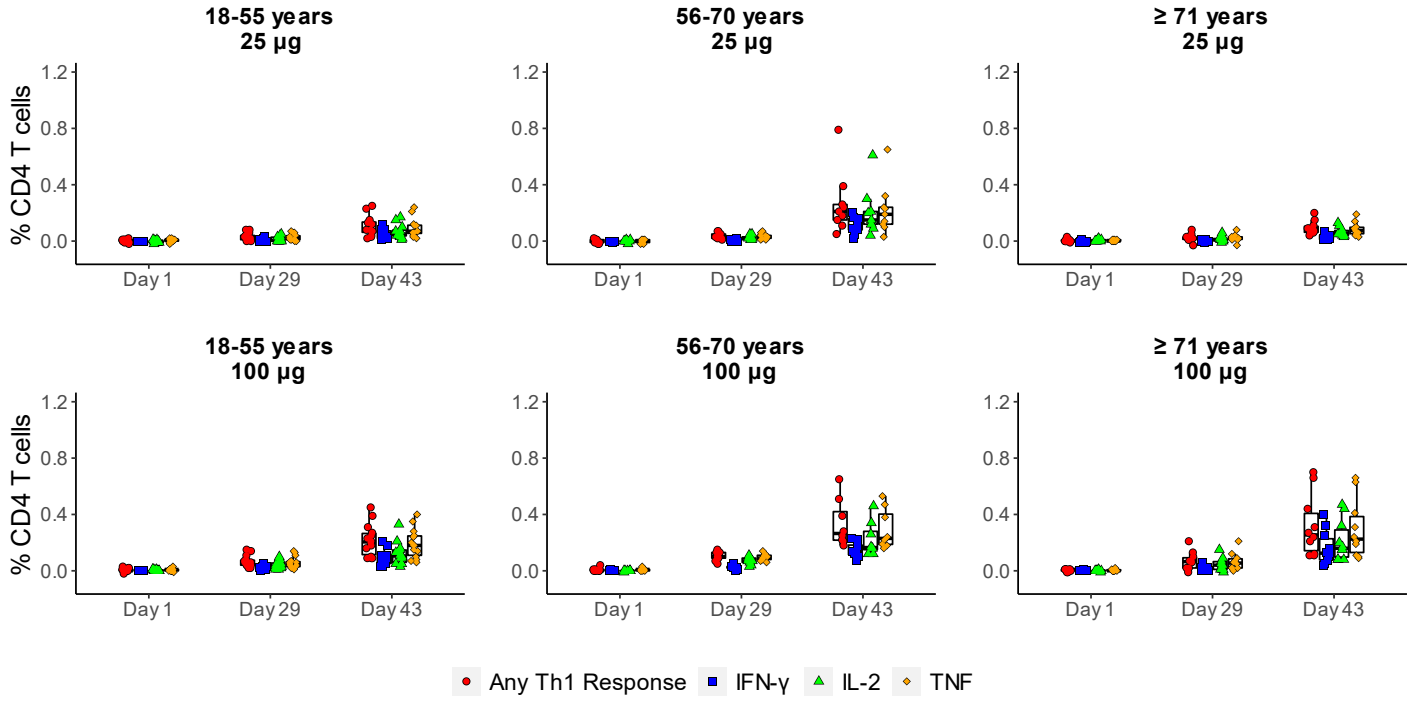
Figure 327: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Distribution by Time Point and Variant, Prototype, Overall – Per Protocol Population

Figure 328: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Distribution by Time Point and Variant, Prototype, Younger Cohort – mITT Population

Figure 329: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Distribution by Time Point and Variant, Prototype, Younger Cohort – Per Protocol Population

Figure 330: Serum IgG Binding Assay Area Under the Curve Measured by ECLIA 10-plex Distribution by Time Point and Variant, Prototype, Older Cohort – mITT Population

Figure 650: Percentages of CD4 T Cells Expressing Th1 Cytokines S1 Peptide Pool, Overall - mITT Population



Implementation Note:

Figure shown is an example. Have one plot for each of the 6 treatment arms. Along the x-axis should be each of the study days (Days 1, 15, 91, 181, and 271 for 1 dose treatment arms and Days 1, 15, 57, 71, 147, 237, and 327 for 2 dose treatment arms).

Figures with Similar Format:

Figure 651: Percentages of CD4 T Cells Expressing Th1 Cytokines S1 Peptide Pool, Overall - Per Protocol Population

Figure 652: Percentages of CD4 T Cells Expressing Th2 Cytokines S1 Peptide Pool, Overall - mITT Population

Figure 653: Percentages of CD4 T Cells Expressing Th2 Cytokines S1 Peptide Pool, Overall - Per Protocol Population

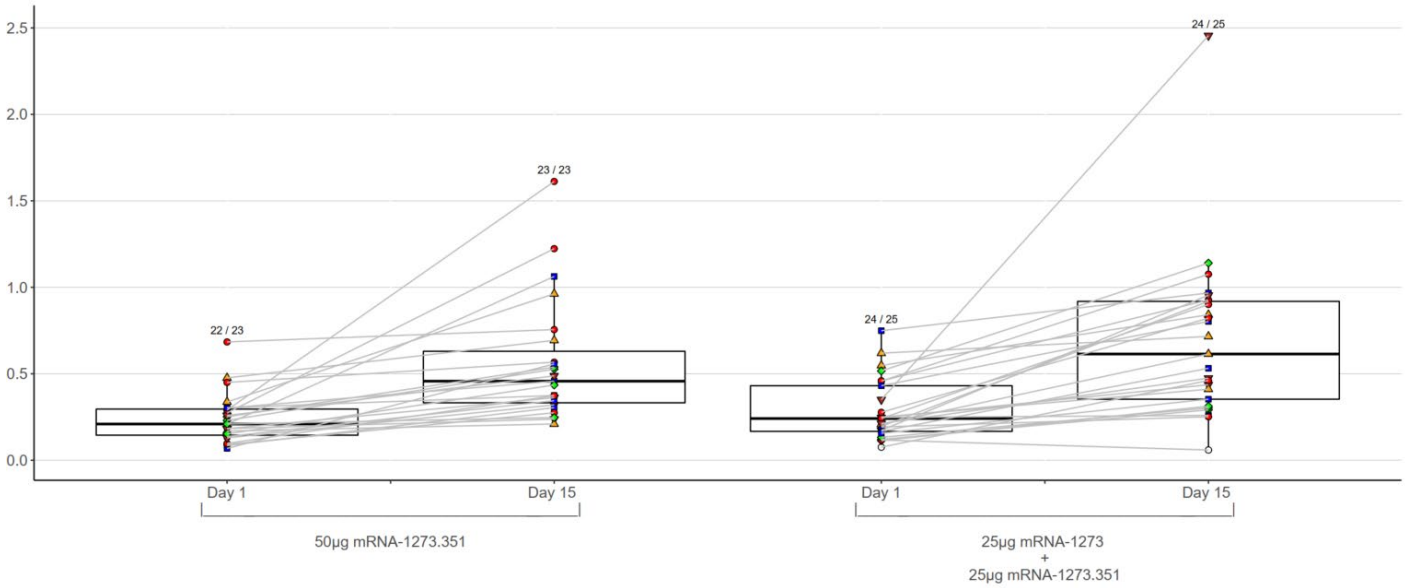
Figure 654: Percentages of CD4 T Cells Expressing Th1 Cytokines S2 Peptide Pool, Overall - mITT Population

Figure 655: Percentages of CD4 T Cells Expressing Th1 Cytokines S2 Peptide Pool, Overall - Per Protocol Population

Figure 656: Percentages of CD4 T Cells Expressing Th2 Cytokines S2 Peptide Pool, Overall - mITT Population

Figure 657: Percentages of CD4 T Cells Expressing Th2 Cytokines S2 Peptide Pool, Overall - Per Protocol Population

Figure 758: Distribution of Percent of IgG B-cells expressing RBD Prototype-Beta by timepoint and Vaccination arm, Overall - mITT Population



Figures with similar format:

Figure 759: Distribution of Percent of IgG B-cells expressing RBD Prototype-Beta by timepoint and Vaccination arm, Overall – Per Protocol Population

Figure 760: Distribution of Percent of IgG B-cells expressing RBD Prototype-Delta by timepoint and Vaccination arm, Overall – mITT Population

Figure 761: Distribution of Percent of IgG B-cells expressing RBD Prototype-Delta by timepoint and Vaccination arm, Overall – Per Protocol Population

Figure 762: Distribution of Percent of IgG B-cells expressing RBD Prototype-Beta-Delta by timepoint and Vaccination arm, Overall – mITT Population

Figure 763: Distribution of Percent of IgG B-cells expressing RBD Prototype-Beta-Delta by timepoint and Vaccination arm, Overall – Per Protocol Population

Figure 764: Distribution of Percent of IgG B-cells expressing RBD Prototype-Omicron by timepoint and Vaccination arm, Overall – mITT Population

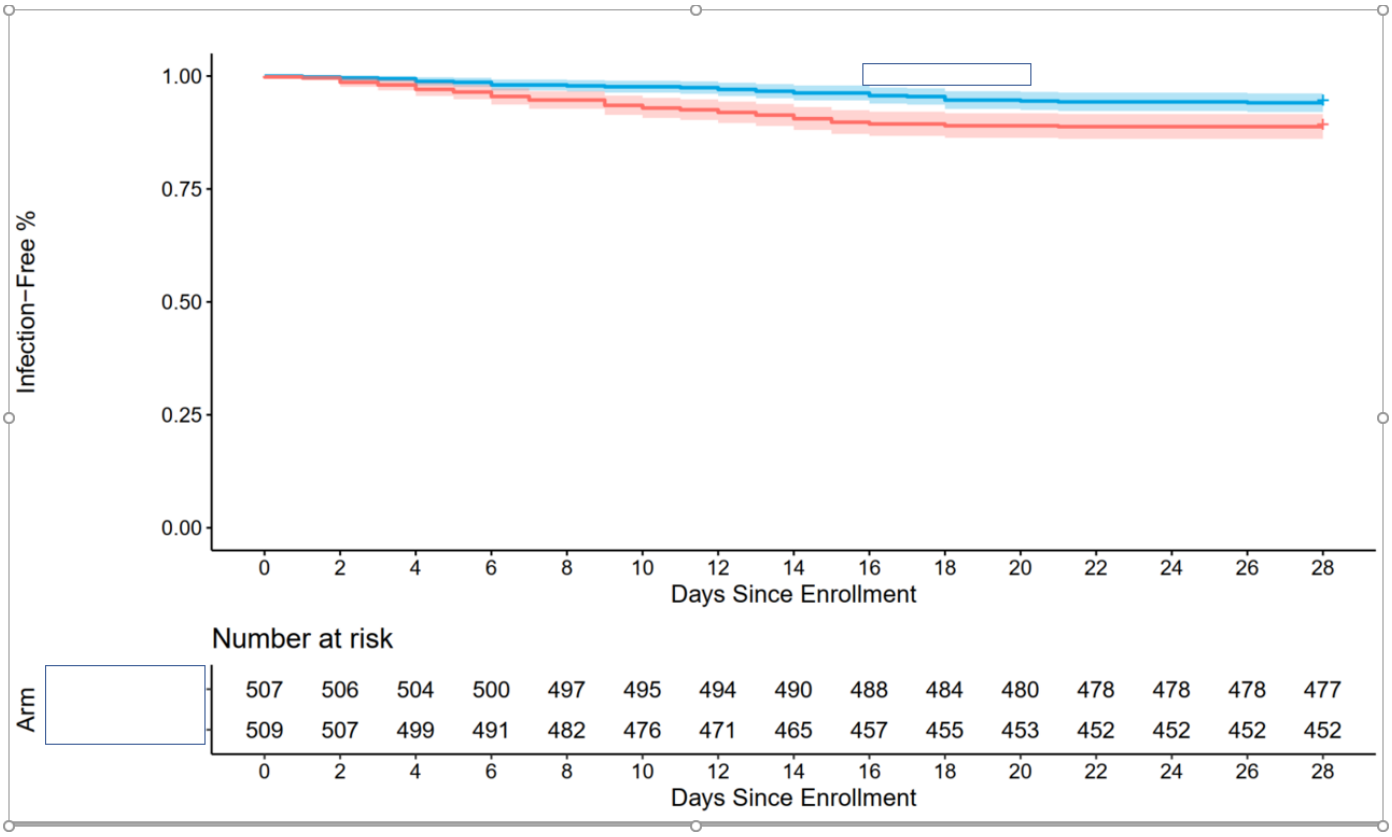
Figure 765: Distribution of Percent of IgG B-cells expressing RBD Prototype-Omicron by timepoint and Vaccination arm, Overall – Per Protocol Population

Figure 766: Distribution of Percent of IgG B-cells expressing RBD Prototype-Omicron-Beta by timepoint and Vaccination arm, Overall – mITT Population

Figure 767: Distribution of Percent of IgG B-cells expressing RBD Prototype-Omicron-Beta by timepoint and Vaccination arm, Overall – Per Protocol Population

Figure 768: Distribution of Percent of IgG B-cells expressing RBD Prototype-Omicron-Delta-Beta by timepoint and Vaccination arm, Overall – mITT Population

Figure 1010: Time to Infection Kaplan-Meier Curve by Vaccination Group, Overall - mITT Population



Implementation Note: A separate curve will be shown for each vaccination group.

Figures with Similar Format:

Figure 1011: Time to Infection Kaplan-Meier Curve by Vaccination Group, Younger Cohort- mITT Population

Figure 1012: Time to Infection Kaplan-Meier Curve by Vaccination Group, Older Cohort - mITT Population

Figure 1013: Time to Infection Kaplan-Meier Curve by Vaccination Group, Infected Cohort (By Self-report or N-protein)- mITT Population

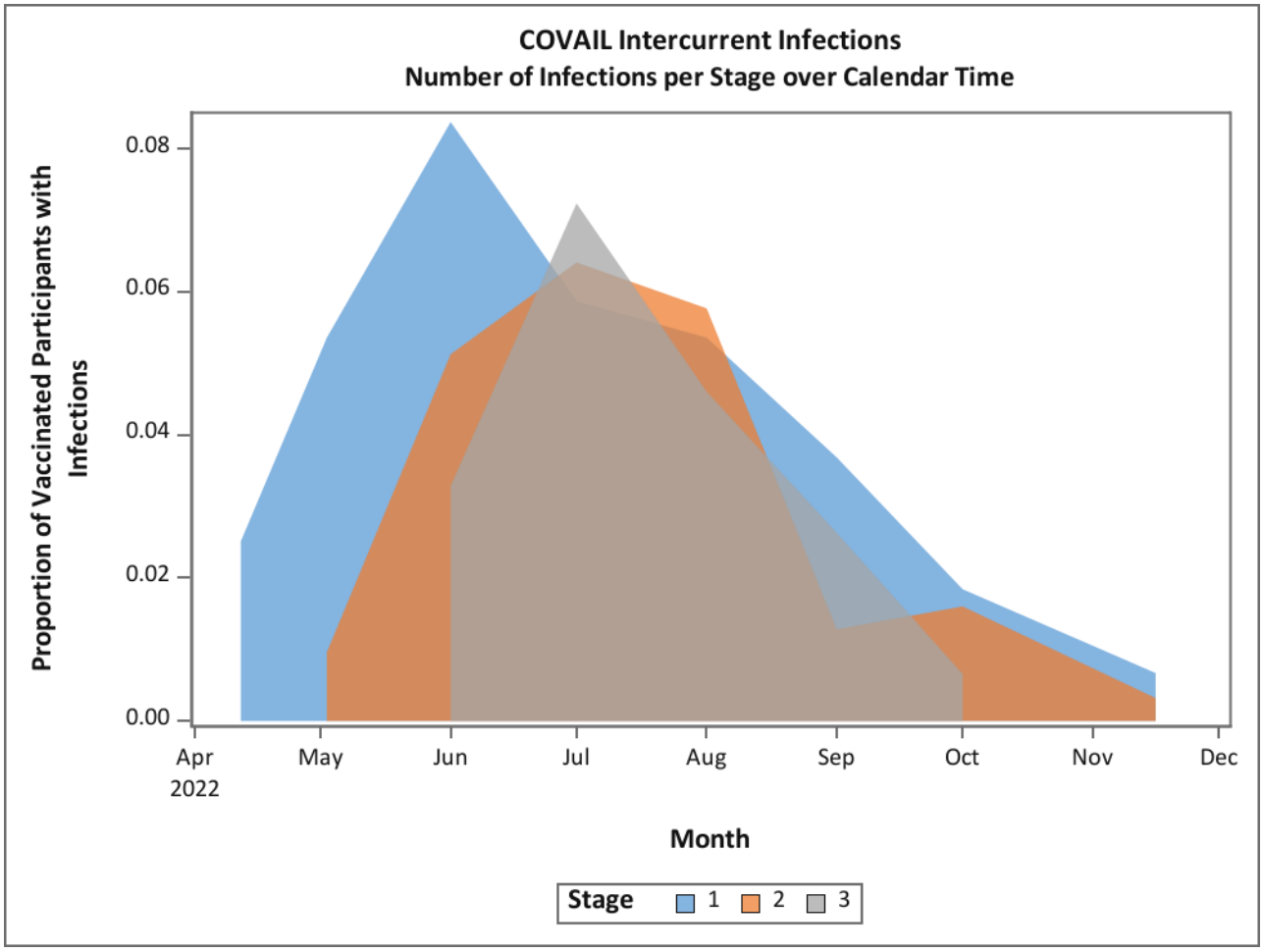
Figure 1014: Time to Infection Kaplan-Meier Curve by Vaccination Group, Uninfected Cohort (By Self-report or N-protein) - mITT Population

Figure 1015: Time to Infection Kaplan-Meier Curve by Vaccination Group, Younger Infected Cohort (By Self-report or N-protein) - mITT Population

Figure 1016: Time to Infection Kaplan-Meier Curve by Vaccination Group, Younger Uninfected Cohort (By Self-report or N-protein) - mITT Population

Figure 1019: Summary of Breakthrough Infections by PANGO Call and Treatment Group, Prototype – Safety Population

[Implementation Note: Figure will be color coded by PANGO Call.]



Figures with Similar Format:

Figure 1020: Summary of Breakthrough Infections by PANGO Call and Treatment Group, 1 Dose Beta + Omicron – Safety Population

Figure 1021: Summary of Breakthrough Infections by PANGO Call and Treatment Group, 2 Dose Beta + Omicron – Safety Population

Figure 1022: Summary of Breakthrough Infections by PANGO Call and Treatment Group, Delta + Omicron – Safety Population

Figure 1023: Summary of Breakthrough Infections by PANGO Call and Treatment Group, Omicron – Safety Population

Figure 1024: Summary of Breakthrough Infections by PANGO Call and Treatment Group, Omicron + Prototype – Safety Population

14.3.1.1 Solicited Adverse Events

Figure 1025: Maximum Severity of Solicited Systemic Symptoms per Subject by Day Post Vaccination and Treatment Group – Dose 1

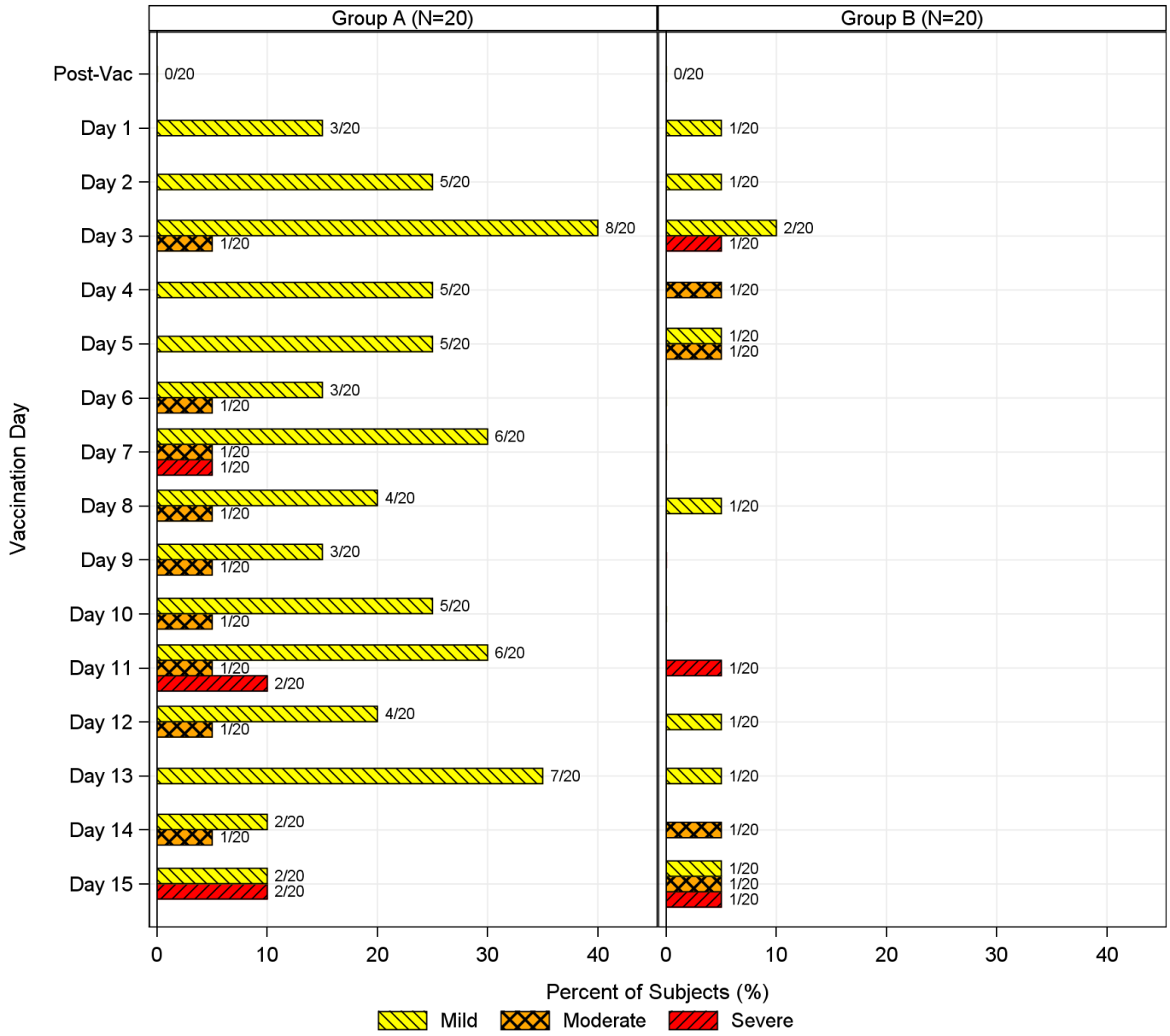


Figure with Similar Format:

Figure 1026: Maximum Severity of Solicited Systemic Symptoms per Subject by Day Post Vaccination and Treatment Group – Dose 2

Figure 1027: Maximum Severity of Solicited Local Symptoms per Subject by Day Post Vaccination and Treatment Group – Dose 1

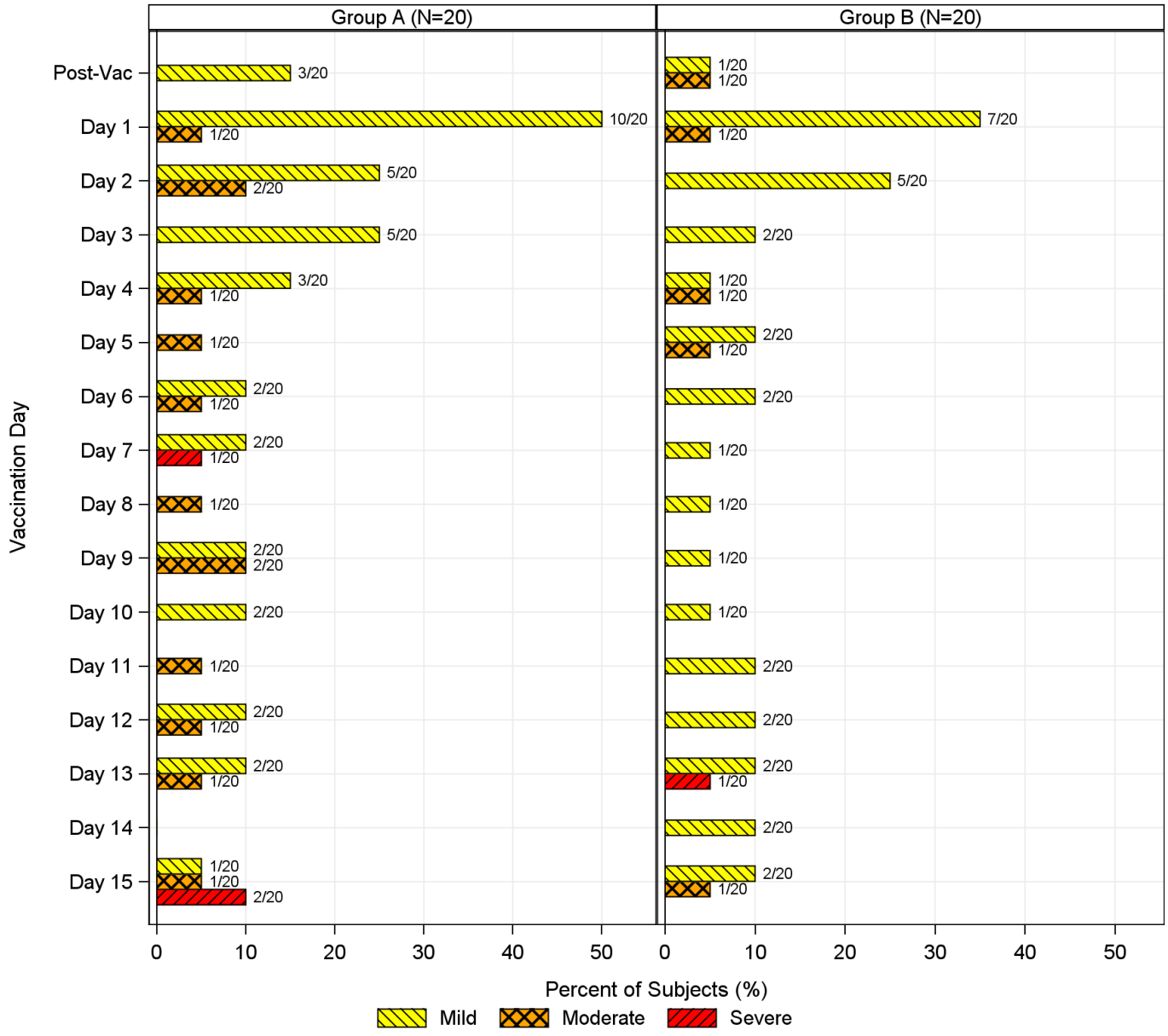
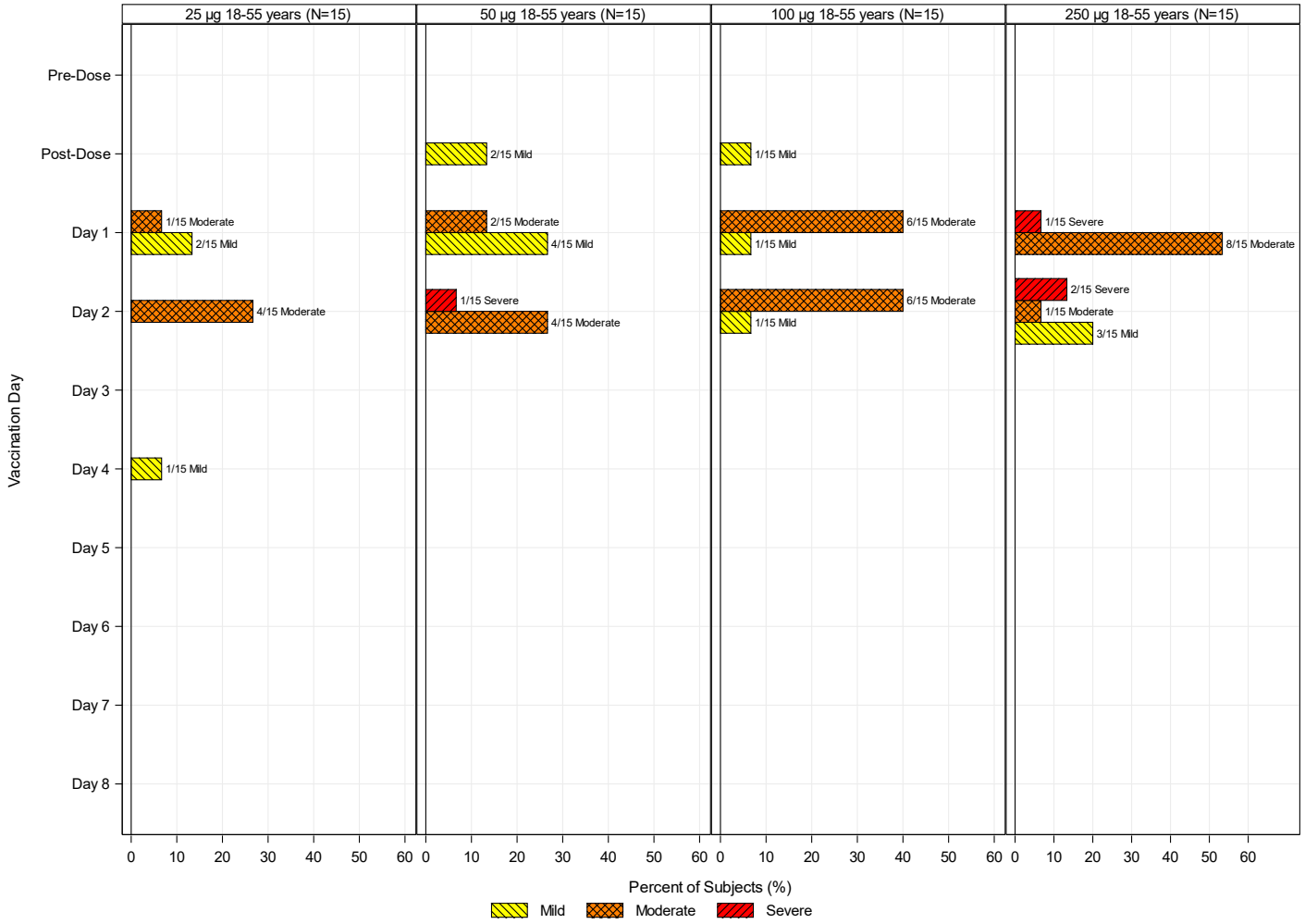


Figure with Similar Format:

Figure 1028: Maximum Severity of Solicited Local Symptoms per Subject by Day Post Vaccination and Treatment Group – Dose 2

Figure 1029: Onset of Solicited Systemic Symptoms by Days Post Vaccination and Treatment Group – Dose 1

[Implementation Note: Have a panel for each treatment group.]



Figures with Similar Format:

Figure 1030: Onset of Solicited Systemic Symptoms by Days Post Vaccination and Treatment Group – Dose 2

Figure 1031: Onset of Solicited Local Symptoms by Days Post Vaccination and Treatment Group – Dose 1

Figure 1032: Onset of Solicited Local Symptoms by Days Post Vaccination and Treatment Group – Dose 2

Figure 1033: Solicited Symptoms by Days Post Vaccination and Treatment Group– Arthralgia

Figures with Similar Format:

Figure 1034: Solicited Symptoms by Days Post Vaccination and Treatment Group– Chills

Figure 1035: Solicited Symptoms by Days Post Vaccination and Treatment Group– Erythema

Figure 1036: Solicited Symptoms by Days Post Vaccination and Treatment Group– Erythema (mm)

Figure 1037: Solicited Symptoms by Days Post Vaccination and Treatment Group– Fatigue

Figure 1038: Solicited Symptoms by Days Post Vaccination and Treatment Group– Fever

Figure 1039: Solicited Symptoms by Days Post Vaccination and Treatment Group– Headache

Figure 1040: Solicited Symptoms by Days Post Vaccination and Treatment Group– Induration

Figure 1041: Solicited Symptoms by Days Post Vaccination and Treatment Group– Induration (mm)

Figure 1042: Solicited Symptoms by Days Post Vaccination and Treatment Group– Myalgia

Figure 1043: Solicited Symptoms by Days Post Vaccination and Treatment Group– Nausea

Figure 1044: Solicited Symptoms by Days Post Vaccination and Treatment Group– Pain

14.3.1.2 Unsolicited Adverse Events

Figure 1045: Frequency of Adverse Events by MedDRA System Organ Class and Severity

[Implementation Note: Have a panel for each treatment group for Dose 1 and a seventh panel for Dose 2.]

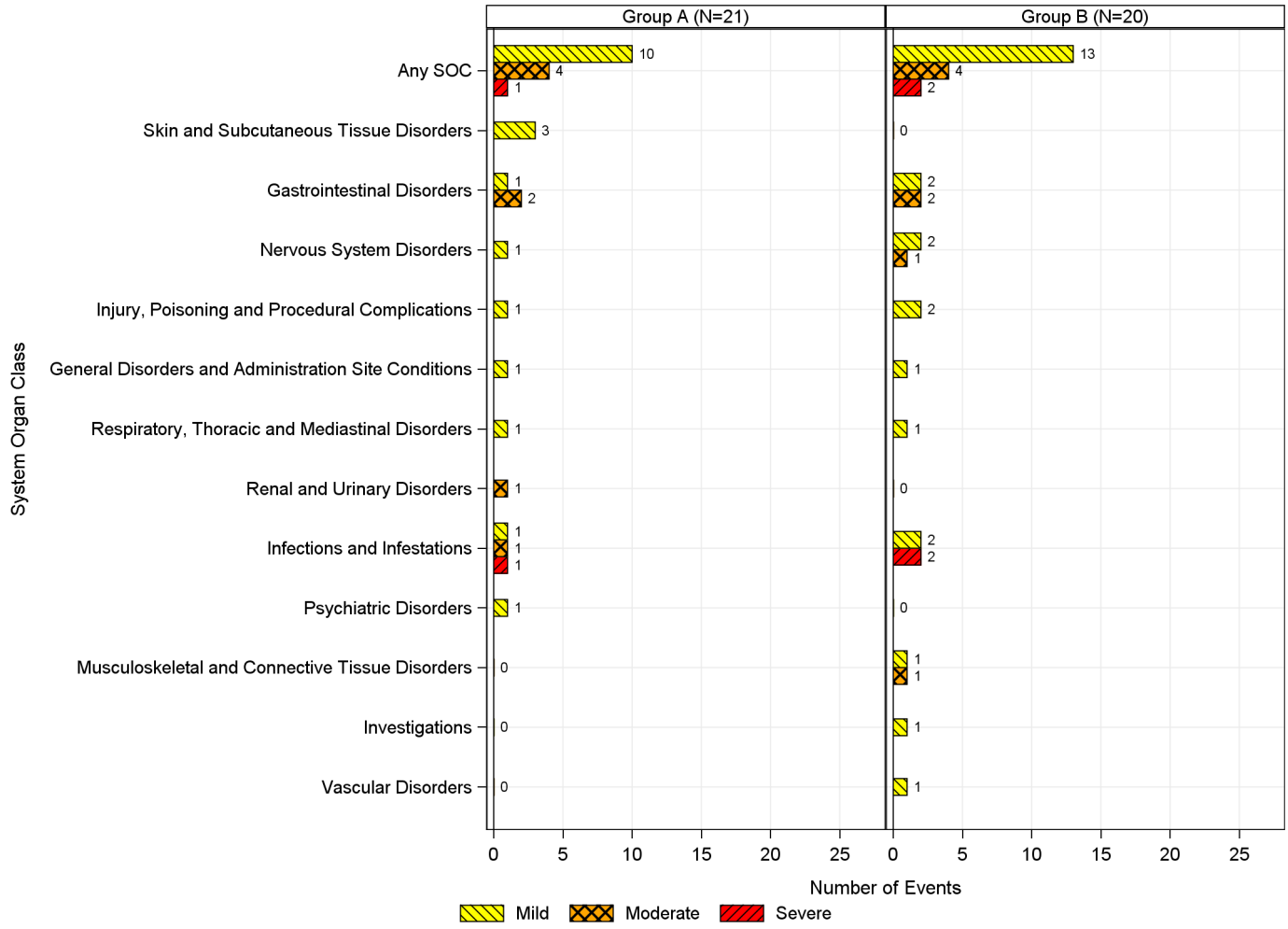
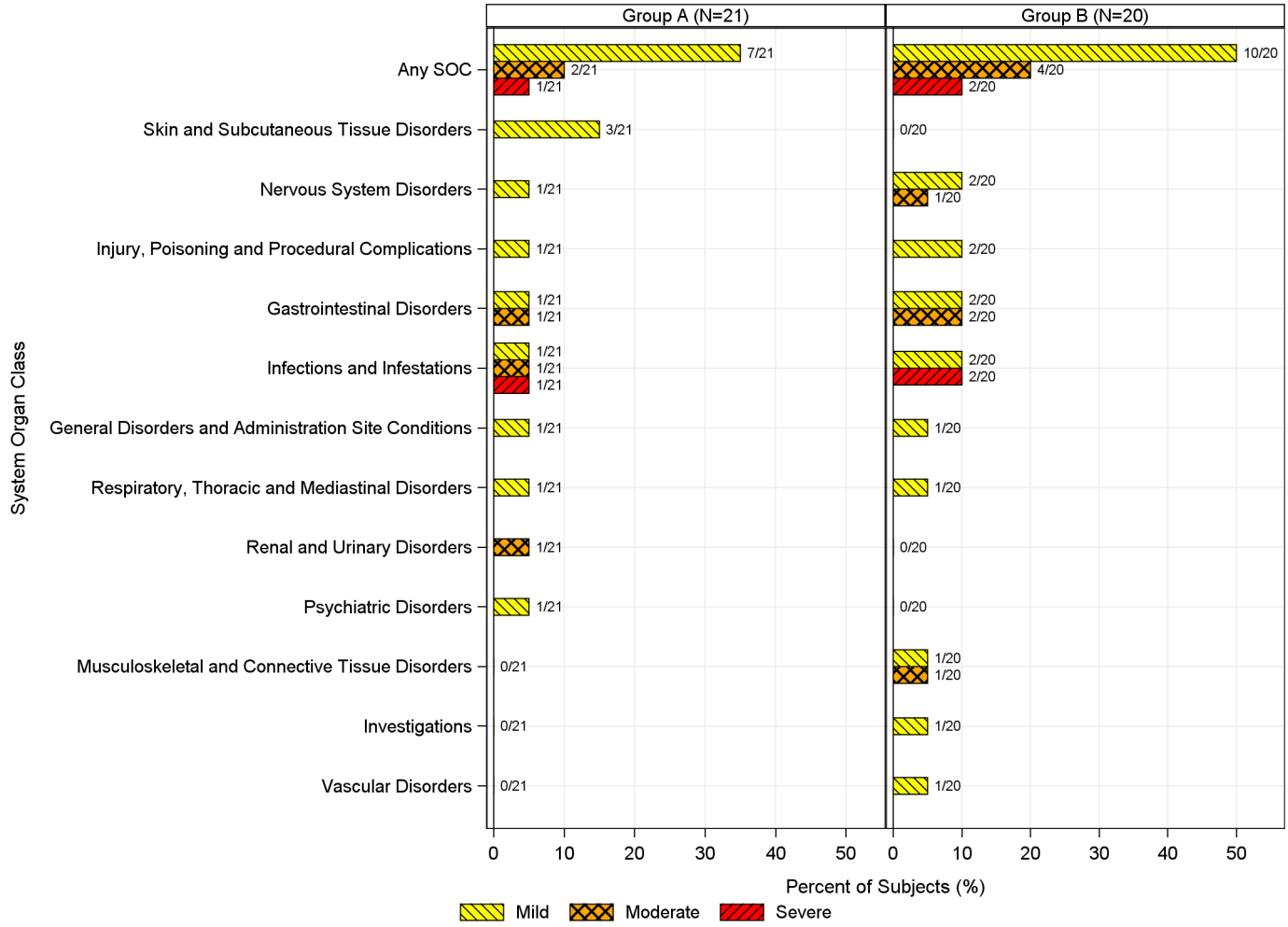


Figure 1046: Incidence of Adverse Events by MedDRA® System Organ Class and Maximum Severity

[Implementation Note: Have a panel for each treatment group for Dose 1 and a seventh panel for Dose 2]



14.3.5 Displays of Laboratory Results

Not Applicable.

APPENDIX 3. LISTINGS MOCK-UPS

LISTINGS

Listing 1: **16.1.6: Listing of Subjects Receiving Investigational Product**

(not included in SAP, but this is a placeholder for the CSR)

16.2 Database Listings by Subject

16.2.1 Discontinued Subjects

Listing 2: 16.2.1: Early Terminations or Discontinued Subjects

Vaccination Group	Subject ID	Category	Reason for Early Termination or Treatment Discontinuation	Study Day

16.2.2 Protocol Deviations

Listing 3: 16.2.2.1: Subject-Specific Protocol Deviations

Vaccination Group	Subject ID	DV Number	Deviation	Deviation Category	Study Day	Reason for Deviation	Deviation Resulted in AE?	Deviation Resulted in Subject Termination?	Deviation Affected Product Stability?	Deviation Resolution	Comments

Listing 4: 16.2.2.2: Non-Subject-Specific Protocol Deviations

Site	Start Date	Deviation	End Date	Reason for Deviation	Deviation Resulted in Subject Termination?	Deviation Affected Product Stability?	Deviation Category	Deviation Resolution	Comments

16.2.3 Subjects Excluded from the Efficacy Analysis

Listing 5: 16.2.3: Subjects Excluded from Analysis Populations

Vaccination Group	Subject ID	Analyses in which Subject is Included	Analyses from which Subject is Excluded	Results Available?	Reason Subject Excluded
		[e.g., Safety, ITT, PP]	[e.g., Safety, ITT, PP, Day x]		

Note: "Yes" in the "Results available" column indicates that available data were removed from the analysis. "No" indicates that no data were available for inclusion in the analysis.

16.2.4 Demographic Data

Listing 6: 16.2.4.1: Demographic Data

Vaccination Group	Subject ID	Sex	Age at Enrollment (years)	Ethnicity	Race	BMI	Time Between First and Second Booster (Days)	Time Between Covid Infection and Second Booster (Days)	Time Between Covid Infection or First Booster and Second Booster (Days)

Listing 7: 16.2.4.2: Pre-Existing and Concurrent Medical Conditions

Vaccination Group	Subject ID	MH Number	Medical History Term	Condition Start Day	Condition End Day	MedDRA System Organ Class	MedDRA Preferred Term

16.2.5 Compliance and/or Drug Concentration Data (if available)

Not Applicable.

16.2.6 Individual Immunogenicity Response Data

Listing 8: 16.2.6: Individual Immunogenicity Response Data

Vaccination Group	Subject ID	Planned Time Point	Actual Study Day	Assay	Units	Results

Listing 9: 16.2.6: Individual T-cell Response Data

Vaccination Group	Subject ID	Planned Time Point	Actual Study Day	T-Cell	Peptide Pool	Cytokine	Adjusted Percent	Responder (Y/N)

Listing 10: 16.2.6: Individual B-cell Response Data

Vaccination Group	Subject ID	Planned Time Point	Actual Study Day	Probe	Percent

Listing 11: 16.2.6: Individual Sequencing Data

Vaccination Group	Subject ID	Planned Time Point	Actual Study Day	PANGO

16.2.7 Adverse Events

Listing 12: 16.2.7.1: Solicited Events – Systemic Symptoms

Vaccination Group	Subject ID	Dose Number	Post Dose Day	Assessment[a]	Symptom	Severity	Attributed to Alternate Etiology?[b]	Alternate Etiology
				MA				
				Clinic				

[a] MA = Data reported by subject on the Memory Aid and reviewed by clinic staff and reported in Solicited Events eCRF.
[b] Grade 3 events only.
Note: Clinic = Data collected by clinic staff during physical exam or symptom assessment (treatment administration record, in-clinic assessment, etc.)

Listing 13: 16.2.7.2: Solicited Events – Local Symptoms

Treatment Group	Subject ID	Dose Number	Post Dose Day	Assessment[a]	Symptom	Severity
				MA		
				Clinic		

[a] MA = Data reported by subject on the Memory Aid and reviewed by clinic staff and reported in Solicited Events eCRF.
Note: Clinic = Data collected by clinic staff during physical exam or symptom assessment (treatment administration record, in-clinic assessment, etc.)

Listing 14: 16.2.7.3: Unsolicited Adverse Events

Adverse Event	Associated with Dose No.	No. of Days Post Associated Dose (Duration)	Severity	SAE?	Relationship to Study Treatment	In Not Related, Alternative Etiology	Action Taken with Study Treatment	Subject Discontinued Due to AE	Outcome	MedDRA System Organ Class	MedDRA Preferred Term
Treatment Group: , Subject ID: , AE Number:											
Comments:											
Treatment Group: , Subject ID: , AE Number:											
Comments:											
Note: For additional details about SAEs, see Figure: xx.											

16.2.8 Individual Laboratory Measurements

Not Applicable.

16.2.9 Vital Signs and Physical Exam Findings

Listing 15: 16.2.9.1: Vital Signs

Treatment Group	Subject ID	Planned Time Point	Actual Study Day	Temperature (°C)	Systolic Blood Pressure (mmHg)	Diastolic Blood Pressure (mmHg)	Heart Rate (beats/min)	Respiratory Rate (breaths/min)	Weight (kg)	Height (cm)

Listing 16: 16.2.9.2: Physical Exam Findings

Treatment Group	Subject ID	Planned Time Point	Actual Study Day	Body System	Abnormal Finding	Reported as an AE? (AE Description; Number)

16.2.10 Concomitant Medications

Listing 17: 16.2.10: Concomitant Medications

Treatment Group	Subject ID	CM Number	Medication	Medication Start Day	Medication End Day	Indication	Taken for an AE? (AE Description; Number)	Taken for a condition on Medical History? (MH Description; Number)	ATC Level 1 (ATC Level 2)

16.2.11 Pregnancy Reports

Listing 18: 16.2.11.1: Pregnancy Reports – Maternal Information

Treatment Group	Subject ID	Pregnancy Number	Study Day Corresponding to Estimated Date of Conception	Source of Maternal Information	Pregnancy Status	Mother's Pre-Pregnancy BMI	Mother's Weight Gain During Pregnancy	Tobacco, Alcohol, or Drug Use During Pregnancy?	Medications During Pregnancy?	Maternal Complications During Pregnancy?	Maternal Complications During Labor, Delivery, or Post-Partum?
Note: Maternal Complications are included in the Adverse Event listing. Medications taken during pregnancy are included in the Concomitant Medications Listing.											

Listing 19: 16.2.11.2: Pregnancy Reports – Gravida and Para

			Live Births												
Subject ID	Pregnancy Number	Gravida	Extremely PB[a]	Very Early PB[a]	Early PB[a]	Late PB[a]	Early TB[b]	Full TB[b]	Late TB[b]	Post TB[b]	Still Births	Spontaneous Abortion/ Miscarriage	Elective Abortions	Therapeutic Abortions	Major Congenital Anomaly with Previous Pregnancy?
Note: Gravida includes the current pregnancy, para events do not.															

[a] Preterm Birth
[b] Term Birth

Listing 20: 16.2.11.3: Pregnancy Reports – Live Birth Outcomes

Subject ID	Pregnancy Number	Fetus Number	Pregnancy Outcome (for this Fetus)	Fetal Distress During Labor and Delivery?	Delivery Method	Gestational Age at Live Birth	Size for Gestational Age	Apgar Score, 1 minute	Apgar Score, 5 minutes	Cord pH	Congenital Anomalies?	Illnesses/ Hospitalizations within 1 Month of Birth?
Note: Congenital Anomalies are included in the Adverse Event listing.												

Listing 21: 16.2.11.4: Pregnancy Reports – Still Birth Outcomes

Subject ID	Date of Initial Report	Fetus Number	Pregnancy Outcome (for this Fetus)	Fetal Distress During Labor and Delivery?	Delivery Method	Gestational Age at Still Birth	Size for Gestational Age	Cord pH	Congenital Anomalies?	Autopsy Performed?	If Autopsy, Etiology for Still Birth Identified?

Listing 22: 16.2.11.5: Pregnancy Reports – Spontaneous, Elective, or Therapeutic Abortion Outcomes

Subject ID	Date of Initial Report	Fetus Number	Pregnancy Outcome (for this Fetus)	Gestational Age at Termination	Abnormality in Product of Conception?	Reason for Therapeutic Abortion