

PASS INFORMATION

Title	VAC4EU Postauthorisation Safety Study of BIMERVAX® Vaccine in Europe
Protocol version identifier	Final Protocol Version 3.0
Date	16 October 2025
HMA-EMA Catalogue of RWD Studies number	EUPAS1000000321
Active substance	SARS-CoV-2 virus recombinant spike (S) protein receptor binding domain (RBD) fusion dimer: the original formulation is a heterodimer (covering B.1.351 – B.1.1.7 strains); the adapted formulations are homodimers (Omicron XBB.1.16 – XBB.1.16 strain; Omicron LP.8.1 – LP.8.1 strain) (Anatomical Therapeutic Chemical (ATC) Code J07BN)
Medicinal product	BIMERVAX® emulsion for injection COVID-19 vaccine, recombinant, adjuvanted The term BIMERVAX® includes all variations of the vaccine that may be distributed during the conduct of this study
Product reference	EU number: EU/1/22/1709
Procedure number	EMA number: EMEA/H/C/006058/0000
Marketing authorisation holder (MAH)	HIPRA Human Health, S.L.U. Avda. la Selva, 135, 17170 Amer (Girona) Spain
Joint PASS	No
Research question and objectives	The research question is: Is there a difference in the risk of selected adverse events of special interest (AESIs) after vaccination with BIMERVAX® compared with vaccination with other vaccines for the same indication? The primary study objectives are as follows: <ul style="list-style-type: none"> To characterise recipients of BIMERVAX® in relation to demographics and clinical characteristics at the time of vaccination, including the following: pregnancy status, age of childbearing potential, immunocompromised status, comorbidities, presence of autoimmune and inflammatory

	<p>disorders, and interaction with other vaccines (influenza).</p> <ul style="list-style-type: none"> • To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other coronavirus disease 2019 (COVID-19) vaccines with the same indication, using a cohort design. • To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using a self-controlled risk interval design. <p>The secondary objectives (study size allowing) are:</p> <ul style="list-style-type: none"> • To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other COVID-19 vaccines with the same indication, using a cohort design in subgroups defined by the following baseline variables: pregnancy status, immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time. • To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using a self-controlled risk interval (SCRI) design in subgroups defined by the following baseline variables: immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time.
<p>Country(-ies) of study</p>	<p>The country currently planned for is Spain (ES). Other European countries are under evaluation.</p>
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Marketing Authorisation Holder

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Project Title: VAC4EU Postauthorisation Safety Study of BIMERVAX[®] Vaccine in Europe

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1. TABLE OF CONTENTS

1. TABLE OF CONTENTS.....	6
2. LIST OF ABBREVIATIONS.....	9
3. RESPONSIBLE PARTIES.....	11
4. ABSTRACT.....	13
5. AMENDMENTS AND UPDATES.....	15
6. MILESTONES AND TIMELINE	16
7. RATIONALE AND BACKGROUND.....	17
8. RESEARCH QUESTION AND OBJECTIVES	18
9. RESEARCH METHODS	19
9.1. Study Design	19
9.1.1. Vaccine Utilisation Study	19
9.1.2. Matched Cohort Design.....	19
9.1.3. Self-controlled Risk Interval Design	22
9.2. Setting	24
9.2.1. Source Population	24
9.2.2. Inclusion Criteria	24
9.2.3. Exclusion Criteria	25
9.2.4. Study Period.....	25
9.3. Variables	25
9.3.1. Exposure	25
9.3.2. Outcomes	27
9.3.3. Covariates	32
9.3.4. Subgroups	36
9.4. Data Sources.....	36
9.4.1. EpiChron (Spain).....	37
9.4.2. SIDIAP (Spain).....	37
9.4.3. VID (Spain)	37
9.5. Study Size	37
9.6. Data Management	39
9.6.1. Record Retention	40
9.6.2. Data Extraction	41
9.6.3. Data Processing and Transformation.....	41

9.6.4. Data Access	41
9.7. Data Analysis	41
9.7.1. Vaccine Utilisation Study	43
9.7.2. Matched Cohort Design.....	43
9.7.3. Self-controlled Risk Interval Design Study.....	47
9.7.4. Handling of Small Cell Counts.....	48
9.8. Quality Control.....	48
9.8.1. RTI-HS as Coordinating Centre	48
9.8.2. EpiChron (Spain).....	49
9.8.3. SIDIAP (Spain).....	49
9.8.4. VID (Spain)	49
9.9. Limitations of the Research Methods.....	50
10. PROTECTION OF HUMAN SUBJECTS	52
10.1. EpiChron	52
10.2. SIDIAP	52
10.3. VID	52
11. MANAGEMENT AND REPORTING OF ADVERSE EVENTS/ADVERSE REACTIONS	53
11.1. Other Good Research Practice	53
12. PLANS FOR DISSEMINATING AND COMMUNICATING STUDY RESULTS	54
13. REFERENCES	55

LIST OF TABLES

Table 1. Safety Outcomes: Adverse Events of Special Interest With Estimated Risk Intervals and Preferred Study Design.....28

Table 2. Confidence Interval Limits for AESI Risks in the Comparator Group for Different Scenarios of True Risk Ratio and of Study Sizes.....38

Table 3. Maximum Follow-up for Each Study Report By Data Source.....42

Table 4. Small Cell Count Rules in Each Data Source.....48

LIST OF FIGURES

Figure 1 Matched Cohort Study Design.....20

Figure 2. Self-controlled Risk Interval Study Design.....23

Figure 3. Data Management Plan.....40

2. LIST OF ABBREVIATIONS

Abbreviation	Definition
ACCESS	vACCine covid-19 monitoring readinESS
AESI	adverse event of special interest
BMI	body mass index
CDM	common data model
CI	confidence interval
CONSORT	Consolidated Standards of Reporting Trials
COVID-19	coronavirus disease 2019
DPT	diphtheria, tetanus, pertussis
DRE	Digital Research Environment
DVT	deep vein thrombosis
EHR	electronic health record
EMA	European Medicines Agency
ENCePP	European Network of Centres for Pharmacoepidemiology and Pharmacovigilance
ES	Spain
ETL	extraction, transformation, and loading
EU	European Union
FAIR principles	findable, accessible, interoperable, re-usable
FDA	Food and Drug Administration
FISABIO	Foundation for the Promotion of Health and Biomedical Research of Valencia Region
FR	France
GDPR	General Data Protection Regulation
GPP	Good Pharmacoepidemiology Practices
GVP	Guidelines on Good Pharmacovigilance Practices
HMA-EMA Catalogue	Heads of Medicines Agencies-European Medicines Agency Catalogue of RWD Studies
ICD-10	<i>International Classification of Diseases, Tenth Revision</i>
ICD-9	<i>International Classification of Diseases, Ninth Revision</i>
IRB	institutional review board
ISPE	International Society for Pharmacoepidemiology
MAH	marketing authorisation holder
MBDS	Minimum Basic Data Set at Hospital Discharge [VID]
MMR	measles-mumps-rubella vaccine
mRNA	messenger RNA
NA	not applicable
OQ	Office of Quality

Abbreviation	Definition
PASS	postauthorisation safety study
PRAC	Pharmacovigilance Risk Assessment Committee
QC	quality control
Qn yyyy	quarter of the calendar year
RMP	risk management plan
RTI	RTI International
RTI-HS	RTI Health Solutions
RT-PCR	reverse transcription polymerase chain reaction
RWD	real-world data
SAP	statistical analysis plan
SARS-CoV-2	severe acute respiratory syndrome coronavirus 2
SCRI	self-controlled risk interval
SES	socioeconomic status
SI-DEP	National Population Screening Information System
SIDIAP	Information System for Research in Primary Care (Sistema d'Informació per al Desenvolupament de la Investigació en Atenció Primària) Spain
SNOMED-CT	Systemized Nomenclature of Medicine-Clinical Terms
SOP	standard operating procedure
STROBE	Strengthening the Reporting of Observational Studies in Epidemiology
UK	United Kingdom
UMCU	University Medical Center Utrecht
VAC4EU	Vaccine Monitoring Collaboration for Europe (study network)
VID	Valencia Health System Integrated Database (Spain)
VIS	Vaccine Information System

3. RESPONSIBLE PARTIES

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VAC4EU Postauthorisation Safety Study of BIMERVAX® Vaccine in Europe

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4. ABSTRACT

Title: VAC4EU Postauthorisation Safety Study of BIMERVAX[®] Vaccine in Europe

Rationale and background: The coronavirus disease 2019 (COVID-19) HIPRA vaccine BIMERVAX[®] is a recombinant protein-based bivalent variant vaccine intended for use in individuals 12 years of age or older. The term BIMERVAX[®] includes all variations of the vaccine that may be distributed during the conduct of this study. In March 2023, the European Commission granted marketing authorisation of BIMERVAX[®] vaccine for use in the European Union [1]. Efficient and timely monitoring of the safety of the vaccine and its subsequent adaptations is needed in Europe; hence, a postauthorisation safety study (PASS) is a postauthorisation measure to the European Medicines Agency (EMA).

Research question and objectives:

Research question: Is there a difference in the risk of selected adverse events of special interest (AESIs) after vaccination with BIMERVAX[®] compared with vaccination by other vaccines for the same indication?

Primary objectives:

- To characterise recipients of BIMERVAX[®] in relation to demographics and clinical characteristics at the time of vaccination, including the following: pregnancy status, age of childbearing potential, immunocompromised status, comorbidities, presence of autoimmune and inflammatory disorders, and interaction with other vaccines (influenza).
- To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other COVID-19 vaccines with the same indication, using a cohort design.
- To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using a self-controlled risk interval (SCRI) design.

Secondary objectives (study size allowing):

- To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other COVID-19 vaccines with the same indication, using a cohort design in subgroups defined by the following baseline variables: pregnancy status, immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time.
- To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using an SCRI design in subgroups defined by the following baseline variables: immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time.

Study design:

The study will comprise:

- A vaccine utilisation study component, which will use a descriptive study design to characterise individuals at the time of vaccination
- A component on comparative safety studies, including:
 - A cohort design to estimate the incidence of AESIs after receiving a BIMERVAX[®] vaccine dose compared with the incidence in a comparator group vaccinated by other COVID-19 vaccines.
 - A self-controlled risk interval design to evaluate the risk of AESIs in a time interval following the receipt of a BIMERVAX[®] vaccine (the risk interval) compared with the risk of the same AESI during a subsequent post-risk time interval (the control interval).

Population: The eligible population for the vaccine utilisation study will be all individuals actively enrolled in each of the selected European health data sources for at least 12 months before receiving a dose of the BIMERVAX[®] vaccine within the study period. For the comparative safety studies, the main eligibility criterion will be receiving BIMERVAX[®] or other COVID-19 vaccine at baseline (matched cohort design) or receiving BIMERVAX[®] and have experienced an AESI during the risk or control interval (self-controlled risk interval design). The study period will begin from the date of first availability of the BIMERVAX[®] original vaccine in each participating data source/country and will end 36 months (48 months for pregnancy outcomes) after the start of data collection. The start of data collection will be anchored on the threshold of a total of 4,000 BIMERVAX[®] doses administered across the participating data sources.

Variables:

- In the vaccine utilisation study, the following variables will be measured at the time of vaccination: demographics; pregnancy status and trimester of pregnancy, as feasible; immunocompromised status; comorbidities that may determine frailty; autoimmunity, and inflammatory conditions; prior COVID-19 vaccination (brand, doses); prior use of other vaccines (influenza); comedications; and COVID-19 history.
- In the comparative safety studies, exposures will be based on recorded prescription, dispensing, or administration of COVID-19 vaccines during the study period. The outcomes will be based on the BIMERVAX[®] risk management plan that included AESIs proposed by the ACCESS project for a cohort and an SCRI study design. Key confounders will include demographics, COVID-19 history, vaccinations, personal lifestyle characteristics, comorbidities, comedications, immunocompromising conditions, and others. Subgroups will be defined by baseline variables, such as immunocompromised status, vaccinations, and others.

Data sources: The planned data sources for this study, pending confirmation of vaccine rollout, are EpiChron (Spain), Information System for Research in Primary Care (SIDIAP) (Spain), and Valencia Health System Integrated Database (VID) (Spain). Rollout in other European countries will be monitored to evaluate other potential data sources.

Study size: The study size for both the vaccine utilisation study and the comparative safety studies will be determined by the uptake of BIMERVAX[®] in the participating data sources during the study period.

Data analysis: The vaccine utilisation study will summarise the variables of interest at the time of vaccination using standard measures of central tendency and of dispersion for continuous variables as well as counts and percentages for categorical variables.

The comparative safety cohort study will use matching and inverse probability weighting to adjust for the measured baseline confounders. Outcomes will be treated as time-to-event variables and will be analysed accordingly. Effect estimates will be provided as risk ratios and as risk differences scales.

The SCRI study will compare the risk of each AESI during a prespecified period following the index date (the “risk interval” during which there is a hypothesised increased risk of the outcome) with that of a self-matched “control interval,” used to assess the baseline risk of the outcome.

Milestones:

Key milestones are as follows:

- Protocol submission: 14 August 2023
- Protocol regulatory endorsement (v1.1): 25 April 2024
- Protocol regulatory endorsement (v2.0): 5 June 2025
- Protocol regulatory endorsement (v3.0): estimated Q4 2025-Q1 2026
- Progress report: 16 July 2024
- Final study report: 36 months after administration of at least 4,000 BIMERVAX[®] doses

5. AMENDMENTS AND UPDATES

None.

6. MILESTONES AND TIMELINE

The start of data collection (i.e., the date from which data extraction starts [2]) will occur once a total of 4,000 BIMERVAX[®] doses is reached across the participating data sources. A total of 4,000 BIMERVAX[®] doses is a threshold where observational data will start generating informative and complementary evidence to existing randomised clinical trials, which analysed a total of 3,480 individuals. Therefore, the start of the data collection and the consecutive milestones will be anchored to this threshold.

Milestone	Date
Protocol submission to EMA PRAC (v1.0)	14 August 2023
Protocol regulatory endorsement (v1.1)	25 April 2024
Protocol regulatory endorsement (v2.0)	5 June 2025
Protocol regulatory endorsement (v3.0)	Estimated Q4 2025-Q1 2026
Registration in the HMA-EMA Catalogue	21 October 2024
Start of data collection ^a	Estimated Q3 2026 (will be anchored on the administration of at least 4,000 doses of BIMERVAX [®]) ^b
Study progress report	16 July 2024
Interim report 1	Estimated Q3 2027 (12 months after the start of data collection)
Interim report 2	Estimated Q3 2028 (24 months after the start of data collection)
Data extraction for the final report (before pregnancy outcomes update)	Estimated Q4 2028
Final report of study results (before pregnancy outcomes update)	Estimated Q3 2029 (36 months after the start of data collection)
End of data collection ^c	Estimated Q4 2029
Final report of study results (with pregnancy outcomes update)	Estimated Q3 2030 (48 months after the start of data collection)

HMA-EMA Catalogue = Heads of Medicines Agencies–European Medicines Agency Catalogue of RWD Studies;
 PRAC = Pharmacovigilance Risk Assessment Committee; Qn yyyy = quarter of the calendar year.

Note: Study implementation contracts between the sponsor and research organisation(s) and approvals by data protection, data custodian, ethics, and scientific review bodies are pending. Timelines may be impacted by approvals of these bodies, duration of contract reviews, and availability of data and staff at research institutions once contracts and approvals are finalised.

^a Start of data collection is “the date from which information on the first study subject is first recorded in the study data set or, in the case of secondary use of data, the date from which data extraction starts” [2].

^b Refers to doses from the adapted and original vaccines. The rollout of the BIMERVAX adapted vaccine to be used for the 2025-2026 autumn-winter vaccination campaign in Spain is expected by Q4 2025. First use of the original vaccine in Spain occurred during 2023.

^c End of data collection is “the date from which the analytical data set is completely available” [2].

7. RATIONALE AND BACKGROUND

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the cause of coronavirus disease 2019 (COVID-19), led to a global pandemic. The World Health Organization views COVID-19 as a major threat and considers crucial, among other measures, the administration of vaccine to high-risk groups [3]. BIMERVAX[®] is a recombinant protein-based bivalent variant vaccine developed by HIPRA and is intended for use for active immunisation against COVID-19.

In March 2023, the European Commission granted marketing authorisation of BIMERVAX[®] (targeting SARS-CoV-2 B.1.351 and B.1.1.7 strains) for use in the European Union (EU) as a booster vaccine in people aged 16 years or older who have previously been vaccinated with a messenger RNA (mRNA) COVID-19 vaccine [1]. In October 2024, the Committee for Medicinal Products for Human Use (CHMP) of the European Medicines Agency (EMA) recommended the marketing authorisation of BIMERVAX[®] XBB.1.16 (targeting Omicron XBB.1.16 strain) with an indication for active immunisation (i.e., as primo vaccination and as a booster) in individuals aged 16 years or older [4]. In September 2025, the European Commission approved the updated composition of BIMERVAX[®] targeting the new SARS-CoV-2 LP.8.1 variant and extended the indication to include individuals aged 12 years or older [5]. In this protocol, the term BIMERVAX[®] includes all variations of the vaccine that may be distributed during the conduct of this study.

The results of laboratory-based and clinical studies [6-8] showed that a BIMERVAX[®] booster dose triggered the production of higher levels of antibodies against the Beta and Omicron variants of SARS-CoV-2 and comparable levels against the Delta variant when compared with a Comirnaty (Pfizer-BioNTech) booster dose. Therefore, BIMERVAX[®] is expected to be at least as effective as Comirnaty at restoring protection against COVID-19 [1]. The BIMERVAX[®] safety profile was also comparable to that of other COVID-19 vaccines. Based on these results, the Committee for Medicinal Products for Human Use concluded that sufficiently robust data on the quality and safety of the vaccine were available and recommended its marketing authorisation in the EU [1]. To gain a more complete understanding, safety monitoring of the BIMERVAX[®] vaccine is needed in European countries.

This protocol was prepared based on the EU risk management plan (RMP) Version 2.0 reviewed by the EMA Pharmacovigilance Risk Assessment Committee (PRAC) [9]. According to the EU RMP, the safety events of special concern for BIMERVAX[®] include pericarditis, myocarditis, and vaccine-associated enhanced disease, including vaccine-associated enhanced respiratory disease. Areas of missing information include the use of BIMERVAX[®] in pregnancy and while breastfeeding, in frail individuals with comorbidities, in interaction with other vaccines, and long-term safety. These areas of missing information will be addressed by analysing the corresponding population subgroups and by estimating the risk of adverse events of special interest (AESIs) up to 365 days of follow-up to assess long-term safety.

As part of the RMP, this protocol describes the postauthorisation safety study (PASS) to be conducted within the Vaccine Monitoring Collaboration for Europe (VAC4EU) study network. This PASS will evaluate the risk of safety concerns and AESIs, as defined in the approved EU RMP, following immunisation in the real-world setting. The PASS has 2 components—a vaccine utilisation study and a comparative safety study—that will be conducted in a staggered-phase

approach. The vaccine utilisation study will characterise individuals receiving BIMERVAX[®] vaccine. The comparative safety study will comprise 2 sub-studies: a cohort study and a self-controlled risk interval (SCRI) study (a subtype of the self-controlled case series design). The cohort study will evaluate the risk of adverse events due to use of BIMERVAX[®] vaccine compared with that of other COVID-19 vaccines with the same indication, whereas the SCRI study will evaluate the risk of adverse events following receipt of a BIMERVAX[®] vaccine compared with the risk of AESIs in a later period not preceded by any COVID-19 vaccination. Given the evolving nature of the SARS-CoV-2 virus, the vaccine's composition may periodically be updated. This will be addressed via subgroup analyses ([Section 9.3.4](#)).

This PASS is a commitment to the EMA and complies with the European Network of Centres for Pharmacoepidemiology and Pharmacovigilance (ENCePP) code of conduct [10]. This protocol follows the structure and contents as included in the EMA's *Guidelines on Good Pharmacovigilance Practices (GVP), Module VIII—Post-Authorisation Safety Studies*.

8. RESEARCH QUESTION AND OBJECTIVES

To evaluate the safety of the BIMERVAX[®] vaccine, this study will address the following research question: Is there a difference in the risk of selected AESIs after vaccination with BIMERVAX[®] compared with vaccination by other vaccines for the same indication?

The primary study objectives are as follows:

- To characterise recipients of BIMERVAX[®] in relation to demographics and clinical characteristics at the time of vaccination, including the following: pregnancy status, age of childbearing potential, immunocompromised status, comorbidities, presence of autoimmune and inflammatory disorders, and interaction with other vaccines (influenza)
- To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other COVID-19 vaccines with the same indication, using a cohort design
- To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using an SCRI design

The secondary objectives (study size allowing) are as follows:

- To estimate the risk ratio and risk difference of prespecified AESIs comparing recipients of BIMERVAX[®] with recipients of other COVID-19 vaccines with the same indication, using a cohort design in subgroups defined by the following baseline variables: pregnancy status, immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time
- To estimate the incidence rate ratio of selected AESIs comparing a prespecified risk interval following BIMERVAX[®] vaccination with a later post-risk interval, using an SCRI design in subgroups defined by the following baseline variables:

immunocompromised status, frailty due to comorbidities, presence of autoimmune or inflammatory disorders, prior use of influenza vaccine and calendar time

9. RESEARCH METHODS

9.1. Study Design

This will be a non-interventional multi-database study based on the secondary use of healthcare data from different European data sources within the VAC4EU network. The comparative safety study will have 2 components: a matched cohort design and an SCRI design, which will be implemented for specific outcomes (specified in [Table 1](#)). Both designs will follow vACCine covid-19 monitoring readinESS (ACCESS) specifications for vaccine safety studies [11]. The study period will begin from the date of first availability of the BIMERVAX[®] original vaccine in each participating data source/country and will end 36 months (48 months for pregnancy outcomes) after the start of data collection. The start of data collection will be anchored on the threshold of a total of 4,000 BIMERVAX[®] doses administered across the participant data sources ([Section 9.2.4](#)); the lookback period for selected covariates will be all available data history.

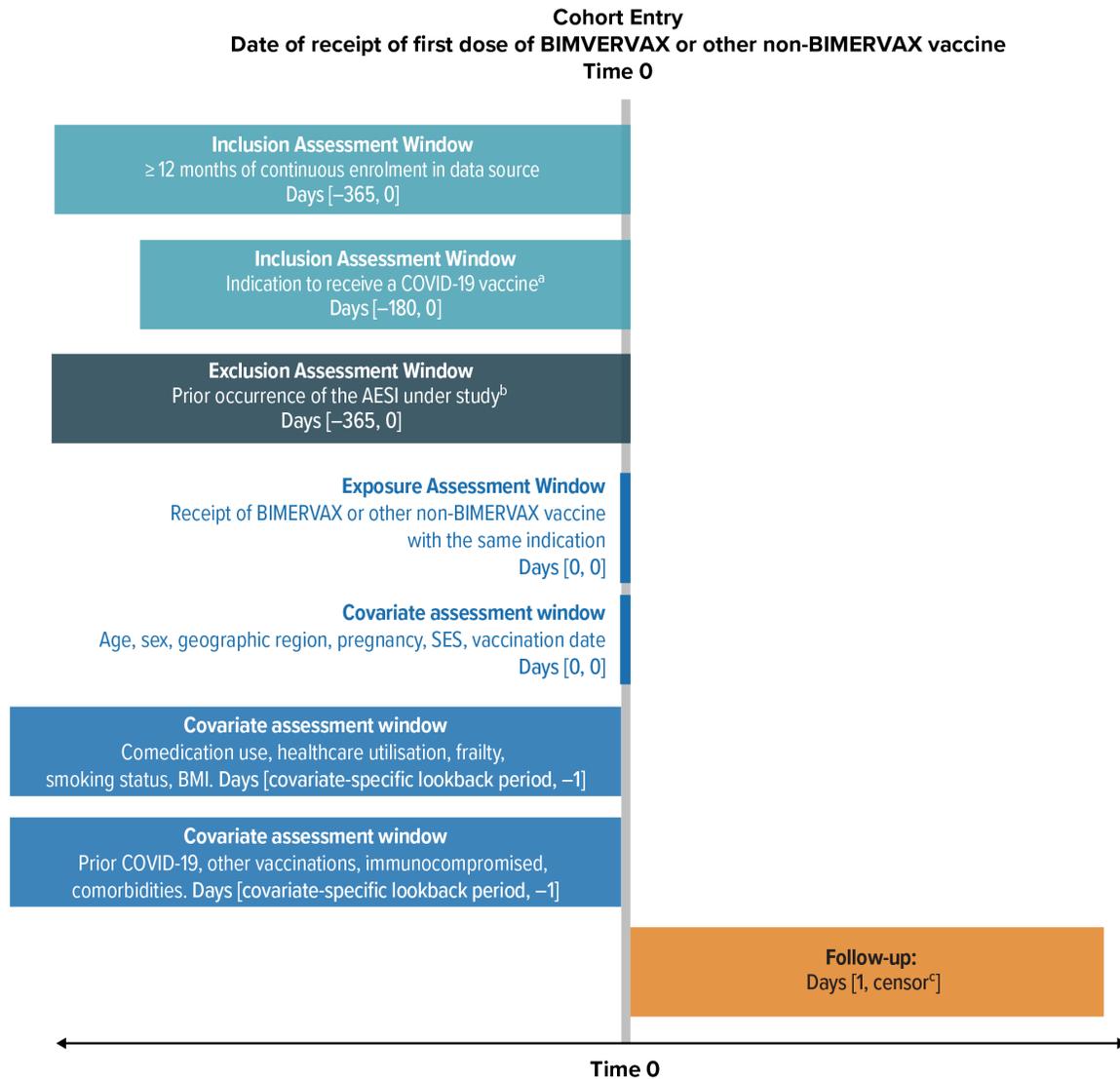
9.1.1. Vaccine Utilisation Study

The vaccine utilisation study will be a descriptive exercise [12]. All subjects receiving BIMERVAX[®] will be characterised at the time of the first BIMERVAX[®] vaccination recorded in the study databases within the study period, and their subsequent vaccination trajectories will be described.

9.1.2. Matched Cohort Design

The matched cohort design ([Figure 1](#)) will be a causal inference exercise [12]. It will estimate the risk of all listed AESIs ([Section 9.3.2](#)) after receipt of BIMERVAX[®] (exposed group) and will compare it with the risk of those AESIs in individuals who received non-BIMERVAX[®] COVID-19 vaccines (comparator group).

Figure 1 Matched Cohort Study Design



AESI = adverse event of special interest; BMI = body mass index; COVID-19 = coronavirus disease 2019; SES = socioeconomic status.

^a Individuals are eligible to receive a COVID-19 vaccine if they are aged 12 years or older. Individuals will be included in the study if at least 6 months have elapsed since a prior COVID-19 vaccination, in the case they received it.

^b Prior occurrence of the AESI under study within the past year will be an exclusion criterion for all AESIs except type 1 diabetes, which will be an exclusion if occurring at any time before time zero.

^c Censoring will happen at the end of the study period, occurrence of the AESI under analysis, death, or disenrolment from the data source, whichever is first. Additionally, individuals will be censored as per the strategies described in [Section 9.7.2.6](#).

Source: Figure template from Schneeweiss et al. [13].

9.1.2.1. Causal Contrast or Estimand

The causal contrast will be the observational analogue of a per-protocol effect, i.e., the effect under complete adherence to the following vaccination strategies and under no infection by SARS-CoV-2:

- Receive 1 dose of BIMERVAX[®] vaccine. Individuals can subsequently receive other COVID-19 vaccinations as per local policies
- Receive 1 dose of another COVID-19 vaccine. Individuals subsequently can receive other COVID-19 vaccinations as per local policies, using any brand but BIMERVAX[®].

9.1.2.2. Time Zero or Baseline

Time zero (baseline) will be defined as the time at which the exposure status is assigned, when inclusion and exclusion criteria are applied, and when the follow-up for study outcomes will start [14-17], and will be operationalised as follows:

- BIMERVAX[®] group: date of BIMERVAX[®] administration
- Non-BIMERVAX[®] COVID-19 vaccine group: date of administration of the non-BIMERVAX[®] vaccine, matched to date of BIMERVAX[®] in the corresponding match

9.1.2.3. Matching Process

The matching process will aim at being similar to those for prior applications of observational studies comparing head-to-head vaccines for COVID-19 [18-20]. The cohort study will match individuals vaccinated with non-BIMERVAX[®] COVID-19 vaccines to individuals vaccinated with BIMERVAX[®] in a 1:1 ratio, using the following variables:

- Calendar date of BIMERVAX[®] dose (time zero); granularity (e.g., week, month, trimester) to be defined in the statistical analysis plan (SAP)
- Age, in 3-year groups
- Sex, exact matching
- Geographic location, as available for each data source, exact matching; level of granularity to be defined in the SAP
- Having received a COVID-19 vaccine in the past (received any COVID-19 vaccine vs. did not receive any COVID-19 vaccine), exact matching
- Pregnancy status, exact matching on the following levels:
 - Not pregnant
 - Pregnant and pregnancy records are categorised as “red” by the ConcePTION Pregnancy Algorithm [21]

- Pregnant and pregnancy records are categorised as other than “red” by the ConcePTION Pregnancy Algorithm [21]
- If pregnant (regardless of the category assigned by the ConcePTION Pregnancy Algorithm [21]), the exact number of weeks since the first day of the last menstrual period (LMP)

Subjects with missing data for the matching variables will not be included in the analysis. Pregnancy status and number of weeks since LMP will be imputed following the ConcePTION Pregnancy Algorithm [21]. Lack of record of an mRNA vaccination will be interpreted as not having received any mRNA vaccine in the past.

Matching variables (i.e., age, geographic location at time zero) will be assessed at time zero. The selection of variables will be tailored based on availability of the variable in each data source and their distribution in the boosted population.

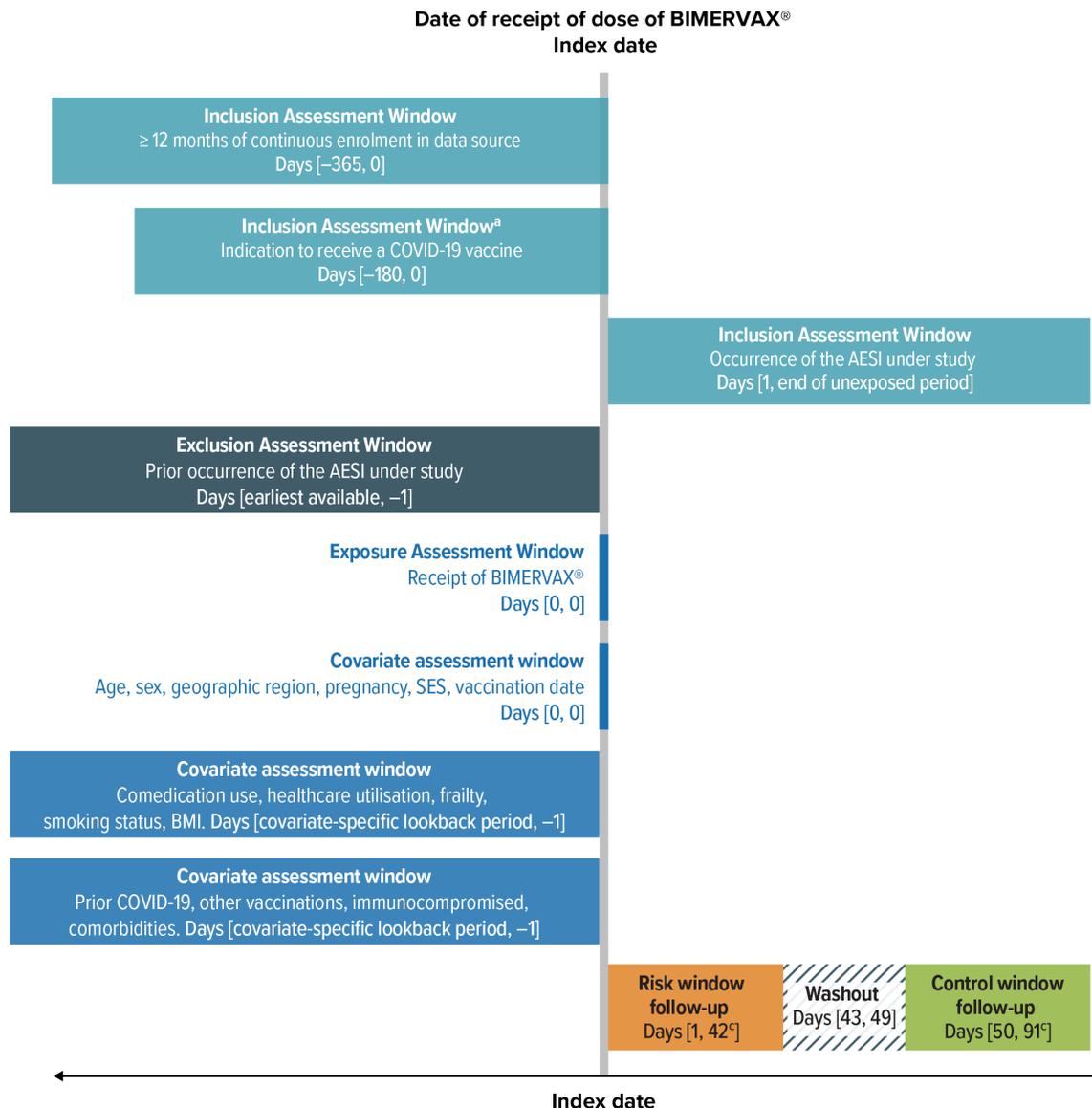
9.1.2.4. Follow-up

Individuals will be followed from time zero until the end of the study period (36 months after the start of data collection), occurrence of the AESI under analysis, death, or disenrolment from the data source, whichever occurs first (further details on censoring criteria are specified in [Section 9.7.2.6](#)). For pregnancy outcomes, the end of the study period will be 48 months after the start of data collection.

9.1.3. Self-controlled Risk Interval Design

The SCRI study design will be a causal inference exercise [12]. The SCRI design ([Figure 2](#)) will be used to compare the occurrence of specific AESIs during a risk interval following receipt of BIMERVAX[®] with the occurrence of the same specific AESI during a post-risk control interval; this will only be done for AESIs for which the SCRI is the recommended design [22,23].

Figure 2. Self-controlled Risk Interval Study Design



AESI = adverse event of special interest; BMI = body mass index; COVID-19 = coronavirus disease 2019; SES = socioeconomic status.

^a Individuals are eligible to receive a COVID-19 vaccine if they are aged 12 years or older. Individuals will be included in the study if at least 6 months have elapsed since a prior COVID-19 vaccination, in the case they received it.

^c Example of an AESI with a risk and control interval of 42-day length and a 7-day washout interval.

Figure template source: Schneeweiss et al. [13].

AESIs that are appropriate for this study design (see [Section 9.3.2, Outcomes](#)):

- Are rare, with a transient risk after exposure
- Have a constant event rate within the observation periods
- Their occurrence does not alter the duration of the observation window

The index date in the SCRI design will be the date of vaccination. The risk of each AESI during a prespecified period following BIMERVAX[®] vaccination (“risk interval”) will be compared with the occurrence of the same AESI in a later interval (“control interval”), in the same individual (Figure 2). The risk and control intervals will be of the same length with a washout period between them. A sensitivity analysis will use a control interval of a different length, 127 days (Section 9.7.3.5).

The risk intervals proposed for each AESI and the AESIs that will be analysed using the SCRI design are summarised in Section 9.3.2.

The use of a control interval after the risk interval (as opposed to use of a control interval before the risk interval) avoids bias from outcomes affecting the probability of exposure (e.g., the outcome is a contraindication for exposure or delays exposure) (Figure 2).

9.2. Setting

9.2.1. Source Population

The source population will comprise all individuals actively enrolled in each of the selected European health data sources who receive a dose of BIMERVAX[®] vaccine within the study period. The study population will include all eligible individuals from the source population as per the eligibility criteria detailed below.

9.2.2. Inclusion Criteria

9.2.2.1. Vaccine Utilisation Study

Individuals must meet the following criteria for inclusion in the vaccine utilisation study:

- Have received a dose of BIMERVAX[®]
- Have a minimum of 12 months of continuous enrolment in the data source by the time they received the first dose of BIMERVAX[®]

Although BIMERVAX[®] is indicated for individuals aged 12 years or older, this vaccine utilisation study will not have any age restriction in order to describe any off-label use and to gather additional information from a population not included in the clinical trials.

9.2.2.2. Matched Cohort Design

Individuals must meet all the following criteria at time zero (Section 9.1.2.2) to be eligible for inclusion in the cohort study:

- Have received 1 dose of BIMERVAX[®] vaccine or 1 dose of another COVID-19 vaccine authorised for the same indication
- Be 12 years of age or older
- Have received the most recent administration of a COVID-19 vaccine at least 6 months ago

- Have a minimum of 12 months of continuous enrolment in the data source
- Have complete information on the matching variables

9.2.2.3. Self-controlled Risk Interval Design

Individuals must meet all the following criteria at the index date for inclusion in the SCRI design:

- Have received a dose of BIMERVAX[®] (this will be the index date when the rest of the inclusion criteria will be evaluated)
- Be 12 years of age or older
- Have received the last administration of a COVID-19 vaccine at least 6 months ago
- Have experienced the specific AESI during the risk or control interval
- Have at least 1 day of data accrual in both the risk and control intervals
- Have a minimum of 12 months of continuous enrolment in the data source

9.2.3. Exclusion Criteria

9.2.3.1. Vaccine Utilisation Study

Individuals who have received a dose of BIMERVAX[®] in the past will be excluded.

9.2.3.2. Cohort Design and Self-controlled Risk Interval Design

Individuals who have had a diagnosis of the specific AESI being analysed within 1 year before time zero (cohort design) or before the index date (SCRI design) will be excluded to distinguish the recording of previous events from true new events. For type 1 diabetes, individuals will be excluded if they receive a diagnosis at any time before time zero.

9.2.4. Study Period

For all studies, the study period will begin from the date of first availability of the BIMERVAX[®] original vaccine in each participating data source/country and will end 36 months (48 months for pregnancy outcomes) after the start of data collection. The start of data collection will be anchored on the threshold of a total of 4,000 BIMERVAX[®] doses administered across the participating data sources.

9.3. Variables

9.3.1. Exposure

9.3.1.1. Vaccine Utilisation Study

All individuals who receive a first dose of BIMERVAX[®] will be considered exposed and will be characterised in the vaccine utilisation study.

9.3.1.2. Matched Cohort Design

The exposure strategies will be as follows (see [Section 9.1.2.2](#) for the definition of time zero):

- **BIMERVAX[®] group:** Receive 1 dose of BIMERVAX[®] vaccine. Individuals subsequently can receive other COVID-19 vaccinations as per local policies.
- **Non-BIMERVAX[®] vaccine group:** Receive 1 dose of a COVID-19 vaccine approved for the same indication as BIMERVAX[®]. Individuals can subsequently receive other COVID-19 vaccinations as per local policies, using any brand except BIMERVAX[®].

9.3.1.3. Self-controlled Risk Interval Design

All participants in the SCRI will have received BIMERVAX[®]. They will be considered exposed during the risk interval and unexposed during the control interval ([Section 9.1.3](#)).

9.3.1.4. Exposure Assessment

For all study designs, exposure status will be assessed from recorded prescriptions, dispensing, or administration data for BIMERVAX[®] and other COVID-19 vaccines. The type of vaccine received and date of vaccination should be obtained from all possible sources that capture COVID-19 vaccination, such as pharmacy dispensing records, general practice records, immunisation registers, vaccination records, medical records, or other secondary data sources. Depending on the data source, vaccines may be identified via nationally used product codes where possible.

Each contributing dataset will identify vaccination as follows:

- **EpiChron – Aragon data sources (Spain):** The Aragon Health System (Aragon, Spain) has implemented a specific vaccination register embedded in the electronic health record (EHR) system. COVID-19 vaccination is systematically recorded in this register by healthcare professionals. This register will contain all relevant information regarding the vaccination process, such as the patient’s identifier; date of administration and due date for next dose, if applicable; centre of administration; part of the body where the vaccine was administered; name of the vaccine; brand (laboratory); dose; and vaccination criterion (risk group to which the patient belongs). There is also a free-text section in which healthcare professionals can include their observations (e.g., presence or not of an allergic reaction).
- **Information System for Research in Primary Care, SIDIAP (Spain):** SIDIAP will have information available on COVID-19 vaccines administered to individuals linked to a unique and anonymous identifier for all 8 million individuals under the Catalan Institute of Health–Primary Care teams. The information will come from electronic medical records. For each patient, SIDIAP will have data on centre and date of administration; dose; brand; reasons for vaccination (e.g., risk group); and other information related to vaccination.
- **Valencia Health System Integrated Database, VID (Spain):** Data on vaccine exposure may be obtained from the Vaccine Information System (VIS), which includes

information on vaccine type, manufacturer, number of doses, batch numbers, location, administration date, and, if applicable, risk groups, all linked with the population information database. Information in the VIS is updated daily as all vaccinations in Valencia are delivered by the regional public health system, automatically recorded in the system, and transferred to the vaccination registry. Recording and availability of vaccination information in the region of Valencia are expected to be complete in the vaccination registry used for this study.

9.3.2. Outcomes

The outcomes will be those AESIs agreed upon in the current BIMERVAX® EU RMP. [Table 1](#) lists these AESIs, indicates which events are deemed suitable for analysis using the cohort and/or SCRI analysis, and outlines the proposed risk intervals. The proposed risk intervals are based on available evidence suggesting that any biological effect of a vaccine is expected to occur during the proposed risk intervals.

Table 1. Safety Outcomes: Adverse Events of Special Interest With Estimated Risk Intervals and Preferred Study Design

Body system/ classification	AESI	Preferred study design according to ACCESS protocol	Risk interval (days)^a	Reference
Neurologic	Guillain-Barré syndrome	Cohort/SCRI	1-42	Based on Yih et al. [24] and BEST Initiative [25]
	Acute disseminated encephalomyelitis	Cohort/SCRI	1-42	Based on BEST Initiative [25]
	Transverse myelitis	Cohort/SCRI	1-90	Based on BEST Initiative [25]
	Encephalopathy	Cohort/SCRI ^b	1-21	Based on case reports of outcome following receipt of a COVID-19 vaccine [26]
	Aseptic meningitis, meningoencephalitis	Cohort/SCRI	1-42	Based on Yih et al. [24]
	Generalised convulsion (seizures)	Cohort/SCRI	0-2	Based on Yih et al. [24] and BEST Initiative [25]
	Facial nerve palsy, Bell's palsy	Cohort/SCRI ^b	1-42	Based on Yih et al. [24] and BEST Initiative [25]
	Narcolepsy	Cohort	1-42	Based on BEST Initiative [25]
	Anosmia, ageusia	Cohort/SCRI	1-42	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
Immunologic	Anaphylaxis	Cohort/SCRI	0-2	Based on Yih et al. [24] and BEST Initiative [25]
	Multisystem inflammatory syndrome	Cohort/SCRI	1-42	Based on BEST Initiative [25]
	Acute aseptic arthritis	Cohort/SCRI	1-42	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
	Subacute thyroiditis	Cohort ^b	1-365	Published risk intervals for autoimmune disorders were applied to similar autoimmune rheumatic conditions (i.e., thyroiditis) as done in a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Diabetes mellitus (type 1) ^c	Cohort	1-365	No consensus evidence for a risk interval was identified; defaulted to 365 days as done in a previous VAC4EU COVID-19 vaccine PASS protocol [27]

Body system/ classification	AESI	Preferred study design according to ACCESS protocol	Risk interval (days)^a	Reference
	Diabetes mellitus (any type)	Cohort	1-365	No consensus evidence for a risk interval was identified; defaulted to 365 days as done in a previous VAC4EU COVID-19 vaccine PASS protocol [27]
Cardiologic	Acute cardiac injury (including microangiopathy, heart failure, stress cardiomyopathy, coronary artery disease, arrhythmia, myocarditis/pericarditis)	Cohort/SCRI	1-42	Based on the BEST Initiative [25]’s published risk intervals for myocarditis and pericarditis, the same risk intervals were applied to other acute cardiac injuries
Haematologic	Coagulation disorders (including DVT, pulmonary embolus, cerebrovascular stroke, limb ischaemia, cerebral venous sinus thrombosis, haemorrhagic disease)	Cohort/SCRI	1-28	Based on the BEST Initiative [25]’s published risk intervals for DVT and pulmonary embolism, the same risk intervals were applied to other cardiovascular and haematological disorders characterised by damage to the blood vessels and/or arteries and clotting
	Disseminated intravascular coagulation	Cohort/SCRI ^b	1-28	Based on BEST Initiative [25]
	Thrombocytopenia	Cohort/SCRI	1-42	Based on Liu et al. [29]
	Immune thrombocytopenia, thrombosis with thrombocytopenia syndrome	Cohort/SCRI ^b	1-42	Based on BEST Initiative [25]
	Single organ cutaneous vasculitis	Cohort/SCRI	1-28	Based on the BEST Initiative [25]’s published risk intervals for DVT and pulmonary embolism, the same risk intervals were applied to other cardiovascular and haematological disorders characterised by damage to the blood vessels and/or arteries and clotting

Body system/ classification	AESI	Preferred study design according to ACCESS protocol	Risk interval (days)^a	Reference
Dermatologic	Erythema multiforme	Cohort/SCRI	1-28	Based on the BEST Initiative [25]’s published risk intervals for DVT and pulmonary embolism, the same risk intervals were applied to other haematological disorders characterised by damage to the blood vessels and/or arteries and clotting
	Chilblain-like lesions	Cohort/SCRI	1-28	Based on the BEST Initiative [25]’s published risk intervals for DVT and pulmonary embolism, the same risk intervals were applied to other haematological disorders characterised by damage to the blood vessels and/or arteries and clotting
Respiratory	Acute respiratory distress syndrome	Cohort/SCRI	1-28	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
Renal	Acute kidney injury	Cohort/SCRI	1-14	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
Hepato- gastrointestinal	Acute liver injury	Cohort/SCRI	1-14	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
	Acute pancreatitis	Cohort ^b	1-365	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
	Appendicitis	Cohort/SCRI ^b	1-42	Based on BEST Initiative [25]
Musculoskeletal	Rhabdomyolysis	Cohort/SCRI ^b	1-42	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]
Death	Death (any causes)	Cohort	1-365	No consensus evidence for a risk interval was identified; defaulted to 1 calendar year as done in a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Sudden death	Cohort	1-6	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [28]

Body system/ classification	AESI	Preferred study design according to ACCESS protocol	Risk interval (days) ^a	Reference
Pregnancy and neonatal outcomes	Spontaneous abortion, stillbirth	Cohort	At delivery	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Foetal growth restriction	Cohort	Any time during pregnancy	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Preterm birth	Cohort	At delivery	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Major congenital anomalies	Cohort	1 year after birth	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Microcephaly	Cohort	At delivery	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Neonatal death	Cohort	At delivery	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Gestational diabetes	Cohort	Any time during pregnancy	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Preeclampsia	Cohort	After 20 weeks of gestation	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
	Maternal death	Cohort	Any time during pregnancy	Based on a previous VAC4EU COVID-19 vaccine PASS protocol [27]
Reproductive system and breast disorders	Menstrual disorder	Cohort ^b	1-365	No consensus evidence for a risk interval was identified; defaulted to 1 calendar year

ACCESS = vACCine covid-19 monitoring readinESS; AESI = adverse event of special interest; COVID-19 = coronavirus disease 2019; DVT = deep vein thrombosis; FDA = Food and Drug Administration; PASS = postauthorisation safety study; SCRI = self-controlled risk interval; VAC4EU = Vaccine Monitoring Collaboration for Europe (study network).

^a Day 0 corresponds to day of receipt of a vaccine dose.

^b Preferred study design is unspecified in the ACCESS protocol but was assumed as per the description of suitable outcomes for SCRI in [Section 9.1.3](#).

^c In the ACCESS report [30], this AESI is specified as “Diabetes (type 1 and broader),” which will be operationalised as 2 outcomes—“Diabetes type 1” and “Diabetes of any type”—for completeness.

9.3.2.1. Outcome Identification, by Data Source

Outcome definition relies on the accuracy of codes and algorithms to identify outcomes in the data available in each data source. To reduce the probability of outcome misclassification and reconcile differences across terminologies in the different data sources, standard algorithms for each outcome definition will be applied to participant data sources, based on the results of the ACCESS project [31] and its updates. The ACCESS algorithms will be adapted to each data source according to the information components (e.g., primary care, secondary care, hospital registries) and coding systems (e.g., Systemized Nomenclature of Medicine-Clinical Terms [SNOMED-CT], the International Classification of Diseases, Ninth Revision [ICD-9], and the International Classification of Diseases, Tenth Revision [ICD-10]) available in each data source, as specified in the ACCESS project [31]. Multiple algorithms for the same outcome may be included in the analysis for some AESIs to assess the potential impact of differential misclassification.

9.3.3. Covariates

The following variables will be assessed at time zero and as available in each of the contributing data sources. They will be used to characterise populations (Sections 9.7.2.2 and 9.7.3.1), to define subgroups (Sections 9.7.2.4 and 9.7.3.3), and to control for confounding (Section 9.7.2.5). The corresponding lookback periods are defined in the SAP. Conditions considered by the US Centers for Disease Control and Prevention (CDC) to place the patient at “higher risk (conclusive)” for severe illness from COVID-19 [32] are marked with an asterisk (*).

- Demographics
- Age (grouped using the following categories [used to report background incidence rates from ACCESS: ≤ 17, 18-29, 30-39, 40-49, 50-59, 60-65, 66-69, 70-79, ≥ 80 years])
- Sex
- Pregnancy* status and pregnancy trimester
 - For pregnant women:
 - Gestational age, defined as the number of weeks from LMP to time zero (continuous variable)
 - Quality of the pregnancy records, categorised as described in the ConcePTION common data model [21]: “green,” “yellow,” “blue,” or “red.” Based on results from diagnostic reports on the quality of pregnancy records produced by the ConcePTION algorithm and feedback from each data source; sensitivity analyses will be considered.
- Geographic region as available in each contributing data source; granularity level to be defined in the SAP
- Socioeconomic status as available in each contributing data source (e.g., housing, employment, income)

- Date of vaccination
- Months of continuous enrolment in the data source
- COVID-19 history
 - Previous diagnosis of or positive test for COVID-19
 - Previous visit to the emergency department because of COVID-19
 - Previous hospital admission because of COVID-19
- COVID-19 vaccination history
 - Time since last COVID-19 vaccination
 - Prior number of doses of each of the COVID-19 vaccines approved during the study period, e.g., mRNA-1273, ChAdOx1-S, Ad26.COV2.S, Nuvaxovid, BNT162b2, BIMERVAX®
- Personal lifestyle characteristics
 - Smoking* status
 - Body mass index*
- Comorbidities
 - Asthma*
 - History of anaphylaxis
 - History of allergies
 - Diabetes mellitus (types 1 and 2)*
 - Hypertension
 - Cardiovascular disease*
 - Cerebrovascular disease*
 - Chronic respiratory disease (bronchiectasis, chronic obstructive pulmonary disease, interstitial lung disease, pulmonary embolism, pulmonary hypertension)*
 - Chronic kidney disease*
 - Chronic liver disease (cirrhosis, non-alcoholic fatty liver disease, alcoholic liver disease, autoimmune hepatitis)*
 - Cancer*
 - Cystic fibrosis*

- Dementia*
- Autoimmune disorders
- Influenza infection or other respiratory infections
- Charlson Comorbidity Index (component morbidities will be reported)
- Mental health conditions (depression, schizophrenia)*
- Obesity*
- Tuberculosis*
- Immunocompromising conditions
 - Immunodeficiencies*
 - Immunosuppressant medication use*
 - Human immunodeficiency virus* and other immunosuppressing conditions
 - Solid organ or blood stem cell transplantation*
- Comedication use during the year before time zero
 - Analgesics
 - Antibiotics
 - Antiviral medications
 - Corticosteroids
 - Non-steroidal anti-inflammatory drugs
 - Psychotropics
 - Statins
 - Novel oral anticoagulants
 - Warfarin
- Healthcare utilisation in the year and in the 2 weeks before time zero
 - Number of hospitalisations
 - Number of emergency department visits
 - Primary care utilisation
 - Cancer screening

- Other vaccinations, against:
 - Influenza
 - Pneumococcus
 - DPT (diphtheria, tetanus, pertussis)
 - Trivalent Oral Polio (polio)
 - Trivalent MMR (measles, mumps, and rubella)
 - Haemophilus influenzae type B
 - Hepatitis B virus
 - Varicella zoster virus
 - Herpes-zoster virus
 - Human papilloma virus
 - Meningococcus
 - Rotavirus
- Surrogates of frailty (as available); use of frailty scores [33,34] as a summary of these variables will be considered:
 - Paralysis
 - Parkinson's disease
 - Skin ulcer
 - Weakness
 - Fatigue
 - Undernutrition
 - Repeated falls
 - Stroke/brain injury
 - Ambulance transport
 - Dementia or cognitive impairment
 - Difficulty walking
 - Psychiatric illness

- Sepsis
- Heart failure
- Podiatric care
- Bladder incontinence
- Diabetes complications
- Osteoarthritis
- Coagulation deficiencies
- Vertigo
- Lipid abnormalities
- Functional decline
 - Use of devices associated with loss of autonomy (e.g., wheelchair, cane, oxygen, medical bed, deafness equipment, orthopaedic support and shoes)
 - Daily physiotherapy or nursing act
 - Living institution

9.3.4. Subgroups

Subgroups will be defined by the following baseline variables:

- Pregnancy status
- Immunocompromised status
- Frail subjects with comorbidities (e.g., chronic obstructive pulmonary disease, diabetes, chronic neurological disease, cardiovascular disorders)
- Presence of autoimmune and inflammatory disorders
- Prior use (concomitant or within the vaccination campaign/season) of influenza vaccine
- Calendar time. Periods corresponding to the use of original BIMERVAX[®] and adaptations targeting new variants of SARS-CoV-2 will be analysed separately.

If the size of the subgroup is adequate, a formal comparison will be implemented; otherwise, a description of the estimated risk of AESIs in that subgroup will be provided.

9.4. Data Sources

The timing and countries/regions where BIMERVAX[®] will be available are, at this time, unknown. The marketing authorisation holder (MAH) anticipates that BIMERVAX[®] may be

supplied to Spain. This study currently aims to use the data sources described in the subsequent sections. Additional potential data sources will be monitored.

9.4.1. EpiChron (Spain)

The EpiChron Cohort Study links sociodemographic and clinical anonymised information for all inhabitants of the Aragon region of Spain and was built from the BIGAN platform. The Aragon BIGAN platform integrates a technical infrastructure and a data lake gathering individual patient data from the regional health service information systems, including primary care, specialised care, hospitalisations, emergency department visits, drug prescriptions, image diagnoses, laboratory tests, diagnostics, vaccinations, medical history, and demographics from users of the public health system of Aragon, which comprises approximately 2 million individuals with historic data and an active population of 1.3 million individuals.

9.4.2. SIDIAP (Spain)

The Information System for the Improvement of Research in Primary Care (SIDIAP) includes data from 328 primary care centres managed by the Catalan Health Institute in Catalonia, Spain. The data source contains pseudo-anonymised records for > 8 million people since 2006, with 5.8 million people active in June 2021 (75% of the Catalan population). SIDIAP is representative of the general population living in Catalonia in terms of age, sex, and geographic distribution [35]. SIDIAP includes data on clinical and referral events registered by primary healthcare professionals and administrative staff in EHRs, demographic information, community pharmacy invoicing data, specialist referrals, and primary care laboratory test results. SIDIAP data can be linked to other data sources and registers at the local and national levels.

9.4.3. VID (Spain)

VID is a set of population-wide electronic databases covering residents of the Valencia region in Spain, representing approximately 5 million individuals [36]. All information in the VID databases can be linked at the individual level through a single personal identification number. The different VID databases collate information on health system coverage (e.g., health system entitlement, insurance modality), sociodemographic data (e.g., sex, age, geographic location), and data from the mortality registry (e.g., date of death) as well as data on primary care and specialised outpatient care (e.g., outpatient consultations, hospitalisations, emergency care, diagnoses, surgeries, critical care, social work), outpatient pharmaceutical prescriptions and dispensing, and clinical and administrative information (e.g., on all hospital admissions and ambulatory procedures, including public-private hospitals). The VID databases use either the ICD-9 or ICD-10 for coding diagnosis.

All databases included in the VID are updated frequently (every 1 to 3 months), except the Minimum Basic Data Set at Hospital Discharge (MBDS), which includes a summary of hospital admissions and is updated every 6 months.

9.5. Study Size

Study size will be determined by the uptake of BIMERVAX® in the contributing countries and data sources during the study period. The width of the 95% confidence intervals (CIs) [37] for different potential values of the true risk ratio of the AESIs is presented in [Table 2](#), under different risk scenarios in the unvaccinated population and sample sizes, assuming complete follow-up, both for the cohort study design and the SCRI study design.

Table 2. Confidence Interval Limits for AESI Risks in the Comparator Group for Different Scenarios of True Risk Ratio and of Study Sizes

Number of individuals per group	AESI risk in comparator group	Risk ratio	Matched cohort design		SCRI design	
			Lower bound of 95% CI	Upper bound of 95% CI	Lower bound of 95% CI	Upper bound of 95% CI
10,000	1 per 100,000	2	0.00	> 1,000	0.00	> 1,000
10,000	1 per 100,000	5	0.01	> 1,000	0.00	> 1,000
10,000	1 per 100,000	10	0.02	> 1,000	0.00	> 1,000
10,000	10 per 100,000	2	0.18	22.05	0.03	127.85
10,000	10 per 100,000	5	0.58	42.79	0.03	961.58
10,000	10 per 100,000	10	1.28	78.11	0.01	> 1,000
10,000	100 per 100,000	2	0.94	4.27	0.54	7.45
10,000	100 per 100,000	5	2.54	9.85	0.95	26.38
10,000	100 per 100,000	10	5.22	19.15	1.16	86.36
50,000	1 per 100,000	2	0.07	59.62	0.01	715.54
50,000	1 per 100,000	5	0.24	104.15	0.00	> 1,000
50,000	1 per 100,000	10	0.55	183.04	0.00	> 1,000
50,000	10 per 100,000	2	0.68	5.85	0.31	12.84
50,000	10 per 100,000	5	1.91	13.06	0.48	52.53
50,000	10 per 100,000	10	3.99	25.07	0.47	210.94
50,000	100 per 100,000	2	1.42	2.81	1.11	3.60
50,000	100 per 100,000	5	3.69	6.77	2.38	10.52
50,000	100 per 100,000	10	7.48	13.37	3.81	26.23
100,000	1 per 100,000	2	0.18	22.06	0.03	127.85
100,000	1 per 100,000	5	0.58	42.80	0.03	961.58
100,000	1 per 100,000	10	1.28	78.12	0.01	9,139.22
100,000	10 per 100,000	2	0.94	4.27	0.54	7.45
100,000	10 per 100,000	5	2.54	9.86	0.95	26.38
100,000	10 per 100,000	10	5.22	19.16	1.16	86.36
100,000	100 per 100,000	2	1.57	2.54	1.32	3.03
100,000	100 per 100,000	5	4.03	6.20	2.96	8.46
100,000	100 per 100,000	10	8.14	12.28	5.06	19.77

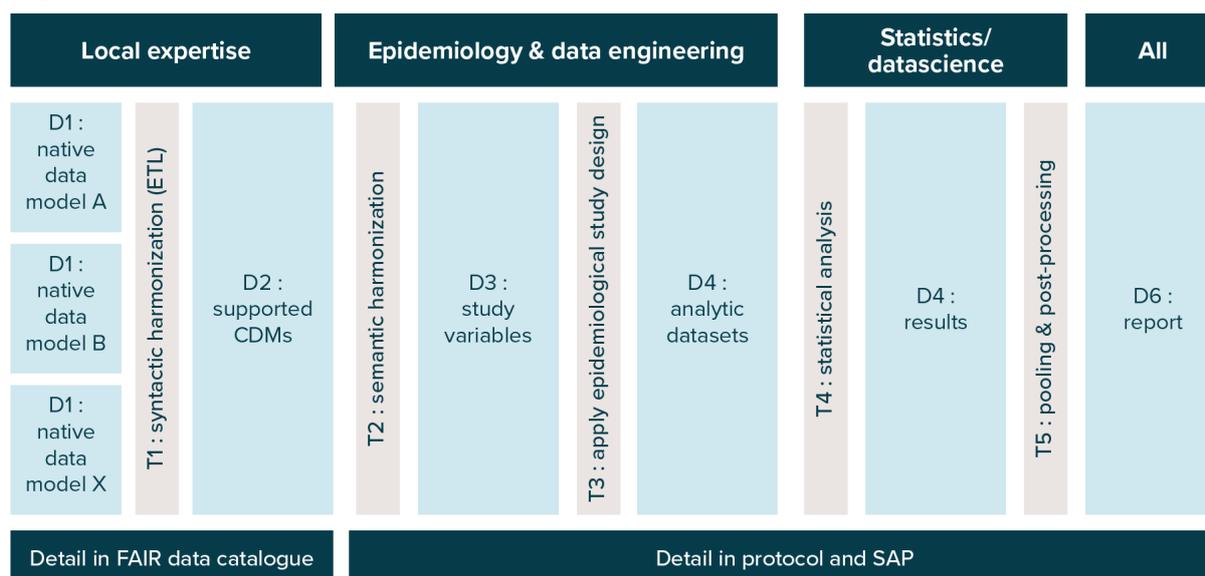
AESI = adverse event of special interest; CI = confidence interval; SCRI = self-controlled risk interval.

9.6. Data Management

This study will be conducted in a distributed manner using a common protocol, the ConcePTION common data model (CDM), and common analytics programs using existing healthcare data. The following transformation steps (T) will be implemented:

- T1: Extraction, transformation, and loading (ETL) of data to a CDM. To harmonise the structure of the data sets stored and maintained by each research partner providing data access, a shared syntactic foundation will be used and each research partner will create script to perform the transformation into the CDM. The CDM that will be used was developed during the IMI-ConcePTION project [38,39]. In this CDM, data are represented in a common structure, but the content of the data remains in its original format. The ETL design for each study will be shared in a searchable catalogue that meets the FAIR principles: findable, accessible, interoperable, and re-usable. The VAC4EU FAIR data catalogue is a meta-data management tool designed to contain searchable meta-data describing organisations that can provide access to specific data sources. Data quality checks will be conducted to measure the integrity of the ETL as well as internal consistency within the context of the CDM (see [Section 9.8](#)).
- T2: To reconcile differences between terminologies, a shared semantic foundation will be built for the definition of the events to be analysed by collecting relevant concepts in a structured fashion using a standardised event definition template. The CodeMapper tool was used to create diagnosis code lists based on completed event definition templates for each AESI and comorbid risk condition in the ACCESS project [40]. Based on the relevant diagnostic medical codes and keywords, as well as other relevant concepts (e.g., medications), 1 or more algorithms will be constructed (typically 1 sensitive, or broad, algorithm and 1 specific, or narrow, algorithm) to operationalise the identification and measurement of each event. These algorithms may differ between data sources, as the components involved in the study variables may differ. Manual review of electronic records will be conducted for a sample of the events. Specifications for both ETL and semantic harmonisation will be shared in the catalogue.
- T3: Following conversion to harmonised study variable sets, R programs for the application of the specific design will be created.
- T4: Programs for the calculation of incidence and prevalence and comparative analysis estimates, if needed, will be distributed to research partners for local deployment. The aggregated results produced by these scripts will then be uploaded to the Digital Research Environment (DRE; [myDRE – Trusted Research Environment](#)). The DRE is a cloud-based, globally available research environment where data are stored and organised securely and where researchers can collaborate. The DRE will be made available through University Medical Center Utrecht (UMCU)/ (<https://www.andrea-cloud.eu/>).
- T5: Pooled analysis will occur in the DRE and creation of tabulated results (post-processing) will occur locally using SAS ([Figure 3](#)).

Figure 3. Data Management Plan



CDM = common data model; D_n = data type; ETL = extraction, transformation, and loading; FAIR = findable, accessible, interoperable, re-usable; SAP = statistical analysis plan; T_n = transformation step; VAC4EU = Vaccine Monitoring Collaboration for Europe (study network).

Source: Figure from Cid Royo et al. [41]

9.6.1. Record Retention

The final study aggregated results sets will be archived and stored on the DRE. Validation of the quality control (QC) of the statistical analyses will be documented. RTI-HS will archive on a specific and secured central drive, the final study protocol and any amendments, the final SAP, statistical programs, and output files. Study records or documents may also include the analysis files, syntaxes (usually stored at the data source site), ETL specifications, and output from data quality checks.

To enable evaluation or inspections/audits from regulatory authorities or HIPRA, research partners providing data access agree to keep all study-related records, including the identity of all participating subjects (sufficient information to link records, for example, case report forms, hospital records), copies of all case report forms, safety reporting forms, source documents, detailed records of treatment disposition, and adequate documentation of relevant correspondence (e.g., letters, meeting minutes, telephone call reports). The records should be retained by research partners according to local regulations or as specified in the vendor contract, whichever is the longest. Research partners must ensure that the records continue to be stored securely for as long as they are retained.

If, for any reason, RTI-HS becomes unable to continue to retain study records for the required period, HIPRA should be prospectively notified. In this case, the study records must be transferred to a designee acceptable to HIPRA.

Study records must be kept for up to 15 years after completion or discontinuation of the study, unless RTI-HS, and HIPRA have expressly agreed to a different retention via a separate written agreement. Records must be retained for longer than 15 years if required by applicable local regulations.

9.6.2. Data Extraction

Each research partner providing data access will create ETL specifications using the standard ConcePTION ETL design template. After completion of this template and review by study statisticians or epidemiologists, each research partner will extract the relevant study data locally using its software (e.g., Stata, SAS, R, Oracle). These data will be loaded into the CDM structure in csv format. These data remain local (Figure 3).

9.6.3. Data Processing and Transformation

The central scripts will first transform the data from the syntactically harmonised CDM to semantically harmonised study variables (Figure 3). Subsequently, scripts to conduct analysis against semantically harmonised study variables will be distributed and run locally to produce aggregated results. The scripts for these processing and analysis steps will be developed and tested centrally and sent to the research partners.

The scripts will be structured in a modular format to ensure transparency. Functions to be used in the modules will be either standard packages or packages specifically designed, developed, and tested for multi-database studies. Scripts will be double coded in SAS or R, and quality checks will be thoroughly documented.

The research partners will run the scripts locally and send aggregated analysis results to the DRE using a secure file transfer protocol. In the DRE, results will be pooled (if needed) for final reporting.

All final statistical computations will be performed using R or SAS. Research partners will have access to the workspace for script verification.

9.6.4. Data Access

Within the DRE, each project-specific area will consist of a separate secure folder called a workspace. Each workspace will be completely secure, and researchers will be in full control of their data. Each workspace will have its own list of users, which will be managed by its administrators.

The DRE architecture will allow researchers to use a solution within the boundaries of data management rules and regulations. Although General Data Protection Regulation and Good (Clinical) Research Practice still apply to researchers, the DRE offers tools to better control and monitor which activities take place within projects.

All researchers who need access to the DRE will be granted access to study-specific secure workspaces. Access to a workspace is only possible with double authentication using an identification code and password together with the user's mobile phone for authentication.

Selected researchers with access to the workspace within the DRE will be able to upload files. File downloads will be possible only after requesting and receiving permission from a workspace member with an "owner" role.

9.7. Data Analysis

Detailed methodology for summary and statistical analyses of data collected in this study will be documented in the SAP, which will be dated, filed, and maintained by the sponsor. The SAP may modify or update the plans outlined in the protocol; any major modifications of

primary endpoint definitions or their analyses will be detailed in a protocol amendment. No specific hypotheses will be tested during the study described in this protocol.

The progress report (submitted on 16 July 2024, 3 months after V1.1 protocol endorsement by the EMA) described the status of project start-up and subsequent activities. The report also identified challenges and proposals for addressing them.

Interim report 1 will provide a description of the cohorts and crude risks of AESIs in the BIMERVAX® and comparator cohorts. Interim report 2 will include all the analyses from interim report 1 based on updated data cuts; additionally, if study size allows, the report will also include the comparative analysis of AESIs in the main cohort. The final report will include all the analyses described below based on available information at the time of the corresponding data extraction.

The final report will be submitted 36 months after the start of data collection and will contain all the analyses described in this protocol. An updated final study report providing results on pregnancy outcomes will be submitted 48 months after the start of data collection. The study periods to be included in each interim report will depend on the data source, linkages, lag times, and time required to obtain the data by the research institutions. [Table 3](#) provides estimations of the available information for each deliverable. In addition, for the first interim report, the study period may be affected by the time needed to allow for protocol endorsement by the EMA, contracting between research institutions, writing of the SAP, data extraction, analysis, and reporting.

Table 3. Maximum Follow-up for Each Study Report By Data Source

Data sources	Time lag for data updates	Interim report 1 (Q3 2027) ^a	Interim report 2 (Q3 2028) ^a	Final report (Q3 2029) ^a
EpiChron (ES)	≈ 6 months	≈ 6 months	≈ 18 months (6 + 12)	≈ 30 months (6 + 24)
SIDIAP (ES)	≈ 6 months	≈ 6 months	≈ 18 months (6 + 12)	≈ 30 months (6 + 24)
VID (ES)	≈ 6 months	≈ 6 months	≈ 18 months (6 + 12)	≈ 30 months (6 + 24)

ES = Spain; SIDIAP = Information System for Research in Primary Care (Spain); VID = Valencia Health System Integrated Database (Spain).

^a Based on administration of at least 4,000 doses of BIMERVAX® expected in Q3 2026. First use of the original vaccine in Spain occurred during 2023.

9.7.1. Vaccine Utilisation Study

This study will describe all covariates (see [Section 9.3.3](#)) at the time of receipt of the first BIMERVAX[®] dose. An additional category for age, corresponding to age of childbearing potential, will be created for women. For continuous variables, means, standard deviations, medians, and other quartiles will be estimated. For categorical variables, counts and proportions will be estimated. The missingness of variables will also be described. Further details will be described in the SAP.

To describe the subsequent vaccination trajectories, the following will be computed:

- Counts and percentages of individuals receiving a subsequent COVID-19 vaccine
- Brand of subsequent COVID-19 vaccine
- Time to administration of subsequent COVID-19 vaccine

Graphical representation via a Sankey plot will be considered.

9.7.2. Matched Cohort Design

Comparative analyses will be performed if at least 3 events are observed per exposure group in each data source.

9.7.2.1. Exposure Assignment and Follow-up

The exposures under study are outlined in [Section 9.3.1](#). Individuals will be assigned to each vaccination category according to their data at time zero, as outlined below:

- BIMERVAX[®] group: eligible individuals will be assigned to this group when they receive a dose of BIMERVAX[®].
- Non-BIMERVAX[®] vaccine group: eligible individuals will be assigned to this group when they receive a dose of any COVID-19 vaccine that is not BIMERVAX[®]. Individuals will be censored if and when they receive a dose of BIMERVAX[®] during follow-up.

Individuals will be followed for incident AESIs from time zero (see [Section 9.1.2.2](#)) until the censoring described above, SARS-CoV-2 infection ([Section 9.7.2.6](#)), death, administrative end of follow-up, or end of the study period ([Section 9.7.2.4](#)), whichever occurs first.

The same individual could therefore be eligible for inclusion in both groups—the BIMERVAX[®] vaccine group and non-BIMERVAX[®] vaccine group—at different points in time provided that they fulfil the eligibility criteria at baseline.

9.7.2.2. Descriptive Statistics

The distributions of baseline characteristics at time zero by exposure group will be calculated to describe the study cohort and illustrate differences between the groups. For continuous variables, means, standard deviations (SDs), medians, and other quartiles will be estimated. For categorical variables, counts and proportions will be estimated. The missingness of

variables will also be described. Additionally, to describe the subsequent vaccination trajectories, the following will be computed:

- Counts and percentages of individuals receiving a subsequent COVID-19 vaccine
- Brand of subsequent COVID-19 vaccine
- Time to administration of subsequent COVID-19 vaccine

Further details will be described in the SAP.

To describe the relative imbalance of characteristics between the exposed and comparator groups, absolute standardised differences will be calculated for each baseline characteristic [42,43]. An overall standardised difference across all levels will be calculated for multilevel categorical variables [43].

9.7.2.3. Crude Outcome Measures

The risk of the study outcomes will be estimated at the end of the risk interval and at 90-day intervals up to 365 days of follow-up (Table 1, Section 9.3.2) using the 1–Kaplan-Meier estimator. Effect estimates will be calculated both as risk differences and risk ratios for those exposed to BIMERVAX[®] compared with those exposed to a comparator vaccine. All estimates will be bounded with a percentile-based 95% CI.

Time to outcome will be defined as the time from the baseline date (time zero) until the occurrence of the outcome or censoring (Section 9.1.2.2 and Section 9.1.2.4). The variance will be computed using approaches that account for autocorrelation (e.g., the robust estimator or via bootstrapping) [44].

9.7.2.4. Subgroup Analyses

If the sample size allows for informative comparative analyses, the subgroups defined in Section 9.3.4 will be analysed.

9.7.2.5. Adjustment for Baseline Imbalances

To account for potential residual baseline confounding after matching, propensity score methods will be used to estimate the adjusted risks, effect estimates, and their corresponding 95% CIs. Specifically, the propensity score (i.e., the probability of receiving BIMERVAX[®] conditional on baseline covariates listed in Section 9.3.2.1) will be used to construct inverse probability weights [45]. More details, including the variable selection and construction of weights, will be provided in the SAP. Given the 7- to 14-day time lag for immunity to build following receipt of a COVID-19 vaccine dose, the incidence of COVID-19 hospitalisations in the first 7 days after baseline will be evaluated as a negative control outcome for baseline exchangeability [19]. Baseline covariate balance after matching and weighting will be assessed by evaluating the standardised mean difference for continuous [42] and categorical [43] variables.

9.7.2.6. Censoring to Estimate the Direct Effect on AESIs Under Complete Follow-up and Under Complete Adherence to the Vaccination Strategies

Many of the observed or hypothetical post-vaccination AESIs may also be associated with COVID-19 infection. Previous studies that evaluated the association between various aspects of COVID-19 infection (e.g., COVID-19 hospitalisation, diagnosis, positive test) and select AESIs showed increased risks of acute kidney injury and arrhythmia [46], deep vein thrombosis/pulmonary embolism [46,47], intracranial haemorrhage [46], myocardial infarction [46-49], ischaemic stroke [47-49], and myocarditis/pericarditis [46] in various populations.

The primary objective of this study specifies the effect to be estimated as vaccination with BIMERVAX® versus vaccination with a COVID-19 vaccine other than BIMERVAX® (i.e., the *direct* effect) (Section 8). The study focuses on the direct effect because of its safety nature. Thus, its aim is to evaluate the effects of BIMERVAX® on the incidence of AESIs, which are not mediated by the vaccine's preventive effect on infection. If we assessed the *total* effect (i.e., both the effect that is mediated by the vaccine's preventive effect on infection plus the direct effect on the AESIs), we might observe that, compared with other vaccines, BIMERVAX® protects against medical complications of SARS-CoV-2 infections (e.g., respiratory distress) because BIMERVAX® protects against infection with SARS-CoV-2, which in turn causes the corresponding medical complications. For example, if respiratory distress were an AESI, the effect of BIMERVAX® on this AESI could potentially be masked by the protective effect of BIMERVAX® against COVID-19 [18].

In addition, if the study estimated the total effect (as opposed to the direct effect), the incidence of events mediated by COVID-19 infection would depend on the background rate of COVID-19 infection in the study population, which would make the effect estimates highly dependent on the level of pandemic activity during the follow-up period. A limitation of this approach is that some infections may not be documented, which would mean that some of the estimated direct effects may be mediated through COVID-19 infection prevention. The total effect will be assessed by a sensitivity analysis (Section 9.7.2.9).

The following censoring will be applied to estimate the direct effect under complete follow-up and complete adherence to the vaccination strategies. The corresponding assumptions for validity are outlined as follows:

- *Censoring of the matched pair when either member has a documented COVID-19 infection.* This censoring will be implemented to estimate the effect of BIMERVAX® compared with other COVID-19 vaccines on the incidence of AESIs that is not mediated by the preventive effect on infection (i.e., the controlled direct effect). This approach assumes that uncensored individuals will have a similar risk for the AESI as that of censored individuals if they had not been infected, conditional on the baseline covariates that were adjusted for (via matching and weighting).
- *Censoring of the matched pair when either member is lost to follow-up (i.e., disenrolls from the data source).* This censoring will be implemented to estimate the effect under complete follow-up. This approach assumes that uncensored individuals will have a similar risk for the AESI as individuals who were disenrolled from the data source if they had remained in follow-up, conditional on the baseline covariates that were adjusted for (via matching and weighting).

- *Censoring of the matched pair when the individual in the comparator group receives a dose of BIMERVAX[®].* This censoring will be implemented to estimate the effect under complete adherence to the vaccination strategies. This approach assumes that the risk of the AESI for individuals who did not deviate from the vaccination strategy would be similar to that for individuals who deviated from the vaccination strategy, had they not deviated, conditional on the baseline covariates that were adjusted for (via matching and weighting).

9.7.2.7. Missing Data Handling

Several approaches for handling missing data will be considered (e.g., inverse probability weighting of the complete case population, complete case analysis) based on the amount of missing data and the most reasonable assumption on the pattern of how the data are missing. Additional details on when and which method will be used will be described in the SAP.

9.7.2.8. Meta-Analysis

A combined risk ratio estimate and its 95% CI will be estimated at the end of the risk interval for each AESI using the DerSimonian-Laird random effects approach [50]. The standard error for each risk ratio will be estimated by the sample SD of the bootstrap replications [51].

Heterogeneity of the estimated effects across data sources will be assessed using the I^2 statistic [52]. Regardless of the value of the I^2 statistic, effect estimates (with the highest level of adjustment implemented) will be meta-analysed across databases; however, the I^2 statistic and consistency of the direction of the effects will be taken into consideration to interpret the meta-analysis results.

The meta-analysis will be performed for the matched population analyses, for sensitivity analyses of the total effect, for sensitivity analyses of the non-matched population, and for the subgroup of the non-matched population analyses, when conducted.

9.7.2.9. Sensitivity Analyses

The following sensitivity analyses will be implemented:

- Analysis to estimate the total effect of BIMERVAX[®] vaccination on the AESIs (as opposed to the main analysis, which estimates the controlled direct effect) by not censoring the pair if a component is diagnosed with a COVID-19 infection. This analysis will estimate the total effect of the vaccines on potential adverse events (AEs) through all causal pathways between the vaccines and outcomes, including those potentially mediated by infection (i.e., these risks capture complications arising both from the vaccines themselves and from the incident infections that they are intended to prevent). Differences from the main analysis should be minimal if SARS-CoV-2 virus circulation is low [18].
- Analysis to estimate the direct effect of BIMERVAX[®] vaccination on the incidence of pneumonia. This analysis will gauge the amount of unreported SARS-CoV-2 infections, because pneumonia is not expected to be a complication of any COVID-19 vaccination [18].
- Analysis to avoid discarding information by matching. In the main analysis, individuals vaccinated with BIMERVAX[®] for whom a match is not found by the proposed matching variables will be discarded from the analysis. If the number of

exposed individuals or outcomes is scarce, matching can contribute to imprecise effect estimates. In this situation, a sensitivity analysis will be considered in which all eligible vaccinees are included and baseline characteristics are adjusted for via inverse probability weighting. Other than the absence of matching and the construction of baseline weights using models that include the matching variables in addition to the variables of the weights used in the main analysis, the remaining analytical procedures will be the same as those in the main analysis.

9.7.3. Self-controlled Risk Interval Design Study

9.7.3.1. Descriptive Statistics

The distributions of subjects' characteristics at the time of vaccination with BIMERVAX® will be calculated to characterise the study sample. Means, SDs, and quartiles will be estimated for continuous variables. Counts and proportions will be estimated for categorical variables. The missingness of variables will also be described.

9.7.3.2. Measures of Association

Conditional Poisson regression will be used to estimate incidence rate ratios and their corresponding 95% CIs. AESIs for which the SCRI design will be used and their risk intervals are specified in [Table 1](#). The control intervals will be the same length as the risk intervals for each AESI and will begin after a 7-day washout period that will separate the risk and control intervals; more details will be provided in the SAP.

The SCRI inherently adjusts for both measured and unmeasured time constant factors, such as sex and chronic health conditions with onset before the start of follow-up. Time-varying confounders may be included as covariates in regression models.

9.7.3.3. Subgroup Analysis

If the sample size allows for informative analyses, subgroups as defined in [Section 9.3.4](#) (except for the pregnancy status subgroup) will be analysed.

9.7.3.4. Meta-Analysis

For the SCRI design, a combined incidence rate ratio estimate and its 95% CI will be estimated for each AESI using the DerSimonian-Laird random effects approach [50].

Heterogeneity of the estimated effects across data sources will be assessed using the I^2 statistic [52]. Regardless of the value of the I^2 statistic, effect estimates will be meta-analysed across databases, but the I^2 statistic and consistency of the direction of the effect estimates will be taken into consideration to interpret the meta-analysis results.

The meta-analysis will be performed for the SCRI main risk and control intervals and for the sensitivity analysis with an extended control interval.

9.7.3.5. Sensitivity Analysis

A sensitivity analysis of the SCRI study will be implemented by extending the proposed control intervals to 127 days. This analysis can increase the precision of the effect estimates.

9.7.4. Handling of Small Cell Counts

Some of the analyses may be limited due to a small number of events and/or data privacy–driven cell count restrictions at a research partner (see [Table 4](#)).

The possibility of unintentional (deductive) disclosure arises when cells with small numbers of subjects are quoted. When reporting data, the policy is that no cell should contain fewer than 5 events. In EpiChron and SIDIAP, zero values can be reported. When distributed outside the research team and the client, the exact number of events will be replaced by < 5 or ≤ 10 , as appropriate, and other cells (such as person-years) will be masked to avoid back calculation, if needed.

Table 4. Small Cell Count Rules in Each Data Source

Rule type	EpiChron	SIDIAP, Catalonia	VID, Valencia
Numbers to be masked	1-4	1-4	NA
Text used	< 5	< 5	NA
Possible to share with research partners	Yes	Yes	Yes
Possible to share with HIPRA, which submits report to regulatory authorities	No	No	Yes
Comments	NA	NA	There must be no identifiable information to be shared

NA = not applicable; SIDIAP = Information System for Research in Primary Care (Spain); VID = Valencia Health System Integrated Database (Spain).

9.8. Quality Control

9.8.1. RTI-HS as Coordinating Centre

Standard operating procedures or guidance documents at the participating institutions will be used to guide the conduct of the study.

At RTI Health Solutions (RTI-HS), these procedures include internal quality audits, rules for secure and confidential data storage, methods to maintain and archive project documents, QC procedures for programming, standards for writing analysis plans, and requirements for senior scientific review. All key study documents, such as the analysis plan, abstraction forms, and study reports, will undergo QC review, senior scientific review, and editorial review.

Experienced RTI-HS programmers will perform the ETL. To ensure the integrity and quality of the study results, RTI-HS will follow the programming validation life cycle process for all analyses. This includes QC programs, logs, and output for accuracy according to relevant standard operating procedures. All programs will be independently reviewed by a second programmer/analyst.

For RTI-HS, an independent Office of Quality (OQ) will perform audits and assessments that involve various aspects of the project, including, but not limited to, education and training documentation, data entry and data transfer procedures and documentation, and institutional review board (IRB) documentation. Such audits will be conducted by the OQ according to

established criteria in standard operating procedures and other applicable procedures. Standard procedures will be in place to restore files in the event of a hardware or software failure.

A quality assurance audit of this study may be conducted by the sponsor or the sponsor's designees.

Appropriate data storage and archiving procedures will be followed with periodic back-up of files. Standard procedures will be in place to restore files in the event of a hardware or software failure at each research centre.

Two members from the independent VAC4EU scientific advisory board will provide independent external review of key study documents, such as the protocol, statistical analysis plans, and reports. This review will focus on scientific soundness and interpretation of the results from reports and publications. The peer review process with the external experts, appointed and contracted by VAC4EU, will support scientific quality, independence, and transparency. Their comments will be made available to all parties involved in the study.

9.8.2. EpiChron (Spain)

The EpiChron Cohort will be built from the BIGAN platform, which integrates a technical infrastructure and a data lake, collecting individual patient data from the regional health service information systems. The BIGAN platform includes several mechanisms to control and improve the quality of data, mainly in the ETL processes for capture and persistence in the data lake. These mechanisms include validation rules (e.g., for dates and time intervals) and cross-checks with master tables, requiring that certain coded data exist in a standardised dictionary. Analyses of the distribution of variables will also be carried out periodically to detect “outliers” that identify errors in the data capture or transformation processes. Generally, records that do not pass the quality assurance procedures are kept in a “holding” area for review and decision to discard or reprocess. The resulting databases will be pseudonymised to encrypt individual-level identification codes, protecting individuals' privacy, and complying with data protection laws. They will be stored on a central computer server, with access restricted to members of the research group, via a 2-step authentication process. The research group will comprise a multidisciplinary qualified team, including public health specialists, epidemiologists, clinicians, pharmacists, statisticians, and data managers, who are all trained in data management and patient data protection.

9.8.3. SIDIAP (Spain)

Quality control processes will be implemented at each phase of the data flow cycle. The QC checks will be performed at the extraction and uploading steps. To assess data completeness, the presence of elements will be described by geographical area, registering physician, time, and the distribution of values. Data accuracy will be assessed by validity checks on outliers, out of range values, formatting errors, and logical date incompatibilities. Completeness and accuracy measures will be used to inform decisions on the required transformations to improve data quality (e.g., harmonisation, normalisation, clean-up) and the fitness for purpose of the data for use in this study.

9.8.4. VID (Spain)

Once the final version of the protocol is available, The Foundation for the Promotion of Health and Biomedical Research of Valencia Region (FISABIO) will develop its own version of the protocol, outlining the tasks to be performed by the research team. This protocol, along

with the original version, must receive approval from the Research Ethics Committee. Once approval from the Research Ethics Committee is obtained, it is necessary to submit all the documentation to the PROSIGA Committee of the Conselleria de Sanitat. Through meetings with the research team, this Committee grants authorisation for data usage and sets the data extraction process.

Next, raw data will be extracted in text file format and will undergo a data quality check. Data will be stored on secure servers at FISABIO in accordance with Spanish and data protection requirements and ensuring that no identifiable data will be stored longer than required.

All procedures that will be implemented for data collection, storage, protection, retention, and destruction will comply with national and EU legislation. The research team will stay up to date with the detailed provisions of the EU General Data Protection Regulation (GDPR), which came into effect in May 2018 and which will supersede national legislation within the EU Member States.

9.9. Limitations of the Research Methods

This study is subject to limitations related to both the study design and to the use of secondary healthcare data.

A data-related limitation of this study is the reliance on the accuracy of codes and algorithms to identify outcomes. Exposure identification may be based on immunisation registers, pharmacy dispensing records, general practice records, medical records, or other secondary data sources. The ability to identify specific COVID-19 vaccine products and dates of vaccination in these data sources is described in [Section 9.3.1](#). Errors in the recording of the brand of the vaccine administered could lead to exposure misclassification, although such errors are unlikely and not necessarily differential by vaccine brand. It is possible that vaccination of individuals outside the healthcare system will not be recorded in secondary data sources, although this should not affect either the matched cohort design (in which both exposure groups are vaccinated) or the SCRI design (in which the control risk interval is adjacent to the exposure period for the same individual). This study requires 12 months of enrolment in the data source before study start to be eligible, to properly characterise individuals based on at least 12 months of data history. Because the data will arise from European public health systems in which individuals are enrolled for a lifetime, with the exception of moving away from the covered geography, we expect that data history will be available well beyond 12 months before study start for the majority of individuals.

A limitation of the cohort design is the potential for residual or unmeasured baseline confounding. Such confounding can occur if the reasons for receiving a specific COVID-19 vaccine brand (i.e., BIMERVAX[®] vs. non-BIMERVAX[®]) are associated with the probability of an AESI occurrence, and those reasons (or their surrogates) are not accurately measured and/or adjusted for. A prior study evaluating the comparative safety of different COVID-19 vaccines achieved good confounding control with a design akin to our matched cohort [18]. Of note, much less confounding is expected when recipients of different vaccines are compared than when vaccinated and unvaccinated individuals are compared. The SCRI, which compares a time period following vaccination with BIMERVAX[®] versus a subsequent time period, automatically adjusts for time-invariant confounders. However, the SCRI is not well suited to study outcomes with gradual onset, long latency, or risk intervals that are not

well known. It also may be subject to bias for outcomes that affect the probability of exposure.

The matching procedure in the cohort design produces a study population (i.e., a set of matched pairs) with a distribution of matching variables representative of those who received BIMERVAX[®] by matching comparator individuals to exposed individuals based on a prespecified set of baseline variables. Therefore, the cohort design will estimate the average causal effect in BIMERVAX[®] recipients (i.e., in a population that has the distribution of matching variables of the BIMERVAX[®] recipients). The application of further adjustment via inverse probability weighting will not change the estimand (the causal effect in a population that has the distribution of matching variables of the BIMERVAX[®] recipients). The average causal effect in the BIMERVAX[®] recipients and the average causal effect in the whole vaccinated population (with and without BIMERVAX[®]) should differ only (apart from random variation) if effect modification by any baseline variable exists. This possibility will have to be considered when comparing effect estimates with those from other studies

In the main analysis, we propose to estimate a controlled direct effect of the vaccines on potential AEs not mediated by infection, by censoring individuals if and when they are diagnosed with a SARS-CoV-2 infection. That is, these risks reflect potential complications arising only from the vaccines themselves. This analysis assumes a complete capture of SARS-CoV-2 infection. If that is not the case (e.g., because infections are underdiagnosed or because infections are diagnosed but not recorded), identified effects can be a mix of true harmful effects plus lower efficacy. We propose to study “pneumonia” because it is not expected to be an adverse event of vaccination but can capture vaccine effectiveness and will serve as an indirect marker of undocumented SARS-CoV-2 infections. Additionally, we propose a sensitivity analysis in which individuals are not censored in the event of SARS-CoV-2 infection. This analysis will estimate the total effect of the vaccines on potential AESIs through all causal pathways between the vaccines and outcomes, including those potentially mediated by infection [18]. In times of low circulation of the SARS-CoV-2 virus, the difference between the controlled direct effect and the total effect should be negligible.

A study design–related limitation of both the cohort and SCRI designs is that any uncertainty regarding risk intervals will lead to misclassification and attenuation of risk estimates. Adverse events remote from the vaccination date are less likely to be a vaccine effect, but if remote person-time is not assessed, then there is a risk of misclassifying the outcome. The estimation of cumulative incidence curves with a time zero aligned with the exposure assignment and eligibility assessment lessens the impact of unknown risk intervals because they evaluate the whole available follow-up [14].

This PASS study evaluates AESIs that tend to be rare, and COVID-19 vaccination may end up being recommended for individuals who are elderly and/or ill, which may decrease the study size. Additionally, the proposed cohort design, which is based on matching, may discard exposed individuals for whom a match was not found. These outcomes could lead to imprecise and poorly informative effect estimates. To mitigate this potential limitation, our matched cohort design will allow for multiple eligibility. Additionally, a proposed sensitivity analysis would analyse all eligible individuals, regardless of whether a match was found for them.

The outcomes “enhanced COVID-19 disease” (meaning a maladaptive immune response to SARS-CoV-2 infection) and “vaccine-associated enhanced disease” (meaning a maladaptive immune response to SARS-CoV-2 infection promoted by vaccination) will not be evaluated

in this study, because immune maladaptation cannot be measured or surrogated within the study data sources. COVID-19 disease and its severity will be studied in the companion postauthorisation effectiveness study sponsored by the MAH. Likewise, the subgroup analysis during breastfeeding and lactation cannot be studied due to lack of data on this status.

There is uncertainty about the uptake of a new COVID-19 vaccination in the context of the COVID-19 pandemic emergency ending and multiple other options for vaccination becoming available. This situation could contribute to decreased precision of estimates, especially for subgroups (e.g., pregnant women) and certain sensitivity analyses.

10. PROTECTION OF HUMAN SUBJECTS

This is a non-interventional study using secondary data collection and does not pose any risks for individuals. All data collected in the study will be de-identified with no breach of confidentiality with regard to personal identifiers or health information. Each data source research partner will apply for an independent ethics committee review according to local regulations; in addition, RTI-HS as the coordinating centre will obtain approval or exemption from the RTI International IRB.

Data protection and privacy regulations will be observed in collecting, forwarding, processing, and storing data from study participants.

10.1. EpiChron

EpiChron will submit the final study protocol (and the potential updates and/or amendments) to the Research Ethics Committee of the Autonomous Community of Aragon (CEICA; <https://www.iacs.es/investigacion/comite-de-etica-de-la-investigacion-de-aragon-ceica/>) for approval. EpiChron will also submit the protocol and a data management plan to the IACS Biocomputing Unit to assess and verify the availability of the requested data in the BIGAN platform; its adequacy for the project; and compliance with all security, privacy, and data minimisation requirements required by current regulations. Access to pseudonymised data will then be regularly granted only for the specific purposes of this study.

10.2. SIDIAP

A 5-step procedure will take place before approval of the study is granted: (1) the researcher(s) must send an application to the SIDIAP team (standardised form available at <https://www.sidiap.org/index.php/en/solicituds-en> and in the study protocol); (2) the application is approved by SIDIAP's Scientific Committee, which will evaluate the scientific quality and feasibility of the proposal; (3) the study protocol is approved by the Clinical Research Ethics Committee of IDIAP-Jordi Gol; (4) the principal investigator or coordinator of the study must sign a Good Practice form and, in some cases, an agreement between parties is needed; and (5) a meeting between the research team and the SIDIAP team will be arranged to discuss the procedures and set the data extraction process. Further information is available online (<https://www.sidiap.org/index.php/en/solicituds-en>).

10.3. VID

Once the final version of the protocol is available, FISABIO will develop its own version of the protocol, outlining the tasks to be performed by the research team. This protocol, along with the original version, must receive approval from the Research Ethics Committee. Once approval from the Research Ethics Committee is obtained, it is necessary to submit all the

documentation to the PROSIGA Committee of the Conselleria de Sanitat. Through meetings with the research team, this Committee grants authorisation for data usage and sets the data extraction process.

11. MANAGEMENT AND REPORTING OF ADVERSE EVENTS/ADVERSE REACTIONS

For non-interventional study designs that are based on secondary use of data, such as studies based on medical chart reviews or EHRs, systematic reviews or meta-analyses, reporting of adverse events/adverse drug reactions is not required. Reports of adverse events/adverse drug reactions should be summarised only in the study report, where applicable [53].

According to the EMA *Guideline on Good Pharmacovigilance Practices (GVP), Module VI – Collection, Management and Submission of Reports of Suspected Adverse Reactions to Medicinal Products (Rev 2)* [53]:

“For non-interventional study designs, which are based on secondary use of data, adverse reactions reporting is not required. All adverse events/reactions should be summarized in the final study report.”

Module VIII – Post-Authorisation Safety Studies (Rev 3) echoes this approach. Legislation in the EU further states that for certain study designs, such as cohort studies, particularly those involving EHRs, it may not be feasible to make a causality assessment at the individual case level.

11.1. Other Good Research Practice

This study adheres to the *Guidelines for Good Pharmacoepidemiology Practices (GPP)* [54] and has been designed in line with the ENCePP *Guide on Methodological Standards in Pharmacoepidemiology* [55]. The *ENCePP Checklist for Study Protocols* [56] has been completed (see [Annex 2](#)).

The study is a PASS and will comply with the definition of the non-interventional (observational) study referred to in the International Council for Harmonisation of Technical Requirements for Registration of Pharmaceuticals for Human Use tripartite guideline *Pharmacovigilance Planning E2E* and provided in the EMA *Guideline on Good Pharmacovigilance Practices (GVP) Module VIII: Post-Authorisation Safety Studies*, as well as with the 2012 EU pharmacovigilance legislation, adopted on 19 June 2012 [57]. The study will comply with the study reporting requirements specified in Module VIII Section VIII.B.6.3.1, Progress reports, and VIII.B.6.3.2, Final study report, of the *Guideline on Good Pharmacovigilance Practices*.

In alignment with GVP Module VIII [2], Section VIII.B.2, Study registration, the study and its updated protocol will be registered in the HMA-EMA Catalogue (currently registered with EU PAS number EUPAS000000321) before the start of data collection [58]. At completion, the final report, or its summary, will be posted.

The research team and study sponsor will adhere to the principles of transparency and independence in the ENCePP Code of Conduct [10].

The research team will apply for the ENCePP Study Seal [59].

12. PLANS FOR DISSEMINATING AND COMMUNICATING STUDY RESULTS

The study protocol, study progress reports, and interim and final study reports will be included in regulatory communications in line with the RMP, Periodic Safety Update Reports, and other regulatory reporting requirements. Study reports will be prepared using a template following the GVP Module VIII Section B.6.3 [2]. [Section 9.7](#) details the content of the study reports.

In its *Guidelines for Good Pharmacoepidemiology Practices (GPP)* [54], the International Society for Pharmacoepidemiology (ISPE) contends that “...*there is an ethical obligation to disseminate findings of potential scientific or public health importance*”; for example, results pertaining to the safety of a marketed medication. “...*the marketing authorisation holder should communicate to the Agency and the competent authorities of the Member States in which the product is authorised the final manuscript of the article within two weeks after first acceptance for publication.*”

Study results will be submitted for publication following guidelines, including those for authorship, established by the International Committee of Medical Journal Editors [60]. When reporting results of this study, the appropriate Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) checklist will be followed [61]. The Consolidated Standards of Reporting Trials (CONSORT) statement [62] refers to randomised studies, but provides useful guidance applicable to non-randomised studies as well.

Communication via appropriate scientific venues (e.g., the International Society for Pharmacoepidemiology) will be considered.

In alignment with the EMA *GVP Module VIII: Post-Authorisation Safety Studies* [2], Section VIII.B.5, and the *ENCePP Code of Conduct* [10], the MAH and the investigator will agree upon a publication policy allowing the principal investigator to independently prepare publications based on the study results, irrespective of data ownership. The MAH will be entitled to view the results and interpretations included in the manuscript and provide comments prior to submission of the manuscript for publication. The MAH and the research team are aware that the MAH should communicate to the Agency and the competent authorities of the Member States in which the product is authorised the final manuscript of the article within 2 weeks after first acceptance for publication [2].

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ANNEX 1 LIST OF STAND-ALONE DOCUMENTS

None.

ANNEX 2 ENCePP CHECKLIST FOR STUDY PROTOCOLS

Doc.Ref. EMA/540136/2009

ENCEPP Checklist for Study Protocols (Revision 4)

Adopted by the ENCePP Steering Group on 15/10/2018

The [European Network of Centres for Pharmacoepidemiology and Pharmacovigilance \(ENCEPP\)](#) welcomes innovative designs and new methods of research. This Checklist has been developed by ENCePP to stimulate consideration of important principles when designing and writing a pharmacoepidemiological or pharmacovigilance study protocol. The Checklist is intended to promote the quality of such studies, not their uniformity. The user is also referred to the [ENCEPP Guide on Methodological Standards in Pharmacoepidemiology](#), which reviews and gives direct electronic access to guidance for research in pharmacoepidemiology and pharmacovigilance.

For each question of the Checklist, the investigator should indicate whether or not it has been addressed in the study protocol. If the answer is “Yes,” the section number of the protocol where this issue has been discussed should be specified. It is possible that some questions do not apply to a particular study (for example, in the case of an innovative study design). In this case, the answer ‘N/A’ (Not Applicable) can be checked and the “Comments” field included for each section should be used to explain why. The “Comments” field can also be used to elaborate on a “No” answer.

This Checklist should be included as an Annex by marketing authorisation holders when submitting the protocol of a non-interventional postauthorisation safety study (PASS) to a regulatory authority (see the [Guidance on the format and content of the protocol of non-interventional post-authorisation safety studies](#)). The Checklist is a supporting document and does not replace the format of the protocol for PASS presented in the Guidance and Module VIII of the Good pharmacovigilance practices (GVP).

Study title: VAC4EU Postauthorisation Safety Study of BIMERVAX® Vaccine in Europe

HMA-EMA Catalogue of RWD Studies number: EUPAS1000000321

Study reference number (if applicable):

Section 1: Milestones	Yes	No	N/A	Section number
1.1 Does the protocol specify timelines for				
1.1.1 Start of data collection ¹	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6
1.1.2 End of data collection ²	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6
1.1.3 Progress report(s)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6
1.1.4 Interim report(s)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6
1.1.5 Registration in the EU PAS Register [®]	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6

¹ Date from which information on the first study is first recorded in the study dataset or, in the case of secondary use of data, the date from which data extraction starts.

² Date from which the analytical dataset is completely available.

<u>Section 1: Milestones</u>	Yes	No	N/A	Section number
1.1.6 Final report of study results	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	6

Comments:

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<u>Section 2: Research question</u>	Yes	No	N/A	Section number
2.1 Does the formulation of the research question and objectives clearly explain:	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	8
2.1.1 Why the study is conducted? (e.g., to address an important public health concern, a risk identified in the risk management plan, an emerging safety issue)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
2.1.2 The objective(s) of the study?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
2.1.3 The target population? (i.e., population or subgroup to whom the study results are intended to be generalised)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
2.1.4 Which hypothesis(-es) is (are) to be tested?	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	
2.1.5 If applicable, that there is no <i>a priori</i> hypothesis?	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	

Comments:

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<u>Section 3: Study design</u>	Yes	No	N/A	Section number
3.1 Is the study design described? (e.g., cohort, case-control, cross-sectional, other design)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1
3.2 Does the protocol specify whether the study is based on primary, secondary or combined data collection?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1
3.3 Does the protocol specify measures of occurrence? (e.g., rate, risk, prevalence)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1.1, 9.7.1
3.4 Does the protocol specify measure(s) of association? (e.g., relative risk, odds ratio, excess risk, incidence rate ratio, hazard ratio, number needed to harm [NNH])	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1.2, 9.7.2.3
3.5 Does the protocol describe the approach for the collection and reporting of adverse events/adverse reactions? (e.g., adverse events that will not be collected in case of primary data collection)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	11

Comments:

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<u>Section 4: Source and study populations</u>	Yes	No	N/A	Section number
4.1 Is the source population described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.2.1
4.2 Is the planned study population defined in terms of:				9.2.2
4.2.1 Study time period	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
4.2.2 Age and sex	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
4.2.3 Country of origin	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
4.2.4 Disease/indication	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
4.2.5 Duration of follow-up	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	

Section 4: Source and study populations		Yes	No	N/A	Section number
4.3	Does the protocol define how the study population will be sampled from the source population? (e.g., event or inclusion/exclusion criteria)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.2.2 9.2.3

Comments:

The planned study population is defined by the detailed inclusion and exclusion criteria.

Section 5: Exposure definition and measurement		Yes	No	N/A	Section number
5.1	Does the protocol describe how the study exposure is defined and measured? (e.g., operational details for defining and categorising exposure, measurement of dose and duration of drug exposure)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1
5.2	Does the protocol address the validity of the exposure measurement? (e.g., precision, accuracy, use of validation sub-study)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.4
5.3	Is exposure categorised according to time windows?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.4
5.4	Is intensity of exposure addressed? (e.g., dose, duration)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.4
5.5	Is exposure categorised based on biological mechanism of action and taking into account the pharmacokinetics and pharmacodynamics of the drug?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.4
5.6	Is (are) an appropriate comparator(s) identified?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.2

Comments:

Exposure assessments are data source dependant.

Section 6: Outcome definition and measurement		Yes	No	N/A	Section number
6.1	Does the protocol specify the primary and secondary (if applicable) outcome(s) to be investigated?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.2
6.2	Does the protocol describe how the outcomes are defined and measured?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.2.1
6.3	Does the protocol address the validity of outcome measurement? (e.g., precision, accuracy, sensitivity, specificity, positive predictive value, use of validation sub-study)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.2
6.4	Does the protocol describe specific outcomes relevant for Health Technology Assessment? (e.g., HRQOL, QALYs, DALYS, healthcare services utilisation, burden of disease or treatment, compliance, disease management)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.2

Comments:

Given the long list of outcomes, further details on the definition, measurement, and validity of outcomes will be provided in the SAP for each contributing data source.

Section 7: Bias		Yes	No	N/A	Section number
7.1	Does the protocol address ways to measure confounding? (e.g., confounding by indication)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.5
7.2	Does the protocol address selection bias? (e.g., healthy user/adherer bias)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1.2.2
7.3	Does the protocol address information bias? (e.g., misclassification of exposure and outcomes, time-related bias)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.1.2.2

Comments:

The explicit definition of time zero in [Section 9.1.2.2](#) and the alignment of exposure assignment and start of follow-up prevents selection bias and time-related bias.

Section 8: Effect measure modification	Yes	No	N/A	Section number
8.1 Does the protocol address effect modifiers? (e.g., collection of data on known effect modifiers, <u>subgroup analyses</u> , anticipated direction of effect)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.4

Comments:

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Section 9: Data sources	Yes	No	N/A	Section number
9.1 Does the protocol describe the data source(s) used in the study for the ascertainment of:				
9.1.1 Exposure? (e.g., pharmacy dispensing, general practice prescribing, claims data, self-report, face-to-face interview)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.1.4
9.1.2 Outcomes? (e.g., clinical records, laboratory markers or values, claims data, self-report, patient interview including scales and questionnaires, vital statistics)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.3.2.1
9.1.3 Covariates and other characteristics?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.2 Does the protocol describe the information available from the data source(s) on:				
9.2.1 Exposure? (e.g., date of dispensing, drug quantity, dose, number of days of supply prescription, daily dosage, prescriber)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.2.2 Outcomes? (e.g., date of occurrence, multiple event, severity measures related to event)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.2.3 Covariates and other characteristics? (e.g., age, sex, clinical and drug use history, comorbidity, comedications, lifestyle)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.3 Is a coding system described for:				
9.3.1 Exposure? (e.g., WHO Drug Dictionary, Anatomical Therapeutic Chemical (ATC) Classification System)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.3.2 Outcomes? (e.g., International Classification of Diseases (ICD), Medical Dictionary for Regulatory Activities (MedDRA))	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.3.3 Covariates and other characteristics?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.4
9.4 Is a linkage method between data sources described? (e.g., based on a unique identifier or other)	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	

Comments:

Research partners confirmed the availability of the required information in their data sources prior to engaging in the study. Details regarding the coding systems or linkages available for each data source have been provided in [Section 9.4](#) when relevant.

Section 10: Analysis plan	Yes	No	N/A	Section number
10.1 Are the statistical methods and the reason for their choice described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7
10.2 Is study size and/or statistical precision estimated?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.5
10.3 Are descriptive analyses included?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.1
10.4 Are stratified analyses included?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.4

<u>Section 10: Analysis plan</u>	Yes	No	N/A	Section number
10.5 Does the plan describe methods for analytic control of confounding?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.5
10.6 Does the plan describe methods for analytic control of outcome misclassification?	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	9.9
10.7 Does the plan describe methods for handling missing data?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.7
10.8 Are relevant sensitivity analyses described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.7.2.9

Comments:

Outcome misclassification is a data-related limitation acknowledged in [Section 9.9](#).

<u>Section 11: Data management and quality control</u>	Yes	No	N/A	Section number
11.1 Does the protocol provide information on data storage? (e.g., software and IT environment, database maintenance and anti-fraud protection, archiving)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.8
11.2 Are methods of quality assurance described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.8
11.3 Is there a system in place for independent review of study results?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.8

Comments:

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<u>Section 12: Limitations</u>	Yes	No	N/A	Section number
12.1 Does the protocol discuss the impact on the study results of: 12.1.1 Selection bias? 12.1.2 Information bias? 12.1.3 Residual/unmeasured confounding? (e.g., anticipated direction and magnitude of such biases, validation sub-study, use of validation and external data, analytical methods)	<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/>	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>	9.9
12.2 Does the protocol discuss study feasibility? (e.g., study size, anticipated exposure uptake, duration of follow-up in a cohort study, patient recruitment, precision of the estimates)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	9.9

Comments:

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<u>Section 13: Ethical issues</u>	Yes	No	N/A	Section number
13.1 Have requirements of Ethics Committee/ Institutional Review Board been described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	10
13.2 Has any outcome of an ethical review procedure been addressed?	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	
13.3 Have data protection requirements been described?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	10

Comments:

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<u>Section 14: Amendments and deviations</u>	Yes	No	N/A	Section number
14.1 Does the protocol include a section to document amendments and deviations?	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	

Comments:

<u>Section 15: Plans for communication of study results</u>	Yes	No	N/A	Section number
15.1 Are plans described for communicating study results (e.g., to regulatory authorities)?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	12
15.2 Are plans described for disseminating study results externally, including publication?	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	12

Comments:

Name of the main author of the protocol: _____



Date: 16 October 2025



Signature: _____

