The global health and economic value of COVID-19 vaccination

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Technical Appendix

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S1. DERIVATION OF THE VALUE FORMULA

We take the broad value of COVID-19 vaccination (CV) to be the sum of monetized quality-adjusted life year (QALY) gains, gross domestic product (GDP) gains, and averted direct and indirect costs. The following is a formal derivation of this value formula. Let a denote age, $\bar{a}$ denote current age, and 99 be the maximum age. Let lifetime utility U from age $a = \bar{a}$ onwards be given by:

$$U = \sum_{a=\bar{a}}^{99} \frac{s(a) * q(a) * u\left(y^f(a)\right)}{(1+\rho)^{a-\bar{a}}} \qquad (S1)$$

In this expression, for each age $a \geq \bar{a}$, the numerator in the summand is period utility at that age and is the product of the survival probability $s(a)$ (i.e., the probability of being alive at age a conditional on being alive at age $\bar{a}$), health utility $q(a)$ (an index between 0 and 1 representing health-related quality of life where 1 corresponds to perfect health and 0 corresponds to death), and economic utility $u(y^f(a))$. Economic utility u is in turn a function of full income $y^f(a)$, which is the sum of earnings and the value of unpaid work. The annual rate of time preference for discounting period utility is ρ See a similar specification of lifetime utility in Murphy and Topel (2006).

Health at age a is summarized by the product $s(a) * q(a)$ (i.e., by the first two terms of period utility) where $s(a)$ captures the quantity aspect of health and $q(a)$ captures the quality aspect, or

equivalently, the mortality and morbidity aspects respectively. Note that in the special case where $y^f(a)$ is constant (i.e., it becomes y^f), then U would simplify to:

$$U = u(y^f) * Q \tag{S2}$$

where:

$$Q = \sum_{a=\bar{a}}^{99} \frac{s(a) * q(a)}{(1+\rho)^{a-\bar{a}}} \tag{S3}$$

Q is a measure referred to as "lifetime quality-adjusted life years" or lifetime QALYs, a measure of lifetime health.

Returning to the general case represented by equation $(S1)$, assume that a shock such as the COVID-19 pandemic can have an impact on age-specific health, an impact we denote $\Delta(s(a) * q(a))$. Assume this shock can have an impact on age-specific full income, an impact we denote $\Delta y^f(a)$. Then the shock's impact on lifetime utility, which we denote ΔU, can be approximated by:

$$\Delta U \approx \sum_{a=\bar{a}}^{99} \left\{ \frac{u\left(y^f(a)\right) * \Delta\left(s(a) * q(a)\right)}{(1+\rho)^{a-\bar{a}}} + \frac{s(a) * q(a) * u'\left(y^f(a)\right) * \Delta y^f(a)}{(1+\rho)^{a-\bar{a}}} \right\} \tag{S4}$$

In words, we can say that the shock's impact on lifetime utility can be approximated by sum of two terms. The first term is the impact on utility of the shock-induced impact on health holding full income fixed, and the second is the impact on utility of the shock-induced impact on full income holding health fixed.

Assume that prior to the shock, full income was constant (i.e., age invariant), so $y^f(a) = y^f(\bar{a})$ for $a \geq \bar{a}$. Assume as well that the shock affects full income only in the current period (so that the COVID-19 pandemic has no long-term economic effects) so $\Delta y^f(a) = 0$ for $a \neq \bar{a}$. Then we have:

$$\Delta U \approx u\left(y^f(\bar{a})\right) \sum_{a=\bar{a}}^{99} \left\{ \frac{\Delta\left(s(a) * q(a)\right)}{(1+\rho)^{a-\bar{a}}} \right\} + s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right) * \Delta y^f(\bar{a}) \qquad (S5)$$

Denote the impact of the shock on lifetime health by:

$$\Delta Q = \sum_{a=\bar{a}}^{99} \left\{ \frac{\Delta\left(s(a) * q(a)\right)}{(1+\rho)^{a-\bar{a}}} \right\} \qquad (S6)$$

So:

$$\Delta U \approx u\left(y^f(\bar{a})\right) * \Delta Q + s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right) * \Delta y^f(\bar{a}) \qquad (S7)$$

We convert the impact of the shock on lifetime utility into willingness-to-pay (WTP) by dividing ΔU by the expected marginal utility of full income at age $a = \bar{a}$, which is $s(\bar{a}) * q(\bar{a}) * u'(y^f(\bar{a}))$:

$$\frac{\Delta U}{s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right)} \approx \frac{u\left(y^f(\bar{a})\right)}{s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right)} * \Delta Q + \Delta y^f(\bar{a}) \qquad (S8)$$

Observe that $s(\bar{a}) * q(\bar{a}) < 1$ since people in the general population typically face some mortality risk and less than perfect health in every age of life. This implies:

$$\frac{u\left(y^f(\bar{a})\right)}{s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right)} > \frac{u\left(y^f(\bar{a})\right)}{u'\left(y^f(\bar{a})\right)} \qquad (S9)$$

Observe as well that simple algebra implies:

$$\frac{u\left(y^f(\bar{a})\right)}{u'\left(y^f(\bar{a})\right)} = \frac{\frac{u}{y^f}}{u'} * y^f \qquad (S10)$$

The ratio $\frac{u/y^f}{u'}$ is the ratio of average utility of full income to the marginal utility of full income. So long as consumer surplus is positive (which we assume is typically the case), this ratio exceeds 1, which implies that:

$$\frac{\frac{u}{y^f}}{u'} * y^f > y^f \quad (S11)$$

The above inequalities imply that:

$$\frac{\Delta U}{s(\bar{a}) * q(\bar{a}) * u'\left(y^f(\bar{a})\right)} > y^f * \Delta Q + \Delta y^f(\bar{a}) \quad (S12)$$

Thus, we find that the WTP for the policy can be conservatively approximated by the product of full income (a conservative estimate of WTP per QALY) and the QALY impacts of the policy while the second term equals the policy-induced impact on full income. Since we can interpret COVID-19 as a negative shock and COVID-19 vaccination as a reduction in the magnitude of that shock, the above equation shows we can value COVID-19 vaccination by valuing its QALY gains at full income and adding to that the value of its impact on full income. For simplicity, we limit the shock's impact on full income to just its impact on resources, ignoring its impact on leisure. We consider resources with market value (i.e., per capita GDP (PCGDP) and direct costs) and resources with no market value (i.e., the unpaid work component of indirect costs; we ignore the paid component of indirect costs because these are already part of PCGDP).

S2. REGRESSION ANALYSIS

The regression analysis is conducted in Excel, Stata 17, and Python 3.11.

S2.1. Regression versus modeling

Our valuation approach relies on regressions for estimating vaccination's impact on infections, deaths, and GDP. In equations (1)-(4) of the article, we specify our regression models that estimate such impacts.

Regressions are standard for analyzing macroeconomic outcomes like GDP, but less so for disease-related outcomes like infections and deaths, where much of the literature uses epidemiological models such as compartmental susceptible-exposed-infectious-recovered (SEIR) models. To see how model- and regression-based approaches differ, assume a highly simplified setting in which outcome y (e.g., deaths) is a function f of an exogenous variable x (e.g., real-world vaccine effectiveness, inclusive of potential herd effects) and vaccination v: $y = f(x, v)$. Assume the functional form f and the value of x are uncertain; we have two data points (v_1, y_1) and (v_2, y_2) where (v_1, y_1) represents the status quo. We seek an estimate $\hat{y}_3$ of the outcome y_3 associated with a counterfactual vaccination level v_3. A model-based approach would derive estimates $\hat{f}$ (perhaps by specifying a particular SEIR model with a simplified population demographic structure) and $\hat{x}$ (e.g., perhaps by assuming that real-world vaccine effectiveness equals trial efficacy), and compute $\hat{y}_3^m = \hat{f}(\hat{x}, v_3)$. Such approach is subject to the problems of modeling uncertainty (the risk that $\hat{f} \neq f$, e.g., the model's population structure is too simple) and parameter uncertainty (the risk that $\hat{x} \neq x$, e.g., real-world vaccine effectiveness differs from trial efficacy).

In contrast, the regression approach relies on data on y, v and sets $\hat{\beta} \equiv \frac{y_1 - y_2}{v_1 - v_2}$ and $\hat{y}_3^r = y_1 - \hat{\beta} * (v_1 - v_3)$. The relative advantage of regression is that it does not require knowledge or approximations of f, x and yet produces an estimate $\hat{y}_3^r$ that is in some way more sensitive to the true f, x than $\hat{y}_3^m$ of the model-based approach. This is because the data y_1, y_2 that enter the calculation of $\hat{\beta}$ and $\hat{y}_3^r$ are outputs from the true model (i.e., reality itself), and so reflect the workings of the true f, x. Actual deaths, for example, reflect actual population demographic structure and vaccine effectiveness, so $\hat{\beta}$ and $\hat{y}_3$ reflect their workings despite the analysis having made no assumption regarding them. The relative disadvantage of the regression model is that for $\hat{y}_3^r = y_1 - \hat{\beta} * (v_1 - v_3)$ to be a good approximation across all possible data points, the ratio $\frac{y_j - y_k}{v_j - v_k}$ would have to be relatively constant across all possible data point pairs (v_j, y_j) and (v_k, y_k). This, generalizing, requires that the true model be linear in the variables within the regression specification. This characterization generalizes to more complex settings with many data observations, large numbers of exogenous variables, and more complex derivations of $\hat{\beta}$.

S2.2. Study population

Our regression samples consist of 148 countries and other territories (Hong Kong and Palestine) that have at least two quarters of non-missing data for all variables in at least one of the four regression specifications (equations (1)-(4) of the article) and a population of at least one million [1]. The following 38 countries in the IHME COVID-19 database are excluded because they have 2020 populations equal to or less than one million: Andorra, Antigua and Barbuda, Bahamas, Barbados, Belize, Bhutan, Brunei, Cape Verde, Comoros, Dominica, Fiji, Greenland,

Grenada, Guyana, Iceland, Kiribati, Luxembourg, Macao, Maldives, Malta, Marshall Islands, Micronesia, Monaco, Montenegro, Nauru, Palau, Saint Kitts and Nevis, Saint Lucia, Saint Vincent and the Grenadines, Samoa, San Marino, Sao Tome and Principe, Seychelles, Solomon Islands, Suriname, Tonga, Tuvalu, and Vanuatu. The countries and territories in our regression samples are provided in Table S1. Countries and territories (hereafter "countries" for simplicity) in this table are organized by World Health Organization (WHO) region classification and World Bank income group classification [2]. Our study countries cover nearly 98% of the 2019 global population.

We perform our seemingly unrelated regression (SUR) regression for infections and deaths on a balanced panel of 145 countries, each of which has 8 quarterly observations. We perform our quarterly GDP regression on an unbalanced panel of 51 countries, some of which have fewer than 8 (but more than 2) quarterly GDP observations. For the 66 countries without quarterly GDP data but with annual GDP data and vaccination starting in either 2020Q4 or 2021Q1, we estimate a cross-sectional regression There are 31 study countries excluded from the GDP analysis either because they do not have GDP data (seven countries), or they have annual GDP data, but vaccinations started after 2021Q1.

To construct per capita variables, we use annual national population sizes from the United Nations World Population Prospects [1].

S2.3. Time period and horizon

The unit of time in much of our regression analysis is the calendar quarter (e.g., we denote the first quarter of 2020 by 2020Q1). For countries with annual as opposed to quarterly GDP data, the unit of time in their GDP regression analysis is the calendar year. The time horizon extends from the start of the pandemic (2020Q1) to the last quarter before the global dominance of the Omicron variant (2021Q4) inclusive. In the annual GDP regression analysis, the time horizon is 2020-2021.

Given that our regression relies on lagged independent variables and given that our earliest dependent variables are dated in 2020Q1, using such data in the regression requires us to impute values for our lagged independent variables (infections, vaccine doses, and pandemic-related government stringency measures) for 2019Q4 and 2019Q3. We set the values for such lagged independent variables in 2019Q4 and 2019Q3 to their natural values, which is zero before the pandemic.

Table S1. Study countries and territories (n=148)

AFRO (n=38) African Region	AMRO (n=23) Region of the Americas	EMRO (n=21) Eastern Mediterranean Region	EURO (n=44) European Region	SEARO (n=8) South-East Asia Region	WPRO (n=14) Western Pacific Region
Low income	**Low income**	**Low income**	**Middle income**	**Low income**	**Middle income**
Benin*	Haiti*	Afghanistan*	Albania	Nepal	Cambodia
Burkina Faso*	**Middle income**	Somalia*	Armenia**	**Middle income**	China
Central African Republic*	Argentina	**Middle income**	Azerbaijan	Bangladesh	Malaysia
Chad*	Bolivia	Egypt	Belarus	India	Mongolia
Democratic Republic of Congo*	Brazil	Iran	Bosnia and Herzegovina	Indonesia	Papua New Guinea
Ethiopia*	Colombia	Iraq	Bulgaria	Myanmar	Philippines
Gambia	Costa Rica	Jordan	Georgia	Sri Lanka	Vietnam
Guinea	Cuba*	Lebanon*	Kazakhstan	Thailand	**High income**
Liberia*	Dominican Republic	Libya*	Kyrgyzstan*	Timor-Leste	Australia
Madagascar*	Ecuador	Morocco	Moldova*		Hong Kong
Malawi	El Salvador	Pakistan	North Macedonia**		Japan
Mali*	Guatemala	Palestine*	Romania		New Zealand
Mozambique	Honduras	Sudan*	Russia		Singapore
Niger*	Jamaica	Syria*	Serbia		South Korea
Rwanda	Mexico	Tunisia	Turkey		Taiwan
Senegal	Panama	Yemen*	Ukraine		
Sierra Leone	Paraguay	**High income**	Uzbekistan*		
South Sudan*	Peru	Bahrain	**High income**		
Togo	Venezuela*	Kuwait	Austria		
Uganda	**High income**	Oman	Belgium		
Zimbabwe	Canada	Qatar	Croatia		
Middle-income	Chile	Saudi Arabia	Cyprus		
Algeria	Trinidad and Tobago	United Arab Emirates	Czechia		

Angola
Botswana*
Cameroon*
Congo*
Cote d'Ivoire
Equatorial Guinea**
Eswatini*
Gabon
Ghana
Kenya
Lesotho*
Mauritania*
Namibia
Nigeria
South Africa
Zambia
United States
Uruguay
Denmark
Estonia
Finland
France
Germany
Greece
Hungary
Ireland
Israel
Italy
Latvia
Lithuania
Netherlands
Norway
Poland
Portugal
Slovakia
Slovenia
Spain
Sweden
Switzerland
United Kingdom

*Countries excluded from the GDP analysis either because they do not have GDP data, or they have annual GDP data but vaccinations started after 2021Q1.

**Countries excluded from the infections and deaths regressions because they are missing the Government Response Index variable.

S2.4. Regression variable construction

S2.4.1. IHME COVID-19 variables

We derive our estimates of vaccine doses, infections, and deaths from the Institute for Health Metrics and Evaluation (IHME) COVID-19 Projections database whose publicly accessible webpage is at COVID-19 (healthdata.org). In many cases, the IHME builds on data from the Johns Hopkins University (JHU) [3]. The IHME deaths data adjust JHU reported deaths for underreporting based on the IHME's improved estimates of COVID-19 excess mortality. IHME derives its estimates of infections by combining JHU's reported cases and hospitalizations; IHME's adjusted JHU reported deaths; and seroprevalence survey data that IHME adjusts for waning, vaccinations, and reinfection from variants. The major source of the IHME vaccine uptake data was Our World in Data (OWiD). However, the OWiD data mostly lacks brand information. IHME addressed this by modeling vaccine uptake by brand as a stepwise function of predicted vaccine supply, predicted vaccine distribution, and predicted vaccine hesitancy (Kate Gillespie, PhD, email to JP Sevilla on 27 October 2023).

After obtaining a data access license, we downloaded two non-publicly accessible extracts from this database using the link https://clients.ihme.services to the IHME Client Portal on 22 February 2023. The first dataset is an extract from an IHME dataset called "Historical and Projected Covid-19 Data" [5] and contains country-specific daily records of infections, deaths, hospital admissions, intensive-care unit (ICU) beds needed, and numbers of individuals fully vaccinated. Although this extract contains both historical and projected data, the data contained

in this extract that are dated within our study horizon (2020Q1 to 2021Q4) are historical rather than projected.

The second dataset is an extract from an IHME dataset called "Vaccine-coverage-by-manufacturer-quarterly-countries.csv" [5] and consists of country-specific quarterly records of brand-specific doses administered. The variables we use from these extracts, along with their IHME variable names are summarized in Table S2. We note that the licensed data we downloaded from the IHME Client Portal are not identical to the data available on the publicly accessible webpage.

S2.4.1.1. Pfizer-BioNTech and non-Pfizer-BioNTech vaccine doses per capita

Our regressions include, as independent variables, vaccine doses per capita in a given country-quarter, as well as cumulative vaccine doses per capita as of the last day of a given country-quarter. We have separate independent variables for Pfizer-BioNTech and non-Pfizer-BioNTech vaccine doses. We construct these variables from the vaccine coverage variables in Table S2.

The IHME vaccine coverage data provide "total" doses, which span all primary series and booster doses, or, using IHME terminology: first course (dose 1 and dose 2 for two-dose vaccines), daily finished series, daily partial series will complete series, daily partial series will not complete series, daily first booster, and daily second booster. In our analysis, we do not distinguish between primary series or booster doses, or between the different doses of a primary series.

For our estimate of Pfizer-BioNTech vaccine doses administered in a particular country-quarter, we use the Pfizer_BioNTech_total_doses variable for that country-quarter. For our estimate of non-Pfizer-BioNTech vaccine doses administered in a particular country-quarter, we sum the total doses of AstraZeneca, Moderna, Johnson&Johnson, Novavax, Sputnik V, CoronaVac, Sinopharm, CanSinoBio, Covaxin, and Other for that country-quarter.

We construct country-specific cumulative vaccine doses as of the end of a particular quarter as the cumulative sum over the relevant quarterly Pfizer-BioNTech doses and over the quarterly non-Pfizer-BioNTech doses. We compute per capita doses and cumulative doses by dividing the Pfizer-BioNTech and non-Pfizer-BioNTech doses and cumulative doses by the total annual national population.

For each country, we take vaccine doses per capita to be zero for all calendar quarters prior to the first quarter that IHME records non-zero doses for that country.

S2.4.1.2. Extrapolating brand-specific vaccine doses to China

The brand-specific doses for China in the vaccine coverage dataset only include Hong Kong and Macao. The vaccine coverage dataset also contains separate brand-specific doses for Hong Kong and Macao, the sum of which is equal to the corresponding China doses. The “IHME projections” database has separate records for China as a whole (including Hong Kong and

Macao), Hong Kong, and Macao. Using these two databases, we extrapolate brand shares of vaccine doses from the Hong Kong and Macao data to China using the following method:

Step 1. Using the cumulative_all_fully_vaccinated variable in the "IHME projections" database, we compute the number of newly vaccinated people in China, Hong Kong, and Macao. We calculate the number of newly vaccinated people in China by subtracting the Hong Kong and Macao values from China's.

Step 2. We combine the number of newly vaccinated people in China, Hong Kong, and Macao with population data, and compute China's per capita newly vaccinated people, Hong Kong's per capita newly vaccinated people, and Macao's per capita newly vaccinated people.

Step 3. Using the population data, we compute a population-weighted average of Hong Kong's per capita newly vaccinated people and Macao's per capita newly vaccinated people.

Step 4. We construct the ratio of China's per capita newly vaccinated people to the population-weighted average in step 3.

Step 5. We combine the vaccine coverage data for Hong Kong and Macao with population data and compute Hong Kong's per capita brand-specific doses, and Macao's per capita brand-specific doses.

Step 6. We compute a population-weighted average of Hong Kong's per capita brand-specific doses and Macao's per capita brand-specific doses.

Step 7. We multiply the population-weighted average per capita brand-specific doses constructed in Step 6 by the ratio of China's per capita newly vaccinated people to the population-weighted average per capita newly vaccinated people (across Hong Kong and Macao) in step 4.

Table S2. IHME variables used in regression analysis

IHME Variable Name	Description
inf_mean	Daily infections (mean estimate)
inf_cuml_mean	Cumulative infections (mean estimate)
daily_deaths	Daily deaths (raw data with excess mortality scalar applied)
cumulative_deaths	Cumulative deaths (raw data with excess mortality scalar applied)
cumulative_all_fully_vaccinated	Fully vaccinated (one of one and two of two doses)
inf_lower	Daily infections (lower 95% confidence interval)
inf_cuml_lower	Cumulative infections (lower 95% confidence interval)
inf_upper	Daily infections (upper 95% confidence interval)
inf_cuml_upper	Cumulative infections (upper 95% confidence interval)
daily_deaths_unscaled	Daily deaths (raw data without excess mortality scalar applied)
cumulative_deaths_unscaled	Cumulative deaths (raw data without excess mortality scalar applied)
AstraZeneca_total_doses	Quarterly total doses for AstraZeneca
Moderna_total_doses	Quarterly total doses for Moderna
Pfizer_BioNTech_total_doses	Quarterly total doses for Pfizer-BioNTech
Johnson_Johnson_total_doses	Quarterly total doses for Johnson & Johnson
Novavax_total_doses	Quarterly total doses for Novavax
Sputnik_V_total_doses	Quarterly total doses for SputnikV
CoronaVac_total_doses	Quarterly total doses for CoronaVac
Sinopharm_total_doses	Quarterly total doses for SinopharmBeijing
CanSinoBio_total_doses	Quarterly total doses for CanSinoBio
Covaxin_total_doses	Quarterly total doses for Covaxin
Other_total_doses	Quarterly total doses for all other brands

S2.4.1.3. COVID-19 per capita infections and per capita deaths

Approximately 4% of the daily_deaths records in the IHME database have missing values. For countries with such missing values, most of these missing values belong to either the earliest or latest days of that country's daily_deaths records in the IHME database. For such countries, we compare the IHME daily_deaths records with the corresponding deaths records in the Our World in Data (OWiD) database. Where the OWiD data suggest that deaths equal zero during the periods with missing daily_deaths values, we recode the missing daily_deaths to zero. Such recoding accounts for nearly all the missing daily_deaths values. The exceptions are three countries (Kazakhstan, Kyrgyzstan, and Uzbekistan) that have a string of missing values for daily_deaths in the middle of their respective IHME series. We handle these missing values as follows:

- In Kazakhstan, deaths are non-missing from 7/1/2021 to 9/16/2021 and missing from 9/17/2021 to 6/30/2022.
    - Solution: We recoded the missing deaths from 9/17/2021 to 9/30/2021 with the average number of deaths from 9/1/2021 to 9/16/2021. We recoded the missing deaths from 10/1/2021 to 6/30/2022 to zero.
- In Kyrgyzstan, deaths are non-missing from 1/1/2022 to 3/14/2022 and missing from 3/15/2022 to 6/30/2022.

    - Solution: We recoded the missing deaths from 3/15/2022 to 3/31/2022 with the average number of deaths from 3/1/2022 to 3/14/2022. We recoded the missing deaths from 4/1/2022 to 6/30/2022 to zero.
- In Uzbekistan, deaths are non-missing from 1/1/2022 to 2/28/2022 and missing from 3/1/2022 to 6/30/2022.
    - Solution: We recoded the missing deaths from 3/1/2022 to 3/31/2022 with the average number of deaths from 2/1/2022 to 2/28/2022. We recoded the missing deaths from 4/1/2022 to 6/30/2022 to zero.

For some countries, the initial value of the daily deaths variable (i.e., the daily_deaths value with the earliest calendar date) does not equal the initial value of the cumulative deaths variable (i.e., the cumulative_deaths value for that same calendar date). In such case, we recode the initial value of daily_deaths to equal the initial value of cumulative_deaths. We recode similarly where the initial value of daily infections (according to the variable inf_mean) does not equal the initial values of cumulative infections (according to the variable inf_cuml_mean).

We compute a country's quarterly infections and deaths by summing daily infections and deaths within that country-quarter. The IHME data contain projections for China (including Hong Kong and Macao) along with separate projections for Hong Kong and Macao. We calculate quarterly infections and quarterly deaths in China by subtracting the Hong Kong and Macao values for these variables from the corresponding China values. We compute per capita values of quarterly infections and deaths by dividing the variables constructed above by the total 2019 national population.

S2.4.1.4. Natural immunity

We construct a measure of natural immunity as lags of new and cumulative infections per capita. Our natural immunity measures include a one-quarter lag of new infections per capita (i.e., new infections per capita in the previous quarter) and a two-quarter lag of cumulative infections per capita (i.e., cumulative infections per capita two quarters ago).

S2.4.2. GDP shortfall

S2.4.2.1. General approach

We define GDP shortfall as the ratio between a country's GDP ("actual GDP") and the pre-pandemic projections of GDP ("projected GDP").

We divide our sample into two groups. The first group consists of 51 countries with available quarterly actual GDP data, and the second group consists of 66 countries whose only available actual GDP data is annual. We exclude 31 study countries from the GDP analysis either because they do not have GDP data (seven countries), or they have annual GDP data but vaccinations started after 2021Q1.

For the first group of countries, we obtain quarterly actual GDP for the eight quarters from 2020Q1 to 2021Q4 from the International Monetary Fund (IMF) International Financial

Statistics (IFS) dataset [6,7]. For the second group of countries, we obtain annual actual GDP for the years 2020 and 2021 from the April 2023 edition of the IMF's World Economic Outlook (WEO) database [8]. For both groups of countries, we obtain 2019 projections of 2020 and 2021 GDP from the October 2019 edition of the WEO database [9].

All these actual and projected GDP data are denominated in real local currency units (LCUs), with base years that vary by country and by whether the GDP figure is actual or projected (i.e., for a single country, actual GDP for 2021 may be in 2022 LCUs while projected GDP for 2021 may be in 2019 LCUs). We compute a GDP deflator between some year and 2019 equal to the ratio of nominal 2019 GDP to real 2019 GDP denominated in LCUs of that year. (e.g., the GDP deflator for 2021 is the ratio of nominal 2019 GDP to real GDP in 2019 expressed in 2021 LCUs). We obtain the nominal and real 2019 GDP data required to compute these deflators from the WEO database. We then convert all actual and projected GDP data to 2019 LCUs using these GDP deflators.

For the second group of countries, we compute the GDP shortfall for a given year as the ratio of actual to projected GDP for that year. For the first group of countries, actual GDP data is quarterly while projected GDP data is annual. We apply a method from Statistics Canada (2011) described in the next section to convert the annual projections to quarterly projections. Given those quarterly projections, we compute the GDP shortfall for a given quarter as the ratio of actual to projected GDP for that quarter.

This completes the description of the construction of the GDP shortfall variables that enter our regressions. Post-regression calculations of the GDP-related value of vaccination (see Sections S3.2.1.4 and S3.2.2) require estimates of projected GDP during the study period denominated in 2019 United States dollars (USDs). We use 2019 market exchange rates to convert those projections from 2019 LCUs to 2019 USD. We obtain 2010 and 2019 market exchange rates from the IMF IFS [10], the United States Department of the Treasury Bureau of the Fiscal Service [11], and the World Bank Global Economic Monitor (GEM) database [12].

S2.4.2.2. Quarterly projected GDP

For countries with quarterly actual GDP from the IFS database, we assume quarterly projected GDP grows linearly within a calendar year. In other words, and denoting GDP in 2019Q4 by X and 2020Q4 GDP by Y, we assume, where D, E are constants:

$$GDP_{2020Q1} = X + D \quad (S13)$$

$$GDP_{2020Q2} = X + 2D \quad (S14)$$

$$GDP_{2020Q3} = X + 3D \quad (S15)$$

$$GDP_{2020Q4} = Y = X + 4D \quad (S16)$$

$$GDP_{2021Q1} = Y + E \quad (S17)$$

$$GDP_{2021Q2} = Y + 2E \quad (S18)$$

$$GDP_{2021Q3} = Y + 3E \quad (S19)$$

$$GDP_{2021Q4} = Y + 4E \quad (S20)$$

Combining (S13)-(S16) and (S17)-(S20) respectively yield:

$$GDP_{2020} = 4X + 10D \quad (S21)$$

$$GDP_{2021} = 4Y + 10E \quad (S22)$$

Since GDP_{2020} and GDP_{2021} are known data, equations (S13)-(S22) imply that knowing X suffices to identify GDP_{2020Q1} to GDP_{2021Q4}. We therefore derive an estimate of X.

Assuming a constant quarterly growth rate gA from GDP_{2018Q1} to GDP_{2019Q4} (so that, for example, $GDP_{2018Q3} = GDP_{2018Q1} * gA^2$, equation (3) in Statistics Canada (2011) shows that:

$$\frac{GDP_{2019}}{GDP_{2018}} - 1 = \frac{gA^4 + gA^5 + gA^6 + gA^7}{1 + gA + gA^2 + gA^3} - 1 \quad (S23)$$

Since the ratio on the left-hand side of (S23) is known, we use (S23) to numerically compute gA. Similarly, assuming a constant quarterly growth rate gB from GDP_{2019Q1} to GDP_{2020Q4} and using the same Statistics Canada equation (3) shows that:

$$\frac{GDP_{2020}}{GDP_{2019}} - 1 = \frac{gB^4 + gB^5 + gB^6 + gB^7}{1 + gB + gB^2 + gB^3} - 1 \quad (S24)$$

Which we numerically solve for gB. We then take the geometric mean of these two rates: $gC = \sqrt{gA * gB}$. We now take gC as our revised best estimate of the constant growth rate in 2019:

$$GDP_{2019} = GDP_{2019,Q1} + GDP_{2019,Q1} * gC + GDP_{2019,Q1} * gC^2 + GDP_{2019,Q1} * gC^3 \quad (S25)$$

This allows us to estimate $GDP_{2019,Q1}$, which is the only unknown in this equation, and which in turn allows us to set $X = GDP_{2019,Q1} * gC^3$.

S2.4.3. Government Response Index

To measure countries' health and economic response to the pandemic, we use the Government Response Index (GRI) from the Oxford COVID Government Response Tracker (OxCGRT) [13]. The GRI is a composite index of lockdown stringency (regarding schools, workplaces, public events, gatherings, public transport, stay-at-home orders, and internal and international movement), non-pharmaceutical interventions (public information campaigns, testing, contact tracing, and masking), and economic policies (income support, debt/contract relief) on a scale of 0 (no response) to 100 (maximal response). The GRI is available daily. We construct country-quarter-specific values by taking the average of daily values within a country-quarter.

S3. THE IMPACT OF VACCINATION ON INFECTIONS, DEATHS, AND GDP

Using the variables constructed above, we specify regression models that estimate the impact of vaccination on quarterly infections, quarterly deaths, quarterly GDP, and annual GDP. We provide these regression models in equations (1)-(4) of the article, and we present the results of our base-case regression analysis in Table 2 of the article.

As shown in Table 2 of the article, vaccination coefficients generally have the correct sign (negative in the infections and deaths regressions, and positive in the GDP regressions; the exception being two-period-lagged cumulative Pfizer-BioNTech vaccination in the deaths regression) and statistically significant at conventional levels (exceptions: two-period-lagged cumulative Pfizer-BioNTech vaccination in the infections regression (p=0.13), one-period-lagged non-Pfizer vaccination in the quarterly GDP regression (p=0.080), and cumulative non-Pfizer-BioNTech vaccination in the annual GDP regression (p=0.093).

Our vaccination independent variables and the infections and deaths dependent variables are scaled such that the vaccination coefficients constitute estimates of the per capita (percentage-point) reduction in the probability of infection or death of receiving an extra (i.e., marginal) dose. This is in the sense that if everyone received a marginal dose, our independent vaccination variables would rise by 1; that if there were no infections or deaths, the values of the dependent variables would be zero; and that if everyone were to be infected or die, the values of the dependent variables would be at least one. This coefficient differs from vaccine efficacy or effectiveness, which measures the *percentage* as opposed to percentage-point reduction in the probability of infection or death.) Under this interpretation, one-period-lagged Pfizer-BioNTech and non-Pfizer-BioNTech vaccination reduce infection probabilities by 0.19 and 0.16 (or equivalently, by 19 and 16 percentage points), respectively. Reductions are smaller for two-period-lagged cumulative doses: 7 (p=0.13) and 13 percentage points for Pfizer-BioNTech and non-Pfizer-BioNTech, respectively. One-period-lagged vaccination reduces death probabilities by 0.15 and 0.03 percentage-points for Pfizer-BioNTech and non-Pfizer-BioNTech doses,

respectively, and by -0.08% and 0.03% for two-period-lagged cumulative Pfizer-BioNTech and non-Pfizer-BioNTech doses, respectively. While the increased mortality risk from two-period-lagged Pfizer-BioNTech doses is puzzling, such risk is outweighed by the almost-twice-as-large protective effect of one-period-lagged doses, so that doses have the net protective impact (see Table 3 of the article).

GRI has the expected negative and statistically significant coefficient in the infections regression. But it has no explanatory power in the deaths regression (p=0.48), and in the quarterly GDP regression it has an unexpected sign though with a very small coefficient (0.0003) that is statistically significant only at the 10% level (0.0003, p=0.10). The cumulative infections variables have the expected signs and are statistically significant in all four regressions, though the one-period-lagged infections variable is statistically insignificant in the infections and GDP regressions (p=0.84 and p=0.99, respectively), and positive and statistically significant in the deaths regression (which we interpret as reflecting deaths resulting from prior infections). Country- and quarter fixed effects are jointly statistically significant.

Our GDP shortfall dependent variable and vaccination independent variables are scaled so the latter's coefficients are estimates of the percentage-point reduction in the GDP gap that would result from a marginal dose. The summary statistics in Table 1 of the article show that the mean and median of the GDP shortfall across our sample are in the range of 0.96 to 0.97 (i.e., that the pandemic caused GDP to be 3 to 4% lower than expected). The coefficients on one-period-lagged and two-period-lagged-cumulative vaccinations per capita in the quarterly and annual GDP regressions are in the range of 0.02 to 0.08, suggesting a marginal vaccination dose per

capita suffices to completely close the GDP shortfall and bring actual GDP back to expected levels.

Using the coefficients from the estimated regression equations, we measure vaccination impacts relative to a "no vaccination" counterfactual as follows.

Vaccination's impact on infections, deaths, and GDP reflects the difference between (i) the predicted values of the dependent variables at observed vaccination doses (and at observed levels for lagged infections and stringency, and given estimated fixed effects) and (ii) counterfactual predicted values for these variables when doses are set to zero (given estimated fixed effects, but when lagged infections and stringency are themselves adjusted for zero vaccination).

S3.1. Predicted values at observed vaccination doses

The predicted values at observed vaccination doses in a particular country-quarter are the values of the dependent variable predicted by the regression model, given the observed values of the all the independent variables and the estimated coefficients on these variables:

$$\hat{n}_{i,t} = \hat{\delta}_1 v^{p}_{i,t-1} + \hat{\delta}_2 v^{np}_{i,t-1} + \hat{\delta}_3 cv^{p}_{i,t-2} + \hat{\delta}_4 cv^{np}_{i,t-2} + \hat{\delta}_5 n_{i,t-1} + \hat{\delta}_6 cn_{i,t-2} + \hat{\delta}_7 s_{i,t-1} + \hat{\omega}_i + \hat{\lambda}_t \quad (S26)$$

$$\hat{d}_{i,t} = \hat{\gamma}_1 v^{p}_{i,t-1} + \hat{\gamma}_2 v^{np}_{i,t-1} + \hat{\gamma}_3 cv^{p}_{i,t-2} + \hat{\gamma}_4 cv^{np}_{i,t-2} + \hat{\gamma}_5 n_{i,t-1} + \hat{\gamma}_6 cn_{i,t-2} + \hat{\gamma}_7 s_{i,t-1} + \hat{\pi}_i + \hat{\rho}_t \quad (S27)$$

$$\hat{g}_{i,t} = \hat{\beta}_1 v^p_{i,t-1} + \hat{\beta}_2 v^{np}_{i,t-1} + \hat{\beta}_3 cv^p_{i,t-2} + \hat{\beta}_4 cv^{np}_{i,t-2} + \hat{\beta}_5 n_{i,t-1} + \hat{\beta}_6 cn_{i,t-2} + \hat{\beta}_7 s_{i,t-1} + \hat{\mu}_i + \hat{\tau}_t \quad (S28)$$

$$\widehat{g_{i,2021} - g_{i,2020}} = \hat{\alpha}_0 + \hat{\alpha}_1 g_{i,2020} + \hat{\alpha}_2 cv^p_{i,2021Q4} + \hat{\alpha}_3 cv^{np}_{i,2021Q4} + \hat{\alpha}_4 cn_{i,2020Q4} \quad (S29)$$

S3.2. Predicted values under the no vaccination counterfactual

Since we aim to identify the value of all COVID-19 vaccines taken together, and the value of Pfizer-BioNTech vaccines more specifically, we calculate two no-vaccination counterfactuals. First is a "no COVID vaccination" counterfactual, in which we derive predicted values for the dependent variables setting all vaccine dose independent variables of any brand (i.e., $v^p_{i,t-1}, v^{np}_{i,t-1}, cv^p_{i,t-2}, cv^{np}_{i,t-2}, cv^p_{i,2021Q4}, cv^{np}_{i,2021Q4}$) equal to zero. Second is a "no Pfizer-BioNTech vaccination" counterfactual, in which we set only Pfizer-BioNTech vaccine doses (i.e. $v^p_{i,t-1}, cv^p_{i,t-2}, cv^p_{i,2021Q4}$) equal to zero while keeping non-Pfizer-BioNTech vaccine doses (i.e. $v^{np}_{i,t-1}, cv^{np}_{i,t-2}, cv^{np}_{i,2021Q4}$) at their observed levels.

We discuss the construction of these counterfactuals for our quarterly regressions in Section S3.2.1 and for our annual GDP regression in Section S3.2.2.

S3.2.1. Quarterly regressions

For a given country-quarter, our regressions specify the dependent variables as functions of independent variables, which include lagged infections and lagged GRI. However, observed values of these lagged infections and lagged stringency independent variables reflect the impact of observed patterns of vaccination. These observed values for lagged infections and lagged stringency would likely have been lower, for example, if vaccinations even further back in time were higher. Conversely, lagged infections and lagged stringency would likely have been higher than observed if there were no vaccination.

Thus, to compute predicted values of dependent variables under no vaccination scenarios, we should not use observed lagged infections or lagged stringency as independent variables. We should instead use counterfactual estimates of lagged infections and lagged stringency reflecting what would have been the case for these lagged values in the absence of vaccination.

S3.2.1.1. Counterfactual stringency

Denote by q_i the last quarter before the administration of any vaccine doses of any brand and denote by r_i the last quarter before the administration of any Pfizer-BioNTech doses. These variables are subscripted by i because the timing of vaccine introductions varies by country. For example, in the United States (US), vaccinations with any brand began in 2020Q4, so $q_{US} = 2020Q3$. For any country i, the value of the stringency index $s_{i,t}$ for any quarter $t \leq q_i$ reflects real-world stringency in the absence of any vaccination. For example, for the US, the value of the stringency index for any quarter up to an including 2020Q3 reflects stringency in the absence of any vaccination.

For the "no COVID vaccination" counterfactual in country i, we take the counterfactual stringency index for any period from the first quarter of vaccine administration onwards to equal the observed value of the stringency index for the quarter q_i (the superscript $\sim CV$ stands for "no COVID vaccination"):

$$s_{i,t}^{\sim CV} = s_{i,q_i}, t > q_i \quad (S30)$$

Thus, in the case of the US, for all t from 2020Q4 onwards, the counterfactual stringency index equals its observed its value in 2020Q3.

Using similar logic, for the "no Pfizer-BioNTech vaccination" counterfactual, we define the counterfactual stringency index using r_i instead of q_i (the superscript $\sim PV$ stands for "no Pfizer-BioNTech vaccination"):

$$s_{i,t}^{\sim PV} = s_{i,r_i}, t > r_i \quad (S31)$$

S3.2.1.2. Counterfactual natural immunity and infections

For periods up to and including the period with vaccination with any brand first occurs (i.e., for $t \leq q_i + 1$), the predicted values for infections are those that follow from normal regression post-estimation using observed natural immunity and stringency setting all vaccine dose administration variables to zero:

$$\hat{n}_{i,t}^{\sim CV} = \hat{\delta}_5 n_{i,t-1} + \hat{\delta}_6 cn_{i,t-2} + \hat{\delta}_7 s_{i,t-1} + \hat{\omega}_i + \hat{\lambda}_t, \qquad t \leq q_i + 1 \qquad (S32)$$

This is because the lagged values on the right-hand side of this equation all reflect observed values prior to vaccination with any brand, and so are consistent with a "no COVID vaccination" counterfactual.

For later periods, we use lagged predicted counterfactual natural immunity and lagged counterfactual stringency:

$$\hat{n}_{i,t}^{\sim CV} = \hat{\delta}_5 \hat{n}_{i,t-1}^{\sim CV} + \hat{\delta}_6 \widehat{cn}_{i,t-2}^{\sim CV} + \hat{\delta}_7 s_{i,t}^{\sim CV} + \hat{\omega}_i + \hat{\lambda}_t, \qquad t > q_i + 1 \qquad (S33)$$

For the "no Pfizer-BioNTech vaccination" counterfactual, the expressions above are slightly modified:

$$\hat{n}_{i,t}^{\sim PV} = \hat{\delta}_2 v_{i,t-1}^{np} + \hat{\delta}_4 cv_{i,t-2}^{np} + \hat{\delta}_5 n_{i,t-1} + \hat{\delta}_6 cn_{i,t-2} + \hat{\delta}_7 s_{i,t-1} + \hat{\omega}_i + \hat{\lambda}_t, \qquad t \leq r_i + 1 \qquad (S34)$$

$$\hat{n}_{i,t}^{\sim PV} = \hat{\delta}_2 v_{i,t-1}^{np} + \hat{\delta}_4 cv_{i,t-2}^{np} + \hat{\delta}_5 \hat{n}_{i,t-1}^{\sim PV} + \hat{\delta}_6 \widehat{cn}_{i,t-2}^{\sim PV} + \hat{\delta}_7 s_{i,t}^{\sim PV} + \hat{\omega}_i + \hat{\lambda}_t, \qquad t > r_i + 1 \qquad (S35)$$

S3.2.1.3. Counterfactual deaths

Deaths in the no-vaccination counterfactual are estimated as:

$$\hat{d}_{i,t}^{\sim CV} = \hat{\gamma}_5 n_{i,t-1} + \hat{\gamma}_6 cn_{i,t-2} + \hat{\gamma}_7 s_{i,t-1} + \hat{\pi}_i + \hat{\rho}_t, \qquad t \leq q_i + 1 \qquad (S36)$$

$$\hat{d}_{i,t}^{\sim CV} = \hat{\gamma}_5 \hat{n}_{i,t-1}^{\sim CV} + \hat{\gamma}_6 \widehat{cn}_{i,t-2}^{\sim CV} + \hat{\gamma}_7 s_{i,t}^{\sim CV} + \hat{\pi}_i + \hat{\rho}_t, \qquad t > q_i + 1 \qquad (S37)$$

And deaths in the no-Pfizer-BioNTech counterfactual are estimated as:

$$\hat{d}_{i,t}^{\sim PV} = \hat{\gamma}_2 v_{i,t-1}^{np} + \hat{\gamma}_4 cv_{i,t-2}^{np} + \hat{\gamma}_5 n_{i,t-1} + \hat{\gamma}_6 cn_{i,t-2} + \hat{\gamma}_7 s_{i,t-1} + \hat{\pi}_i + \hat{\rho}_t, \qquad t \leq r_i + 1 \ (S38)$$

$$\hat{d}_{i,t}^{\sim PV} = \hat{\gamma}_2 v_{i,t-1}^{np} + \hat{\gamma}_4 cv_{i,t-2}^{np} + \hat{\gamma}_5 \hat{n}_{i,t-1}^{\sim PV} + \hat{\gamma}_6 \widehat{cn}_{i,t-2}^{\sim PV} + \hat{\gamma}_7 s_{i,t}^{\sim PV} + \hat{\pi}_i + \hat{\rho}_t, \qquad t > r_i + 1 \ (S39)$$

S3.2.1.4. Counterfactual GDP

Quarterly GDP shortfall in the no-vaccination counterfactual is estimated as:

$$\hat{g}_{i,t}^{\sim CV} = \hat{\beta}_5 n_{i,t-1} + \hat{\beta}_6 cn_{i,t-2} + \hat{\beta}_7 s_{i,t-1} + \hat{\mu}_i + \hat{\tau}_t, \qquad t \leq q_i + 1 \qquad (S40)$$

$$\hat{g}_{i,t}^{\sim CV} = \hat{\beta}_5 \hat{n}_{i,t-1}^{\sim CV} + \hat{\beta}_6 \widehat{cn}_{i,t-2}^{\sim CV} + \hat{\beta}_7 s_{i,t}^{\sim CV} + \hat{\mu}_i + \hat{\tau}_t, \qquad t > q_i + 1 \qquad (S41)$$

And quarterly GDP shortfall in the no-Pfizer-BioNTech counterfactual is estimated as:

$$\hat{g}_{i,t}^{\sim PV} = \hat{\beta}_2 v_{i,t-1}^{np} + \hat{\beta}_4 cv_{i,t-2}^{np} + \hat{\beta}_5 n_{i,t-1} + \hat{\beta}_6 cn_{i,t-2} + \hat{\beta}_7 s_{i,t-1} + \hat{\mu}_i + \hat{\tau}_t, \qquad t \leq r_i + 1 \ (S42)$$

$$\hat{g}_{i,t}^{\sim PV} = \hat{\beta}_2 v_{i,t-1}^{np} + \hat{\beta}_4 cv_{i,t-2}^{np} + \hat{\beta}_5 \hat{n}_{i,t-1}^{\sim PV} + \hat{\beta}_6 \widehat{cn}_{i,t-2}^{\sim PV} + \hat{\beta}_7 s_{i,t}^{\sim PV} + \hat{\mu}_i + \hat{\tau}_t, \qquad t > r_i + 1 \quad (S43)$$

S3.2.2. Annual GDP regression

The difference between 2021 and 2020 GDP shortfall in the no-COVID vaccination counterfactual is estimated as:

$$\widehat{g_{\iota,2021} - g_{\iota,2020}}^{\sim CV} = \hat{\alpha}_0 + \hat{\alpha}_1 g_{i,2020} + \hat{\alpha}_4 cn_{i,2020Q4} \quad (S44)$$

And the difference between 2021 and 2020 GDP shortfall in the no-Pfizer-BioNTech counterfactual is estimated as:

$$\widehat{g_{\iota,2021} - g_{\iota,2020}}^{\sim PV} = \hat{\alpha}_0 + \hat{\alpha}_1 g_{i,2020} + \hat{\alpha}_3 cv_{i,2021Q4}^{np} + \hat{\alpha}_4 cn_{i,2020Q4} \quad (S45)$$

S3.3. Averted infections, deaths, and GDP loss

S3.3.1. Quarterly regressions

In a particular country-quarter, infections, deaths, and GDP losses averted by CV are given by:

$$averted\ infections_{i,t}^{CV} = \left(\hat{n}_{i,t}^{\sim CV} - \hat{n}_{i,t}\right) * pop_{i,2019} \quad (S46)$$

$$averted\ deaths_{i,t}^{CV} = \left(\hat{d}_{i,t}^{\sim CV} - \hat{d}_{i,t}\right) * pop_{i,2019} \quad (S47)$$

$$GDP\ gain_{i,t}^{CV} = \left(\hat{g}_{i,t}^{\sim CV} - \hat{g}_{i,t}\right) * gdp_{i,t}^{projected} \quad (S48)$$

where $pop_{i,2019}$ represents the national population of country i in 2019 and $gdp_{i,t}^{projected}$ is the pre-pandemic projected GDP (2019 USD) in country i and quarter t.

In a particular country-quarter, infections, deaths, and GDP losses averted by Pfizer-BioNTech are:

$$averted\ infections_{i,t}^{PV} = \left(\hat{n}_{i,t}^{\sim PV} - \hat{n}_{i,t}\right) * pop_{i,2019} \quad (S49)$$

$$averted\ deaths_{i,t}^{PV} = \left(\hat{d}_{i,t}^{\sim PV} - \hat{d}_{i,t}\right) * pop_{i,2019} \quad (S50)$$

$$GDP\ gain_{i,t}^{PV} = \left(\hat{g}_{i,t}^{\sim PV} - \hat{g}_{i,t}\right) * gdp_{i,t}^{projected} \quad (S51)$$

S3.3.2. Annual regression

In a particular country, GDP losses averted by CV (or GDP gains from CV) are:

$$GDP\ gain_{i,2021}^{CV} = \left(\widehat{g_{i,2021} - g_{i,2020}} - \widehat{g_{i,2021} - g_{i,2020}}^{\sim CV}\right) * gdp_{i,2021}^{projected} \quad (S52)$$

And the GDP losses averted by Pfizer-BioNTech vaccination (or GDP gains from Pfizer-BioNTech vaccination) are:

$$GDP\ gain_{i,2021}^{PV} = \left(\widehat{g_{\iota,2021} - g_{\iota,2020}} - \widehat{g_{\iota,2021} - g_{\iota,2020}}^{\sim PV}\right) * gdp_{i,2021}^{projected} \qquad (S53)$$

S3.4. Country and global totals

For a given country, averted infections, averted deaths, and GDP gains are algebraic sums of these quantities across all periods (i.e., quarters or years). Global totals are algebraic sums across countries.

S4. ESTIMATING THE BROAD VALUE OF VACCINATION

To estimate the broad value of vaccination, we first combine the estimates of vaccine-averted infections and deaths defined above with estimates of the QALY losses, direct costs per nonfatal infection and death, and indirect costs per nonfatal infection to estimate the QALYs saved and direct and indirect costs averted by vaccination. We then monetize QALYs saved at the country-specific value of per capita full income. The broad value of CV is the sum of the GDP gains defined above, monetized QALY gains, and averted direct and indirect costs. The global broad value of CV sums up country-level broad values.

In this subsection, we provide our methodology for estimating and monetizing QALY gains and for estimating direct and indirect costs.

S4.1. QALYs

Our regression analysis produces estimates of fatal and nonfatal infections averted by vaccination. This section described our calculations of the QALY loss per fatal infection (Section S4.1.1) and the QALY loss per nonfatal infection (Section S4.1.2). Combining these QALY losses per fatal and nonfatal infection with the number of fatal and nonfatal infections averted by vaccination yields our estimates of the QALY gains from vaccination.

S4.1.1. QALY losses per fatal infection

The QALY loss per fatal infection equals the weighted average of the age-specific QALY loss of per death, where the weights reflect the age distribution of COVID-19 deaths. Section S4.1.1.1 describes the age distribution of COVID-19 deaths and Section S4.1.1.2 describes the age-specific QALY loss per death.

S4.1.1.1. Age distribution of COVID-19 deaths

We derive the age distribution of COVID-19 deaths from the COVerAGE-DB dataset, described in Riffe and Acosta (2021) [14]. This dataset disaggregates cumulative COVID-19 deaths into 5-year age intervals (i.e., 0-4, 5-9, …, 95-99). We aggregate these age groups into a smaller number of age groups: 0-14, 15-24, 25-34, 35-44, 45-54, 55-64, 65-74, and 75-100. We did this in part because these are the age categories in our reference for country- and age-specific general

population health utilities [15], and in part because using these larger age groups produced less noisy age distributions of deaths.

For a given age group, the COVerAGE-DB dataset provides daily cumulative deaths. We take (non-cumulative) deaths on a particular day ("daily deaths") to equal COVerAGE-DB cumulative deaths on that day minus COVerAGE-DB cumulative deaths from the previous day. There are gaps in the COVerAGE-DB data, that is, days for which there are no records in the COVerAGE-DB database. In the case of such gaps, we compute the difference in cumulative deaths on either side of the gap and treat that difference as the number of (non-cumulative) deaths on the day after the gap. Cumulative deaths can decline in the database, which we believe reflects data corrections, which would imply that our calculation of daily deaths would yield negative values. We handle such instances by bottom-coding negative daily death estimates to zero. We then aggregate daily deaths across all the days within a quarter to obtain an estimate of the number of deaths within an age group in a particular quarter.

The age distribution of deaths in a particular quarter consists of the shares of each age group of the total deaths (i.e., the sum of deaths across all age groups) in that quarter.

There are 60 study countries that are not in COVerAGE-DB, and many of the 85 study countries in the database have at least one quarter of missing data. We assign these study countries with missing values to a pool of similar countries with the requisite data, compute the average values across the countries within the pool, and impute these averages to the missing values. We call this the "pooled average method" for imputing missing data.

To construct country pools, we first group countries by the interaction of WHO region and World Bank Income Category, where LIC = low-income country, MIC = middle-income country, and HIC = high-income country). For example, one group consists of AMRO HICs, and another group consists of EURO MICs. We visually inspect the age structures of deaths across the countries within each of these groups, and where these age structures are sufficiently similar across two or more groups, we combine these groups (e.g., we combined all HICs into a single group).[2] Such visual inspection and group aggregation yields the following smaller number of groups:

- All HICs
- AMRO MIC
- EURO MIC
- AFRO LIC, SEARO LIC, AMRO LIC, and AFRO MIC
- EMRO LIC and EMRO MIC
- SEARO MIC and WPRO MIC

We construct quarterly age distributions of deaths within each of these groups. Lastly, we assign these pooled age distributions in death to any country-quarter in the group with missing data.

S4.1.1.2. Age-specific QALY loss per fatal infection

[2] See the GitHub repository for graphs: https://github.com/DataforDecisionsLLC/The-global-health-and-economic-value-of-COVID-19-vaccination

For a given integer age x, QALY losses per death equals discounted quality-adjusted life expectancy (QALE) [16]:

$$QALE(x) = \frac{1}{l(x)} \sum_{u=x}^{100} \frac{L(u) * Q(u)}{(1+r)^{(u-x)}} \quad (S54)$$

This formula uses the following variables:

Table S3. QALE Variables and Definitions

Variable	Definition
$L(u)$	The total number of person-years (out of a reference birth cohort of size 100000) lived between u to $u+1$
$l(x)$	The total number of persons (out of a reference birth cohort of size 100000) alive at the beginning of the age interval (i.e., at age x)
$Q(u)$	The baseline health-related quality of life for persons at age u
r	The annual discount rate

We take the life table variables $L(u)$ and $l(x)$ from the 2019 UN World Population Prospects (UN WPP) [17]. We rely on Szende et al. (2014) [15] for country- and age-specific baseline health utilities $Q(u)$. (See Szende et al. (2014), Table 3.5, which includes country and age-specific baseline health utilities valued on the European VAS scale.) For countries not included in Szende et al. (2014), we use the age-specific baseline health utilities of the country within that study with the closest life expectancy at birth. The annual discount rate, r, is set to 3%, consistent with WHO recommendations [18].

For each of the following age groups, 0-14, 15-24, 25-34, 35-44, 45-54, 55-64, 65-74, and 75-100, we compute an age-group-specific QALY loss per fatal case. This equals the weighted average of the integer-age QALY losses across all integer-ages within that age group. For each integer-age, the weight used in the averaging equals the share of that integer-age's population to the total population in the age group (i.e., the weights sum to one across single ages within an age group) [17].

S4.1.1.3. QALY loss per fatal case

We compute the QALY loss per fatal infection as a weighted average of the age-group-specific QALY losses per death from Section S4.1.1.2, where the weights are the age-group-specific shares of deaths from Section S4.1.1.1. Since these age distributions of deaths vary across quarters within a country, our estimate of QALY loss per fatal infection is country-quarter-specific.

S4.1.2. QALY losses per nonfatal infection

To compute QALY losses per nonfatal infection, we distinguish nonfatal infections by severity levels, compute the number of infections within each severity level (Section S4.1.2.1), compute the QALY loss associated with each severity level (Section S4.1.2.2), and take a weighted average of these QALY losses using the relative probability of each severity level (Section S4.1.2.3).

S4.1.2.1. Severity levels

Following Robinson et al. (2022), we distinguish the following severity levels among nonfatal infections: asymptomatic infections requiring no care, mild infections requiring outpatient care, severe infections requiring hospitalization but not ICU admission, and critical infections requiring ICU admission [19].

We estimate the number of nonfatal infections per severity level from the following IHME variables in Table S4:

Table S4. IHME COVID-19 projections data used in QALY calculations

Variable	description
location_name	Location name
Date	Date of prediction
inf_mean	Daily infections (mean estimate)
daily_deaths	Daily deaths (raw data with excess mortality scalar applied)
icu_beds_mean	Daily COVID-19 ICU beds needed (mean estimate)
admis_mean	Daily COVID-19 hospital admissions (mean estimate)

Institute for Health Metrics and Evaluation (IHME).

For each day, we use *inf_mean* to measure the number of total infections (fatal and nonfatal); we use *daily_deaths* to measure the number of fatal infections (this is only an approximation since deaths on a given day will reflect infections on previous days as opposed to infections on that given day that eventually result in death); we use *admis_mean* to measure the number of severe nonfatal infections (this is only an approximation since *admis_mean* includes infections that may ultimately turn fatal); and we conservatively estimate the number of asymptomatic infections as

19.2% of total infections (Di Fusco et al., 2022, estimate that the asymptomatic proportion of infections falls between 14.8% and 19.2%) [20].

For each day, we estimate the number of critical nonfatal infections as the ratio of the number of ICU beds needed (as measured by *icu_beds_mean*) to the average length of stay (LOS) in those beds. (This is an approximate measure because the *icu_beds_mean* variable does not exclude cases that eventually become fatal; it can be shown that this essentially determines the rolling-average of ICU admissions.) Di Fusco et al. (2021) provide two estimates of LOS in the ICU: 9.6 days for those not requiring invasive mechanical ventilation (IMV) and 18.6 days for those requiring it [21]. Using the sample sizes provided in the article for those not requiring IMV and those requiring it (n = 16496 and n = 21632, respectively), we calculate the sample size weighted average LOS in the ICU as 14.7 days.

For each day, we estimate the number of mild nonfatal infections as a residual value by subtracting that day's asymptomatic infections, severe infections, critical infections, and deaths from the number of total infections.

S4.1.2.2. QALY loss by severity level

To derive QALY losses by severity level, we adopt values from the existing literature with one modification. Robinson et al. (2022) provide estimates of the QALY losses for nonfatal infections of varying severities [19]. We adopt their values for mild and severe infections (0.009 and 0.019, respectively). We adjust their value for critical infections, allowing long COVID to

last for only 18 months rather than the full lifetime which they assume [22]. Using this method, we estimate the QALY loss from a critical infection at 0.232. We assume asymptomatic infections cause no QALY loss.

S4.1.2.3. Average nonfatal QALY loss

The QALY loss per nonfatal infection in a given quarter is a weighted average of the QALY losses for each severity level, where the weights equal the relative sizes of the severity levels across all nonfatal infections in the quarter. This yields country-quarter-specific QALY losses per nonfatal infection.

S4.2. Direct costs per infection

For each country-quarter, we estimate a direct cost per infection. This equals a weighted average of direct costs for infections of different severity levels, where the weights equal the relative probabilities of the different severity levels. The computation of the direct costs for infections of different severity levels is described in Section S4.2.1. The weighting is described in Section S4.2.2. The conversion to base currencies is discussed in Section S4.2.3. The extrapolation of direct costs across countries is discussed in Section S4.2.4.

S4.2.1. Direct costs for infections of different severity levels

We assume no direct cost for asymptomatic infections. We assume a mild infection requires one outpatient visit based on Di Fusco et al. (2022), which found that approximately 94% of symptomatic COVID-19 cases sought outpatient care in the United States [20]. We estimate the cost of such outpatient visit from using the WHO-CHOICE cost of an "outpatient visit in health centers (no beds)" [23].

We estimate the direct costs of a severe infection by multiplying costs per bed day in primary hospitals from WHO-CHOICE by our estimate of the hospital LOS for a severe infection. Our estimate of the LOS for a severe infection is a weighted average of Di Fusco et al.'s (2022) estimates of LOS in a general ward with and without IMV, where the weights reflect rates of IMV use in general wards [20]. We estimate the direct costs of a critical infection by multiplying costs per bed day in tertiary hospitals from WHO-CHOICE by our estimate of the LOS for a critical infection. Our estimate of the LOS for a critical infection is a weighted average of Di Fusco et al.'s (2022) estimates of LOS in an ICU with and without IMV, where the weights reflect rates of IMV use in ICUs; these IMV rates in the general ward and in ICU are from Di Fusco et al. (2022, Table S9) [20]. Since these IMV rates are age-group specific (12-17, 18-29, 30-49, 50-64, 65-74, and 75+), we compute population weighted averages of these age-group specific rates using as weights the 2019 single age population data from United Nations World Population Prospects 2022 [1].

S4.2.2. Aggregating direct costs across severity levels

In a given country-quarter, we calculate the direct cost per COVID-19 infection as a weighted average of the severity-level-specific direct costs from Section S4.2.1. The weights we use are the country-quarter relative shares of the different severity levels across nonfatal infections described in Section S4.1.2.1. Note that though the weights we use consist of our estimates of the relative shares of the different severity levels across nonfatal infections, for simplicity we use the resulting weighted average as our estimate of the direct cost per infection, whether fatal or nonfatal.

S4.2.3. Currency conversions

The WHO-CHOICE data come denominated in 2010 USDs, which we convert to 2019 USDs as follows. First, we convert 2010 USDs to 2010 LCUs using 2010 market exchange rates (LCUs per USDs). Second, we inflate 2010 LCUs to 2019 LCUs using country-specific 2010 and 2019 GDP deflators [9,24]. We used the 2010 and 2018 GDP deflators from the World Bank for Syria, because this country did not have a 2019 GDP deflator. Third, we convert 2019 LCUs to 2019 USDs using 2019 market exchange rates. We obtain 2010 and 2019 market exchange rates from the IMF IFS [10], the United States Department of the Treasury Bureau of the Fiscal Service [11], and the World Bank GEM database [12].

S4.2.4. Extrapolation across countries

There are 28 study countries that are not in the WHO-CHOICE database, and one additional study country (Venezuela) that is in this database but does not have the market exchange rates

needed for the currency conversions described above. We extrapolate costs for an outpatient visit and hospital cost per bed day in 2019 USDs to these 29 countries ("target countries") using an approach we call "nearest neighbor matching." This approach imputes the missing direct cost values from the values of a single similar country (the "nearest neighbor"). The first step in this approach is to construct pools of candidate countries (call these "donor pools" and "donor countries," respectively) with non-missing values for direct costs based on a common WHO region and World Bank income group (hereafter, "region-income" group, e.g., the "Western Pacific High Income" group). In the second step, we select a variable that is closely related to direct costs, and for which target- and donor countries have non-missing values ("matching variable"). Our "matching variable" is 2019 per capita GDP. In the third step, we map each target country to a donor pool based on its region-income group and identify the "nearest neighbor" within the donor pool whose value for 2019 per capita GDP is closest (i.e., has the smallest absolute value difference) to that of the target country. In the last step, we adjust the imputed value for direct costs by multiplying it by the ratio of each target country's 2019 per capita GDP to its donor country's 2019 per capita GDP.

S4.3. Indirect costs due to a nonfatal infection

Indirect costs consist of lost unpaid work due to a nonfatal infection, which we calculate as the product of the average hourly wage, the average daily number of hours spent on unpaid work, and the severity-level-specific number of COVID-19 related workdays lost. This estimate assumes that the number of workdays lost is a valid proxy for the number of days that a patient is also unable to perform unpaid work.

S4.3.1. Hourly wage

We obtain hourly wages from the International Labour Organization (ILO) [25]. This database provides country-specific average hourly earnings of employees aggregated across males and females and across all occupations in 2019 USD for 46 study countries [26]. We extrapolate these hourly earnings to the 95 countries without data using nearest neighbor matching method described in Section S4.2.4 (i.e., pooling countries within WHO region-WB income groups and using 2019 per capita GDP as the matching variable). There are however some WHO region-WB income groups in which no country has 2019 ILO hourly earnings data. For countries in these groups, we use nearest neighbor matching within the global pool using 2019 per capita GDP as the matching variable.

S4.3.2. Unpaid work time (hours per day)

We obtain time use data from Charmes (2019) and Charmes (2015) [27,28]. These studies provide country- and sex-specific minutes per day spent on different time use categories in the working age population. The specific age ranges of the working age population vary by country but tend to start at age 10 or 15, and end at either age 55, 60, 65, or 75. For simplicity, we assume that the time use patterns reported in Charmes (2015, 2019) apply uniformly between the ages of 15 and 64. We use their data on two time use categories: unpaid work and leisure. From Charmes (2019), we use data from Charts 2, 3, 36, and 37. From Charmes (2015), we take data from Charts 3, 13, 14, 24, 25, 33, 34, 49, 50, 58, 59, 67, 68, 76, and 77.

Charmes (2015, 2019) data are sex-disaggregated. We aggregate across sexes using the relative sizes of male and female populations aged 15-64 as weights [29,30]. For consistency, we assume the working-age population includes everyone aged 15-64. We obtain the population distributions from the UN WPP 2022.

Charmes (2019) provides sex-specific estimates of daily unpaid work time in 75 of our study countries. For countries not in Charmes (2019), we impute unpaid work time using a "pooled average method." In the first step of the "pooled average method," we define donor pools using the regional groupings used in Charmes (2019). All but one of the Charmes geographic classifications can be directly found in the UN sub-regions. The exception is Charmes' category "Arab countries". We define all countries on the Arabian Peninsula, except for Israel, as being part of the "Arab countries" group. We classify all other countries based on the UN sub-region, which aligns with the groupings used by Charmes. In the second step, we calculate the average value of daily unpaid work time within the pool and impute this value to the countries within the pool with missing data.

S4.3.3. Unpaid workdays lost due to nonfatal COVID-19

We estimate the number of unpaid workdays lost for mild, severe, and critical nonfatal infections using results from Di Fusco et al. (2022, Table S13) for lost paid work time under the assumption that the latter is a valid proxy for the former [20]. Our estimates are imperfect approximations since we need workdays lost for nonfatal infections while Di Fusco et al., 2022,

provide workdays lost for groups that include both fatal and nonfatal infections [20]. For mild infections we use their estimate of workdays lost in those receiving outpatient care. For severe nonfatal infections, we take a weighted average of workdays lost among patients in the general ward with and without IMV, using IMV rates in the general ward as weights. For critical nonfatal infections, we take a weighted average of workdays lost among patients in the ICU with and without IMV, using IMV rates in the ICU as weights. These IMV rates in the general ward and in ICU are from Di Fusco et al. (2022, Table S9) [20]. Since these IMV rates are age group specific (12-17, 18-29, 30-49, 50-64, 65-74, and 75+), we compute a weighted average of these rates using the relative sizes of these age groups in 2019 according to the United Nations World Population Prospects 2022 [1]. In computing this average, we weight the rate for the 12-17 age group using the relative population size of the ages 15-17, thus assuming that those younger than 15 do not perform any unpaid work.

Based on Di Fusco et al. (2022, Table S9, "Probability of PASC among patients receiving inpatient care"), we assume 45.7% of severe and critical cases experience long COVID [20]. Based on Robinson et al. (2022), we assume severe cases with long COVID lose an additional 45 workdays [19]. Based on Hastie et al. (2022), we assume critical cases with long COVID lose an additional 18 months (548 days) of work [22].

S4.3.4. Unpaid work loss due to nonfatal infection

We calculate unpaid work losses due to nonfatal infection of a given severity level as the product of the average hourly wage, the average daily number of hours spent on unpaid work, and the

severity-level specific number of unpaid workdays lost. Since the duration of critical cases with long COVID is nearly two years, we discount the unpaid work loss for this health state at 3% per year. We calculate unpaid work loss per nonfatal infection as a weighted average of the unpaid work loss for each nonfatal severity level, where the weights equal the relative size of patient groups at the following severity levels: asymptomatic, mild, severe without long COVID, severe with long COVID, critical without long COVID, and critical with long COVID. These weights vary by country-quarter so our estimate of unpaid work loss per nonfatal infection is country-quarter-specific.

S4.4. Averted direct and indirect costs

Given averted deaths and infections, we multiply country-quarter-specific averted infections by country-quarter-specific direct costs to generate an estimate of country-quarter-specific direct costs averted. We sum over all country-quarters to produce a global estimate of averted direct costs.

We also multiply country-quarter-specific averted nonfatal infections (i.e., averted infections minus averted deaths) by country-quarter-specific indirect costs per nonfatal infection. We sum over all country-quarters to produce a global estimate of averted nonfatal indirect costs.

We sum averted direct costs and averted nonfatal indirect costs to produce a global estimate of the averted costs associated with vaccination.

S4.5. Full income

Full income in country i, which we denote by y_i^f, is an annual per capita figure equal to annual earnings plus the value of annual nonmarket time:

$$y_i^f = y_i + w_i * z_i \quad (S55)$$

where y_i, w_i, z_i are country-specific per capita income, hourly wage, and per capita annual nonmarket time, respectively. Nonmarket time consists of time spent on unpaid work and leisure. We describe our unpaid work time data in Section S4.3.2. We use DigitizeIt graph reading software [31] to extract sex-specific daily leisure time from Charmes (2015), which we weight across the sexes using 2019 relative population sizes from UN World Population Prospects 2022. We use the pooled average method described in Section S4.1.1.1 to extrapolate to countries without leisure data in Charmes (2015). The value of nonmarket time equals the product of the hourly wage (Section S4.3.1) and annual nonmarket time.

For per capita earnings, we use gross national income (GNI) per capita from the World Bank national accounts data and OECD National Accounts data files [32]. GNI in the World Bank national accounts data, and OECD National Accounts data files is defined as "the sum of value added by all resident producers plus any product taxes (less subsidies) not included in the valuation of output plus net receipts of primary income (compensation of employees and property income) from abroad." We use GNI per capita denominated in 2019 USDs, which is available for all but five of our study countries (Cuba, South Sudan, Syria, Taiwan, Venezuela).

We extrapolate GNI per capita to these countries using nearest neighbor matching within WHO region-WB income groups using 2019 per capita GDP as the matching variable.

S4.6. Monetized health gains

Given averted deaths and infections, we multiply country-quarter-specific averted deaths by country-quarter-specific QALY losses per fatal infection to generate an estimate of country-quarter-specific QALYs gained through averted deaths. We sum across all country-quarters to produce a global estimate of QALYs gained through averted deaths We also multiply country-quarter-specific averted nonfatal infections (averted infections minus averted deaths) by country-quarter-specific QALY losses per nonfatal infection to generate an estimate of country-quarter-specific QALYs gained through averted nonfatal infections. We sum across all country-quarters to produce a global estimate of QALYs gained through averted nonfatal infections. We sum fatal QALY gains and nonfatal QALY gains to produce an estimate of total QALY gains.

Given QALY gains from averted deaths and nonfatal infections, we monetize these gains by multiplying them by the value of full income (see equation S55).

S4.7. Total value of COVID-19 vaccination

The previous sections describe the estimation of our three primary benefit outcomes:

(i) GDP gains,

(ii) monetized health gains, and

(iii) direct and indirect costs averted.

When added together, these benefit outcomes correspond to the total value of COVID-19 vaccination (VoV) in our study.

S5. OTHER TOPICS

S5.1. Vaccine effectiveness

Using our analytical results, we can generate rough estimates of vaccine effectiveness against infections and deaths. We estimate vaccine effectiveness against infections (deaths) as the ratio of averted infections (deaths) per dose to per capita infections (deaths) in the absence of vaccination.

Averted infections (deaths) per dose are equal to global averted infections (deaths) divided by global doses administered. Global averted infections (deaths) are derived in Table 3 of the article and reported in rows (3) and (4) of Table S5. Averted infections (deaths) per dose are calculated in rows (7) and (8) of Table S5.

Per capita infections (deaths) in the absence of vaccination are equal to global infections (deaths) in the no-vaccination scenario divided by the global population. Since the benefits of vaccination in the numerator of the vaccine effectiveness ratio are only measured in 2021 (i.e., after the vaccine rollouts), the denominator of the ratio only measures global infections (deaths) in the

absence of vaccination in 2021. These values are reported in rows (5) and (6) of Table S5 for infections and deaths, respectively, and the corresponding per capita measures are calculated in rows (9) and (10).

Vaccine effectiveness against infections is the ratio of averted infections per dose in row (7) to per capita infections in the absence of vaccination in 2021 in row (9). These estimates are calculated in row (11) as 0.365 for all vaccine brands and 0.493 for Pfizer-BioNTech. Vaccine effectiveness against deaths is the ratio of averted deaths per dose in row (8) to per capita deaths in the absence of vaccination in 2021 in row (10). These estimates are calculated in row (12) as 0.306 for all vaccine brands and 0.632 for Pfizer-BioNTech.

These effectiveness estimates are considerably lower than published estimates of vaccine efficacy [33]. This is likely because in clinical trials and other settings from which published estimates are derived, societal and policy contexts are relatively similar between the vaccinated and non-vaccinated. In contrast, in our analysis, we allow such contexts to vary so that, e.g., there is greater natural immunity, lockdown stringency, and non-pharmaceutical interventions in the no vaccination counterfactual relative to the actual state of the world with vaccination. This tends to reduce the difference in infections between the actual and counterfactual states, which tends to reduce vaccine effectiveness.

Table S5. Vaccine effectiveness

	All vaccine brands	**Pfizer-BioNTech**
(1) Population	7601912488	7369618671
(2) Doses	6386639570	1001790180
(3) Infections averted by vaccination	1665369941	270715259

(4) Deaths averted by vaccination	4080843	1107206
(5) Infections in the absence of vaccination in 2021	5436267668	4040704409
(6) Deaths in the absence of vaccination in 2021	15863307	12888589
(7) Averted infections per dose = (3)/(2)	0.261	0.270
(8) Averted deaths per dose = (4)/(2)	0.000639	0.00111
(9) Per capita infections in the absence of vaccination in 2021 = (5)/(1)	0.715	0.548
(10) Per capita deaths in the absence of vaccination in 2021 = (6)/(1)	0.002	0.002
(11) Vaccine effectiveness against infections = (7)/(9)	**0.365**	**0.493**
(12) Vaccine effectiveness against deaths = (8)/(10)	**0.306**	**0.632**

S5.2. Sensitivity and scenario analysis

S5.2.1. One-way sensitivity analysis

In one-way sensitivity analysis, we test the robustness of our base-case results to alternative values of COVID-19 infections, COVID-19 deaths, and discount rates. We vary the magnitude of infections using the IHME lower and upper bound estimates of this variable. We change the base-case values of COVID-19 deaths to IHME's daily deaths without the excess mortality scalar applied ("reported deaths"). We change the discount rates to 0% and 6%.

As discussed above, we use the IHME COVID-19 infections and deaths variables to construct the severity levels (asymptomatic, mild, severe, and critical). These severity levels are in turn used to derive QALY losses, direct costs, and unpaid work loss due to disability. Our one-way sensitivity analyses only change the dependent variables in the infections and deaths regressions, and hold fixed all quantities that are affected by the value of infections and deaths through severity splits.

S5.2.2. Probabilistic sensitivity analysis

Our quarterly and annual GDP regressions are both estimated using ordinary least squares with robust standard errors. Our probabilistic sensitivity analysis (PSA) assumes that coefficients estimated from each of these two regressions follow a multivariate normal distribution (MVN) parametrized by a mean vector consisting of the coefficient estimates and a variance-covariance matrix (VCE) of those coefficient estimates. Our deaths and infection regressions are estimated using seemingly unrelated regression and robust standard errors. Under SUR, we have a single large VCE spanning all coefficients of both equations (i.e., the death equation and the infection equation), and the PSA draws 1000 draws from this single large distribution. We therefore take 1000 draws for the SUR model, 1000 draws for the quarterly GDP regression, and 1000 draws for the annual GDP regression (i.e., 3000 draws in all), where each draw yields a new set of coefficient estimates for each of the four regressions (deaths, infections, quarterly GDP, and annual GDP). For each of the four regressions, our simulation yields 1000 vectors of coefficient estimates. For each of the 1000 coefficient vectors, we predict the impact of vaccination, monetize the health gains, calculate averted direct and indirect costs, and compute the total VoV. We use the first (n^{th}) draw of each set to estimate the first (n^{th}) simulated VoV from all vaccination and the first (n^{th}) simulated VoV from Pfizer-BioNTech vaccination. Doing this for all 1000 draws, we produce 1000 simulated VoVs from all vaccination and 1000 simulated VoVs from Pfizer-BioNTech vaccination. We then estimate the 95% CI of the VoV from all vaccination and the 95% CI of the VoV from Pfizer-BioNTech vaccination.

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