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Supplementary Materials for

The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak

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Material and Methods

Global Epidemic and Mobility Model

The Global Epidemic and Mobility Model (GLEAM), an individual-based, stochastic, and spatial epidemic model (*4–7, 38*). GLEAM uses a metapopulation network approach integrated with real-world data where the world is divided into sub-populations centered around major transportation hubs (usually airports). The subpopulations are connected by the flux of individuals traveling daily among them. Population data are obtained from the high-resolution population database of the Gridded Population of the World project from the Socioeconomic Data and Application Center at Columbia University (`sedac.ciesin.columbia.edu`). The model considers geographical cells of 0.25° x 0.25°, corresponding to an approximately 25km x 25km square for cells along Earth's equator. Cells are then grouped into sub-populations defined by a Voronoi-like tessellation of the Earth's surface centered around major transportation hubs in different urban areas. The model includes over 3,200 sub-populations in roughly 200 different countries and territories (numbers vary by year). Sub-populations interact through the mechanistically simulated mobility and commuting patterns of disease carriers. Individuals who travel are randomly sampled from the "origin" population. The detailed algorithm is described in (*5*). The airline transportation data consider daily origin-destination traffic flows from the Official Aviation Guide (OAG) and IATA databases (updated 2019). Ground mobility/commuting flows are derived by the analysis and modeling of data collected from the Offices of Statistics for 30 countries on 5 continents. The full dataset contains about 80,000 administrative regions on 5 continents and over 5 million commuting flow connections between them (*5*).

The disease model within each subpopulation assumes a compartmental representation of the disease under study. The epidemic evolution is modeled using an individual dynamic where transitions are mathematically defined by chain binomial and multinomial processes to preserve the discrete and stochastic nature of the transmission and disease evolution process. Each subpopulation's disease dynamic is coupled with the other subpopulations through the mechanistically simulated travel and commuting patterns of disease carriers. Within each sub-population, the human-to-human transmission of COVID-19 is modeled using a compartmental representation of the disease where individuals can occupy one of the following compartments: Susceptible (S), Latent (L), Infectious (I) and Recovered (R). Susceptible individuals can acquire the virus through contacts with individuals in the infectious compartment, and become latent, meaning they are infected but can not transmit the disease yet. Latent individuals progress to the infectious stage with a rate inversely proportional to the latent period (which we assume to have the same duration as the incubation period), and infectious individuals progress into the removed stage with a rate inversely proportional to the infectious period. The sum of the mean latent and infectious periods defines the generation time. Disease carriers travel during the entire latency and infectious period and are not traveling when they enters the removed stage identifying those who can no longer infect others, meaning they are recovered, isolated, hospitalized, or dead. The model works in discrete time steps, representing a full day, to implement computationally the air travel, the compartmental transitions (where the force of infection takes into account both the infection dynamics and the short-range movement of individuals), and the

partial aggregation of the results at the desired level of geographic resolution. All the technical details of the model have been previously published (*5, 7*). The model is fully stochastic and for each nominally identical initialization (initial conditions and disease model) generates an ensemble of possible epidemic evolutions for epidemic observables, such as newly generated cases, time of arrival of the infection, and number of traveling carriers. Parameter ranges for the latent and infectious period, and generation time are derived from early estimates on the epidemiological characteristics of COVID-19, as well as plausible ranges from the SARS epidemic (*18–23*). In Fig. S1A we report in the table the parameters range explored in the sensitivity analysis of the model.

Calibration. We assume a starting date of the epidemic that falls between 11/15/2019 and 12/1/2019, with 40 cases caused by zoonotic exposure. For each generation time T_g, we perform an Approximate Bayesian Computation to estimate the posterior distribution of the basic reproductive number R_0 of the outbreak. We simulate epidemics with R_0 in the range 1.5 to 4.0, sampled with a uniform prior. This allows us to calculate the distribution $P(D)$ for the evidence D, and for each value of R_0, the likelihood $P(D|R_0)$. From these distributions we can calculate the posterior probability $P(R_0|D)$ of interest (see Fig. S1B). The evidence D is the growth rate of imported COVID-19 cases to international locations during the exponential growth of the epidemic. We select the simulated epidemics that match the observed number of cumulative imported cases by January 23, 2020 with a tolerance accounting for the 40% probability of detecting an importation (*14*). We consider only statistically independent importation events by date of arrival at international destinations (the list of importation events used is provided in Table S1). Then, $P(R_0 = x|D)$ is computed as the number of simulations where $R_0 = x$ and the evidence constraint D is satisfied over the total number of simulations where $R_0 = x$.

Sensitivity Analysis

We have performed an extensive sensitivity analysis to check the robustness of the results. We report here the results obtained by calibrating the model under the same assumptions and show that the obtained results are consistent with the results reported in the main manuscript text and do not alter the considerations offered by our modeling study.

- Long Generation Time. We considered a generation time up to $T_g = 9$ days and analyze the effect of the travel ban on the outbreak sizes in Wuhan and in the remaining areas in Mainland China as well as the effect on the number of international case importations. The model assumptions are the same as what is used in the main text. We assume an epidemic starting date that falls between 11/15/2019 and 12/1/2019, with 40 cases initially caused by zoonotic exposure. The posterior distribution of the reproductive number is estimated using an Approximate Bayesian Computation approach as previously described. We find an average reproductive number $R_0 = 2.6$ [90%CI 2.5-2.8] with a doubling time measured at $T_d = 5$ days. Similar to the parameters used in the main text, introducing a travel ban in Wuhan shows a delay of approximately 3 days occurring for locations in Mainland China other than Wuhan. The projections for Wuhan on the other hand do not change.

- Initial number of zoonotic cases. We have repeated the ABC calibration yielding the posterior distribution of R_0 by using a different number of initial zoonotic cases exploring the range from 20 to 80 cases. We have observed that the variation on the average reproductive number are below the 10% threshold.

- Starting date of the outbreak. We have performed the ABC calibration extending the start of the outbreak to early November. In this case we can look at the joint posterior of the starting date and the reproductive number R_0. The posterior for the starting date is reported in Fig. S1C. The analysis shows that initial start of the outbreak in early December has a likelihood 2 times larger than early November. The mean reproductive number shows a $\approx 9\%$ increase with respect to the baseline.

- Detection rate. We have performed the ABC calibration by varying the overall International case detection rate. The reproductive number posterior distribution yields $R_0 = 2.66$ [90%CI 2.48-2.84] and $R_0 = 2.50$ [90%CI 2.32-2.67] for the detection rate set at 30% and 50%, respectively. The results obtained for the epidemic evolution in Mainland China are consistent with the baseline scenario reported in the main paper.

Real time human mobility data sources

We collected daily travel data starting January 1, 2020 until February 25, 2020 from Baidu Qianxi platform (*39*), which provides three mobility indices (inflow index, outflow index, and intra-city index). The indices are proxies for the number of travelers moving in, out of, and inside a city, respectively. We extracted the mobility outflow index of 27 provinces and 4 municipalities for the current year 2020 and the previous year (same lunar date), and then mapped all provinces and municipalities to the metapopulation structure of the model to estimate the travel flow changes during the epidemic where the travel reduction can be estimated as $travel\ reduction = 1 - \frac{I_{cur}}{I_{pre}}$, where I_{cur} and I_{pre} are the mobility outflow index of current year 2020 and previous year on the same lunar date, respectively. We report the data for Wuhan and Mainland China in Fig. S2.

Exported cases from Wuhan city

As the calibration of our model relies on the tracking of imported cases from Wuhan, we kept track of every importation event in other countries. Due to lack of an official source recording these events, we produce a database as shown in Table S1 combining information from news sources and other published line lists (*16, 17*). As we are interested in individual importation events, family clusters or groups of tourists traveling together were considered as an individual, independent event. For each event we recorded when it was reported and when the individual(s) arrived in a given country. This dataset is incomplete as we rely mostly on news outlets that do not always report all the information we require. It's worth mentioning that the number of cases reflected in this table are not the total number of cases reported in a country. That is we are not keeping track of local transmissions. Since January 30, 2020 many countries have started to bring back their own citizens living in Wuhan. Some of these individuals have been confirmed as a case of COVID-19 after they arrived and were put in isolation. These individuals are not considered in the database.

Parameter	Range
Latency period (mean)	3-6 days
Infectious period (mean)	2-8 days
Generation time T_g	6-11
Starting dates considered in interval	[2019-11-15, 2019-12-01]
Initial number of zoonotic cases	20-80

A

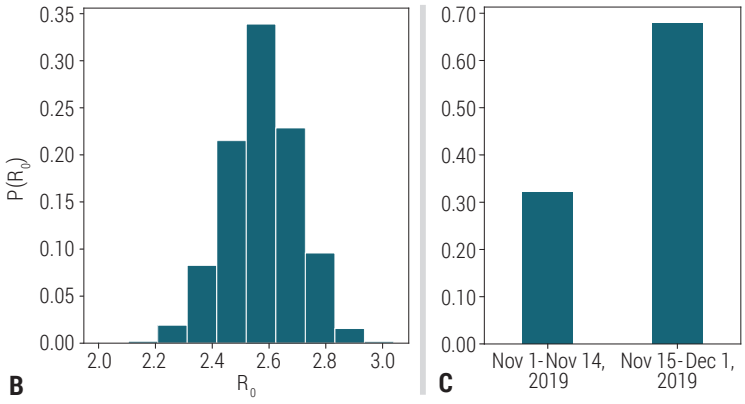

Fig. S1: Sensitivity analysis and Calibration. A) Model parameter's range explored in the sensitivity analysis. B) Posterior distribution of the reproductive number R_0 when the generation time $T_g = 7.5$ and starting date 12/1/2019. C) Posterior distribution of the epidemic starting dates.

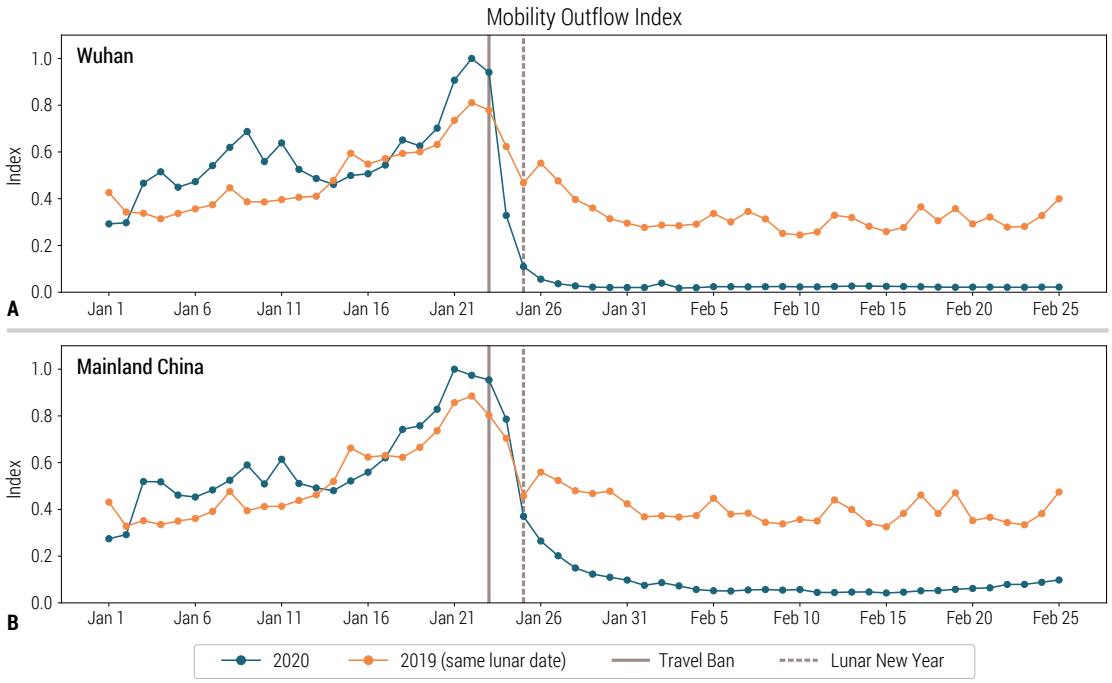

Fig. S2: Real-time mobility data for Mainland China. A) Mobility outflow index for Wuhan during January 1, 2020 and February 25, 2020. B) Mobility outflow index for Mainland China during the same time period. For both figures, blue and orange lines represent mobility outflow indices for 2020 and 2019 (same lunar date), respectively, and the indices are normalized by dividing the maximum value of current year's indices

Date Reported	Date of Arrival	Country	City	Cluster	Ref.
2020-01-24	2020-01-05	Nepal	Kathmandu	No	(*40*)
2020-01-25	2020-01-06	Australia	Sydney	No	(*41*)
2020-01-15	2020-01-06	Japan		No	(*42*)
2020-01-12	2020-01-08	Thailand	Bangkok	No	(*43*)
2020-01-20	2020-01-12	Taiwan	Taiwan	No	(*44*)
2020-01-30	2020-01-13	Japan		No	(*45*)
2020-01-17	2020-01-13	Thailand	Bangkok	No	(*46*)
2020-01-24	2020-01-13	United States of America	Chicago	No	(*47*)
2020-01-23	2020-01-13	Vietnam	Nha Trang	No	(*48*)
2020-01-20	2020-01-15	United States of America		No	(*49*)
2020-02-01	2020-01-16	Vietnam		No	(*50*)
2020-01-29	2020-01-16	United Arab Emirates		Yes	(*51*)
2020-01-28	2020-01-16	France	Paris	No	(*52*)
2020-02-06	2020-01-17	Malaysia	Johor Bahru	No	(*53*)
2020-01-30	2020-01-17	Vietnam		Yes	(*54*)
2020-01-25	2020-01-18	Australia	Sydney	No	(*41*)
2020-01-25	2020-01-18	Japan	Tokyo	No	(*55*)
2020-02-03	2020-01-18	Malaysia	Kuala Lumpur	No	(*56*)
2020-01-27	2020-01-18	Singapore	Singapore	No	(*57*)
2020-01-24	2020-01-18	France	Paris	Yes	(*58*)
2020-01-25	2020-01-19	Australia	Melbourne	No	(*59*)
2020-01-24	2020-01-19	Japan		No	(*60*)
2020-01-20	2020-01-19	Republic of Korea	Seoul	No	(*61*)
2020-01-27	2020-01-19	Sri Lanka	Colombo	No	(*62*)
2020-01-27	2020-01-19	Singapore	Singapore	No	(*63*)
2020-01-28	2020-01-19	Singapore	Singapore	Yes	(*64*)
2020-01-22	2020-01-19	Thailand		No	(*65*)
2020-01-22	2020-01-19	Thailand		No	(*65*)
2020-01-25	2020-01-19	Thailand	Hua Hin	No	(*66*)
2020-01-25	2020-01-20	Australia	Sydney	No	(*41*)
2020-01-28	2020-01-20	Japan		No	(*67*)
2020-01-30	2020-01-20	Japan		No	(*68*)
2020-01-26	2020-01-20	Republic of Korea		No	(*69*)
2020-01-27	2020-01-20	Republic of Korea	Seoul	No	(*70*)
2020-02-02	2020-01-20	Republic of Korea	Suwon	No	(*71*)
2020-01-23	2020-01-20	Malaysia	Johor Bahru	Yes	(*72*)
2020-01-28	2020-01-20	Malaysia	Kuala Lumpur	No	(*73*)
2020-02-05	2020-01-20	Philippines		No	(*74*)
2020-01-23	2020-01-20	Singapore	Singapore	Yes	(*75*)
2020-01-29	2020-01-20	Singapore	Singapore	No	(*76*)
2020-01-29	2020-01-21	Australia		No	(*77*)

2020-01-28	2020-01-21	Japan	Hokkaido	No	(*78*)
2020-02-04	2020-01-21	Japan		Yes	(*79*)
2020-01-30	2020-01-21	Philippines	Santa Cruz	Yes	(*80*)
2020-01-24	2020-01-21	Singapore	Singapore	No	(*81*)
2020-01-30	2020-01-21	Singapore	Singapore	Yes	(*82*)
2020-01-24	2020-01-21	Thailand	Bangkok	No	(*83*)
2020-01-27	2020-01-22	Australia	Sydney	No	(*84*)
2020-01-29	2020-01-22	Australia	Gold Coast	Yes	(*85*)
2020-01-25	2020-01-22	Canada	Toronto	Yes	(*86*)
2020-01-24	2020-01-22	France	Bordeaux	No	(*87*)
2020-01-26	2020-01-22	Japan		Yes	(*88*)
2020-01-30	2020-01-22	Japan		No	(*89*)
2020-01-24	2020-01-22	Republic of Korea		No	(*90*)
2020-01-25	2020-01-22	Malaysia	Johor Bahru	No	(*91*)
2020-01-25	2020-01-22	Singapore	Singapore	Yes	(*92*)
2020-01-30	2020-01-22	Singapore	Singapore	No	(*93*)
2020-01-31	2020-01-22	Singapore	Singapore	No	(*94*)
2020-02-01	2020-01-22	Singapore	Singapore	No	(*95*)
2020-01-27	2020-01-23	Germany	Starnberg	No	(*96*)
2020-01-31	2020-01-23	Canada	London	No	(*97*)
2020-01-29	2020-01-23	Finland	Ivalo	No	(*98*)
2020-01-30	2020-01-23	Italy	Milano	Yes	(*99*)
2020-01-26	2020-01-23	Cambodia	Sihanoukville	No	(*100*)
2020-01-31	2020-01-23	Republic of Korea		No	(*101*)
2020-01-31	2020-01-23	Republic of Korea		No	(*102*)
2020-02-06	2020-01-23	Republic of Korea		No	(*103*)
2020-01-27	2020-01-23	Singapore	Singapore	No	(*104*)
2020-02-02	2020-01-23	United States of America		No	(*105*)
2020-01-31	2020-01-24	Sweden	Jönköping	No	(*106*)
2020-01-31	2020-01-24	United States of America		No	(*107*)
2020-01-31	2020-01-25	Australia		No	(*108*)
2020-02-05	2020-01-25	Malaysia		Yes	(*109*)
2020-01-30	2020-01-26	Singapore	Singapore	No	(*94*)
2020-01-31	2020-01-28	United States of America	Boston	No	(*110*)
2020-02-05	2020-01-30	United States of America		No	(*111*)
2020-02-09	2020-02-01	Malaysia		No	(*112*)

Table S1: Imported cases from Wuhan. We only consider as an importation if the case has a travel history related to Wuhan. Family clusters or groups of people traveling together are considered as one importation event.

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