Routes of importation and spatial dynamics of SARS-CoV-2 variants during localised interventions in Chile

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Supplementary Material

Supporting Text
Figures S1 - S13

Supporting text - Contextualising the COVID-19 and mobility situation in Chile during 2020-2021

Located on the southernmost end of the South American Pacific coast, Chile provides an interesting context to analyse the effects of human mobility and spatial connectivity in the spread of SARS-CoV-2 as it includes highly connected yet largely rural areas. The majority of air travellers enter the country through the Arturo Merino Benítez International Airport, located on the outskirts of its capital city Santiago de Chile (in this work referred to as the Santiago International Airport or SCL for short), which accounted for 99.24% of all travellers entering the country through international flights between October 2020 and December 2021 (the remainder entering through six secondary airports, as shown from publicly available data from the Junta Aeronáutica Civil, Ministerio de Transportes y Telecomunicaciones; http://www.jac.gob.cl/estadisticas/informes-estadisticos-mensuales-del-trafico-aereo/). While this single main port of entry drives registers a large portion of all incoming international travellers, the country also shares a long border with neighbouring Argentina, the longest international land border of South America, covering 5,308km in length; this border features 26 official international border crossings through which substantial numbers of travellers enter Chile, most predominantly into the regions of Atacama in the north (Paso Sico), Coquimbo (Paso Agua Negra) and Valparaíso (Paso Los Libertadores) in central Chile (including Santiago) and Los Lagos (Paso Cardenal Samoré) in the south of the country. Overall, land border passes register up to one third of all international arrivals into Chile (e.g. 652,843 travellers entered Chile from border crossings in 2021 as shown from data obtained through an Information Transparency request, see *Methods*). Internally, Chile has a generally well-developed highway infrastructure and a domestic flight network, but its elongated geography along the north-south axis lends itself to the establishment of remote areas across the national territory with limited human mobility. Approximately 38.62% of the population lives within the Santiago Metropolitan Area, with an additional 15.08% of the population residing in the major urban centres of Valparaíso, Concepción, Temuco and Antofagasta (2017 census data available at https://www.bcn.cl/siit). Population densities tend to be high in the central regions of the country (1); the rest of the country is less densely populated, including large and mostly unpopulated natural parks and remote regions. The vast Atacama Desert in the north and the extreme latitude of the southernmost regions of Chile might discourage the development of large human settlements but incentivise a rich tourism industry.

As with other countries, Chile suffered local COVID-19 epidemic waves throughout 2020 and 2021. The public health response to SARS-CoV-2 in Chile included several key particularities. From a surveillance perspective, the country implemented had been running genomic surveillance since 2020 and implemented a systematic genomic surveillance programme in April 2021 after the emergence of the Alpha and Gamma VOCs amongst others (2); within this broader programme, specific testing was performed on all international returning travellers at the Arturo Merino Benítez International Airport (in this work referred to as the Santiago International Airport or SCL for short). This dedicated testing programme was used not only to inform travellers about their quarantine requirements if they tested positive, but also served as a sentinel system to identify incoming viral lineages and specifically VOIs/VOCs. As non-pharmaceutical interventions (NPIs), Chile implemented a targeted scheme for partial and complete lockdowns and progressive reopening at the *comuna* level (adm3 administrative divisions; n = 346 comunas) called *Paso a paso nos cuidamos* (lit. “Step by step we take care of ourselves”) in July 2020 (3). Comunas were placed in one of five possible lockdown tiers (called ‘steps’, lit. *Pasos*), in order of stringency these are ‘*Cuarentena*’ (Quarantine), ‘*Transición*’ (Transition), ‘*Preparación*’ (Preparation), ‘*Apertura inicial*’ (Initial opening) and ‘*Apertura avanzada*’ (Advanced opening). Limitations within these tiers concerned, amongst other things, the requirement of special permits to enter/leave the comunas or to circulate freely. In practice the different levels of stringency resulted in the following mobility characteristics:

1. The **Quarantine step** limited human mobility throughout the entire week.
2. The **Transition step** limited human mobility only on weekends when the stringency of the higher tier (Quarantine) was maintained.
3. The **Preparation** and **Initial opening steps** share similar mobility regimes, with no restrictions on free circulation in the comuna and the main differences between them concerning specific types of activities permitted and recommendations on numbers of people for gatherings.
4. The **Advanced opening** step results in scenarios with no restrictions.

As such, we re-code the NPI stringency levels into three tiers: ***(1) full lockdown*** (includes comunas in Quarantine step), ***(2) weekend lockdown*** (includes comunas in Transition step) and ***(3) no lockdown*** (includes comunas in the Preparation and Initial opening steps). The scheme provided some degree of autonomy to individual comunas and allowed them to decide when to increase or reduce the lockdown stringency level. This resulted in a highly heterogeneous landscape of the timing and intensity of non-pharmaceutical interventions across the country; the effects of such a spatially heterogeneous implementation of interventions on viral transmission remain unclear.

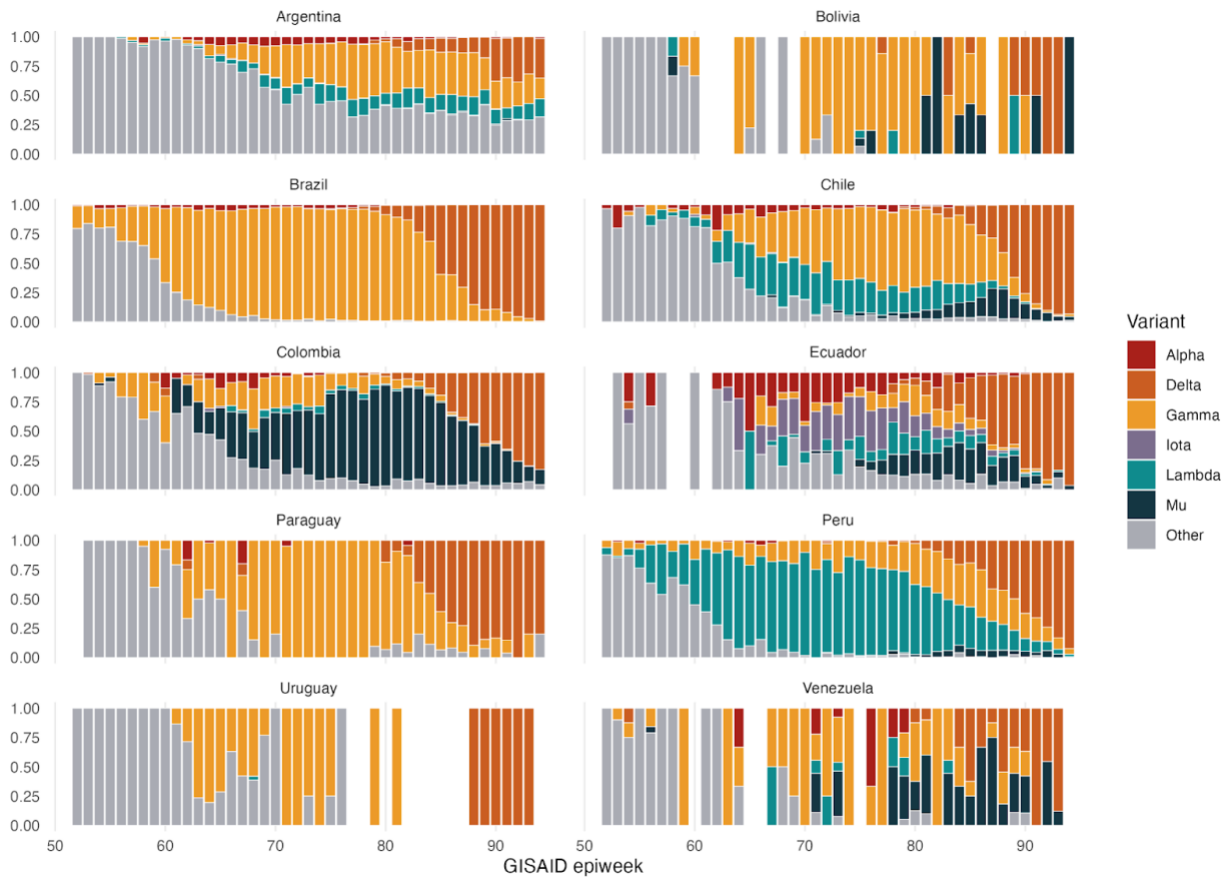

Figure S1. Proportion of SARS-CoV-2 variants detected in South American countries. *The proportion of sequences corresponding to each VOI/VOC per epidemic week (as annotated on GISAID) is shown per country, relative to the total number of sequences generated by each country over that two-week period.*

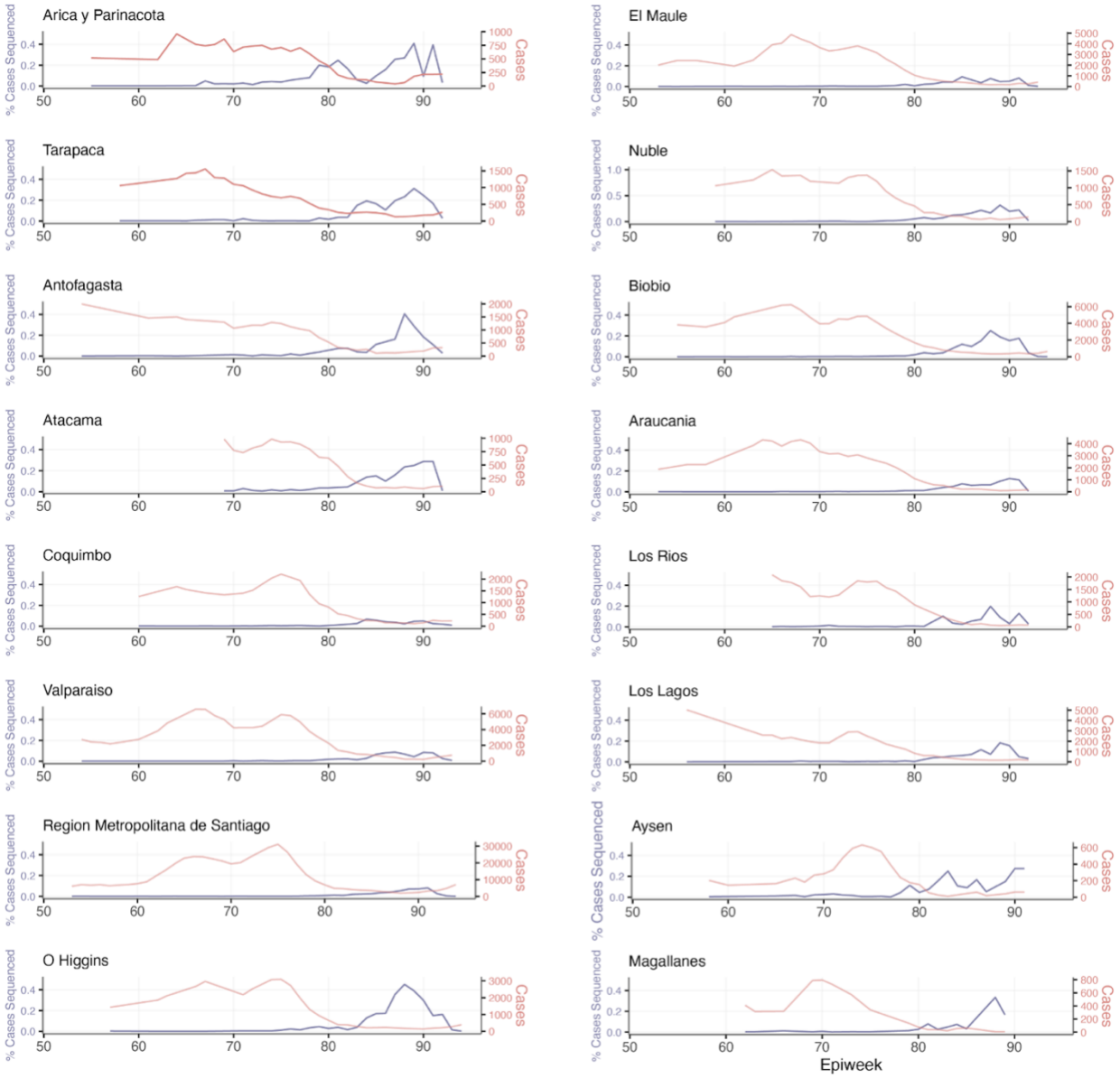

Figure S2. Epidemic trends and sequencing intensity by geographic region in Chile. *Numbers of cases and percentage of cases sequences in 16 geographic regions of Chile per week over 2021.*

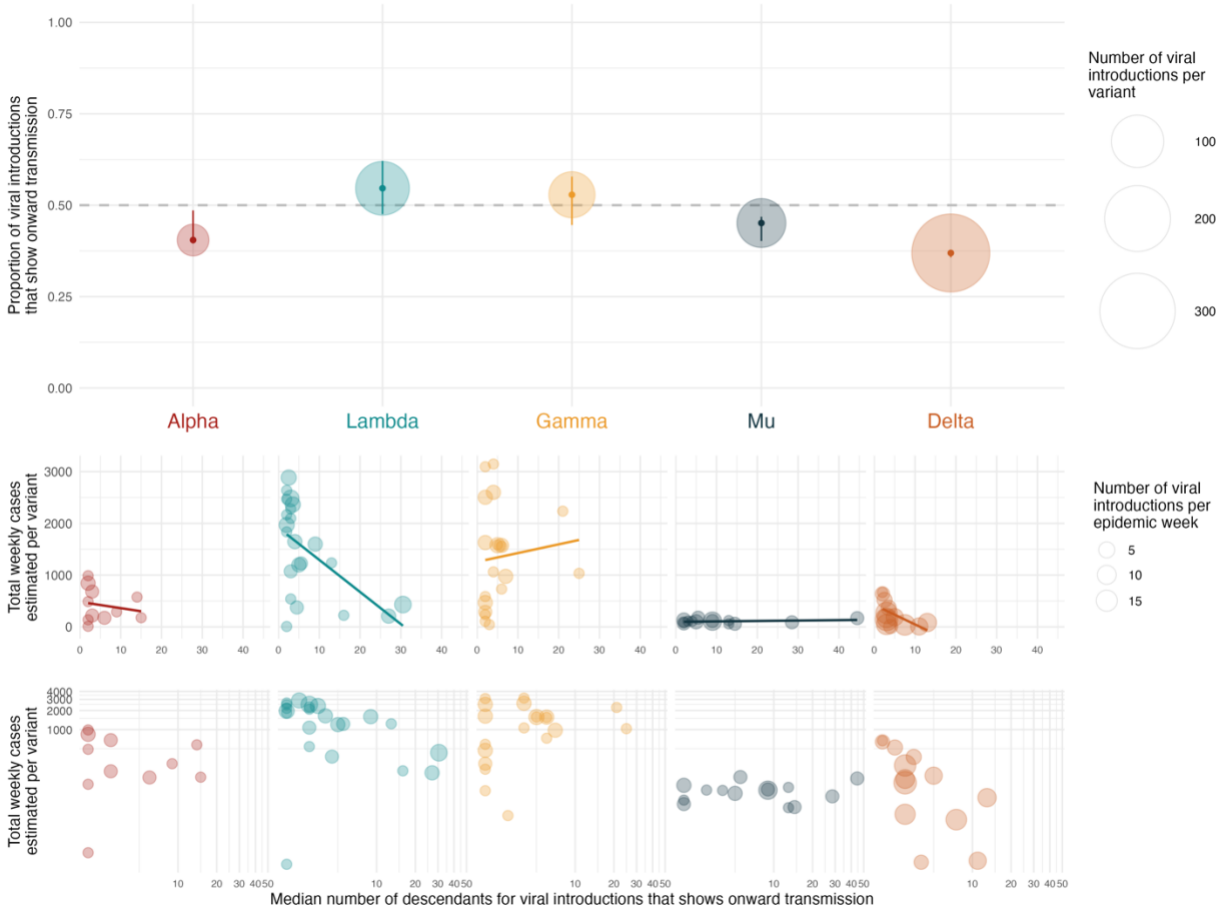

Figure S3. Onward transmission following viral introductions in Chile. *The upper panel shows the proportion of viral introductions that show onward transmission (i.e., importations that leave two or more descendants, also described as transmission lineages) per variant. The middle and lower panels show the median number of descendants of transmission lineages introduced into Chile during each epidemiological week in our study and the numbers of cases attributed to that variant in the same epidemiological week (raw counts in the middle panel and log-transformed estimates in the lower panel). The numbers of importations on each panel are shown by circle sizes; the upper panel shows the total number of importations (regardless of whether these resulted in detectable onwards transmission or not) and the middle and lower panels show the number of importations that did result in detectable onwards transmission per epidemic week.*

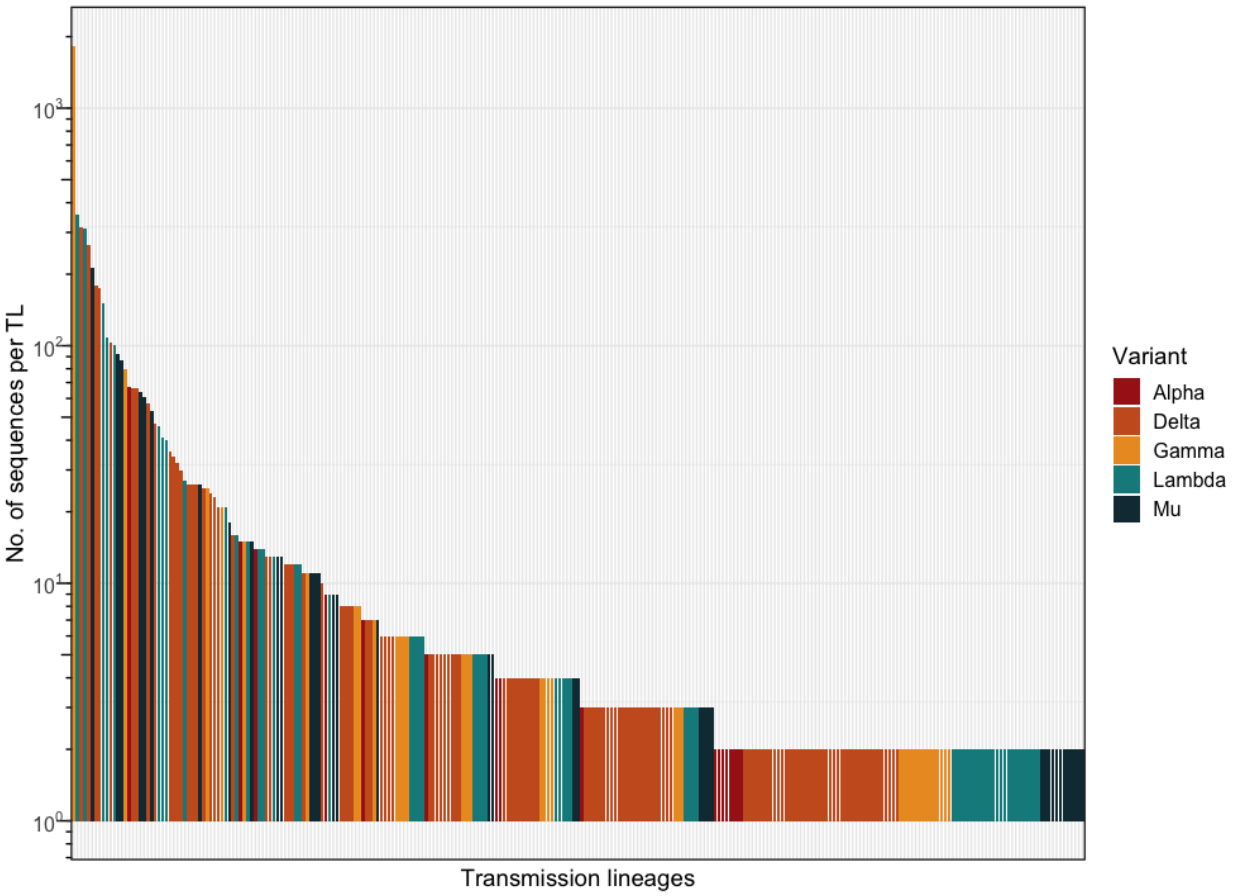

Figure S4. Distribution of transmission lineage sizes. *Distribution of the number of sequences in each transmission lineage inferred from genomic data (includes singleton, i.e. transmission lineages with n = 1 taxa) in Chile coloured by variant. Number of taxa shown on a logarithmic scale.*

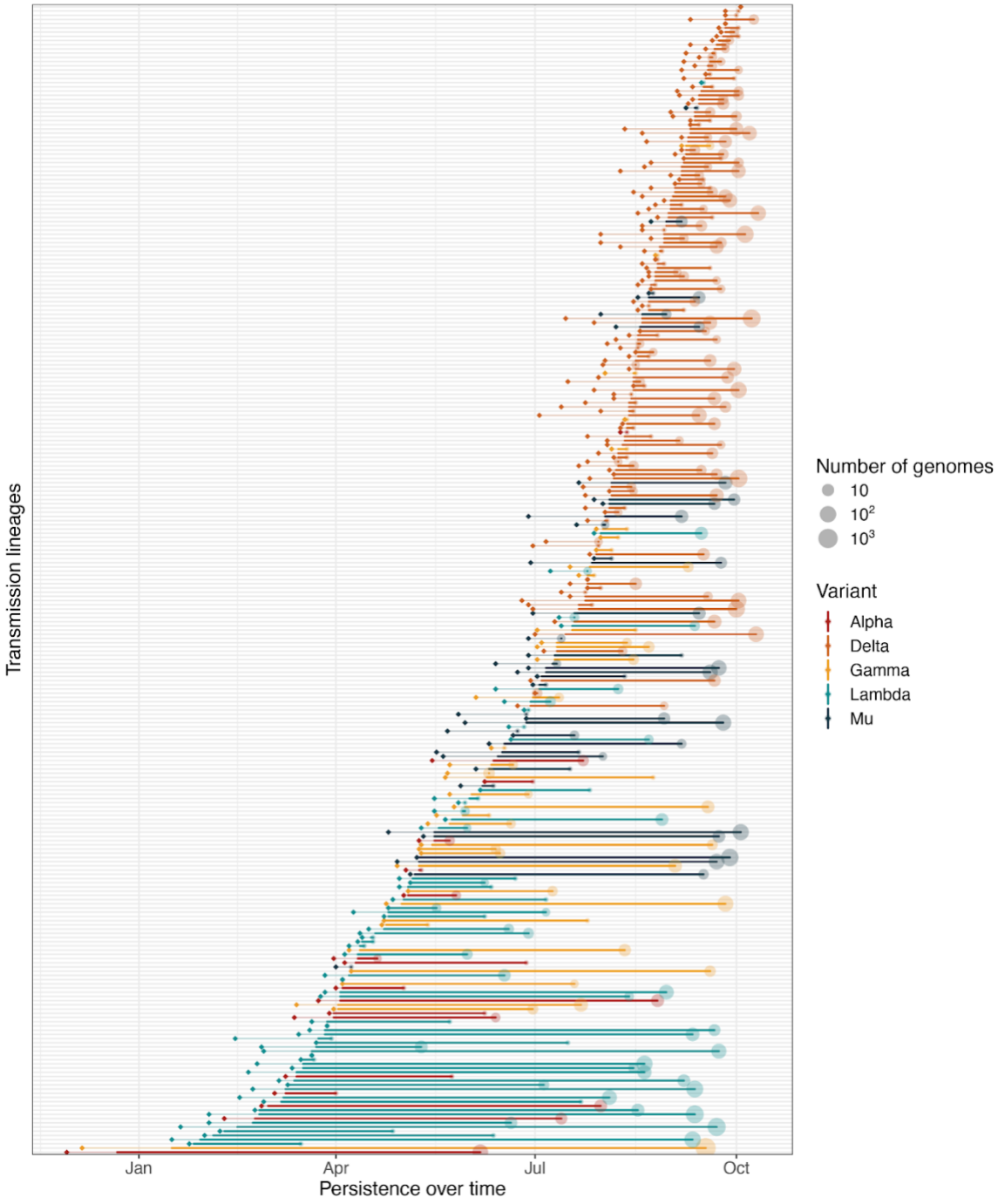

Figure S5. Transmission lineage TMRCAs and persistence over time. *Rows show individual transmission lineages (singletons excluded, i.e. transmission lineages with n = 1 taxa) plotted over the time when they were detected and circulating in Chile. Solid lines show the detection period (time lapse between the collection date of the earliest sequence, referred to as 'first detection', and the collection date of the most recent sequence, referred to as 'last detection'). Faded lines show the detection lag period (time lapse between the inferred transmission lineage TMRCA, shown as diamonds, and the date of first detection). Size of circles on the date of last detection shows the number of sequences for that transmission lineage.*

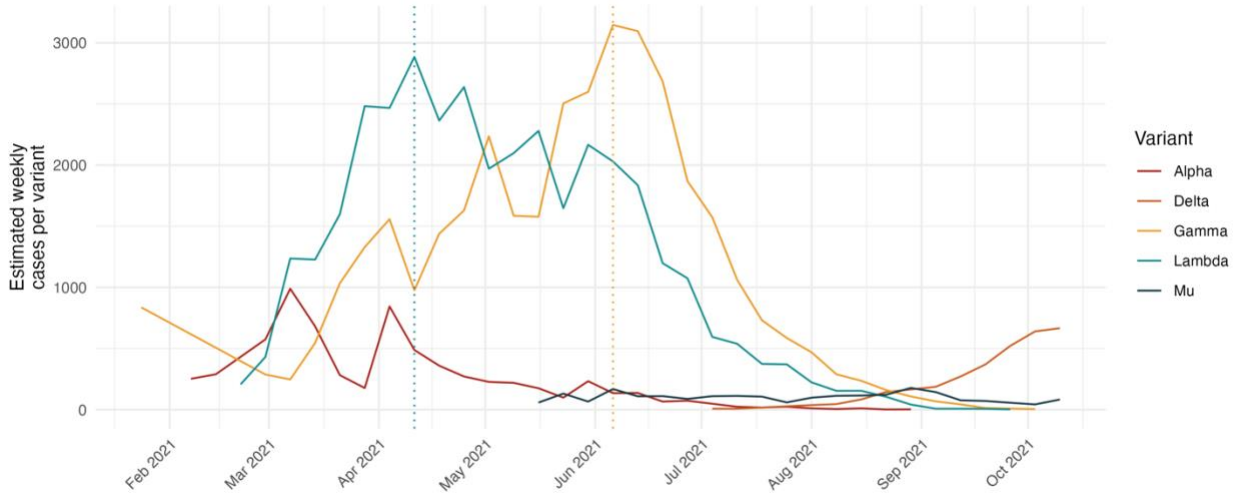

Figure S6. Epidemiological trends of different SARS-CoV-2 variants in Chile. *Number of cases per epidemiological week for each variant is estimated by multiplying the reported cases by the proportion of genome sequences attributed to that specific viral variant from the ISP community surveillance genomic data. Epidemic peaks in 2021 can be predominantly attributed to Lambda cases (April 11) and Gamma cases (June 6), indicated by the dotted vertical lines.*

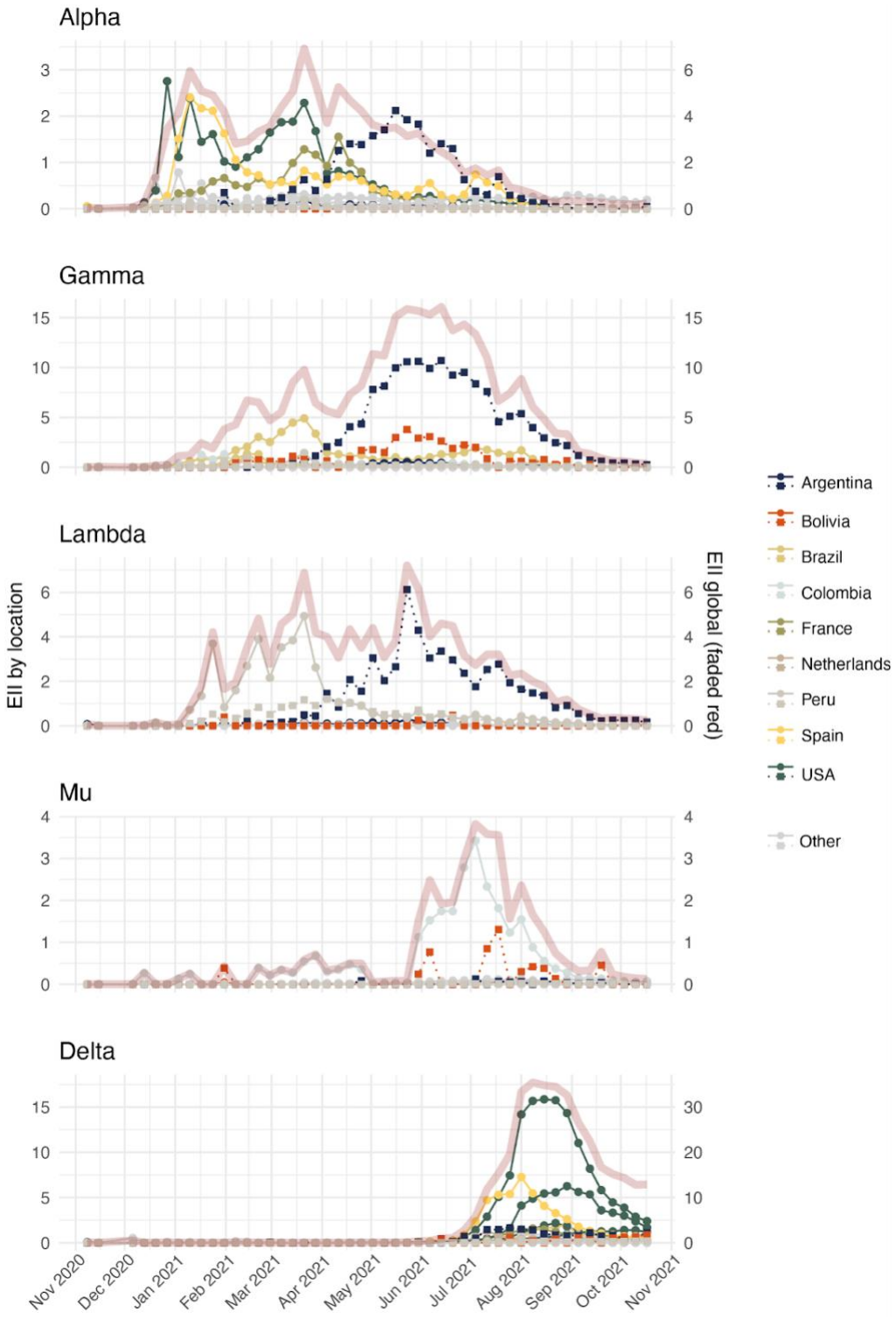

Figure S7. Estimated importation intensity (EII) indices over time. *Time series for the weekly estimated importation intensity (EII) indices from selected states and countries related to Figure 2C. Solid lines with circles show EIIs based on air travel volume (aEII) and dashed lines with squares show EIIs based on land border crossings (lEII). Broad red lines show the combined global EII.*

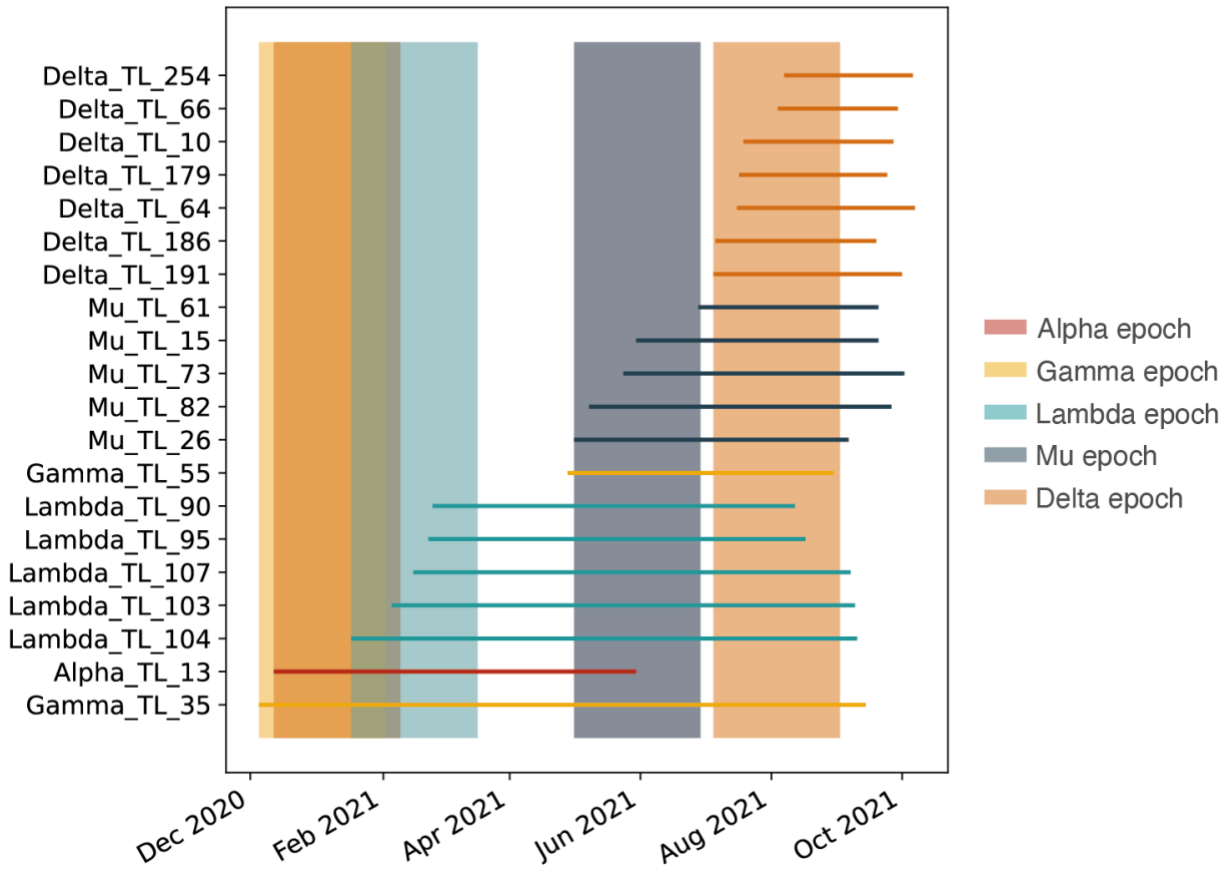

Figure S8. Time of arrival epochs. *Importation dates of the 20 largest SARS-CoV-2 transmission lineages in Chile coloured by variant. Coloured bars show the epoch over which mobility estimates were used to evaluate their effect on viral spread, depending on the dates of the first importation of each variant.*

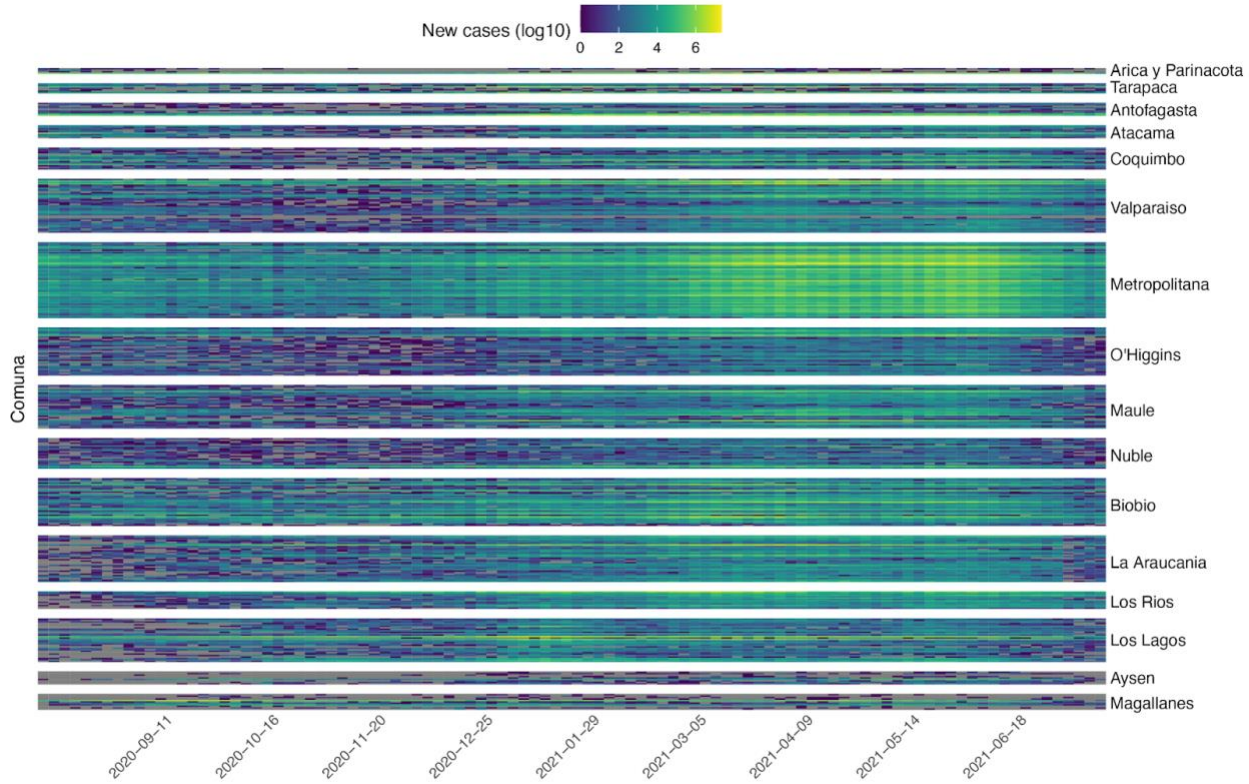

Figure S9. Reported new cases per comuna in Chile. *New cases reported across Chile. Values correspond to dates when epidemiological reports were issued (every 2-4 days_ and do not represent a complete daily time series. Each row represents an individual comuna, and these are grouped by region (Adm1), ordered from north to south.*

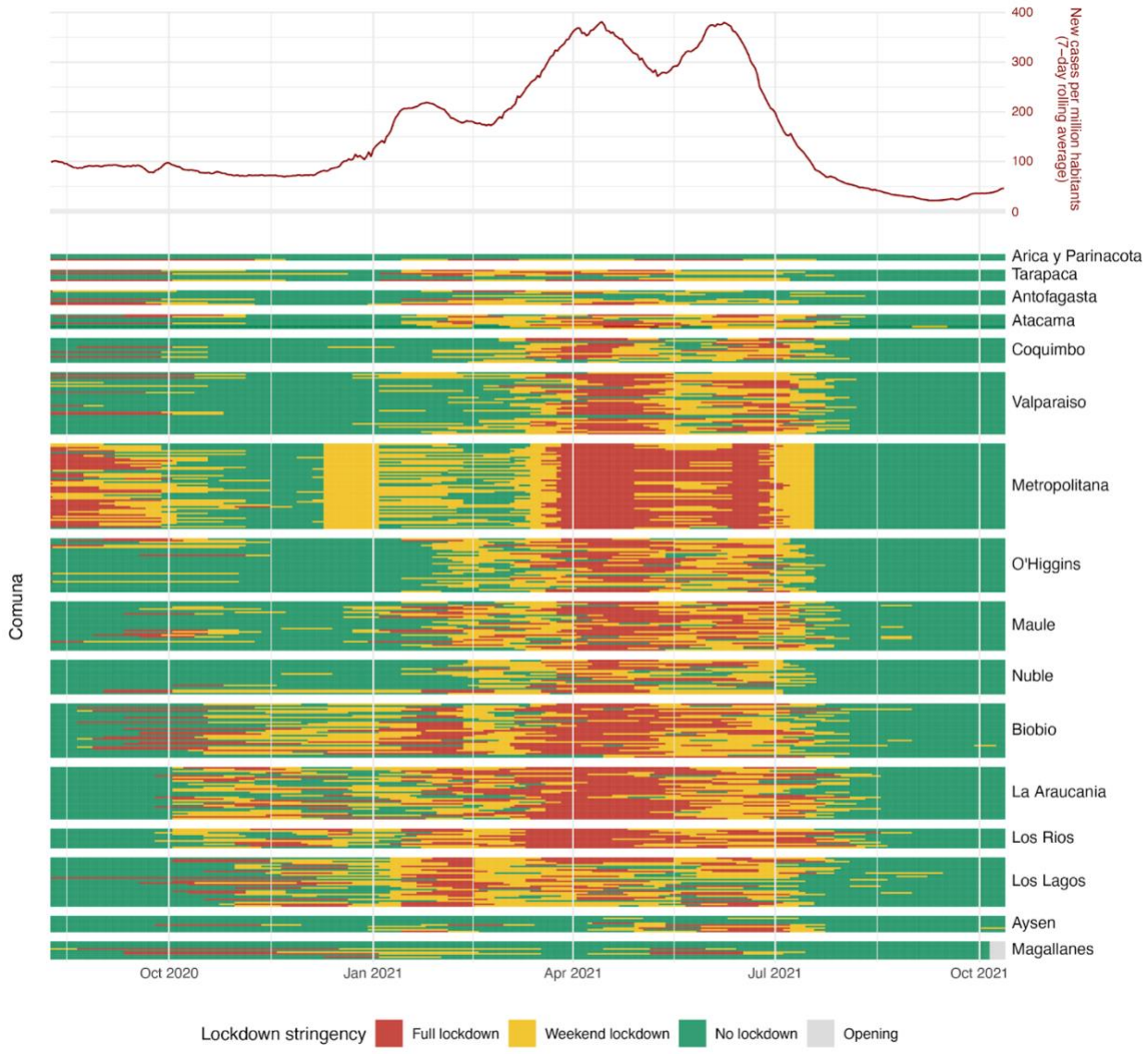

Figure S10. Changes of lockdown stringency in Chile. *Upper panel shows the 7-day rolling average of total new cases in Chile (as reported by Our World in Data). The lower panel shows the daily lockdown stringency based on the number of weeks of the day where mobility restrictions were implemented within the Paso a Paso program. Details about lockdown stringency can be found in the Extended Text S1. Each row represents an individual comuna, and these are grouped by region (Adm1), ordered from north to south.*

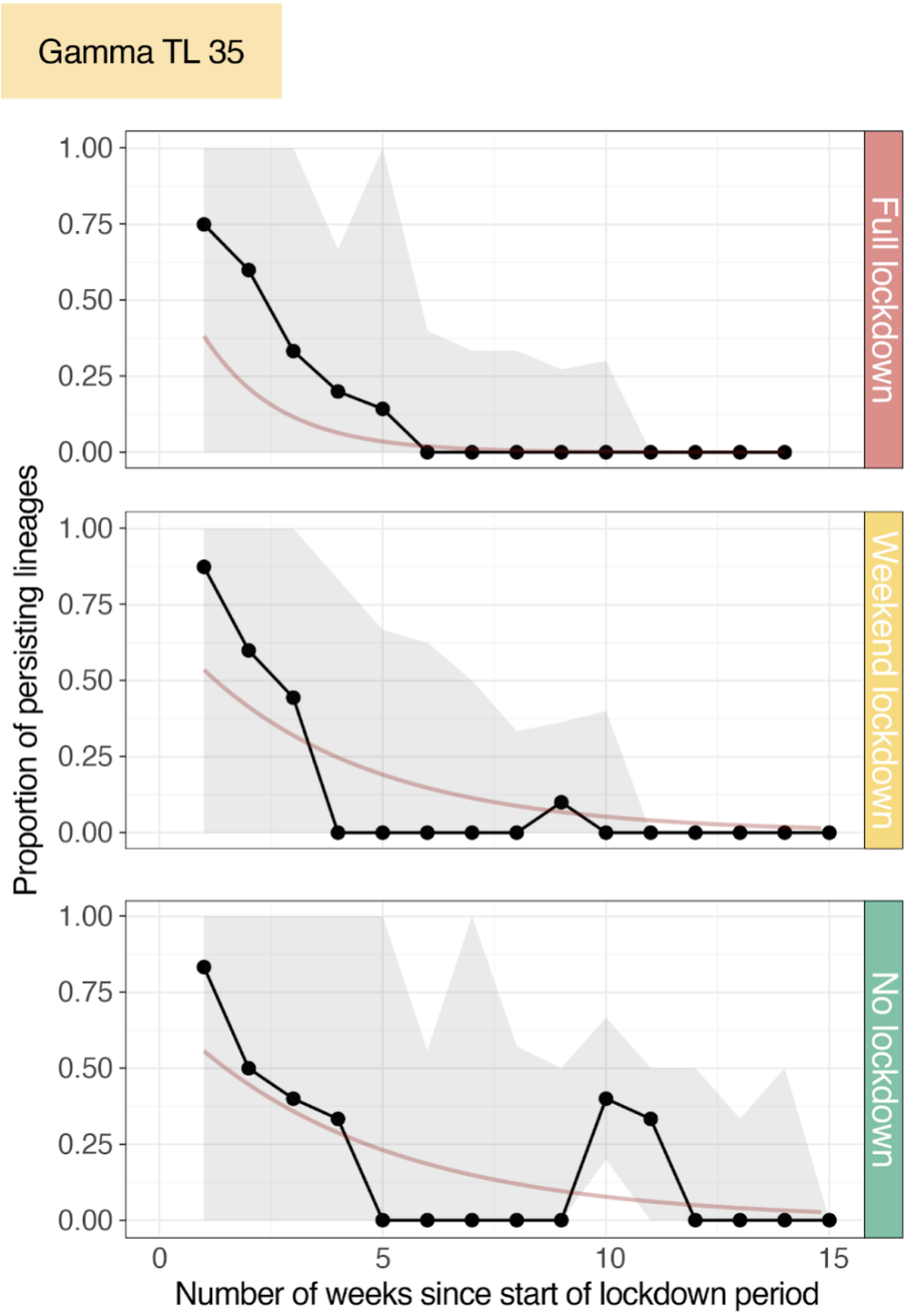

Figure S11. Decay of persisting viral lineages over time. *Proportion of persisting lineages from Gamma TL 35 across the most affected comunas in Chile under different lockdown tiers estimated with PersistenceSummarizer. Persistence was measured on a weekly basis from the start of the lockdown period by calculating the proportion of phylogenetic branches (lineages) that persisted from the beginning of the lockdown. The dark red line shows a fitted exponential function to the median estimates of the persisting lineage proportions. Observations are aggregated over the fourteen comunas with the highest number of viral movements in our data set.*

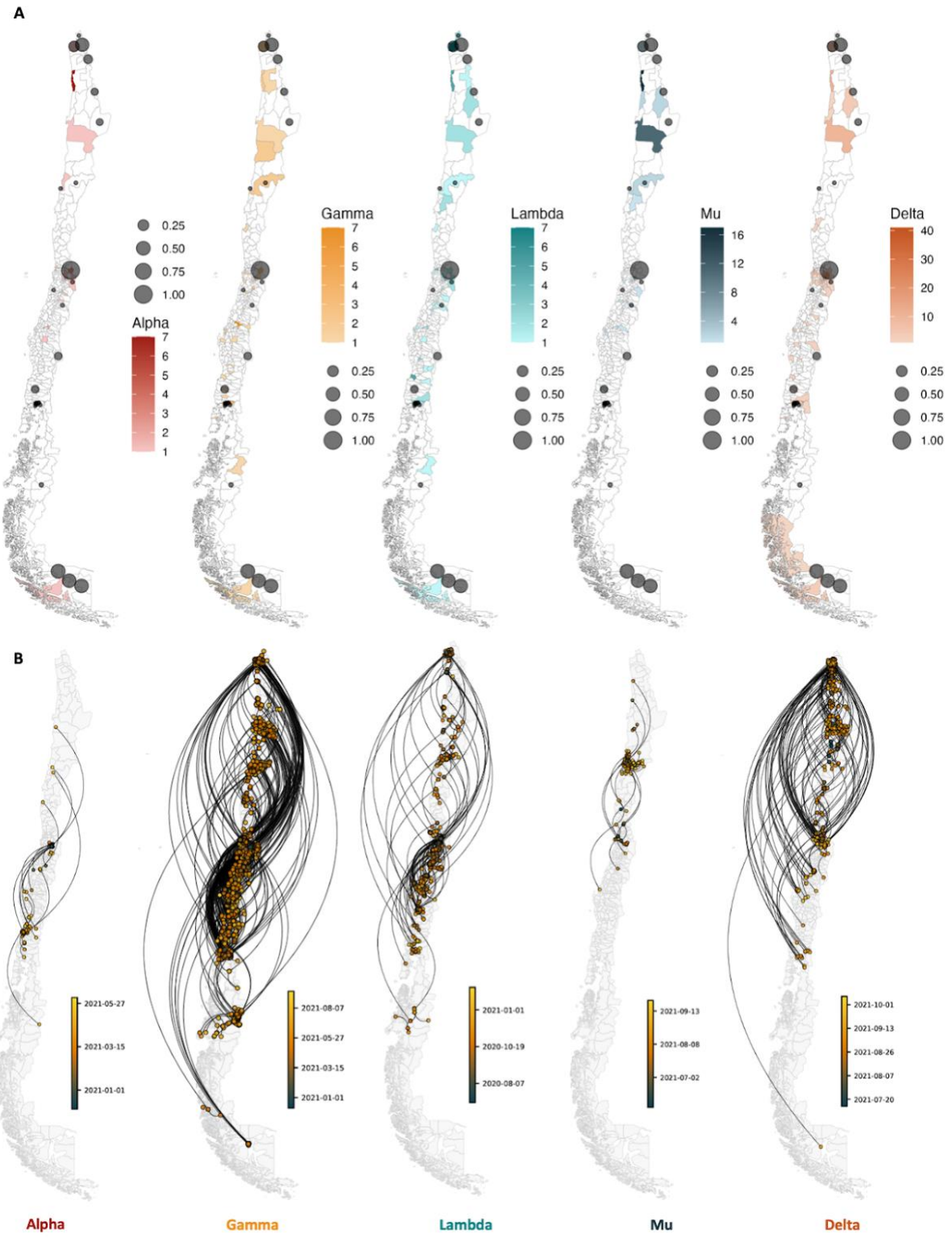

Figure S12. Number of first detection of SARS-CoV-2 introductions into Chile. *Maps show the number of first detections of viral introductions (i.e., location of singletons and earliest sequences for each transmission lineage inferred from genomic data) by comuna (adm3) in Chile. Grey circles show the comunas where the main land border crossings in Chile are located, the radius shows the proportion of crossings that go through each one of these land border crossings.*

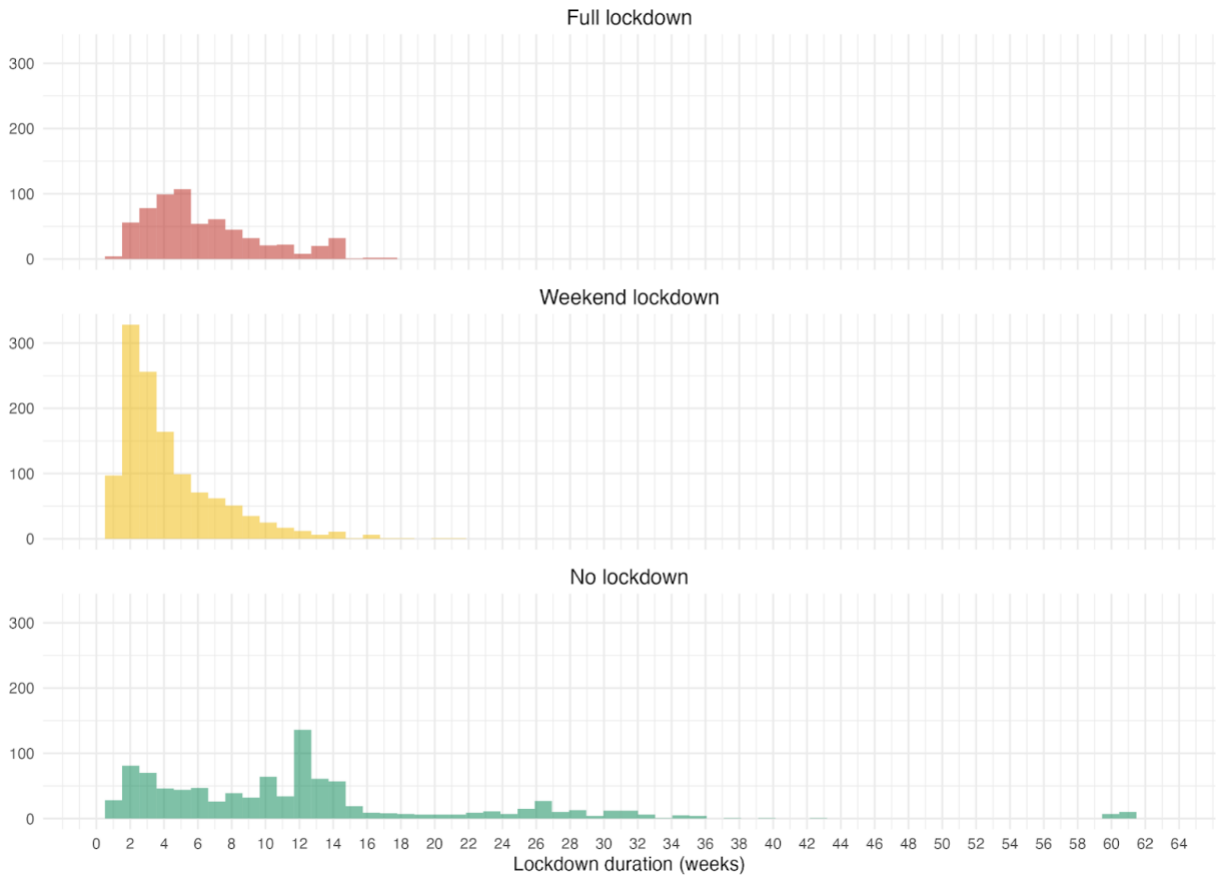

Figure S13. Duration of lockdown tiers in Chile. *Distribution of the continuous number of weeks for which each lockdown tier was implemented. Every individual observation corresponds to a change of lockdown stringency tier in a single comuna, and the number of weeks is counted from the start of that stringency tier to the next change in the stringency tier for that comuna.*

Supplementary references

1. N. C. Bronfman, P. B. Repetto, N. Guerrero, J. V. Castañeda, P. C. Cisternas, Temporal evolution in social vulnerability to natural hazards in Chile. *Nat. Hazards* **107**, 1757–1784 (2021).

2. M. de S. de Chile., Aprueba Proyecto de Vigilancia Genómica de SARS- CoV-2. Ordinario Res.Ex. N°403 (2021).

3. C. L. Gobierno de Chile, Actualización de la Estrategia Gradual "Paso a Paso nos cuidamos" (2021) (June 23, 2023).