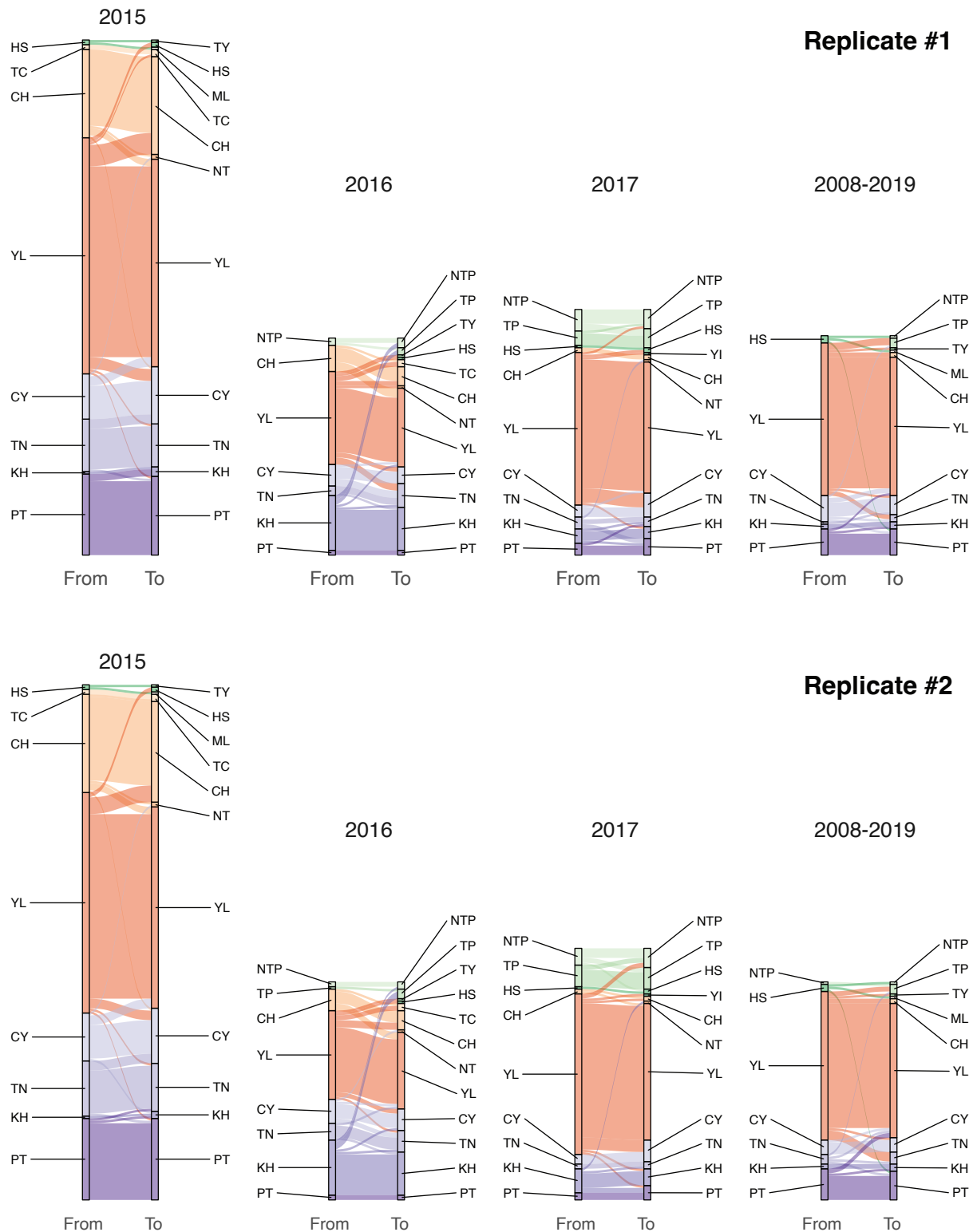


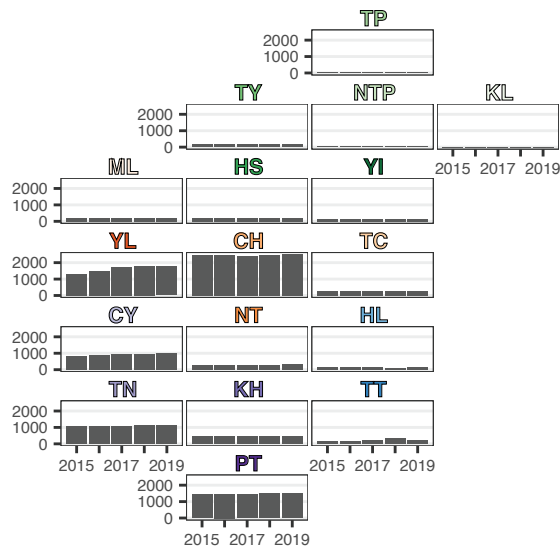
From emergence to endemicity of highly pathogenic H5 avian influenza viruses in Taiwan

Supplementary Information

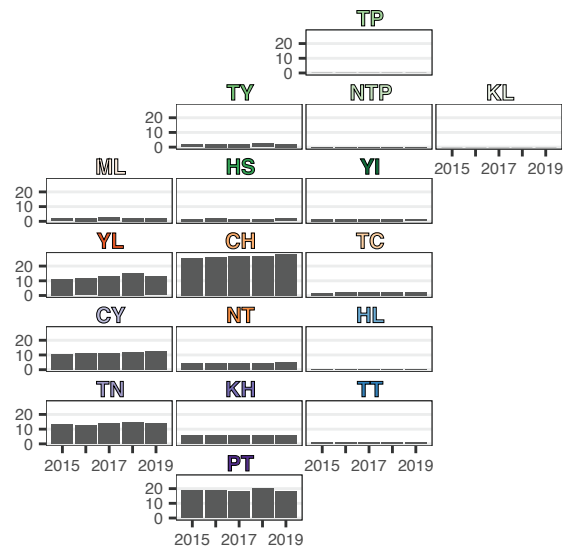


Supplementary Figure 1. Visualisation of the dispersal pattern of the clade 2.3.4.4c virus in discrete geographical divisions. The connected lines represent branches inferred by the continuous phylogeographic approach (see Figure 3), with origin and destination locations determined as county or city-level divisions. The lines were coloured based on the origin. Replicated results from parallel runs are shown.

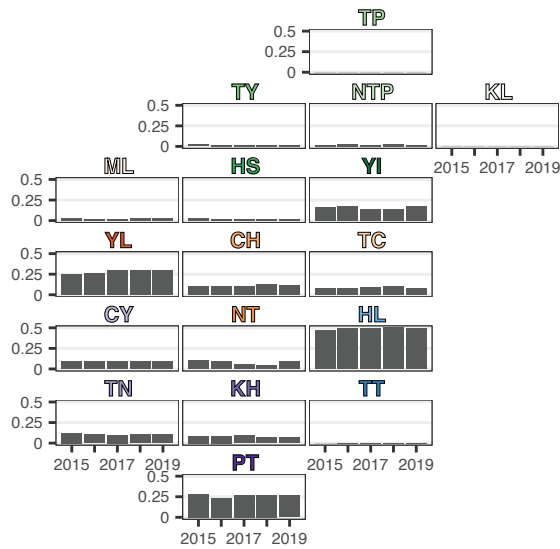
A Poultry farm



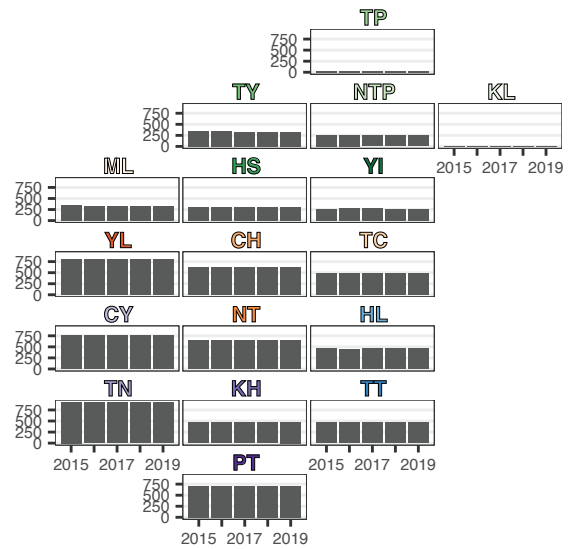
B Poultry population (10⁶)



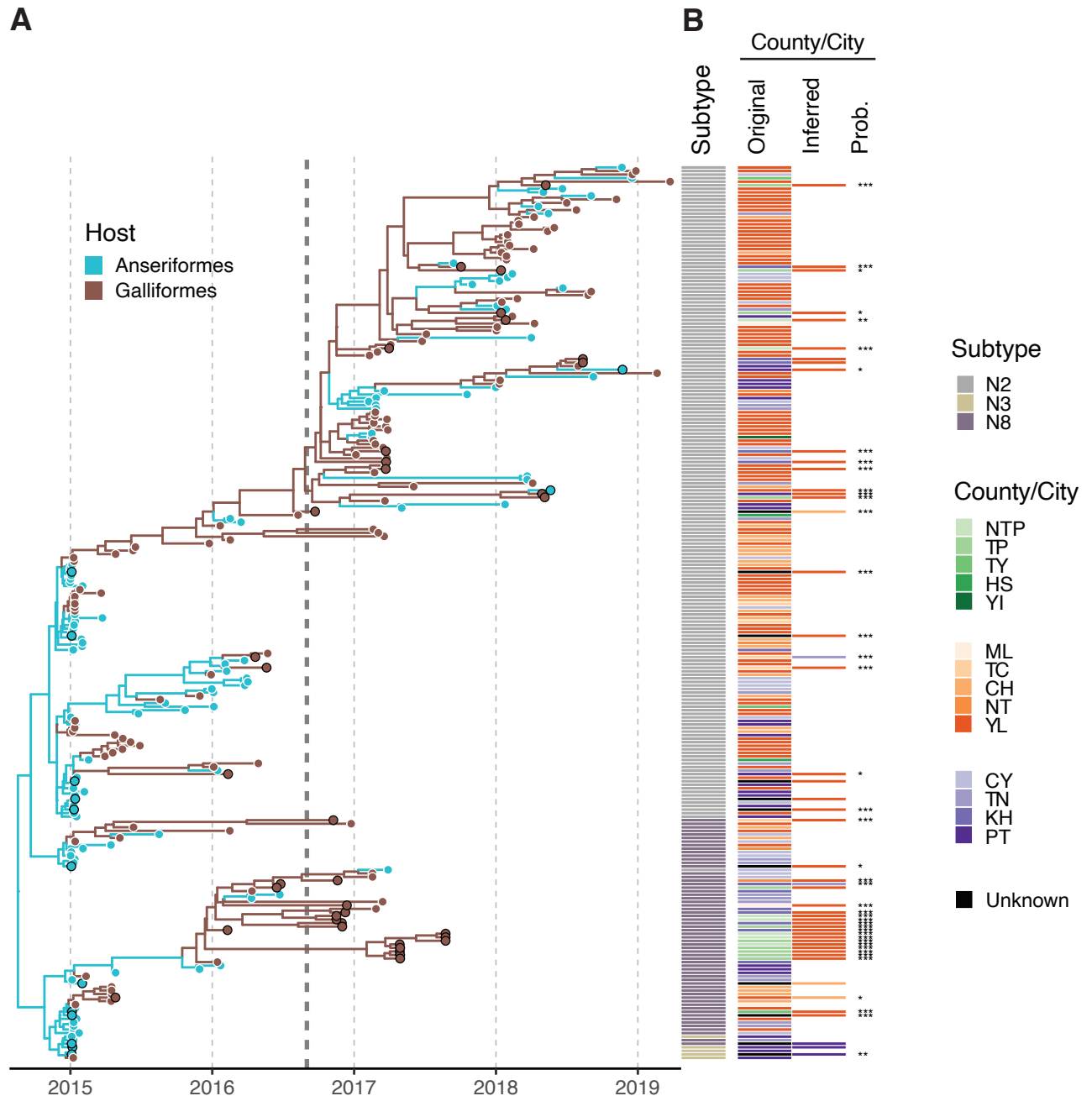
C Poultry heterogeneity



D Cropland area (km²)



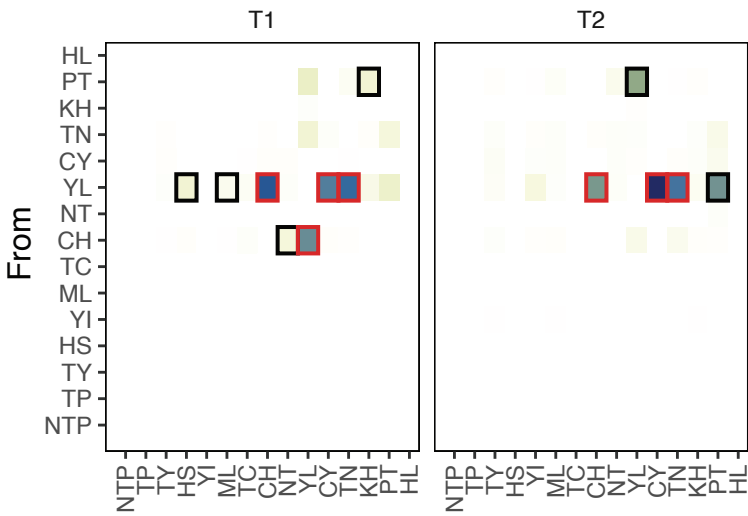
Supplementary Figure 2. Agricultural characteristics of county or city-level administrative areas in Taiwan.



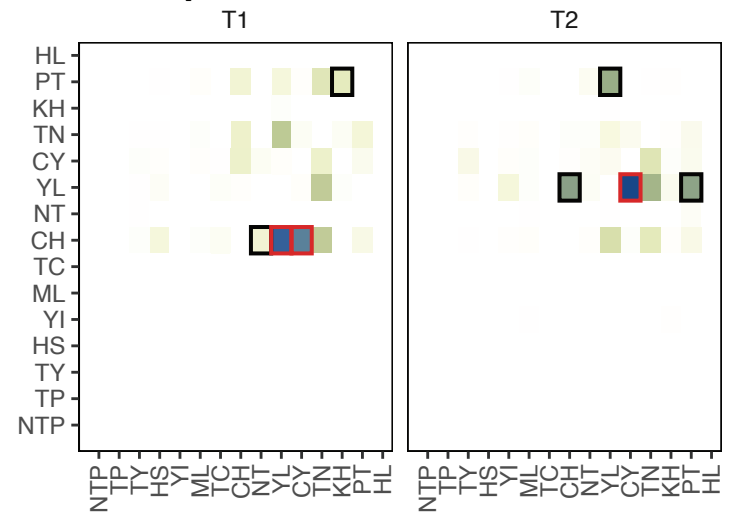
Supplementary Figure 3. Summary of the host and geographical information associated with the genomic data used in this study. (A) The time-scaled phylogeny was reconstructed using the HA genes of the clade 2.3.4.4c virus in Taiwan. The tips on the phylogeny are colored according to the host genera, Galliformes (chicken, turkey and quail) or Anseriformes (duck and goose), logged in the sequence metadata. The branches are colored according to the states inferred on the summarized maximum clade credibility (MCC) tree. The tips with black borders indicate taxa that have uncertain state assignments in geographical analyses. The vertical dashed line denotes September 1st, 2016. (B) The adjacent heatmap shows the NA subtypes and the corresponding collection locations of the tree taxa. The discrete diffusion model was used to estimate the uncertain geographical locations and posterior probabilities. Only the results of samples collected in slaughterhouses/rendering factories and samples lacking geospatial information, which were implemented with state uncertainty, are shown in the 'Inferred' column. The symbols *, ** and *** denote posterior probability > 0.7, 0.8 and 0.9, respectively.



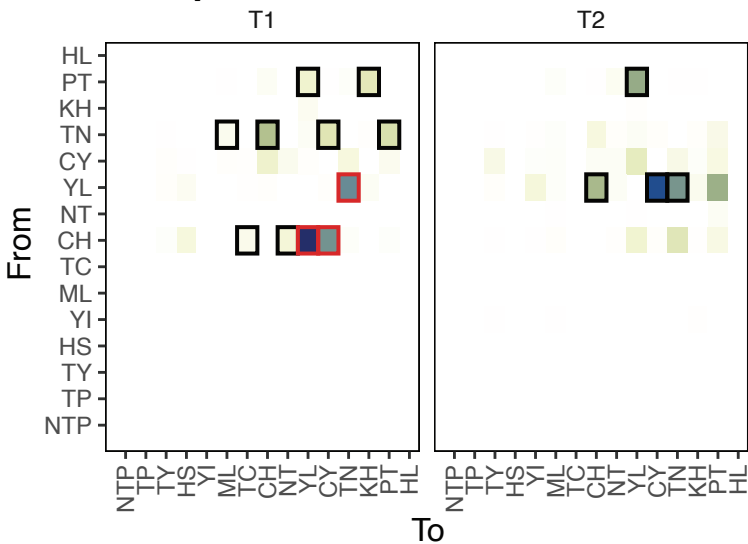
A Full data set



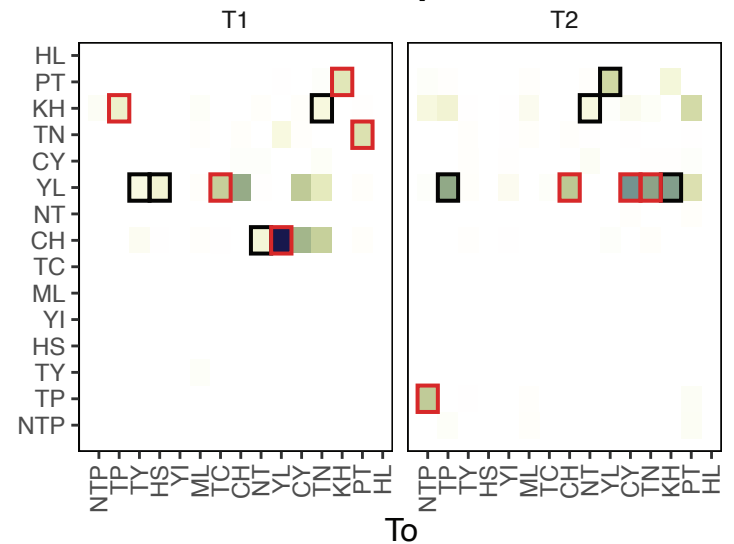
B Subsampled 1



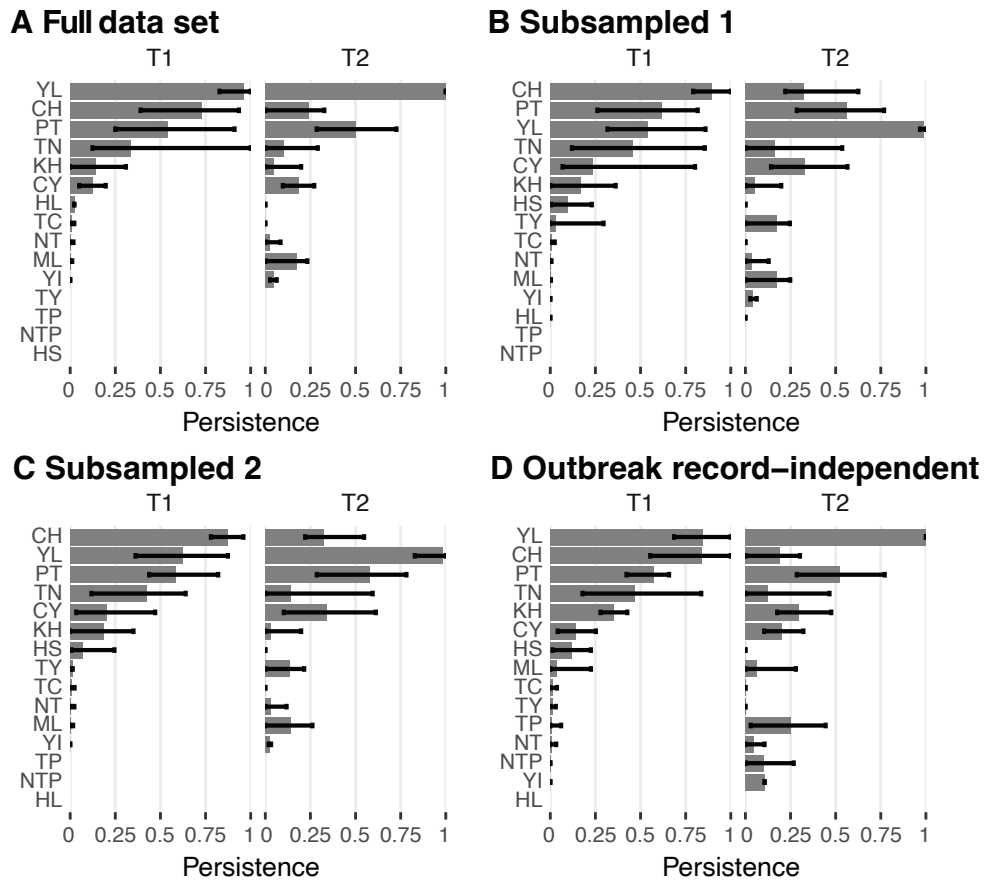
C Subsampled 2



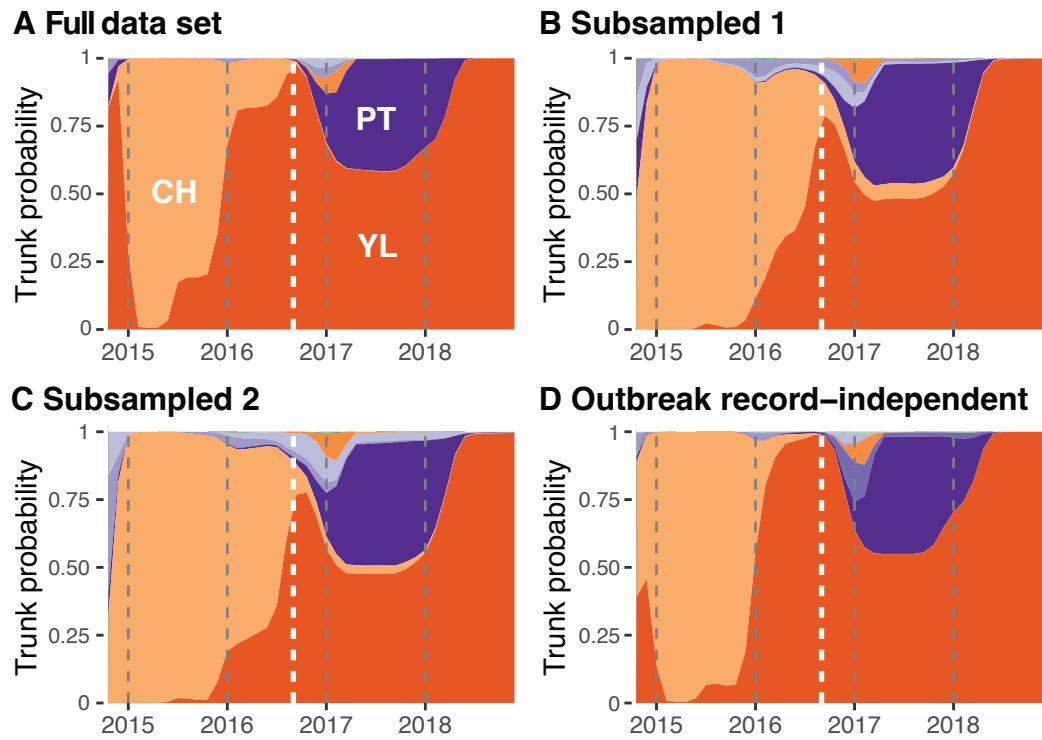
D Outbreak record-independent



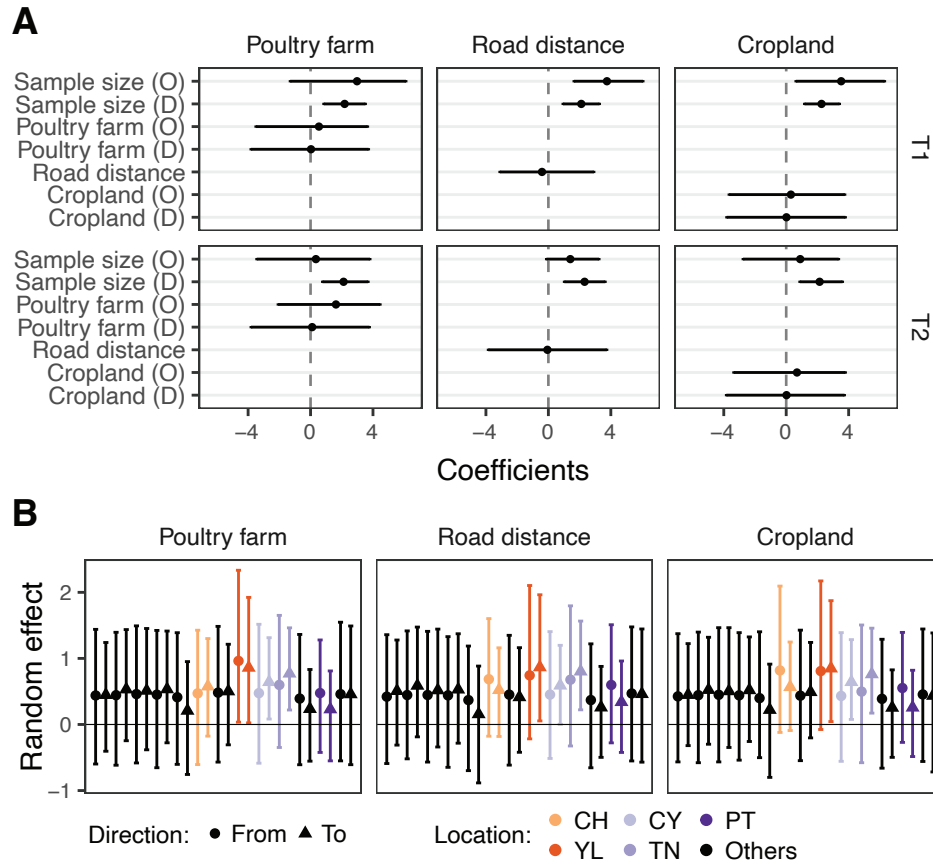
Supplementary Figure 4. Estimated number of transition events between counties/cities in Taiwan inferred by the discrete phylogeographic method. The color of the heatmap reflects the proportions of between-locations Markov jumps to the total jumps in the distinct time period. The directions supported by Bayesian factor (BF) are highlighted by black (>20) or red (>150) edges. Results of a full genomic data set (A), along with two data sets with reduced samples from county YL are shown (B and C). Using the same genomic data as panel (A), Bayesian inference was performed for panel (D) with geographical states assigned independently of outbreak records. The locations were determined by the sequence metadata if available, or using a uniform prior over all isolated counties/cities if the collection site was unknown.



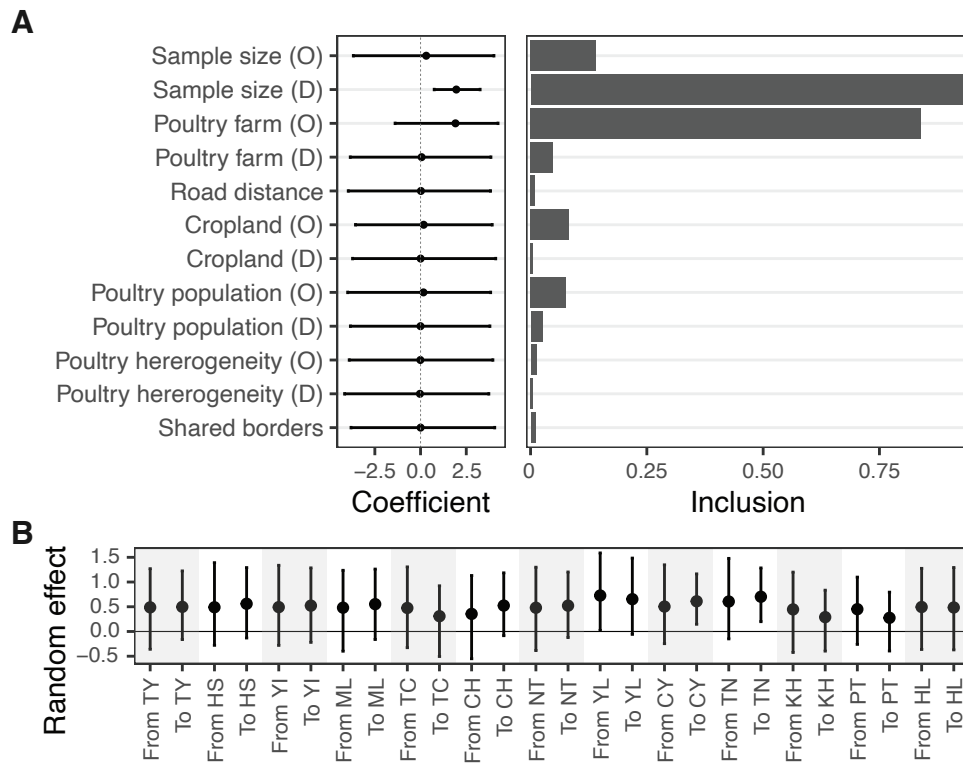
Supplementary Figure 5. Persistence of the virus assessed by the discrete phylogeographic method. To calculate the value for each location, the branch length was unified from branches where both nodes were estimated to share the same state. The unified time interval was presented as a proportion divided by the time span of T1/T2. The mean and 95% HPD of the proportions summarized by 1000 posterior trees are indicated by the bars. The results of the four panels were obtained from the same MCMC runs as the corresponding panels in Supplementary Figure 4.



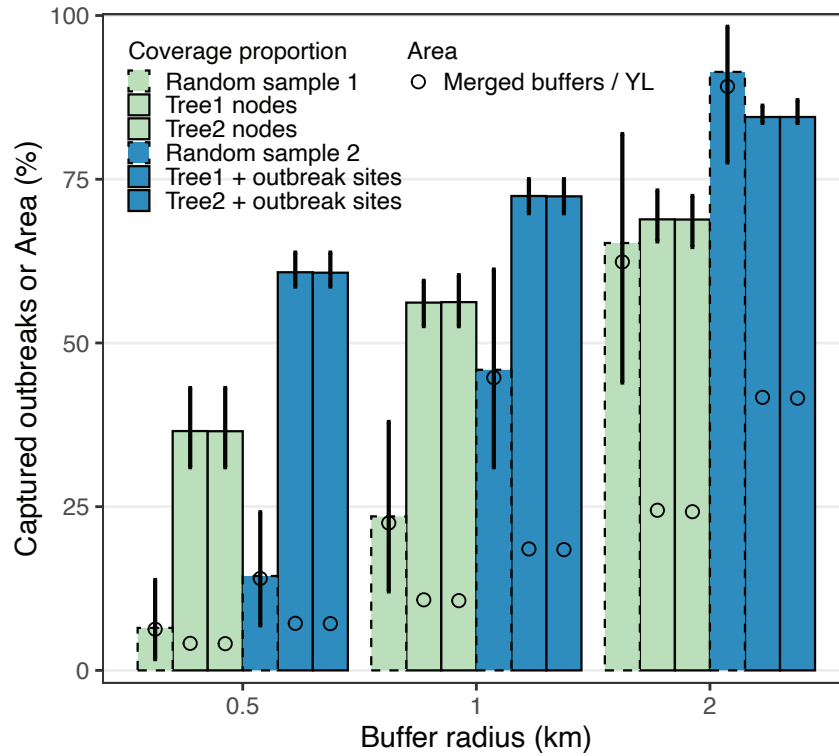
Supplementary Figure 6. Inferred trunk locations of Taiwan clade 2.3.4.4c phylogenies through time in different genetic data sets (A-C) or with a simple geographic state assignment scheme (D). The proportions at each time point indicate the posterior support for viruses circulating in a particular county/city occupying the trunk of the tree. The areas are colored using the same scheme as Figure 2. The white dashed lines indicate the boundary of T1 and T2, September 1st, 2016.



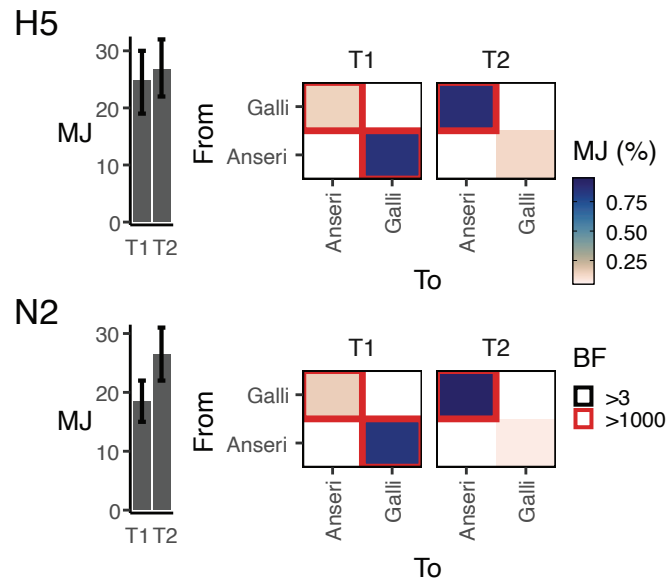
Supplementary Figure 7. Evaluating predictors in reduced models of time-heterogeneous phylogenetic GLM. (A) The conditional effect sizes in models containing respective predictors. The predictor names are denoted by O in parentheses for origin and D for destination. (B) Location-specific random effects in the three models, with high incidence areas colored. The estimates are in log space and presented as mean with 95% HPD interval.



Supplementary Figure 8. Evaluating predictors in a time-homogeneous model. (A) The conditional effect sizes and the inclusion probabilities of predictors estimated by the conventional phylogenetic GLM models. The predictor names are denoted by O in parentheses for origin and D for destination. (B) Location-specific random effects in the GLM model. The estimates are in log space and presented as mean with 95% HPD interval.



Supplementary Figure 9. Impact of buffer radius on evaluating the re-emergence of new outbreaks in county YL. The estimated locations of tree nodes using the continuous phylogenetic method during T2, combined with or without contemporary outbreak sites, served as central points to create buffers with different radius distances on the map. The proportion of new outbreak sites covered by the buffer areas was calculated for each posterior tree. These outbreak sites were reported between 2019 and 2022, after the latest available genetic data. Null models were created by randomly distributing sites in YL with the same number of tree nodes (Random sample 1, green) or tree nodes plus outbreak sites (Random sample 2, blue). The bars show the mean values of two parallel continuous phylogeographic analyses each with 1000 posterior trees, and null models. Error bars indicate 95% credible intervals. The open circle in each bar represents the ratio of the area of merged buffers to the area of YL.



Supplementary Figure 10. Diffusion between host groups. Markov jumps (MJ) and Bayes factors (BF) were estimated by the discrete phylogenetic method. Total MJ counts in different time spans are shown on the left. The heatmaps present the jumps as proportions to the total counts. Anseri refers to the Anseriformes genus and Galli refers to the Galliformes genus. Results based on both HA (H5) and NA (N2) are shown.

Supplementary Table 1. Selection pressure for the surface proteins of H5 avian influenza lineages in Taiwan.

	H5		N2	
	GsGd Clade 2.3.4.4	North American	GsGd Clade 2.3.4.4	North American
dN/dS (ω) (95% CI)	0.204 (0.180-0.230)	0.207 (0.174-0.245)	0.355 (0.316-0.397)	0.233 (0.192-0.279)
Pervasive positively selected sites	131	-	77	-
Episodic positively selected sites	131, 387, 403, 545	17, 102, 137, 155, 317	77, 313, 416, 439	5, 6, 261, 307
No. of fixed sites among selected sites	0	0	0	0

Supplementary Table 2. List of database accession numbers from GenBank and GISAID.

	accession no.	strain name
1	MW333030	duck/Nantou/15A03445-11-20T/2015
2	MW333038	chicken/Changhua/15010120-1/2015
3	MW333046	chicken/Changhua/15010288/2015
4	MW333054	chicken/Changhua/15010324-2/2015
5	MW333062	chicken/Changhua/15010361-1/2015
6	MW333070	chicken/Changhua/15010362-2/2015
7	MW333078	chicken/Changhua/15010363-2/2015
8	MW333086	chicken/Changhua/15040036-1/2015
9	MW333094	chicken/Changhua/15040043-1/2015
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234	KU646885	goose/Taiwan/01031/2015
235	KU646893	goose/Taiwan/01040/2015
236	EPI961922	chicken/Taiwan/u7/2016
237	EPI961933	chicken/Taiwan/x37/2016
238	KP714479	goose/Taiwan/01-003/2015
239	KP714480	goose/Taiwan/01-004/2015
240	KP714481	goose/Taiwan/01-042/2015
241	MW334254	duck/Tainan/16010024-1/2016
242	MW333318	chicken/Kaohsiung/16MB0889/2016
243	MW333638	chicken/Taipei/16060023-1/2016
244	MW333670	chicken/Taipei/17050007-2/2017
245	MW333438	chicken/New_Taipei_City/17090002/2017
246	KU646909	chicken/Taiwan/01174/2015
247	MW334558	goose/Chiayi/18020014-3/2018
248	MW334766	goose/Yunlin/18030020-1/2018
249	MN988773	chicken/Taiwan/A3/2019
250	MN988805	chicken/Taiwan/D9/2019
251	KT388452	goose/Taiwan/TNC2/2015
252	KT388476	goose/Taiwan/TNC5/2015
