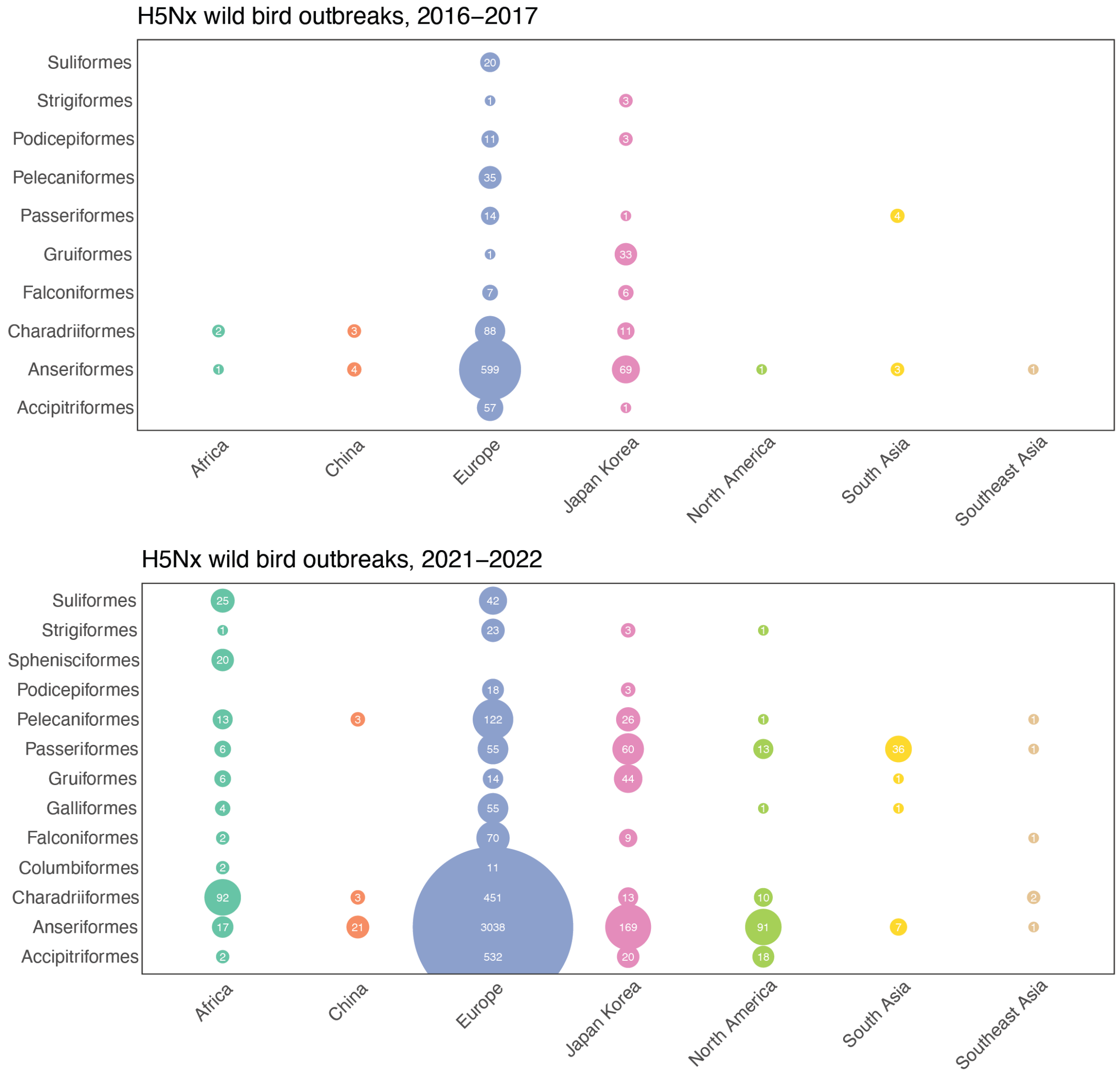
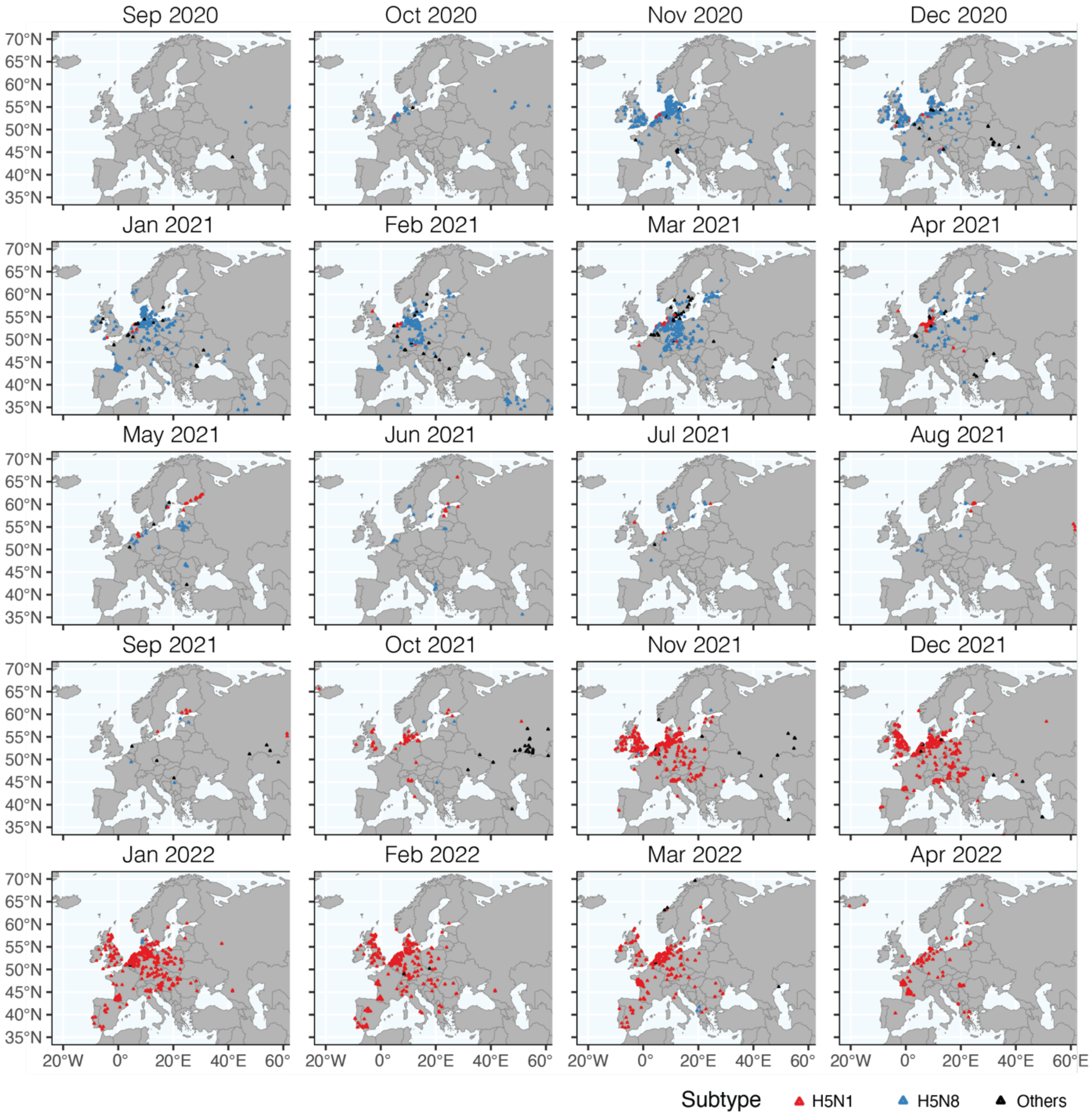
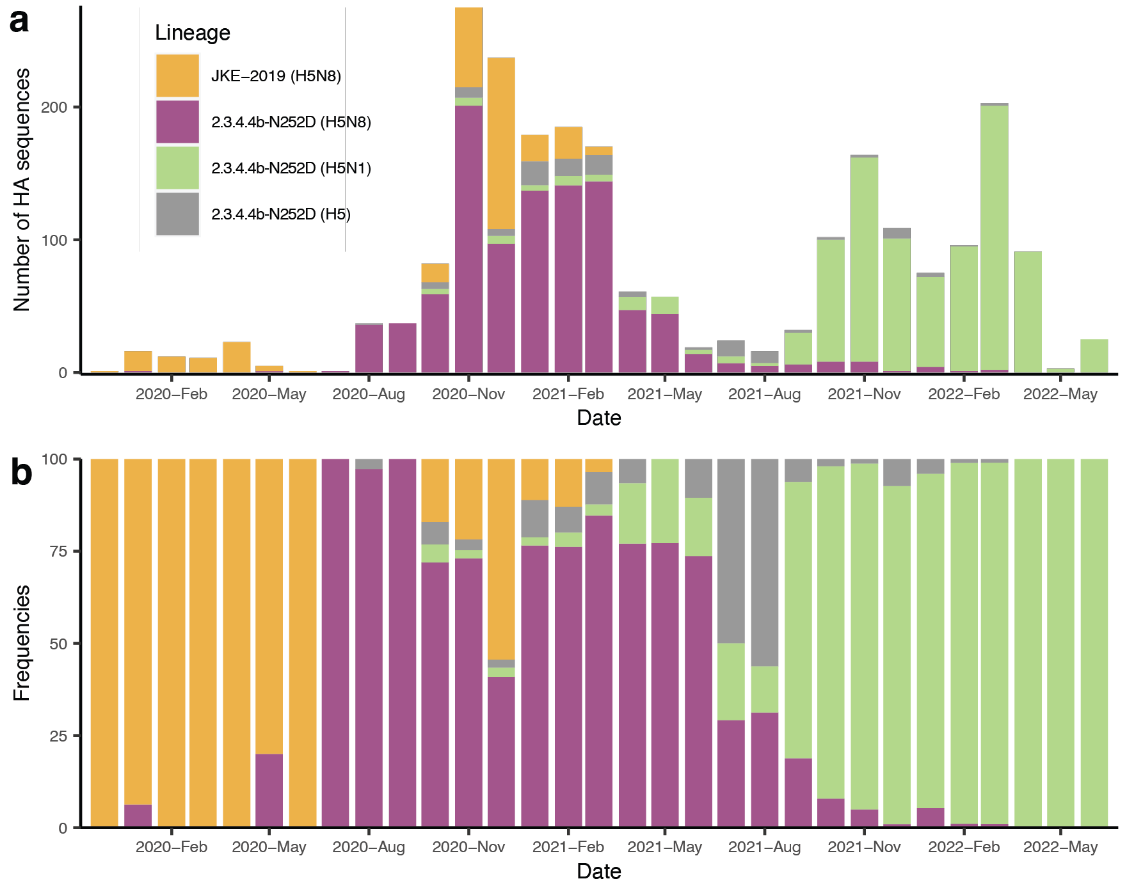


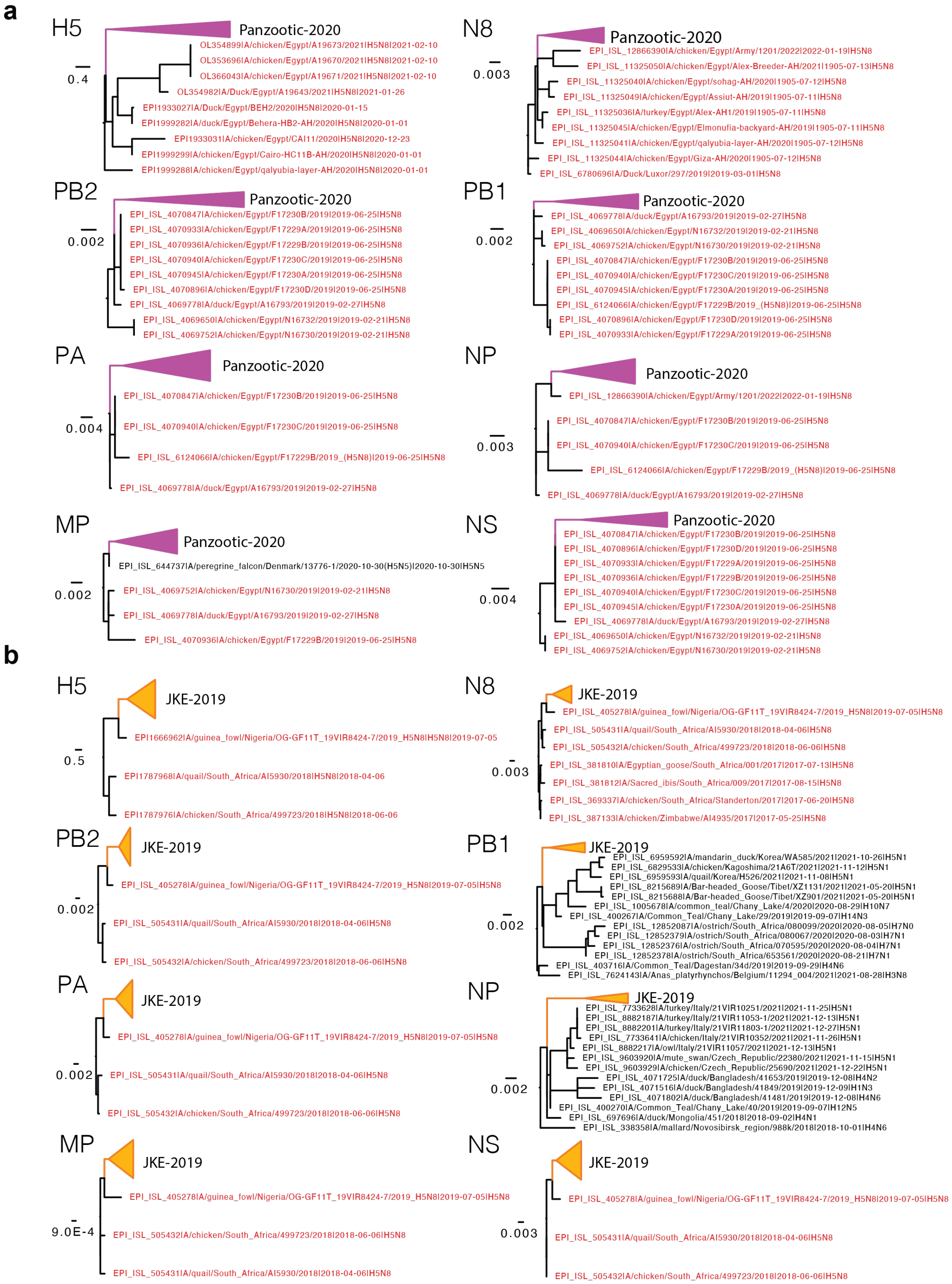
Supplementary Figure 1 | Comparison of affected wild bird species in H5Nx outbreaks between 2016-2017 and 2021-2022.



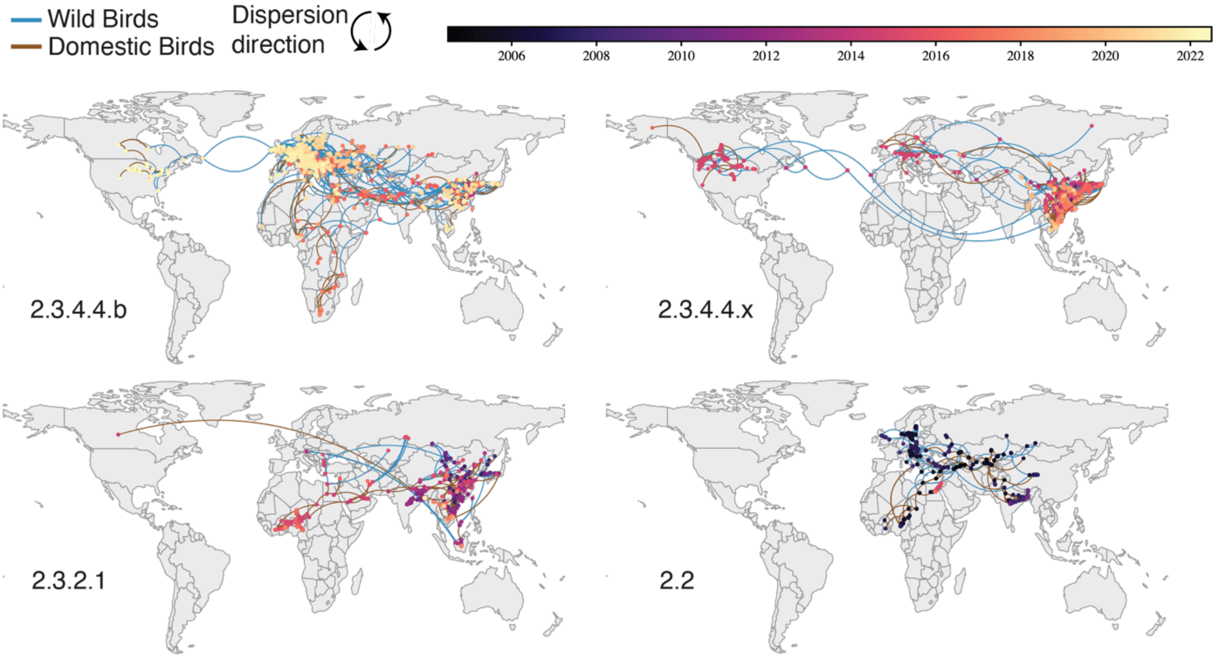
Supplementary Figure 2 | The spatial distribution of FAO outbreaks in Europe during 2020-2022. Dots are colored by subtypes.



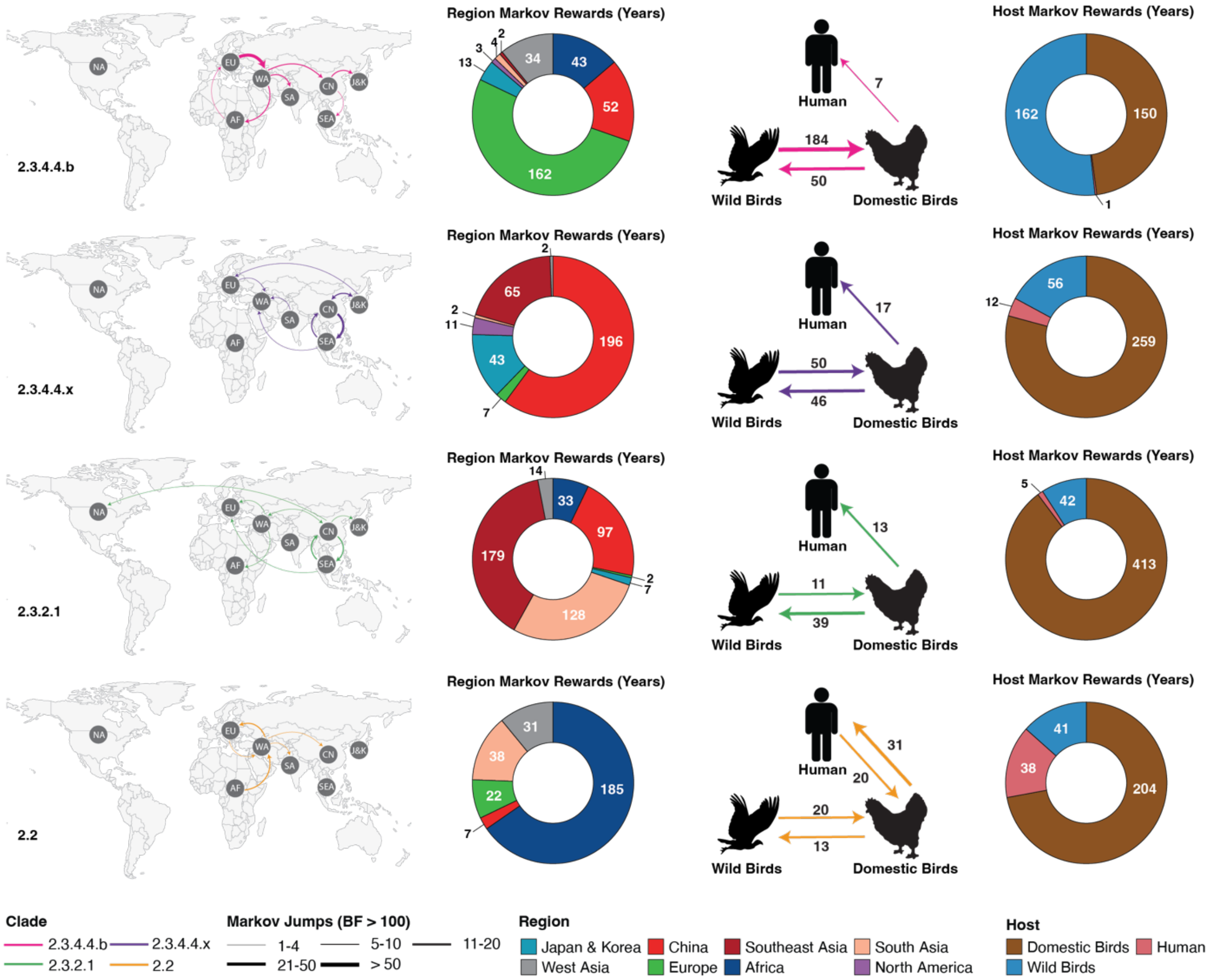
**Supplementary Figure 3 | ** Temporal changes in HPAI H5 lineage predominance. (a) The number of HA sequences colored by lineage since 2020. (b) Proportional lineage distribution by month inferred from (a).



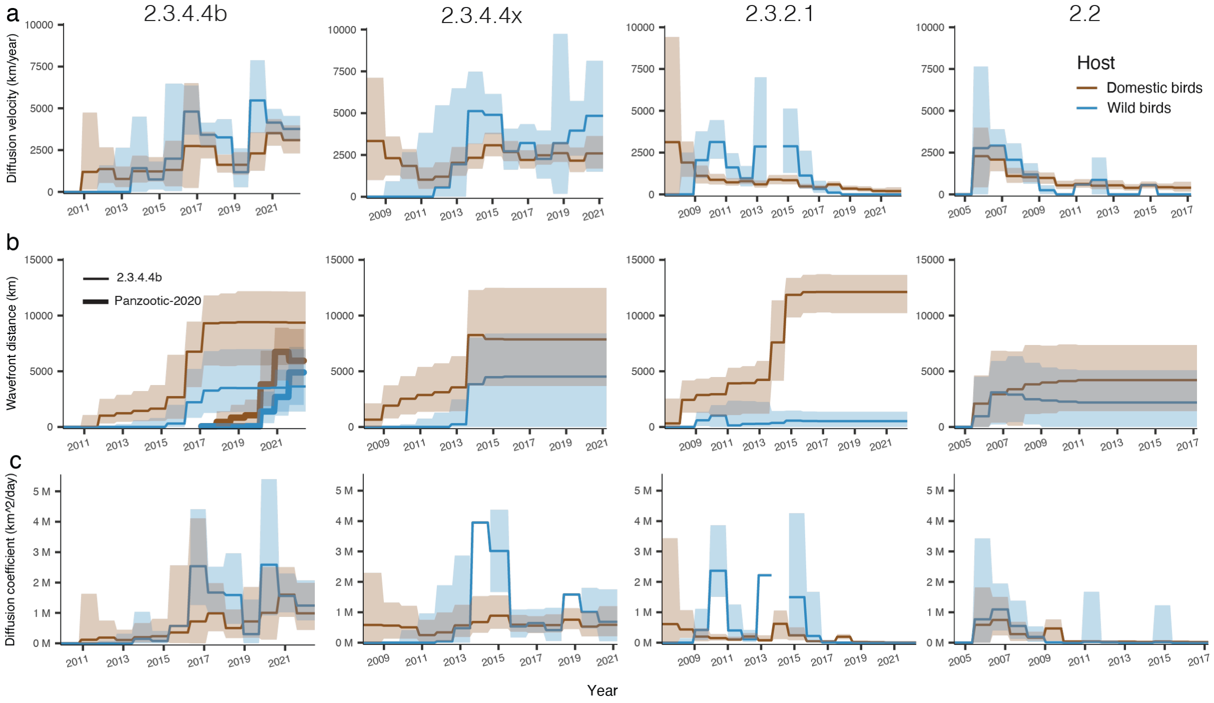
Supplementary Figure 4 | Evolutionary relationships of Panzootic-2020 (including 2020/21 and 2021/22 resurgence) and JKE-2019 lineage. Maximum likelihood tree of Panzootic-2020 (a) and JKE-2019 (b) for eight segments. Samples collected in Africa are highlighted in red.



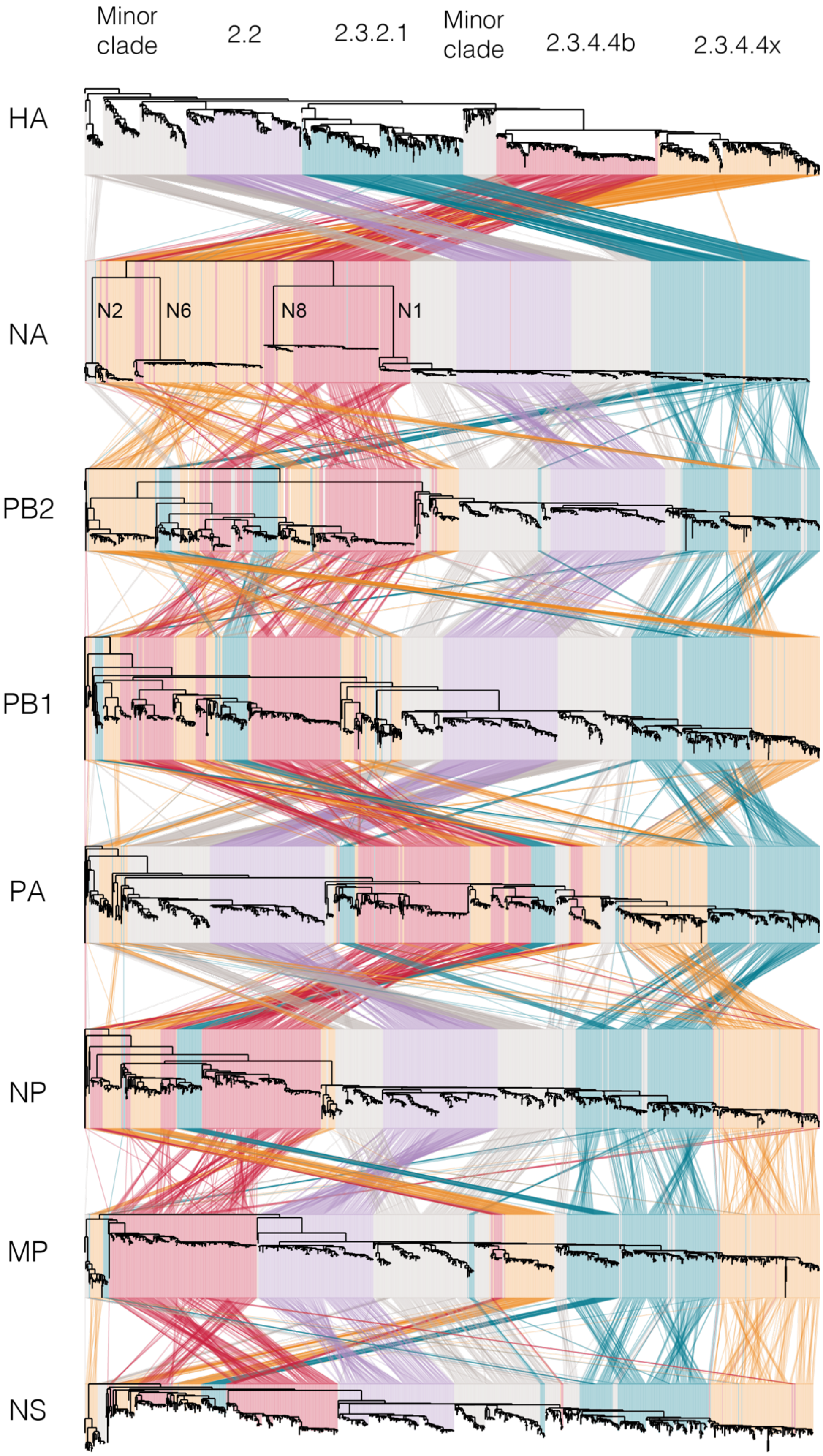
Supplementary Figure 5 | Dynamics of HPAI H5 transmission lineages in clades 2.3.4.4.b, 2.3.4.4.x, 2.3.2.1 and 2.2. Virus lineage movements were inferred by continuous phylogeographic analysis for each clade.



Supplementary Figure 6 | The contrasting geographic and host transmission patterns among HPAI H5 2.3.4.4.b, 2.3.4.4.x, 2.3.2.1 and 2.2 clades inferred from discrete phylogeography. From left to right, the figures represent regional Markov jumps, regional Markov rewards, host Markov jumps and host Markov rewards.



Supplementary Figure 7 l The contrasting spatial epidemiology among HPAI H5 clades 2.3.4.4b, 2.3.4.4x, 2.3.2.1 and 2.2. (a) Viral Diffusion velocity (km/year) of domestic (brown) and wild birds (blue) over time for each clade. (b) Viral wavefront distance (km) of wild and domestic birds over time for each clade. A recalculation of the wavefront distance in the panzootic-2020 clade (including 2020/21 and 2021/22 resurgences, shown in a thick line) was performed, in which Egypt was regarded as the epidemic's origin. (c) Viral Diffusion coefficient (km2/day) over time for each clade. The diffusion velocity and coefficient of wild birds in clade 2.3.2.1 during 2014 are not shown in the plot due to abnormal estimation value, possibly caused by insufficient sampling. The shaded areas denote the 95% confidence interval, in which some extreme values were not shown.



Supplementary Figure 8 | Tanglegram of HPAI H5 virus reassortment. Colored lines connect each virus across all eight genes, showing incongruence between and within major clades.