

Legends to the supplementary materials

Manuscript title: Phylodynamic analysis of the highly pathogenic avian influenza H5N8 epidemic in France, 2016-17

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S1. A heat map depicting multi-collinearity between linear predictors of the viral effective population size N_e GLM during the HPAI H5N8 outbreaks of 2016-17 in southwest France. Each cube depicts the range of the Pearson correlation coefficient (ρ) between a pair of predictors. Darker colour represents stronger positive correlations.

S2. Accession numbers and numbers of sequences of the HPAI H5N8 outbreaks of 2016-17 in southwest France. Source: <https://doi.org/10.3201/eid2702.202920>

S3. Metadata of samples from the HPAI H5N8 outbreaks of 2016-17 in southwest France.

S4. A scatter plot depicting a strong positive Pearson correlation between sample size and case counts in each département during the HPAI H5N8 outbreaks of 2016-17 in southwest France.