To determine human-to-human transmission for zoonotic pathogens, we expanded data from Geoghegan et al. 2016 *PNAS*.

For the 83 missing rows, we screened for information on person-to-person transmission in the following virology texts.

1. Cook, G.C. & Zumla, A. (2009). *Manson’s Tropical Diseases*. Elsevier Health Sciences
2. Maclachlan, N.J. & Dubovi, E.J. (2010). *Fenner’s Veterinary Virology*. Academic Press
3. Leitner, T. (2002). *The Molecular Epidemiology of Human Viruses*. Springer Science & Business Media
4. Strauss, E.G. & Strauss, J.H. (2007). *Viruses and Human Disease*. Academic Press
5. Tabor, E. (2006). *Emerging Viruses in Human Populations*. Elsevier
6. Mahy, B.W.J. (2009). *The Dictionary of Virology*. Academic Press
7. Kaslow, R.A., Stanberry, L.R. & Duc, J.W.L. (2014). *Viral Infections of Humans: Epidemiology and Control*. Springer

We also used a targeted search in GoogleScholar using two strings:

“VIRUS NAME” AND (“human transmission” OR “human-human transmission” OR person-person transmission” OR “human-to-human transmission” OR “person-to-person transmission”)

“VIRUS NAME” AND “transmission”

To determine pathogen release for all zoonotic viruses, we expanded data from Olival et al. 2017, Jones et al. 2008, and Plourde et al. 2017 on transmission mode.

For the 179 rows (excluding viruses with humans as primary reservoirs), we repeated the above screening using the same virology texts and a similar targeted GoogleScholar search:

“VIRUS NAME” AND (“transmission” OR “human exposure” OR “excretion” OR “slaughter” OR “vector”)

Pathogen release was recorded as a set of three binary covariates for whether viral transmission occurs through excretion, slaughter, or vector (categories are not mutually exclusive).