

**Temporal and spatial limitations in global surveillance for bat filoviruses and
henipaviruses: Online Appendix**

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S1. Systematic search

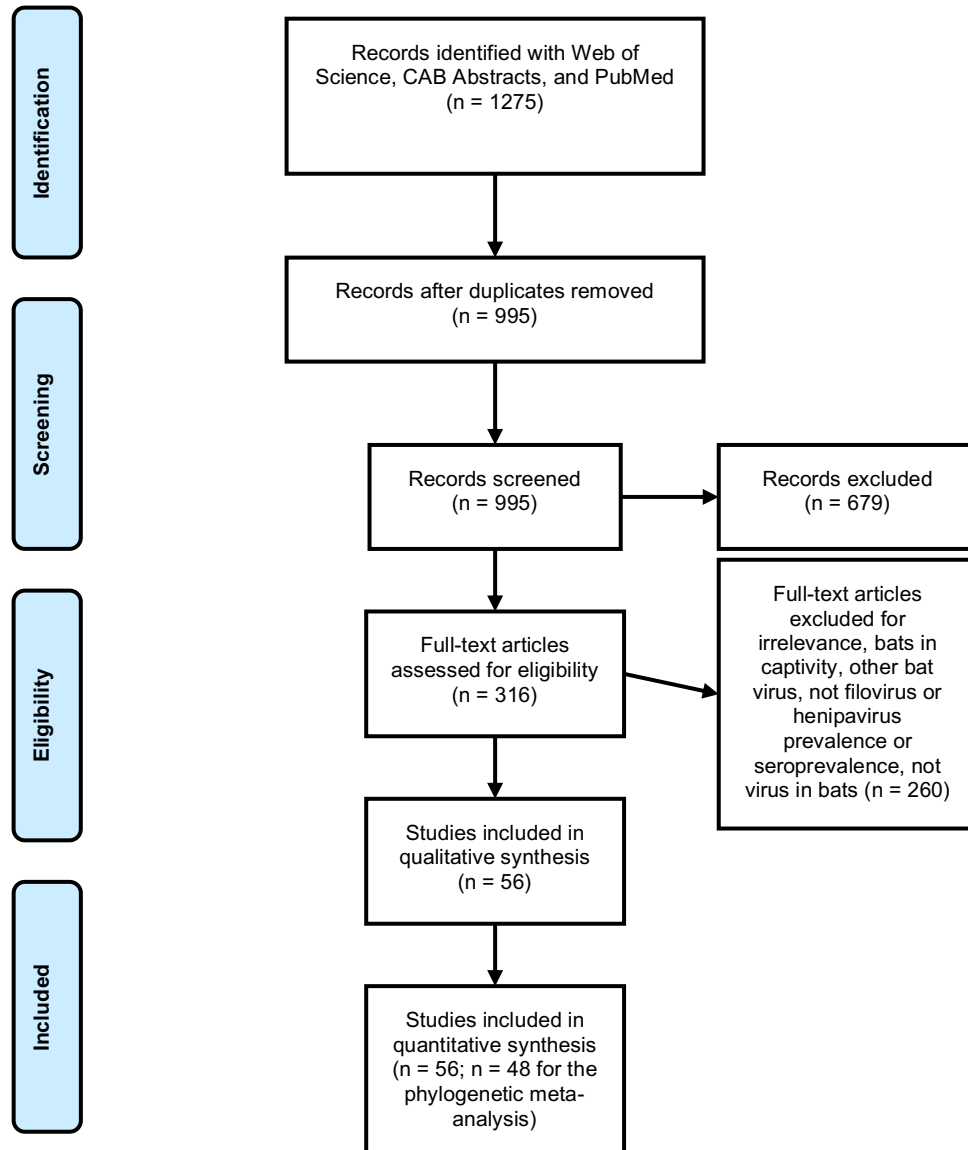
S2. Full reference list

S3. Bat phylogeny

S4. Post-hoc sampling design analysis

S1. Systematic search

Figure S1. The data collection and inclusion process for studies of wild bat filovirus and henipavirus prevalence and seroprevalence (PRISMA diagram). Searches used the following string: (bat* OR Chiroptera*) AND (filovirus OR henipavirus OR "Hendra virus" OR "Nipah virus" OR "Ebola virus" OR "Marburg virus" OR ebolavirus OR marburgvirus). Searches were run during October 2017. Publications were excluded if they did not assess filovirus or henipavirus prevalence or seroprevalence in wild bats or were in languages other than English.



S2. Full reference list

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S4. Post-hoc sampling design analysis

Table S1. Post-hoc analysis for the significant interaction between sampling design, outcome (prevalence or seroprevalence), and viral taxa. Mixed effects models with the same random effects as in the full model were fit to each virus–outcome dataset (filovirus prevalence=129, filovirus seroprevalence=174, henipavirus prevalence=217, henipavirus seroprevalence=210). Effect size and statistical significance were assessed using Wald-type tests for sampling design.

Data subset	Q_2	p
Filovirus prevalence	0.12	0.94
Filovirus seroprevalence	11.53	0.003
Henipavirus prevalence	0.98	0.61
Henipavirus seroprevalence	3.41	0.18