Supplementary Materials for

Wildlife trade drives animal-to-human pathogen transmission over 40 years

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MDAR Reproducibility Checklist

Materials and methods

Taxonomic harmonization. We combined multiple databases on mammals' taxonomy, biogeography, zoonotic pathogens, and trade (Table S1). To assemble these databases, we performed a taxonomic harmonization procedure using, as a reference, the Mammals Diversity Database (MDD), which is the most complete and up-to-date authoritative database on mammal taxonomy (*105*). To harmonize taxonomy across databases, we first matched species names against MDD's accepted names. Then, for species that were not found in MDD, we matched them against all possible synonyms of MDD accepted names using the R package *taxize* (*106*). Species that could not be linked to a MDD species after this step were excluded from further analyses (depending on the dataset, 90-99% of species were matched; Table S2). Because sub-species designations complicate cross-referencing and are subject to frequent reclassifications and disagreements among taxonomists (*107*), we chose to merge them at the species level. Our final dataset listed 6,596 valid mammal species. From this complete dataset, we excluded species listed as extinct in MDD (101 species) and domesticated species (24 species), including their wild relatives (14 species), and *Homo sapiens* (Table S3), leaving 6,456 species in our dataset. We chose to exclude the wild relatives of domesticated species to avoid overestimating the number of zoonotic pathogens in wildlife, as domesticated animals are often recorded under the scientific name of their wild counterparts and this mislabeling could artificially inflate pathogen counts in wild species. The biogeographical origin (Afrotropic, Australasia/Oceania, Indomalaya, Marine, Nearctic, Neotropic, Palearctic) of each species was also extracted from the MDD database.

Host–pathogen association data. To assess whether mammals are known to host pathogens and parasites (hereafter ‘pathogens’) that are also known to infect humans, we used the CLOVER database (*49*) (downloaded on February 29th, 2023), a reconciled aggregate of four extensive host-pathogen associations databases: GMPD 2.0 (Global Mammal Parasite Database (*108*)), EID2 (ENHanCEd Infectious Diseases Database (*109*)), HP3 (Host-Parasite Phylogeny Project (*4*)), and Shaw database (*110*). The CLOVER database has been used in previous studies to assess the occurrence of zoonotic pathogens in mammals (*24*, *25*, *111*) and is the highest quality host-pathogen association dataset to date, as it has been manually cleaned to remove errors and harmonize taxonomy. After taxonomic harmonization and data filtering (e.g., removing extinct and domesticated species), the dataset contained a total of 8,188 unique associations involving zoonotic pathogens, between 1,312 mammal species (incl. humans) and 2,424 pathogens, including 400 viruses 1,509 bacteria, 297 fungi, 148 helminths, and 70 protozoa. Using this information, we calculated the number of zoonotic pathogen species per mammal species.

Research effort. To account for knowledge bias, we assessed research effort by retrieving the number of publications per mammal species using the *easyPubMed* R package (*112*). We computed two indices of research effort per species by searching for keywords in the title and abstract of publications listed in PubMed. First, we calculated the total number of publications per mammal species, based on all possible valid specific Latin names and all possible common names (in English) from MDD (SUPP .xlsx dataset). We used a boolean ‘OR’ between possible species names, and, because our search contained Latin names that are used worldwide, our search string allowed us to detect non-English-language publications. Second, we calculated the proportion of all publications that focused on diseases or pathogens by refining our previous search with the following string: “pathogen* OR zoono* OR 'public health' OR 'emerging infectious disease' OR 'disease' OR parasit* OR virus OR viral OR helminth* OR bacteria* OR fung* OR protozoa OR infect*”. Several words in this string can match many non-English languages (e.g., pathogen*, zoono*, parasit*, virus, infect*) and are thus expected to capture non-English-language publications. We finally computed a unique index of research effort per species (eqn. 1) by multiplying the total number of publications (log-transformed and rescaled to [0-1]; eqn. 2) to the proportion of these publications focusing on diseases and pathogens (logit-transformed and rescaled to [0-1]; eqn. 3). The equation for calculating this index is as followed:

$$RE_i = \mathrm{D'}_i \times \mathrm{T'}_i \tag{1}$$

$$D'_i = \frac{\mathrm{logit}(\mathrm{D}_i) - \min(\mathrm{logit}(\mathrm{D}))}{\max(\mathrm{logit}(\mathrm{D})) - \min(\mathrm{logit}(\mathrm{D}))} \tag{2}$$

$$T'_i = \frac{\log(\mathrm{T}_i + 1) - \min(\log(\mathrm{T} + 1))}{\max(\log(\mathrm{T} + 1)) - \min(\log(\mathrm{T} + 1))} \tag{3}$$

With T_i the total number of publications for species *i*, T'_i the log-transformed and rescaled value of T_i to [0-1], D_i the proportion of all publications that focused on diseases or pathogens for species *i*, D'_i the logit-transformed and rescaled value of D_i to [0-1] (to avoid infinite values, the logit of 0 and 1 were calculated as the logit of 0.025 and 0.975, respectively). RE_i is the index of research effort for species *i*. This index combines the information on the total number of publications and proportion of these publications focused on pathogens and diseases (see Fig. 1a).

Phylogenetic non-independence among species. We used the VertLife database (*113*) to assess evolutionary relationships between mammals (downloaded on February 29th, 2023). Because our dataset included species that were not present in the phylogeny (905 species from 307 genera), we grafted these species following a genus-level imputation approach. Specifically, we identified species missing from the tree but whose genus was represented and randomly inserted them within their respective genus clades using the *phytools* R package. This procedure preserves the overall topology of the tree while ensuring that missing species are placed in phylogenetically plausible positions. Only 10 species were not grafted because their genus was not represented in the tree. These species were excluded from our analyses, decreasing our dataset to 6,446 species.

Synanthropy. We assessed mammals' propensity to live inside or near humans and human settlements using the IUCN Red List database (*39*). A mammal species was listed as synanthropic if it was known to occur in urban areas (habitat code 14.4), rural gardens (14.5), water storage areas (15.1), aquaculture ponds (15.3), wastewater treatment areas (15.6) or canals and drainage channels (15.9). A total of 875 mammal species (out of 6,456) were categorized as synanthropic (14%).

Wild meat usage. We assessed whether mammal species are being used as a food resource by humans using the IUCN Red List database (*39*). This variable does not directly reflect the global trade in wild mammals' meat, but rather the general use of mammal species as a food resource at local, national or international scales. A total of 1,249 mammal species were found to be consumed as wild meat (19%).

Mammals in the legal and illegal global wildlife trade. We used the CITES trade database (*42*) and the LEMIS trade database (*44*) to assess whether species were legally traded or not (following recommendations in characterizing wildlife trade (*114*)). The CITES trade database remains the most comprehensive database on the international wildlife trade in live animals and animal products and contains records for CITES-listed species from 1975 to present (*42*, *46*). The LEMIS trade database compiles records of wildlife and wildlife products imported in the United States between 2000 and 2022 (*43*, *44*, *47*). Although this database is limited to U.S. importations and covers a shorter timespan than the CITES trade database, it covers all species and thus, provides valuable information on the trade in species not listed in CITES Appendices and therefore absent from the CITES trade database. In this work, we considered species traded legally alive or as products, for commercial, personal, medical, scientific, and hunting trophy purposes. These trade purposes represent the majority of CITES and LEMIS trade records (84% and 99%, respectively). To assess which species were being traded illegally, we used Stringham et al. (2021)'s database on wildlife seizures (*45*). This curated database compiles information on illegal trade events recorded by CITES, LEMIS and TRAFFIC between 2010 and 2019. TRAFFIC's database focuses on the illegal wildlife trade and is the most comprehensive repository of wildlife seizures currently available (*48*). Unlike systematic trade declarations such as those in CITES and LEMIS, TRAFFIC data is largely derived from open-source information, such as media and government press releases. Finally, for both legal and illegal trade records, we noted whether the trade was in live animals or animal products (e.g., dead animals, animal parts, or products derived from animals) using CITES and LEMIS trade descriptions (i.e., trade records coded as ‘LIV’ [live animals] or ‘DEA’ [live animals that died during transport] were categorized as live animal trade; all other records were categorized as animal products).

Temporal analysis of the global wildlife trade. The CITES trade database is the only long-term (1975-present) and global compilation of the trade in wild animals (*46*). We used the aggregated version of the CITES trade database (*42*) (Comparative tabulation version 2023.1) to avoid duplicated trade records (e.g., when both importers and exporters report the same trade event). The CITES trade database totals 405,066 records of trade in mammals since 1975 (after taxonomic harmonization). However, we applied several filters to the database, reducing the number of analyzed records to 236,412. First, we chose to consider only the period 1980-2019 (40 years) because the first five years (1975-1979) and the last three years (2020-2022) of recording are incomplete, due to non-systematic recording during the first years (many species were not yet listed in CITES and many countries were not yet parties of CITES before 1980 (*115*)) and a time lag in reporting for the recent years (*42*). We also excluded 1) species that were listed in CITES after 1980 (16% of CITES-listed mammals) because their trade was not reported systematically over the period 1980-2019 and 2) species listed in CITES Appendix III (6% of all CITES-listed mammals) because their trade is not systematically recorded at a global scale as the CITES framework protects (and requires reporting on) them only when they are sourced from some specific countries (*101*). Using this refined dataset, we calculated the number of years that each traded mammal species appeared in trade over the last 40 years.

Statistical analysis. All data processing, statistical analyses and visualizations were performed in R v4.4.3 and RStudio (*116–120*). Generalised linear models were computed using the *glmmTMB* package (*121*). Continuous covariates were scaled (i.e., centered and normalized) in all models. The statistical validity of each model was systematically assessed using the *performance* (*122*) and *DHARMa* (*123*) packages. Whenever a random effect with an estimation very close to zero created a singularity issue (that can hinder model's convergence), the problematic factors were removed from the model to allow a non-singular fit (following package recommendations (*124*)). To control for phylogenetic non-independence among species, we decomposed the mammal phylogenetic tree into orthogonal phylogenetic eigenvectors using the *PVR* package (*125*). These phylogenetic eigenvectors (PEVs) summarize major axes of phylogenetic structure. The first ten PEVs were selected, scaled and included as additional covariates in all GLMs and in the SEM (Fig. S2). To ensure that ten PEVs were sufficient to account for phylogenetic non-independence among species, we systematically tested for phylogenetic signal in the residuals of our models using Blomberg's K (*126*, *127*). We did not include mammals' phylogenetic distance to humans (PDH) in our models because this variable was correlated to several PEVs and created collinearity issues when PDH was included in our models. We used the sjPlot package (*128*) to calculate standardized effect sizes of our GLMs. To estimate predicted response values for specific predictors, we used marginal means computation using the *ggeffects* package (*129*). This method calculates model-based expected values on the response scale, averaging over the distribution of other covariates in the model. To interpret effect sizes, we calculated marginal risk ratios, defined as the ratio of these marginal means between groups of interest (e.g., traded, not traded). Structural equation models were computed using the *piecewiseSEM* package (*130*).

Effect of trade on the probability of sharing pathogens with humans. To assess whether, among all mammal species, traded species are more likely to share pathogens with humans, we used a binomial model (logit link function) with zoonotic host status (i.e., the species shares at least one pathogen with humans or not) as the response variable and trade status (i.e., traded or not) as a predictor (fixed effect). To account for variables that could influence the relationship between trade and zoonotic host status, we added the index of research effort (see eqn. 1-3), synanthropic status (i.e., synanthropic or not) and wild meat status (i.e., consumed as human food or not) as covariates. To account for phylogenetic non-independence among mammals, we used ten PEVs as covariates. These ten eigenvectors accounted for 54% of the total phylogenetic variance. To account for the biogeographical origin of mammal species, we added their biogeographical realm as a random effect on the intercept. Species occurring in two or more biogeographical realms were assigned to the category 'multiple'.

To further test whether the statistical relationship between trade and the probability of sharing pathogens with humans was direct or mediated by wild meat consumption and synanthropy, we used a structural equation model (SEM) (*130*). SEM is a multivariate analysis technique that integrates multiple predictor and response variables into a single directed network of hypothetical causal links, represented through linear equations. SEM enables the estimation of the strength and significance of each relationship in the model (using standardized estimates) while accounting for all specified relationships within the network (*130*), therefore allowing us to account for the potential influence of wild meat consumption and synanthropy on the relationship between trade and the probability of sharing pathogens with humans. Moreover, this modelling technique also allows us to specify networks of interdependence between our variables of interest (zoonotic host status, trade, wild meat consumption and synanthropy) and research effort. Our SEM model consists of the combination of three sub-models, all accounting for the phylogenetic relatedness between species (using PEVs as fixed effects), and for the biogeographical origin of mammal species (using biogeographical realm as a random effect on the intercept). The first sub-model is a Gaussian model with research effort as the response variable and trade status, wild meat consumption status and synanthropy status as predictors. This sub-model results from the hypothesis that species that are traded, consumed as food by humans and synanthropic are more likely to be studied. The second sub-model is a binomial model (logit link function) with trade status as the response and wild meat consumption status and synanthropy status as predictors. This sub-model results from the hypothesis that wild meat consumption and synanthropy increase the probability of being traded. The third sub-model is a binomial model (logit link function) with zoonotic host status as the response and trade status, wild meat consumption status and synanthropy status, and research effort as predictors. This sub-model results from the hypotheses that the probability of being known to share pathogens with humans increases with research effort, synanthropy, use as human food and trade.

Effect of illegal trade and live-animal market on the probability of sharing pathogens with humans. To assess whether, among all mammal species, those occurring in the illegal trade and in the live-animal market were more likely to share pathogens with humans, we expanded our previous model to include these two binary variables. This approach tests whether – even after accounting for the general effect of trade on human-wildlife pathogen sharing – species occurring in the illegal trade and live-animal market are more likely to share pathogen with humans or not. We used an analysis of variance (likelihood ratio test) to assess whether adding these two variables to the initial model significantly improved the model fit.

Effect of time in trade on the number of pathogens shared with humans. We tested whether the number of years that a species has occurred in trade is positively linked to the number of pathogens shared with humans. Here, we focused on mammal species listed in CITES Appendices I and II, that were traded at least once between 1980 and 2019, based on records of the CITES trade database (*42*). Our analysis included 583 mammal species for which international trade events were recorded globally and continuously between 1980 and 2019. We tested whether time in trade is positively associated with zoonotic pathogen richness using a negative binomial model. The response variable was the number of zoonotic pathogens shared with humans (count data, range: 0–84). Our main predictor was time in trade (number of years, range: 1–40), and we included additional fixed effect covariates to control for factors potentially influencing the association between trade and pathogen sharing. These covariates were: synanthropy (binary), use as wild meat (binary), presence in the live animal market (binary), presence in the illegal wildlife trade (binary), research effort (continuous). To account for phylogenetic non-independence between species, we included the first ten phylogenetic eigenvectors (PEVs) as additional covariates. These ten eigenvectors accounted for 71% of the total phylogenetic variance. To account for the biogeographical origin of mammal species, we added their biogeographical realm as a random effect on the intercept.

To estimate the rate at which species share new pathogens with humans as a function of time in trade, we computed the predicted average response (i.e., number of pathogens shared with humans) across the range of the predictor variable (i.e., time in trade) using *ggaverage* from the *ggeffects* package. We then calculated the numerical derivative of this average effect using finite differences, calculated as:

$$f'(x_i) \approx \frac{f(x_i + 1) - f(x_i)}{x_{i+1} - x_i} \quad 4$$

Where $f(x_i)$ is the predicted average effect at the i-th value of the predictor variable. To interpret this rate of change, we calculated its reciprocal ($1/f'(x)$) which represents the number of years in trade needed to observe an increase of 1 in the response variable: the number of pathogens shared with humans. We finally calculated the mean ± CI95% rate of change over the whole range of the predictor variable.

Sensitivity analyses. We assessed the robustness of our results to variations in both the wildlife trade dataset and the host-pathogen association dataset used to test our hypotheses.

1) Sensitivity to wildlife trade dataset

Our first set of analyses (i.e., effect of trade status, trade legality, and market type, on the probability of sharing at least one pathogen with humans; results presented in Fig. 1 and 2) are based on a definition of the legal wildlife trade that depends on two datasets: CITES and LEMIS. To ensure than our conclusions did not change depending on the dataset used, we reran our models by defining trade using CITES only and LEMIS only, and compared the results to those of our main approach that uses both datasets to determine which species are traded. Overall, our conclusions were consistent across datasets (i.e., when trade status was defined using CITES only, LEMIS only, or both combined; Fig. S3-S4). However, using CITES alone slightly underestimated the overall effect of trade on the probability of sharing at least one pathogen with humans (Fig. S3-S4) and slightly overestimated the effect of occurrence in live-animal markets (Fig. S4). This likely reflects the strong overlap between the product and live-animal trades—over 90% of species present in live markets also appear in product markets—and the overrepresentation of live-animal trade in CITES data: 58% of CITES-listed traded species are traded alive, compared with only 23% in LEMIS. Consequently, in CITES data, presence in live and product markets are more strongly correlated, which may hinder detection of the independent contribution of each variable due to redundancy.

2) Sensitivity to host-pathogen associations dataset

Our main analyses rely on the full CLOVER dataset, a hand-curated dataset that covers all types of pathogens and parasites (i.e., viruses, bacteria, fungi, helminths, protozoa). In addition to this main dataset, we repeated our analyses using four alternative datasets: CLOVER-virus (CLOVER dataset with host-virus associations only), CLOVER-noEID2 (CLOVER dataset with exclusion of host-pathogen associations from the EID2 database (*109*)), VIRION (viruses only, see description below) and VIRION-noPREDICT (VIRION dataset with exclusion of host-virus associations from the PREDICT database (*131*, *132*)).

VIRION (*133*), the Global Virome in One Network (accessed on September 16th, 2025 (*134*)) compiles and harmonizes six host-virus associations databases (the four sources of CLOVER (*49*), PREDICT (*131*) and GenBank (*133*)). While CLOVER covers all groups of pathogens and parasites, VIRION focuses only on viruses. However, as a periodically re-compiled database, it is the most up-to-date and comprehensive compilation of vertebrate-virus associations currently available. After taxonomic harmonization and data filtering (e.g., removing extinct and domesticated species), the VIRION dataset contained a total of 11,888 unique associations between 1,525 mammal species (incl. humans) and 983 zoonotic viruses.

Repeating our analyses on the VIRION dataset allowed us to test whether the CLOVER dataset led to the same conclusion as the most comprehensive and up-to-date host-pathogen associations dataset available to date. However, VIRION can only be compared to CLOVER-virus. Moreover, repeating our analyses with the CLOVER-virus and VIRION datasets allowed us to determine whether our findings hold when considering only viruses – the pathogen group that poses the highest pandemic risk in the future (*135*). Repeating our analysis by excluding EID2 records from CLOVER, and PREDICT records from VIRION, allowed us to make sure that our findings held when data sources with known potential biases were removed. For CLOVER, we excluded host-pathogen associations from the EID2 database (one of the four data sources compiled in CLOVER), as EID2 includes a substantial number of records from experimental infections (*109*). These records could introduce artificial host-pathogen associations and potentially inflate the number of species sharing pathogens with humans. For VIRION, we excluded host-virus associations from the PREDICT database (one of the six sources compiled in VIRION), as the PREDICT program preferentially targeted high-risk interfaces (*131*) – including captive animals – which could potentially inflate the number of zoonotic pathogens detected in traded mammals compared to non-traded mammals. All our results remained consistent across host-pathogen associations datasets (Fig. S3-S5).

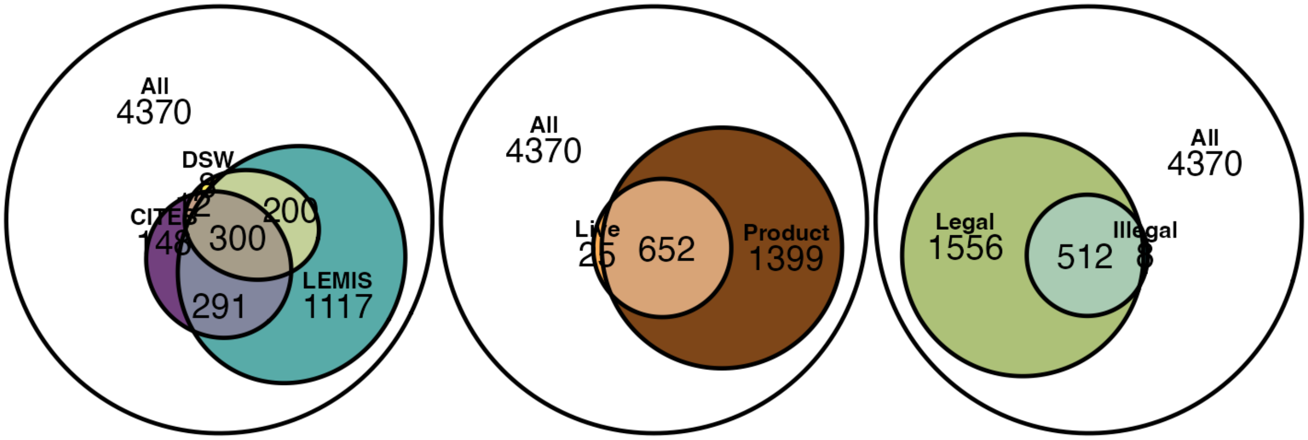

Figure S1

Wild mammal species overlap between trade datasets: CITES (purple), LEMIS (green) and DSW (i.e., illegal trade; yellow); market type: product (brown) and live (orange); and legality: legal (green) and illegal (turquoise).

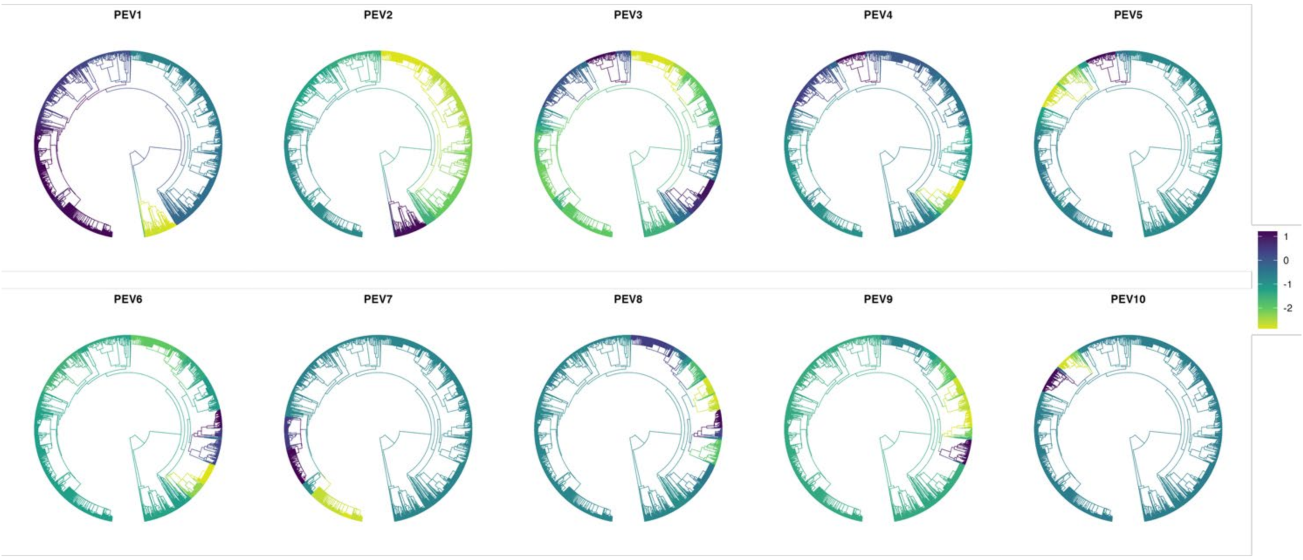

Figure S2

The ten first phylogenetic eigenvectors (scaled) used to control for phylogenetic non-independence in models presented in Tables S4, S6 and S7 (n= 6,446 species), accounting for 54% of all phylogenetic variance.

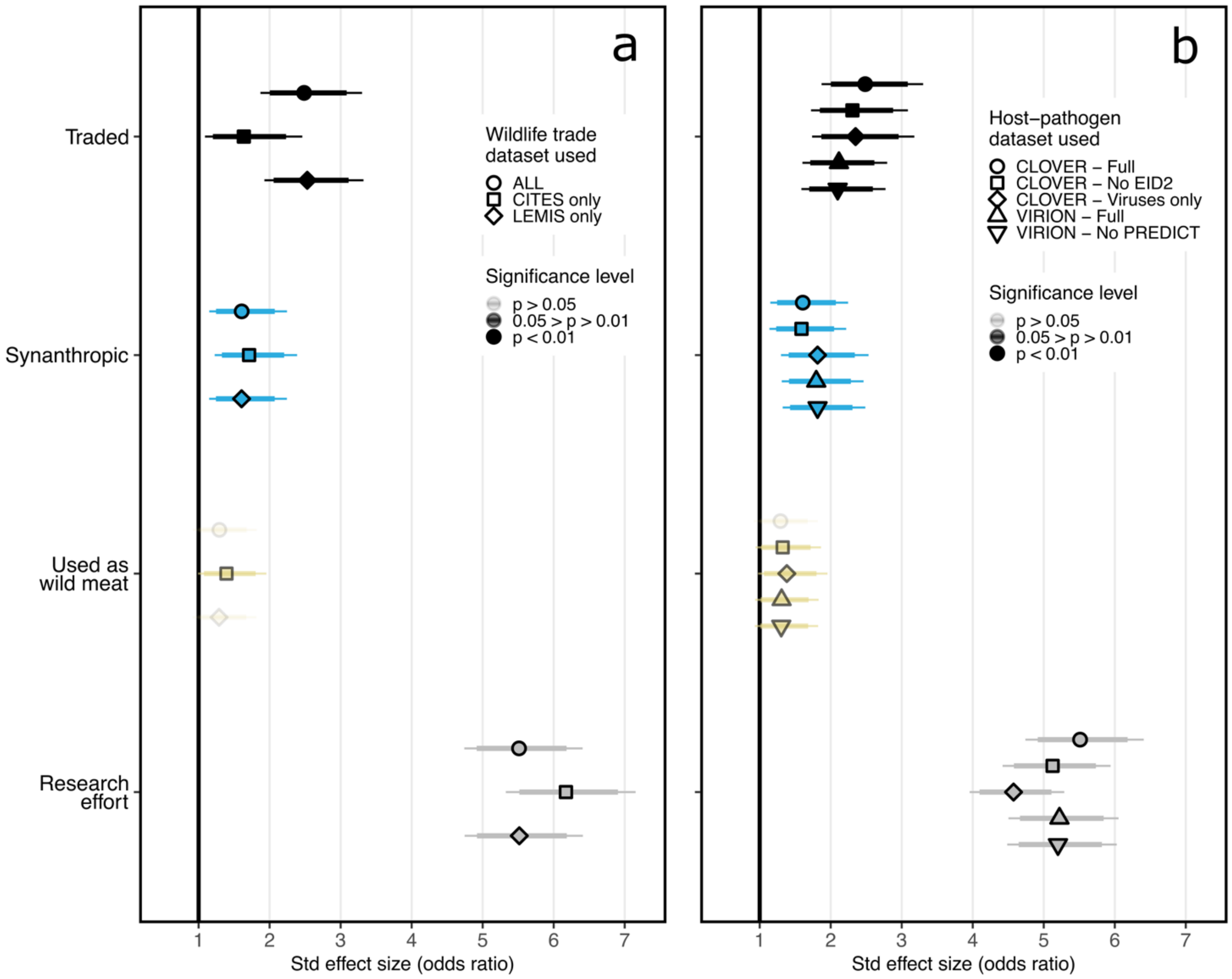

Figure S3

Sensitivity analyses on model presented in Fig. 1 and Table S4. Standardized effect size (mean ± CI95%) of main predictors on the probability of sharing at least one pathogen with humans (n = 6,446). **a**, Sensitivity to the wildlife trade dataset used: CITES only, LEMIS only, all (CITES, LEMIS, and DSW; we did excluded DSW because it is almost entirely included in CITES and LEMIS anyway; see Fig. S1). **b**, Sensitivity to the host-pathogen interaction dataset used: CLOVER, CLOVER – no EID2, CLOVER – virus only, VIRION, VIRION – no PREDICT.

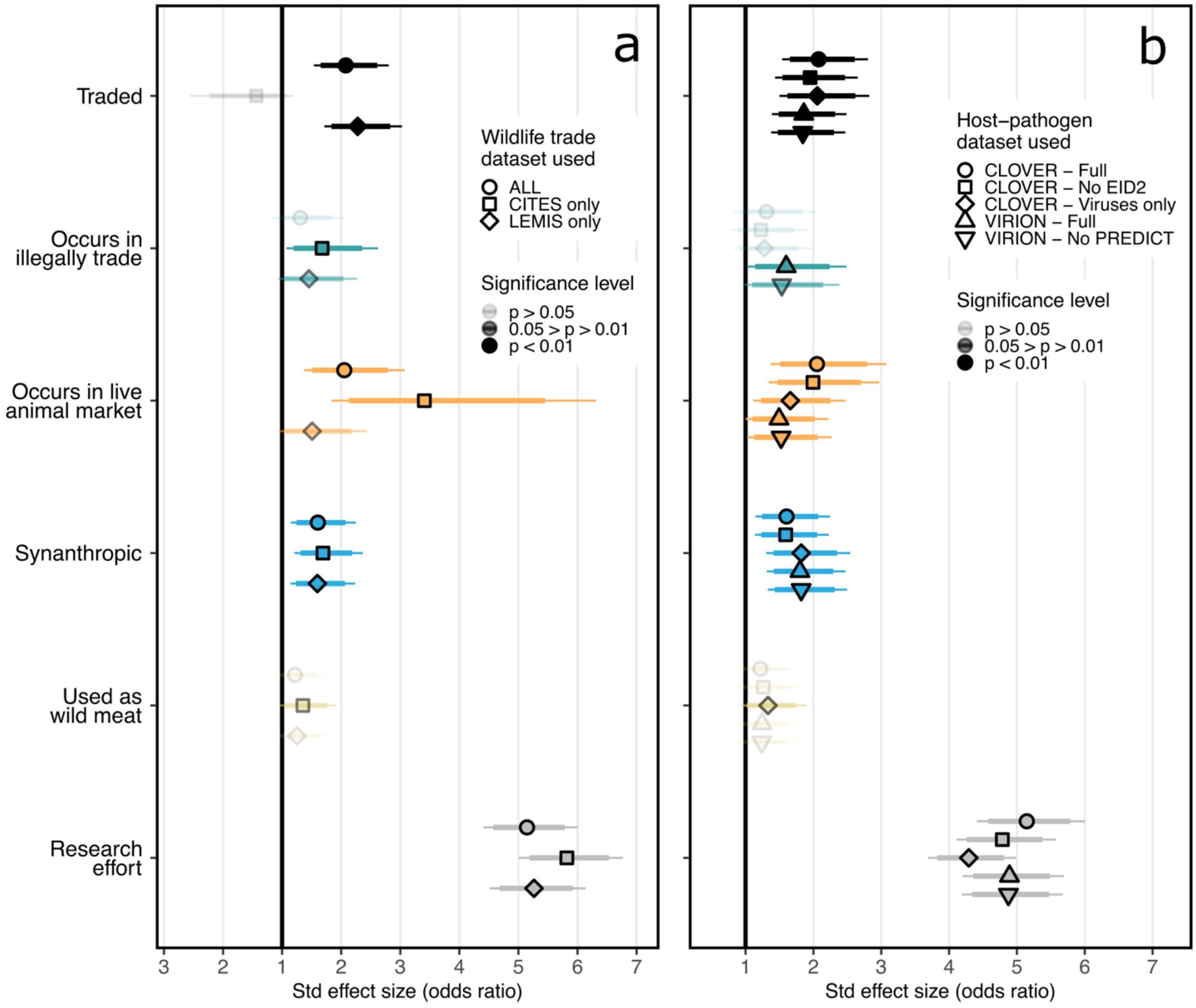

Figure S4

Sensitivity analyses on model presented in Fig. 2 and Table S7. Standardized effect size (mean ± CI95%) of main predictors on the probability of sharing at least one pathogen with humans. **a**, Sensitivity to the wildlife trade dataset used: CITES only, LEMIS only, both. **b**, Sensitivity to the host-pathogen interaction dataset used: CLOVER, CLOVER – no EID2, CLOVER – virus only, VIRION, VIRION – no PREDICT. In panel a, note the tendency for the CITES dataset to amplify the effects of occurrence in illegal trade, live trade, and use as wild meat, at the expense of the overall effect of trade itself. This likely reflects the overrepresentation of illegally traded, live-traded, and wild meat species in the CITES trade database (see Fig. 1a and Fig. 3a), which is expected given its regulatory focus.

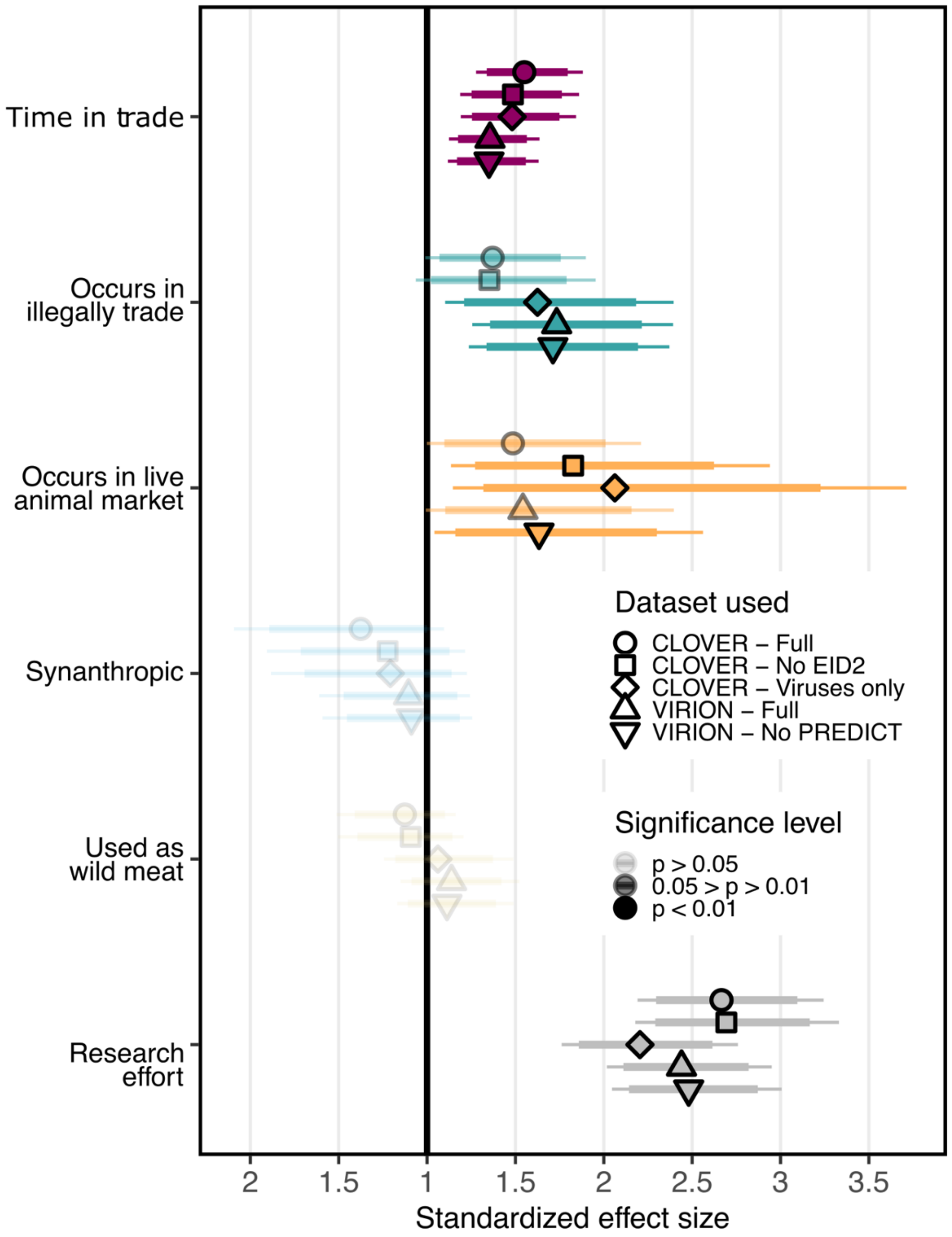

Figure S5

Sensitivity analyses on model presented in Fig. 3 and Table S8 to the host-pathogen interaction dataset used: CLOVER, CLOVER – no EID2, CLOVER – virus only, VIRION, VIRION – no

PREDICT. Standardized effect size (mean ± CI95%) of main predictors on the number of pathogens shared with humans.

Database	**Use**	**Version or access date**	**Link**
Mammals Diversity Database	Taxonomy (reference database)	v1.9.1	https://www.mammaldiversity.org/
CLOVER	Host-pathogen associations	Accessed on February 29th, 2023	https://github.com/viralemergence/clover
VIRION	Host-virus associations	v25 (September 16th, 2025)	https://doi.org/10.5281/zenodo.17128513
CITES checklist	CITES appendices and date of listing	Accessed on June 30th, 2023	https://checklist.cites.org/#/en
CITES trade database	Traded species, Temporal trends in species trade	v2023.1	https://trade.cites.org/
LEMIS	Traded species	v2025	https://figshare.com/s/960af99373aba13791be
IUCN Red list database	Synanthropic species, species used as human food	Accessed on May 1st, 2024 (synanthropy) and July 20th, 2025 (wild meat)	https://www.iucnredlist.org/
VertLife	Mammal phylogeny	Accessed on February 25th, 2023	http://vertlife.org/phylosubsets/
DSW	Illegally traded species	v2021	https://figshare.com/articles/dataset/Dataset_of_seized_wildlife_and_their_intended_uses/14914773?file=28717758

Table S1

List of databases used in this study.

	Initial number of species	**Number of species matched to MDD**	**Matching rate (%)**
CLOVER	1364	1341	98
VIRION	1741	1574	90
CITES	838	783	93
LEMIS	2057	1968	96
DWS	564	554	98
IUCN (synanthropic species)	1770	1746	99
IUCN (wild meat)	1343	1263	94
Mammal phylogeny	5911	5658	96

Table S2

Matching rates with the reference database (MDD) for the eight main sources of information used in this study.

Excluded species	**Reason**
Homo_sapiens	human
Bos_domesticus	domestic
Bos_frontalis	domestic
Bos_grunniens	domestic
Bos_indicus	domestic
Bos_javanicus	domestic
Bos_mutus	domestic
Bos_taurus	domestic
Bubalus_arnee	wild relative to domesticate
Bubalus_bubalis	domestic
Camelus_bactrianus	domestic
Camelus_dromedarius	domestic
Camelus_ferus	wild relative to domesticate
Canis_familiaris	domestic
Canis_lupus	wild relative to domesticate
Capra_aegagrus	wild relative to domesticate
Capra_hircus	domestic
Cavia_porcellus	domestic
Cavia_tschudii	wild relative to domesticate
Equus_africanus	wild relative to domesticate
Equus_asinus	domestic
Equus_caballus	domestic
Equus_ferus	wild relative to domesticate
Felis_catus	domestic
Felis_lybica	wild relative to domesticate
Lama_glama	domestic

Lama_guanicoe	wild relative to domesticate
Lama_pacos	domestic
Lama_vicugna	wild relative to domesticate
Mus_musculus	domestic
Mustela_furo	domestic
Mustela_putorius	wild relative to domesticate
Neogale_vison	domestic
Oryctolagus_cuniculus	domestic
Ovis_aries	domestic
Ovis_gmelini	wild relative to domesticate
Rattus_norvegicus	domestic
Sus_domesticus	domestic
Sus_scrofa	wild relative to domesticate
Antillomys_rayi	extinct
Archaeolemur_edwardsi	extinct
Bettongia_anhydra	extinct
Bettongia_pusilla	extinct
Boromys_offella	extinct
Boromys_torrei	extinct
Bos_primigenius	extinct
Brotomys_voratus	extinct
Caloprymnus_campestris	extinct
Chaeropus_ecaudatus	extinct
Chaeropus_yirratji	extinct
Conilurus_albipes	extinct
Conilurus_capricornensis	extinct
Coryphomys_buehleri	extinct

Coryphomys_musseri	extinct
Cryptoprocta_spelea	extinct
Dusicyon_australis	extinct
Dusicyon_avus	extinct
Geocapromys_caymanensis	extinct
Geocapromys_columbianus	extinct
Geocapromys_thoracatus	extinct
Heteropsomys_insulans	extinct
Hexolobodon_phenax	extinct
Hippopotamus_lemerlei	extinct
Hippopotamus_madagascariensis	extinct
Hippotragus_leucophaeus	extinct
Hydrodamalis_gigas	extinct
Hyperplagiodontia_araeum	extinct
Isolobodon_montanus	extinct
Isolobodon_portoricensis	extinct
Juscelinomys_candango	extinct
Lagorchestes_asomatus	extinct
Lagorchestes_leporides	extinct
Lagostomus_crassus	extinct
Lenomys_grovesi	extinct
Leporillus_apicalis	extinct
Lutra_nippon	extinct
Macrotis_leucura	extinct
Megaladapis_madagascariensis	extinct
Megalomys_desmarestii	extinct
Megalomys_georginae	extinct

Megalomys_luciae	extinct
Megaoryzomys_curioi	extinct
Melomys_rubicola	extinct
Melomys_spechti	extinct
Neogale_macrodon	extinct
Neomonachus_tropicalis	extinct
Nesophontes_edithae	extinct
Nesophontes_hemicingulus	extinct
Nesophontes_hypomicrus	extinct
Nesophontes_major	extinct
Nesophontes_micrus	extinct
Nesophontes_paramicrus	extinct
Nesophontes_zamicrus	extinct
Nesoryzomys_darwini	extinct
Nesoryzomys_indefessus	extinct
Noronhomys_vespuccii	extinct
Notamacropus_greyi	extinct
Notomys_amplus	extinct
Notomys_longicaudatus	extinct
Notomys_macrotis	extinct
Notomys_mordax	extinct
Notomys_robustus	extinct
Oligoryzomys_victus	extinct
Onychogalea_lunata	extinct
Oryzomys_antillarum	extinct
Oryzomys_nelsoni	extinct
Palaeopropithecus_ingens	extinct

Pennatomys_nivalis	extinct
Perameles_eremiana	extinct
Perameles_fasciata	extinct
Perameles_myosuros	extinct
Perameles_notina	extinct
Perameles_papillon	extinct
Peromyscus_pembertoni	extinct
Pipistrellus_murrayi	extinct
Pipistrellus_sturdeei	extinct
Plagiodontia_ipnaeum	extinct
Plagiodontia_spelaeum	extinct
Potorous_platyops	extinct
Prolagus_sardus	extinct
Pseudomys_auritus	extinct
Pseudomys_glaucus	extinct
Pteropus_allenorum	extinct
Pteropus_brunneus	extinct
Pteropus_coxi	extinct
Pteropus_pilosus	extinct
Pteropus_subniger	extinct
Pteropus_tokudae	extinct
Rattus_macleari	extinct
Rattus_nativitatis	extinct
Rattus_sanila	extinct
Rhizoplagiodontia_lemkei	extinct
Rucervus_schomburgki	extinct
Solenodon_arredondoi	extinct

Solenodon_marcanoi	extinct
Solomys_spriggsarum	extinct
Thylacinus_cynocephalus	extinct
Tonatia_saurophila	extinct

Table S3

List of mammal species excluded from the study and reason for exclusion.

Response	**Zoonotic host status**		
Predictors	*Odds Ratios*	*CI 95%*	*p*
(Intercept)	0.06	0.04 – 0.08	**<0.001**
Trade [yes]	2.49	2.00 – 3.08	**<0.001**
Synanthropy [yes]	1.61	1.25 – 2.07	**<0.001**
WildMeat [yes]	1.29	1.00 – 1.67	0.052
Research effort	5.75	5.12 – 6.47	**<0.001**
PEV1	1.03	0.92 – 1.15	0.655
PEV2	0.99	0.89 – 1.11	0.907
PEV3	0.84	0.74 – 0.96	**0.008**
PEV4	1.52	1.31 – 1.77	**<0.001**
PEV5	1.21	1.10 – 1.33	**<0.001**
PEV6	1.13	0.99 – 1.28	0.067
PEV7	1.03	0.92 – 1.16	0.607
PEV8	0.95	0.87 – 1.04	0.285
PEV9	1.03	0.95 – 1.12	0.459
PEV10	1.13	1.01 – 1.27	**0.034**

Random Effects	
σ^2	3.29
$\tau_{00\ \mathrm{BioRealm}}$	0.16
ICC	0.05
N_{BioRealm}	8

Observations	6446
Marginal R^2 / Conditional R^2	0.572 / 0.592
Phylogenetic signal (Blomberg's K)	0.026 (p=0.51)

Table S4

Detailed results for the binomial model (presented in Fig. 1) used to test whether traded species are more likely to share pathogens with humans, based on the full CLOVER dataset. See Fig. S3 for sensibility analyses.

Response	**Zoonotic host status**		
Predictors	*Odds Ratios*	*CI 95%*	*p*
(Intercept)	0.06	0.05 – 0.07	**<0.001**
Trade [yes]	2.72	2.21 – 3.35	**<0.001**
Synanthropy [yes]	1.67	1.32 – 2.12	**<0.001**
WildMeat [yes]	1.24	0.99 – 1.56	0.063
Research effort	5.65	5.05 – 6.32	**<0.001**
Observations	6446		
R^2	0.57		

Table S5

Detailed statistics for the phylogenetic binomial model corresponding to the model presented in Table S4.

Response	**Predictor**	**Estimate**	**Std.Error**	**Crit.Value**	***p***	**Std.Estimate**
r	T	0.7487	0.0243	30.7967	< 0.0001	0.3587
r	W	0.1196	0.0307	3.895	0.0001	0.0484
r	PEV1	-0.0267	0.0106	-2.505	0.0122	-0.0272
r	PEV2	0.039	0.0109	3.5673	0.0004	0.0398
r	PEV3	0.0728	0.0109	6.6541	< 0.0001	0.075
r	PEV4	-0.0068	0.0103	-0.6665	0.5051	-0.0071
r	PEV5	0.0365	0.0101	3.6075	0.0003	0.0375
r	PEV6	0.1824	0.0119	15.3921	< 0.0001	0.1852
r	PEV7	-0.0188	0.0115	-1.6445	0.1001	-0.0193
r	PEV8	0.0385	0.0101	3.7933	0.0001	0.0393
r	PEV9	0.08	0.0101	7.9646	< 0.0001	0.0813
r	PEV10	-0.0045	0.0105	-0.4301	0.6671	-0.0046
T	S	0.8392	0.087	9.6473	< 0.0001	0.1314
T	W	1.0103	0.0855	11.822	< 0.0001	0.1825
T	PEV1	-0.1079	0.0328	-3.2914	0.001	-0.0491
T	PEV2	-0.1195	0.0336	-3.5534	0.0004	-0.0544
T	PEV3	0.194	0.0364	5.3289	< 0.0001	0.0891
T	PEV4	0.164	0.0377	4.3461	< 0.0001	0.0754
T	PEV5	0.2738	0.0316	8.6568	< 0.0001	0.1255
T	PEV6	0.6791	0.0389	17.4756	< 0.0001	0.3074
T	PEV7	-0.0068	0.0365	-0.1877	0.8511	-0.0031
T	PEV8	-0.0706	0.0315	-2.2427	0.0249	-0.0321
T	PEV9	0.0691	0.0317	2.1839	0.029	0.0313
T	PEV10	0.0762	0.0363	2.0993	0.0358	0.0347
Z	T	0.9105	0.1102	8.2615	< 0.0001	0.1495
Z	S	0.4741	0.1299	3.6499	0.0003	0.057
Z	W	0.2566	0.1321	1.9422	0.0521	0.0356
Z	r	1.75	0.0599	29.2129	< 0.0001	0.5997
Z	PEV1	0.0259	0.058	0.4463	0.6554	0.0091
Z	PEV2	-0.0069	0.0587	-0.1168	0.907	-0.0024
Z	PEV3	-0.1736	0.0659	-2.6349	0.0084	-0.0613
Z	PEV4	0.4208	0.0761	5.5265	< 0.0001	0.1487
Z	PEV5	0.1885	0.0484	3.8964	0.0001	0.0664
Z	PEV6	0.1199	0.0655	1.8307	0.0671	0.0417

Z	PEV7	0.0314	0.061	0.5145	0.6069	0.011
Z	PEV8	-0.0503	0.0471	-1.0682	0.2854	-0.0176
Z	PEV9	0.0317	0.0428	0.741	0.4587	0.011
Z	PEV10	0.1224	0.0577	2.122	0.0338	0.0428

Response	**Marginal R^2**	**Conditional R^2**
r	0.29	0.35
T	0.24	0.34
Z	0.57	0.59

Table S6

Detailed statistics for the Structural Equation Model analysis presented in Fig. 1e. Based on full CLOVER dataset. Main effects are highlighted in light blue. Letters code: Z: Shares at least one pathogen with humans; T: Traded; S: Synanthropic; W: Used as wild meat; r: Research effort; PEV: Phylogenetic EigenVector.

Response	**Zoonotic host status**		
Predictors	*Odds Ratios*	*CI*	*p*
(Intercept)	0.06	0.04 – 0.08	**<0.001**
Trade [yes]	2.08	1.65 – 2.61	**<0.001**
Trade live [yes]	2.05	1.51 – 2.79	**<0.001**
Trade illegal [yes]	1.31	0.93 – 1.85	0.126
Synanthropy [yes]	1.6	1.24 – 2.07	**<0.001**
WildMeat [yes]	1.22	0.93 – 1.59	0.147
Research effort	5.36	4.75 – 6.05	**<0.001**
PEV1	1.03	0.92 – 1.16	0.558
PEV2	1	0.89 – 1.12	0.983
PEV3	0.79	0.69 – 0.90	**<0.001**
PEV4	1.48	1.28 – 1.72	**<0.001**
PEV5	1.2	1.09 – 1.33	**<0.001**
PEV6	1.08	0.94 – 1.23	0.278
PEV7	1.01	0.90 – 1.14	0.887
PEV8	0.94	0.85 – 1.03	0.171
PEV9	1.01	0.93 – 1.10	0.802
PEV10	1.15	1.02 – 1.29	**0.019**
Random Effects			
σ^2	3.29		
τ_{00} BioRealm	0.2		

ICC	0.06
N $_{\text{BioRealm}}$	8
Observations	6446
Marginal R^2 / Conditional R^2	0.573 / 0.597
Phylogenetic signal (Blomberg's K)	0.027 (p=0.21)

Table S7

Detailed results for the binomial model (presented in Fig. 2) used to test whether species involved in the lve animal market and illegal trade are more likely to share pathogens with humans. Based on the full CLOVER dataset. See Fig. S4 for sensibility analyses.

Response	**Number of pathogens shared with humans**		
Predictors	*Standardized coefficients*	*CI 95%*	*p*
(Intercept)	0.76	0.56 – 1.02	0.067
Time in trade (scaled)	1.55	1.34 – 1.80	**<0.001**
Synanthropy [yes]	0.73	0.53 – 1.00	0.05
Wild meat [yes]	0.89	0.71 – 1.11	0.3
Trade live [yes]	1.49	1.10 – 2.01	**0.01**
Trade illegal [yes]	1.37	1.07 – 1.76	**0.013**
Research effort (scaled)	2.67	2.30 – 3.10	**<0.001**
PEV1	0.53	0.48 – 0.60	**<0.001**
PEV2	0.85	0.74 – 0.97	**0.016**
PEV3	1.19	1.06 – 1.33	**0.003**
PEV4	1.05	0.87 – 1.26	0.602
PEV5	1.11	1.01 – 1.22	**0.026**
PEV6	1.15	1.03 – 1.28	**0.011**
PEV7	1.24	1.03 – 1.49	**0.026**
PEV8	0.85	0.77 – 0.94	**0.001**
PEV9	1.19	1.01 – 1.39	**0.035**
PEV10	0.97	0.78 – 1.20	0.766
Observations	583		
Dispersion parameter	1.75		
R^2 (delta approximation)	0.77		

Phylogenetic signal (Blomberg's K)	0.018 (p=0.42)

Table S8

Detailed results of the negative binomial model (presented in Fig. 3) used to test whether time in trade predicts the number of pathogens shared using the full CLOVER host-pathogen association dataset (Fig. S5 for visual representation of effect sizes).

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