S2 | **Methods used to analyse articles**

Supporting Information

Methods

In order to assess the research emphasis and approaches used for studying viral host jumps, we focused on four specific viruses: Influenza A (IAV), Severe acute respiratory syndrome coronavirus (SARS-coV), canine parvovirus (CPV) and Venezuelan equine encephalitis virus (VEEV) because these viruses have been: 1) among the most researched on the topic of host jumps, or 2) studied using approaches that we deemed to be extremely fruitful for understanding evolutionary mechanisms of host jumps. We acknowledge that other viruses (e.g., HIV) fall into these categories, and thus emphasize that our goal is not to be comprehensive but to use a few strong examples to point out methodological strengths and weaknesses, data gaps and biases and effective future directions.

Search methodology. We used the Web of Science (WofS) to search for studies that addressed host jumps or changes in host range for each of the four viruses. All searches were conducted on Jan. 20th, 2010 meaning that publications after this date were excluded. Our search query (see below) contained a set of terms that are commonly used in addressing host jumps as well as the name of the specific virus (and variants of this name where necessary). We required that the host jump terms and virus name be in the WofS "Topic" category which includes titles, abstracts and keywords. We refined each search by only selecting journal articles. We emphasize that our search results are not meant to be absolutely quantitative but should be regarded as a sample of the studies that address host jumps. This approach allows us to draw conclusions about the relative effort dedicated towards collecting different types of data and addressing evolutionary hypotheses, which are our goals. Our search query was: (TS=("host jump*" OR "host switch*" OR ("host species" SAME (different OR novel OR new OR alternat*)) OR ("host range" SAME (expan* OR decreas* OR increas* OR change* OR shift)) OR "host specialization" OR "host specificity" OR "cross-species" OR "host transfer" OR "cross-host" OR "species barriers" OR "species tropism" OR "animal-to-human" OR "interspecies trans*" OR "inter-species trans*" OR "zoonotic transm*" OR "host radiation" OR spillover OR "spill over" OR xenotrop*) AND TS=(virus name)).

Criteria for paper selection. We screened the final set of host jump papers for each virus to eliminate inappropriate hits and to subdivide the relevant papers into 3 categories for further analysis. The following papers were eliminated: review articles, book chapters, papers that did not address host range change or host jumps, papers that did not address the specified virus or papers that were in languages other than English, French or German (languages in which the authors are competent). Papers in the final set were scored as (see column Supp. Table 1, column 3): 1) 0 for papers that address host range change or host jumps but do not collect data that would be relevant for testing evolutionary hypotheses, 2) 1 for papers that collect relevant data for addressing evolutionary hypotheses but they do not explicitly test an evolutionary hypothesis nor mention evolutionary processes in the abstract, and 3) 2 for papers that collect data that address evolutionary mechanisms of host range change or host jumps. We classified data as being relevant to addressing evolutionary hypotheses if the study included genetic or phenotypic viral data.

Paper review. Papers in the 0 category were not analyzed further except for being tallied as part of the denominator representing the total set of papers addressing host range change or host jumps. For 1 papers, only the virus type, broad scope of the sampling, type of data and approach were recorded (first 4 sections of Supp. Table 1) abstracts were recorded from information in the abstracts. For 2 papers, the entire paper was used to fill out the data in all of Supp. Table 1. By tallying the number of papers in each category, we calculated the effort on addressing evolutionary hypotheses relative to total effort on host

jumps (2 / 0 + 1 + 2), the effort on addressing evolutionary hypotheses out of total data that are relevant to evolutionary hypotheses (2 / 1 + 2), and the effort on collecting evolutionary-type data relative to total host jump data (2 + 1 / 0 + 1 + 2).

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Influenza[1-49,50-72,2, 44, 63, 73-152]; SARS-coV[66, 87, 153-188], CPV[189-213]; VEEV[214-228]

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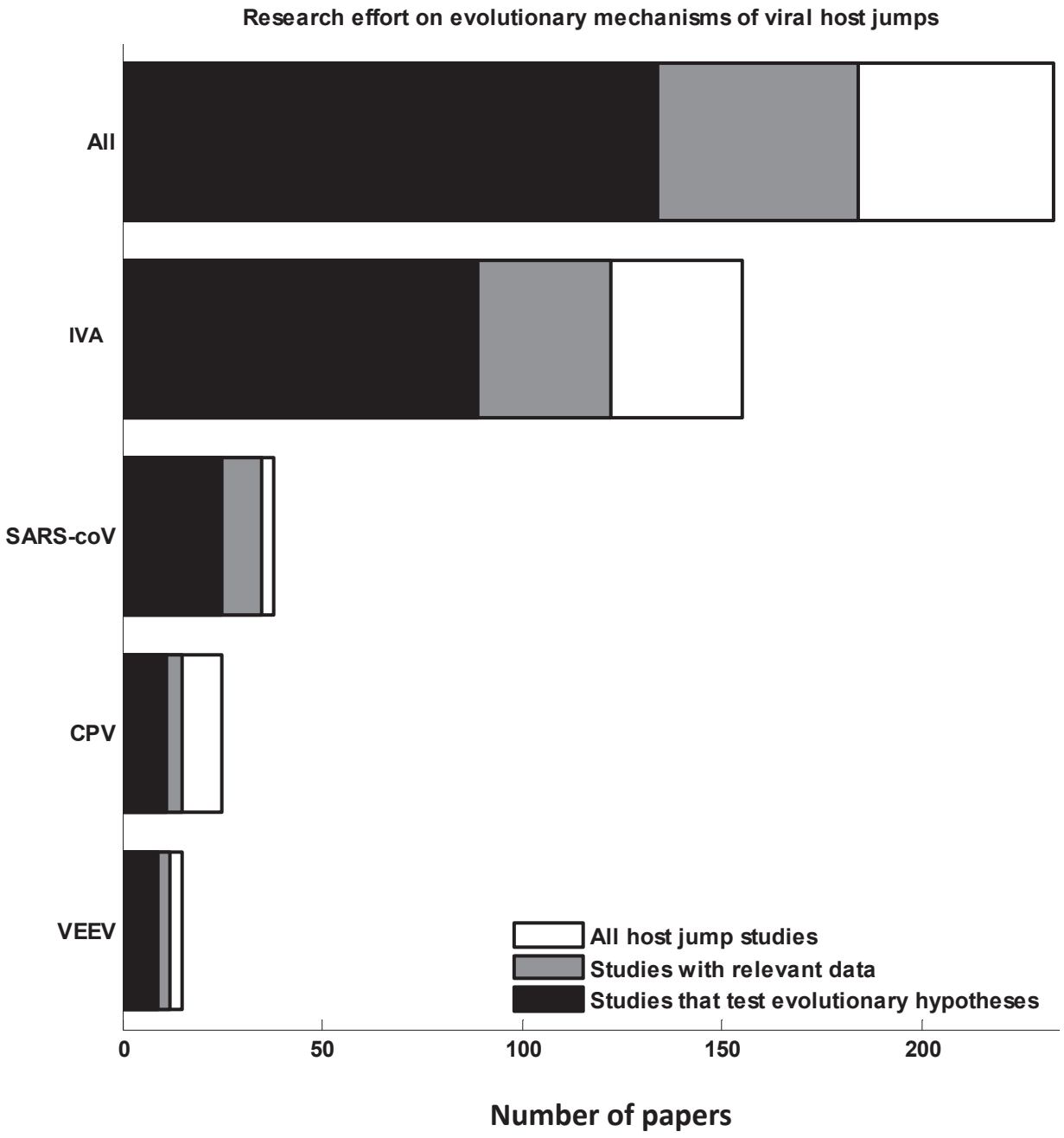
S3 | **Research effort on viral host jumps.**



Total numbers of papers for all 4 viruses combined (All) and each virus individually are shown on the x-axis. Papers were categorized into three broad groups: 1) host jump studies that do not collect evolutionary data (white bars, papers not reviewed), 2) host jump studies that collect evolutionary data but do not interpret the role of evolutionary processes in the host jump (grey bars, broadly reviewed), and 3) host jump studies that collect evolutionary data and explicitly interpret the role of evolutionary processes (black bars, fully reviewed).

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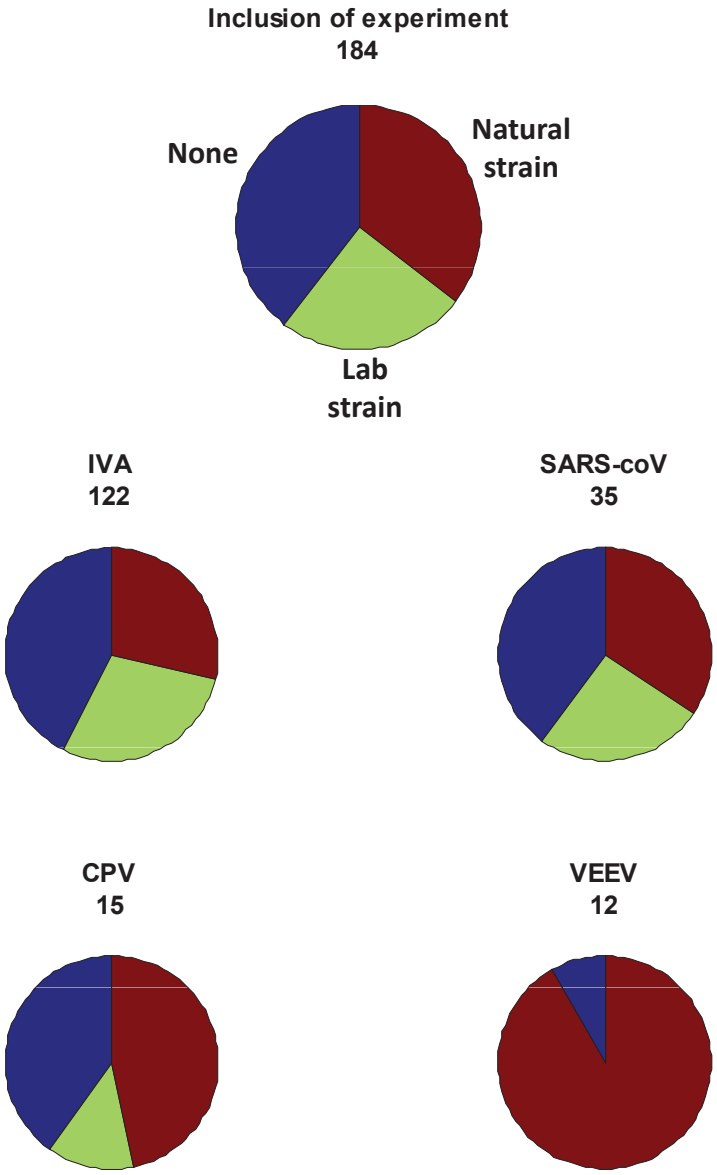
S4 | **Inclusion of experiment in studies with relevant data.**



All studies with relevant data grouped by presence of experiment and whether the target virus was sampled from nature. Studies for all four viruses are combined in the top chart. Three categories are: No experiment (blue), experiment on artificial strains (green, i.e., passaged extensively in the lab) and experiment on natural strains (red). Numbers indicate the total number of papers surveyed.

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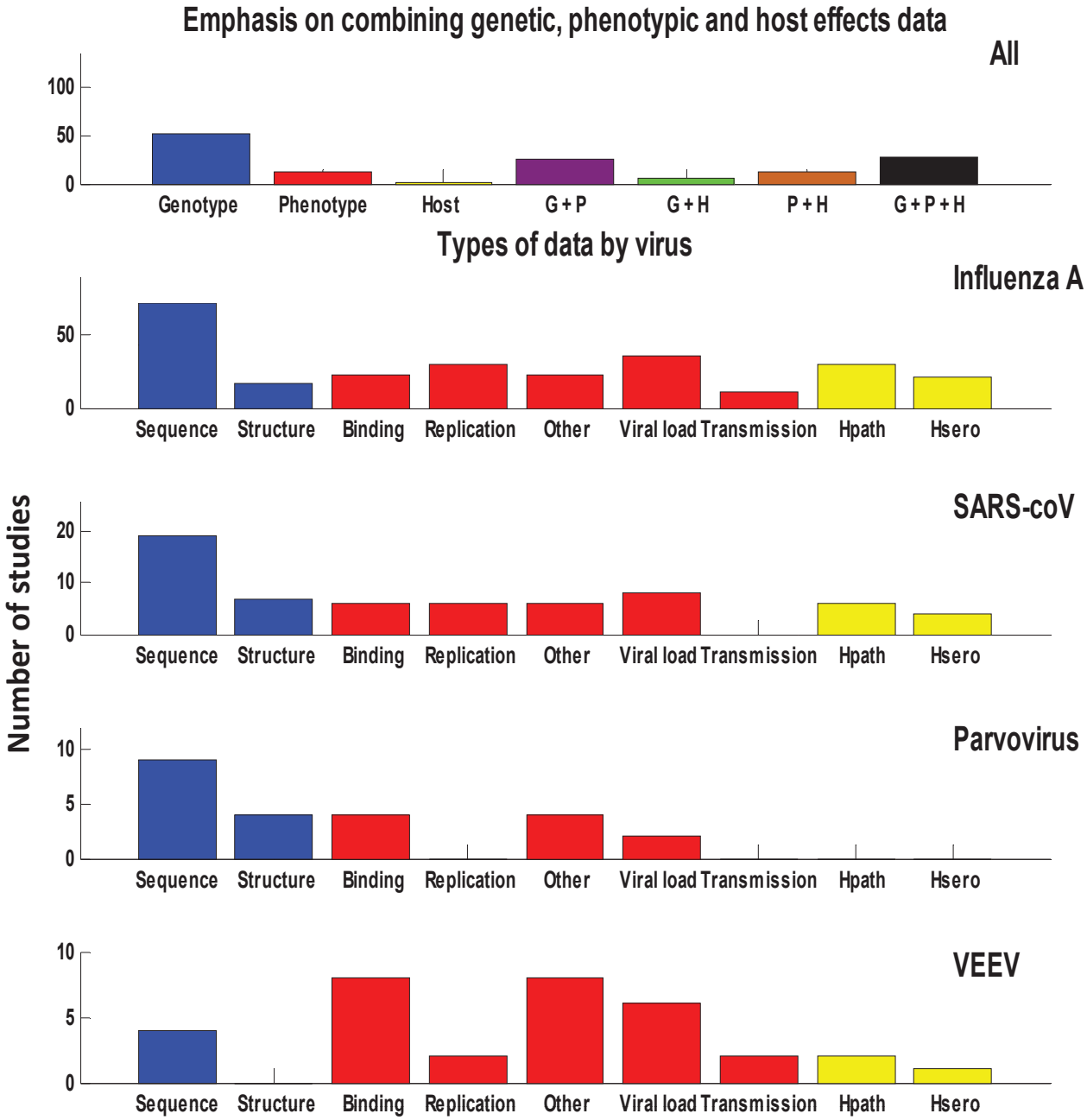
S5 | **Types of data used for analyses of evolutionary processes.**



Studies are grouped by whether they included genetic, phenotypic, host effects data or combinations of these categories (e.g. G+P means that the study includes genotypic and phenotypic data; top plot). Only studies that tested evolutionary hypotheses (black Genetic data (Genotype, blue) includes genetic sequence or protein structure. Phenotype (red) involves mars from Fig. 1) are included. Measurement of a viral trait such as receptor binding, polymerase replication efficiency, withinhost fitness (time course of infectious particles), transmission rate or other. Host (yellow) involves measurement of a host pathology (Hpath) or immune response (Hsero). Categories in top plot are mutually exclusive while categories for each separate virus (second plot to last plot) are not. Genotype (G), Phenotype (P), Host (H). The maximum value for each of the Y-axes is the total number of papers surveyed (134 for All, top).

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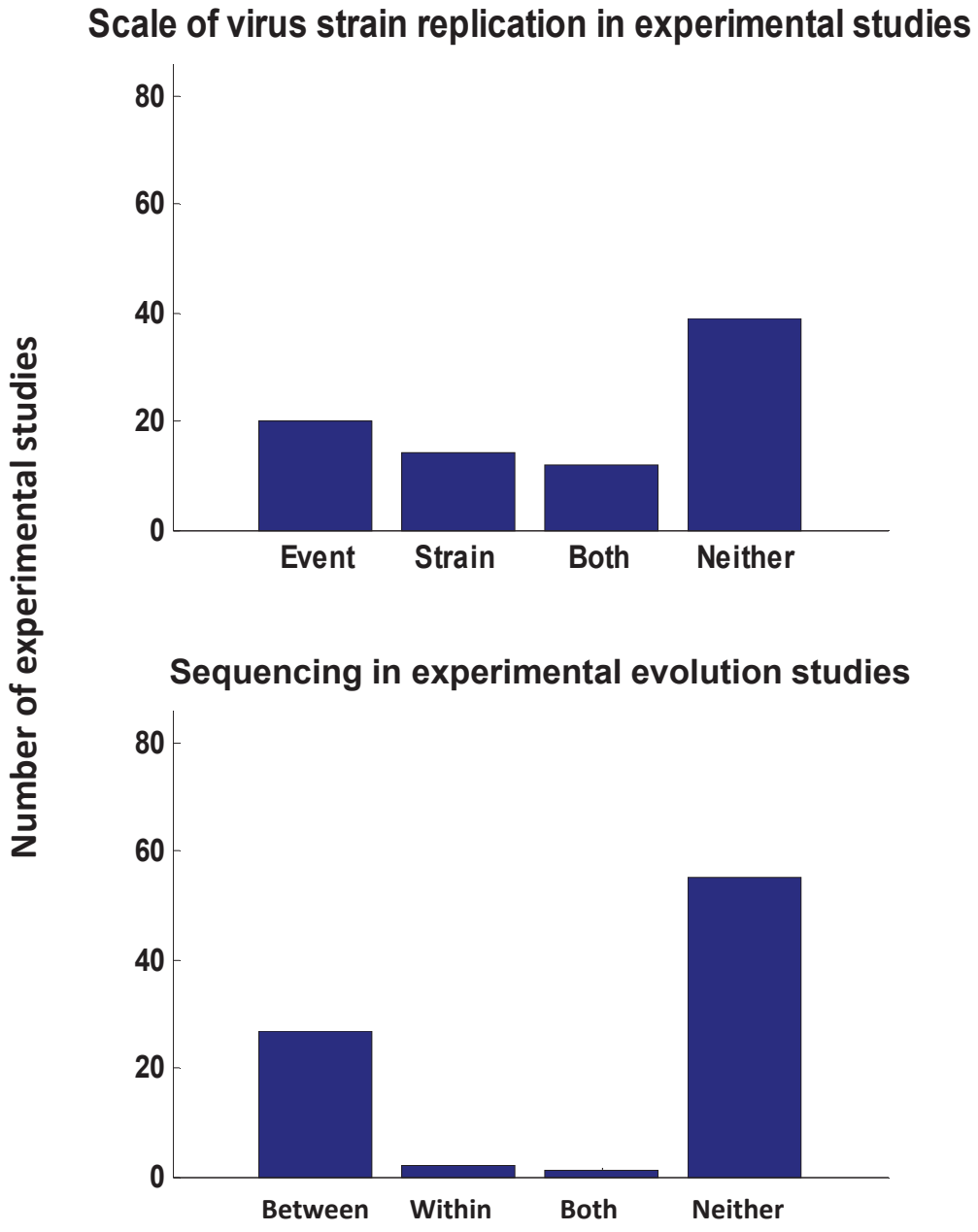
S6 | **Replication and experimental evolution in experimental studies.**



The scale of replication in the design of experimental studies was divided into four categories (top): 1) the study includes data from > 1 host jump event (Event), 2) the study includes > 1 viral strain for a single host jump event (Strain), 3) the study does both 1 and 2 (Both), or 4) the study does not include replication at the scale of the host jump event or strains within and event. The scale of genetic sequencing in experimental studies was categorized as follows (bottom): 1) Sequence viruses from > one time point following replication in > one host or cell culture (Between), 2) Sequence viruses from > one time point during within-host replication (Within), 3) Include both 1 and 2 (Both), or 4) Do not collect sequence data in their experiments (i.e., no experimental evolution). Maximum value on Y-axis is the total number of experimental studies for all viruses.

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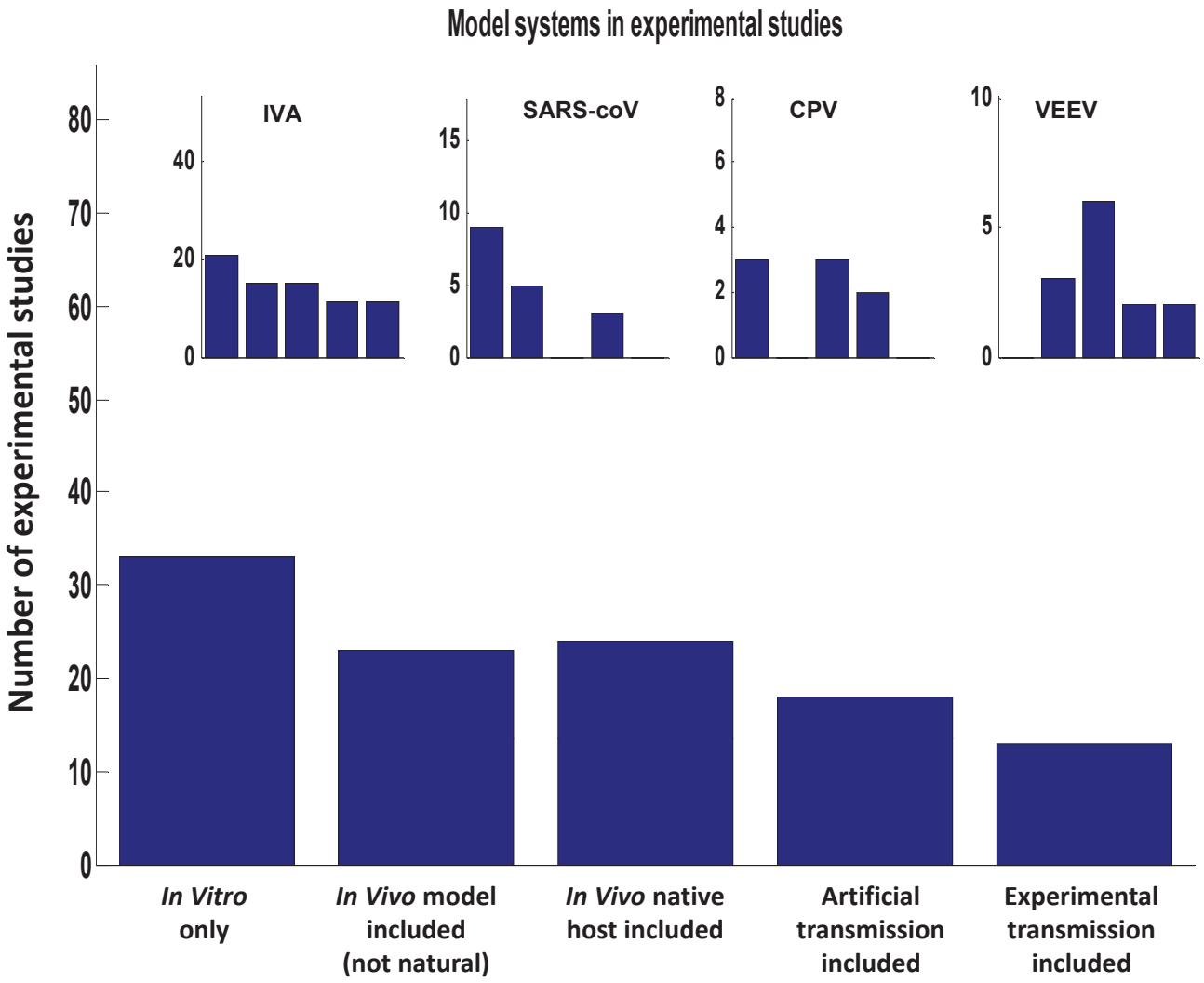
S7 | **Model systems in experimental studies.**



Data for all viruses are shown on the bottom plot. The inset shows the patterns by virus. There are five categories which are not mutually exclusive shown from left to right : 1) The study only uses an in vitro or cell culture-based host model system, 2) The study includes an animal host model that is not a natural component of the host jump system being studied, 3) The study includes an animal host model that is a natural component of the host jump system, 4) The study includes passaging as a form of transmission, 5) The study includes experimental transmission (i.e., hosts are allowed some degree of exposure to one another so that transmission can occur via a natural route). Maximum value on Y-axis is the total number of experimental studies for all viruses.