Supplementary Materials

Results

Supplementary Table S1. Matrix of product-moment correlation among centrality indices. All correlations $P<0.0001$.

	Closeness centrality	Betweenness centrality	Eigenvector centrality
Betweenness centrality	0.1724		
Eigenvector centrality	0.3439	0.6467	
Strength centrality	0.3624	0.2927	0.9907

Supplementary Table S2. Principal component analysis of correlation among centrality indices.

	Factor 1 (Composite centrality)	Factor 2
Percentage of explained variance	0.657	0.217
Closeness centrality	0.512	0.276
Betweenness centrality	0.424	-0.904
Eigenvector centrality	0.524	0.256
Strength centrality	0.532	0.203

Supplementary Table S3. Phylogenetic generalized least squares (GLS) results (i.e., effect of each centrality index on number of viruses reported in each NHP).

	Estimate±1 SE	t	*P*-value	R^2	Lambda
Closeness centrality	0.4477±0.0643	6.9659	<0.0001	0.3311	0.192*
Betweenness centrality	0.1095±0.0061	17.9201	<0.0001	0.7693	0.000
Eigenvector centrality	24.1574±2.1502	11.2350	<0.0001	0.5661	0.354***
Strength centrality	0.1135±0.0100	11.3226	<0.0001	0.5699	0.351***
Composite centrality	3.3226±0.2631	12.6284	<0.0001	0.6228	0.304***

Significance codes for phylogenetic signal (λ): * $P<0.05$; *** $P<0.001$.

Supplementary Table S4. Phylogenetic GLS results on effect of each centrality index on number of viruses reported in each NHP shared with humans.

	Estimate±1 SE	t	*P*-value	R^2	Lambda
Closeness centrality	0.4099±0.0579	7.0824	<0.0001	0.3387	0.181
Betweenness centrality	0.0982±0.0057	17.1101	<0.0001	0.7524	0.000
Eigenvector centrality	22.0750±1.9301	11.4372	<0.0001	0.5749	0.351***
Strength centrality	0.1034±0.0090	11.4533	<0.0001	0.5756	0.339***
Composite centrality	3.0201±0.2374	12.7203	<0.0001	0.6262	0.294***

Significance codes for phylogenetic signal (λ): ***: $P<0.001$.

Controlling for sampling bias in centrality computation.

Host-virus data are sensitive to sampling effort. Consequently, computation of individual centralities can be influenced by the sampling intensity of each primate species. We dealt with this issue by up-weighting the least sampled primate and down-weighting the most sampled primate per edge. For this, we corrected the weight of each edge by:

the Shared Virus Species × 1/(the Sampling Effort of NHP Species 1 × the Sampling Effort of NHP Species 2/Mean (Sampling Effort))

where sampling effort is the number of studies for each NHP species (Gómez et al., 2013).

All four centrality indices showed positive correlations ($0.2295<r<0.9723$, $P<0.05$ in all cases, $n=140$ NHPs; Supplementary Table S5), indicating that they detected similar NHP species as the most central. A single principal component analysis (PCA) factor explained 65.7% of the variance in the indices, which was used as the composite index to assess the centrality of each node (Supplementary Table S2).

Supplementary Table S5. Matrix of product-moment correlations among centrality indices after controlling for sampling bias (all correlations $P<0.05$).

	Closeness centrality	Betweenness centrality	Eigenvector centrality
Betweenness centrality	0.9321		
Eigenvector centrality	0.3441	0.4115	
Strength centrality	0.3571	0.4037	0.9818

Supplementary Table S6. Principal component analysis of correlations among centrality indices after controlling for sampling bias.

	Factor 1 (Composite centrality)	Factor 2
Percentage of explained variance	0.611	0.210
Closeness centrality	0.357	0.701
Betweenness centrality	0.469	0.437
Eigenvector centrality	0.568	-0.401
Strength centrality	0.575	-0.396

Supplementary Table S7. Phylogenetic GLS results on effects of each centrality index on number of viruses reported in each NHP after controlling for sampling bias.

	Estimate±1 SE	t	*P*-value	R^2	Lambda
Closeness centrality	3.9944±0.6121	6.5255	<0.0001	0.3022	0.000
Betweenness centrality	0.0321±0.0054	5.8565	<0.0001	0.7693	0.000
Eigenvector centrality	7.2118±2.8950	2.4911	<0.05	0.0514	0.000
Strength centrality	0.1898±0.0731	2.5981	<0.05	0.0565	0.000
Composite centrality	2.1307±0.4197	5.0773	<0.0001	0.2052	0.000

Significance codes for phylogenetic signal (λ): * $P<0.05$.

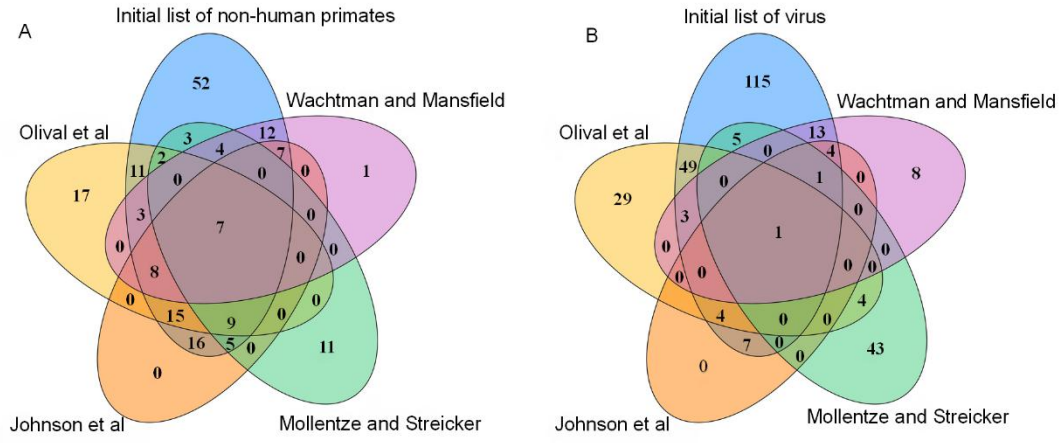
Supplementary Table S8. Phylogenetic GLS results on effects of each centrality index on number of viruses reported in each NHP shared with humans after controlling for sampling bias.

	Estimate±1 SE	t	*P*-value	R^2	Lambda
Closeness centrality	3.7336±0.5466	6.8301	<0.0001	0.3223	0.000
Betweenness centrality	0.0305±0.0048	6.2737	<0.0001	0.2855	0.000
Eigenvector centrality	7.1775±2.6056	2.7547	<0.001	0.5749	0.000
Strength centrality	0.1890±0.0657	2.8769	<0.001	0.0642	0.000
Composite centrality	2.0553±0.3733	5.5055	<0.0001	0.2339	0.000

Significance codes for phylogenetic signal (λ): * $P<0.05$.

Supplementary Table S9. Top 10 NHP species with high composite centrality in network

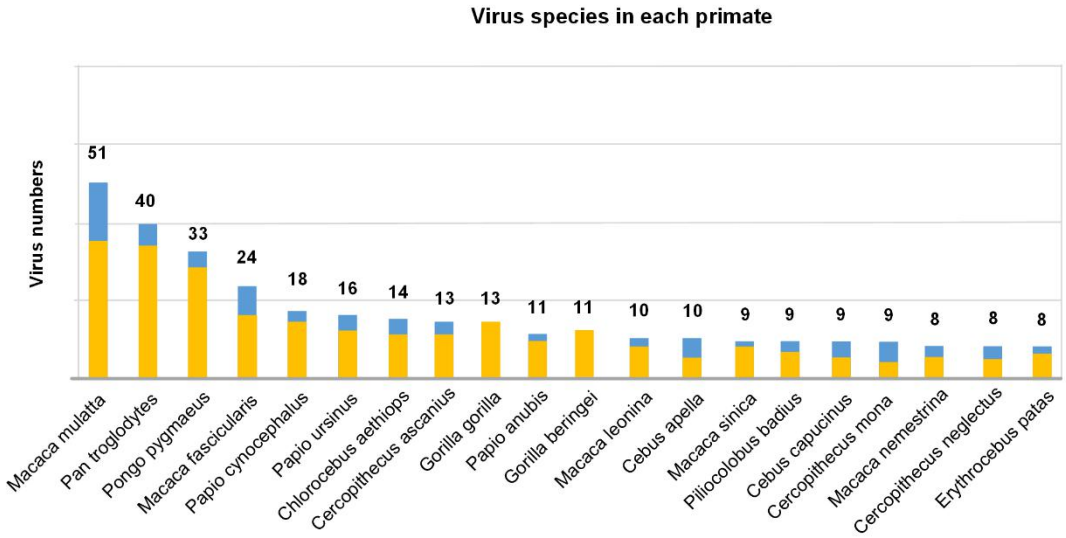
Before controlling for phylogeny and sampling effort	After controlling for phylogeny and sampling effort
Macaca mulatta	*Pan troglodytes*
Pan troglodytes	*Macaca mulatta*
Chlorocebus aethiops	*Macaca fascicularis*
Papio cynocephalus	*Papio cynocephalus*
Allochrocebus lhoesti	*Pongo pygmaeus*
Lophocebus albigena	*Cercopithecus ascanius*
Cercopithecus mitis	*Chlorocebus. aethiops*
Cercopithecus ascanius	*Macaca leonina*
Macaca fascicularis	*Cercopithecus erythrotis*
Cercopithecus neglectus	*Allochrocebus lhoesti*



Supplementary Figure S1. Relationship between data used in this study and public literature.

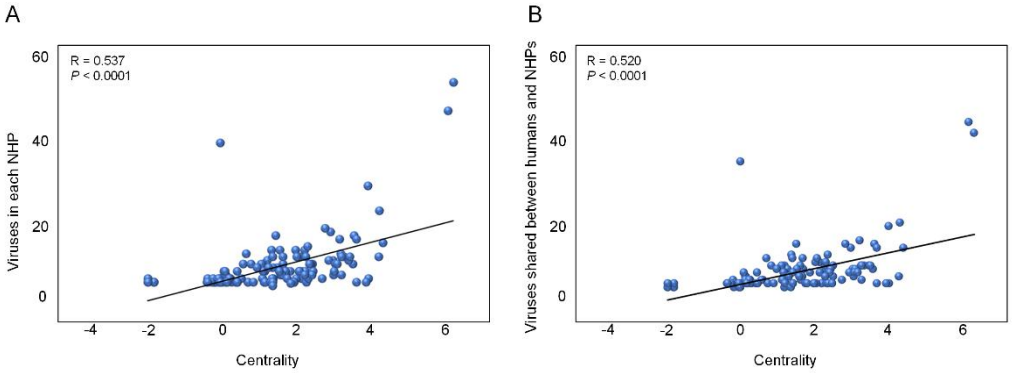
(A) Relationship between listed NHPs in initial dataset and in published literature (Johnson et al., 2020; Mollentze & Streicker, 2020; Olival et al., 2017; Wachtman & Mansfield, 2012).

(B) Relationship between listed viruses in initial dataset and published literature.



Supplementary Figure S2. NHPs with largest number of documented virus infections (top 20).

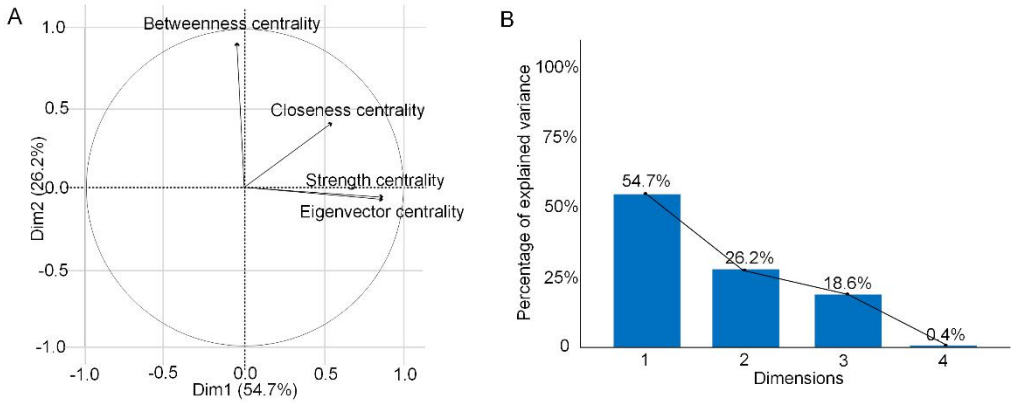
Virus infection in NHPs (top 20), yellow fraction refers to number of viruses reported in humans.



Supplementary Figure S3. Relationship between composite centrality and number of viruses in each NHP.

(A) Relationship between composite centrality and number of viruses in each NHP species.

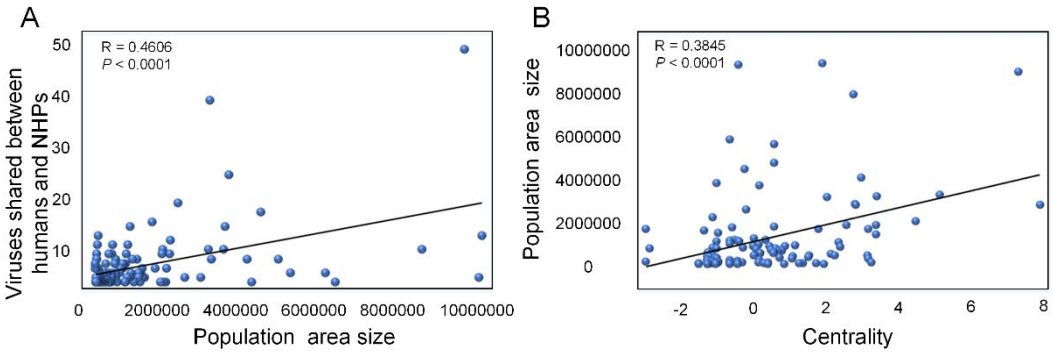
(B) Relationship between composite centrality and number of viruses in each NHP species shared with humans.



Supplementary Figure S4. Principal component analysis of NHP-virus network.

(A) Correlations among four centrality indices in network (i.e., betweenness, strength, eigenvector, and closeness centralities), which all show positive correlations.

(B) Factors found in PCA, with Dim1 factor explaining 54.7% of variance in indices.



Supplementary Figure S5. Relationship between composite centrality and number of virus species and distribution area size in each NHP species.

(A) Relationship between virus species and NHPs and distribution area size in each NHP species.

(B) Relationship between composite centrality and distribution area size in each NHP species.