Supplementary Materials

Supplementary figures S1 ~ S4

Supplementary tables S1 ~ S5

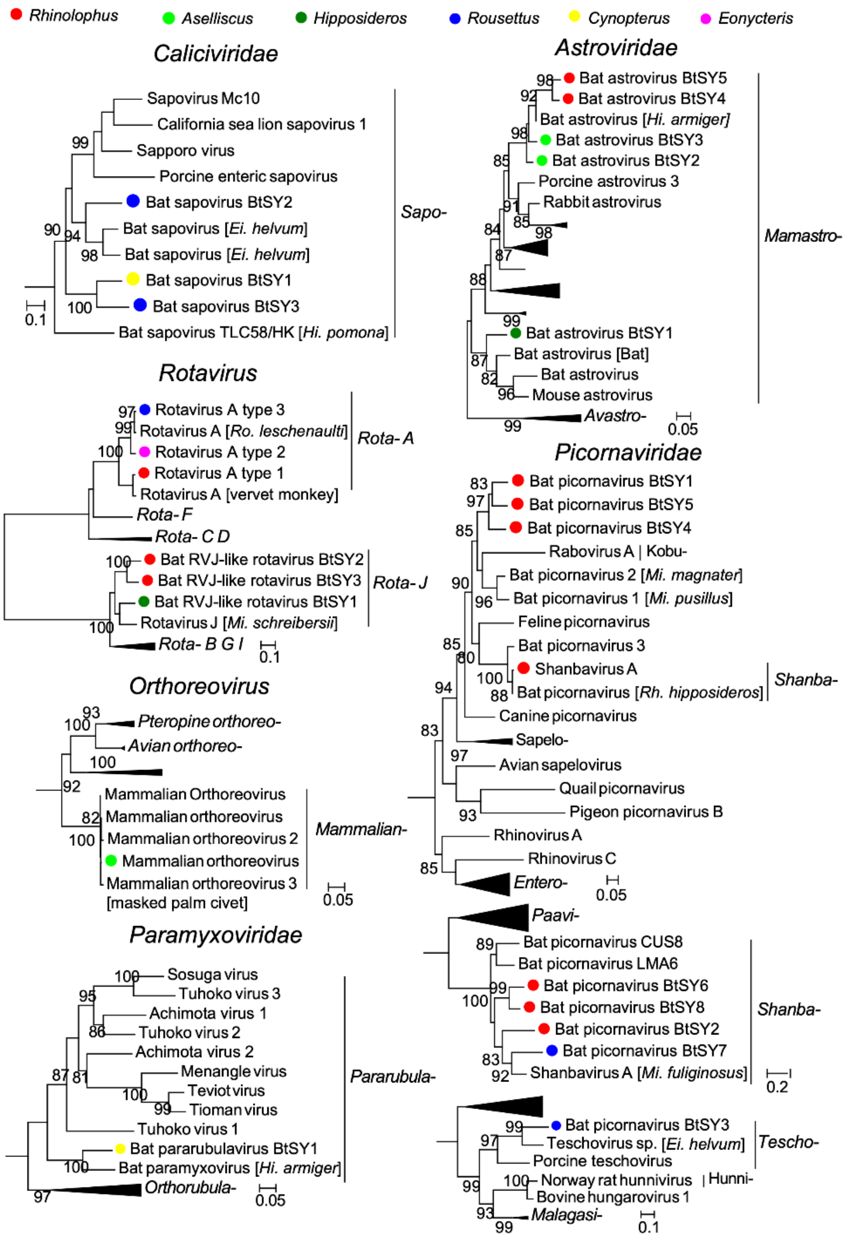

Fig. S1 | The evolutionary relationships of the RNA viruses identified in this study. The phylogenetic trees were estimated using a maximum likelihood method based on the RdRp protein. All trees were midpoint-rooted and the branch length indicates number of nucleotide substitutions per site. For clarity, only support values >80% are shown. Dots indicate viruses detected in our samples and colors represent host genus.

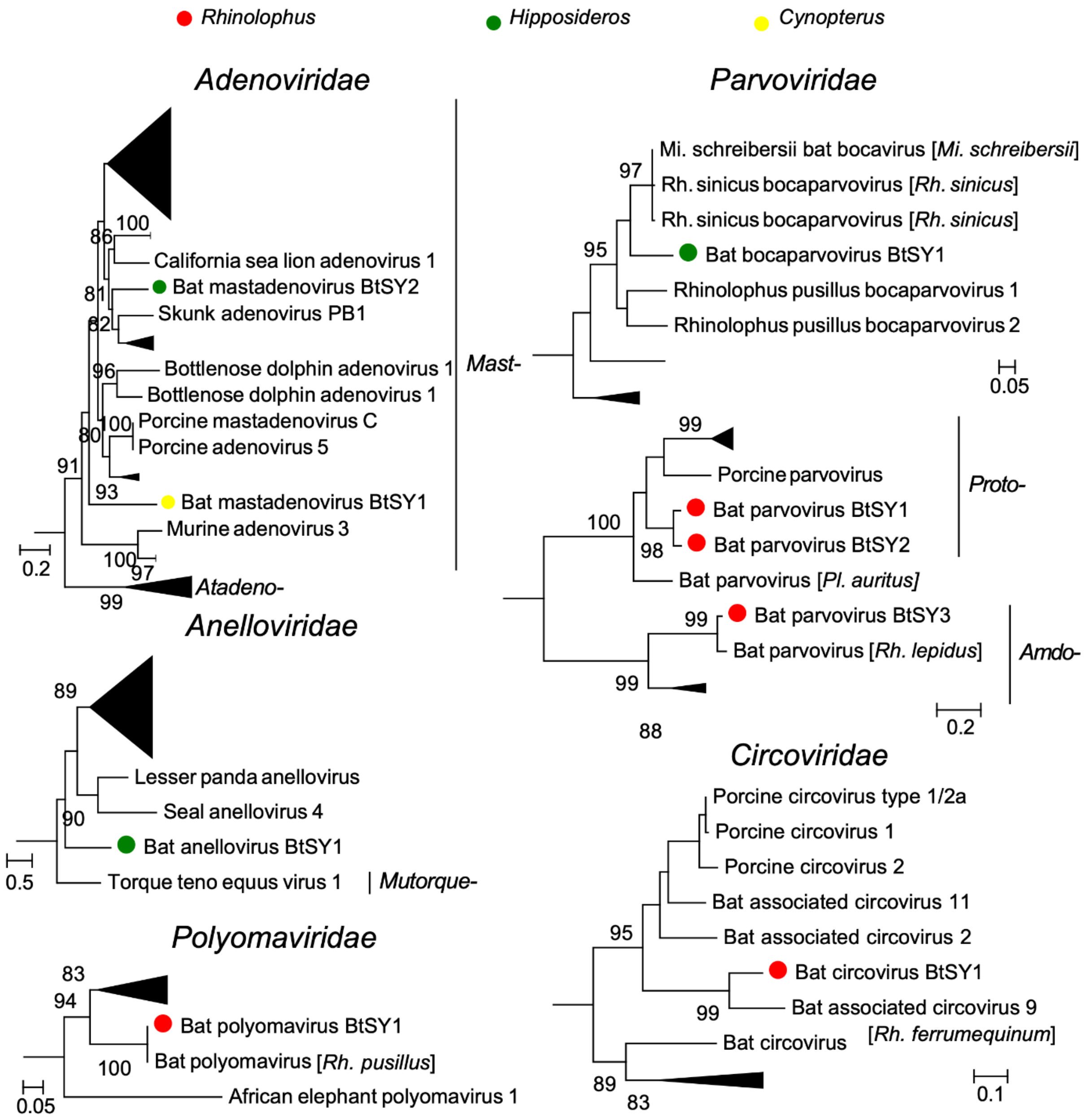

Fig. S2 | The evolutionary relationships of the DNA viruses identified in this study. These phylogenetic trees were estimated using a maximum likelihood method based on DNA pol or LTAg (*Polyomaviridae*), ORF1 (*Anelloviridae*), and NS1 (*Parvoviridae*) protein. All trees were midpoint-rooted, and the branch length indicates number of nucleotide substitutions per site. For clarity, only support values >80% were shown. Dots indicate viruses detected in our samples, and colors represent host genus.

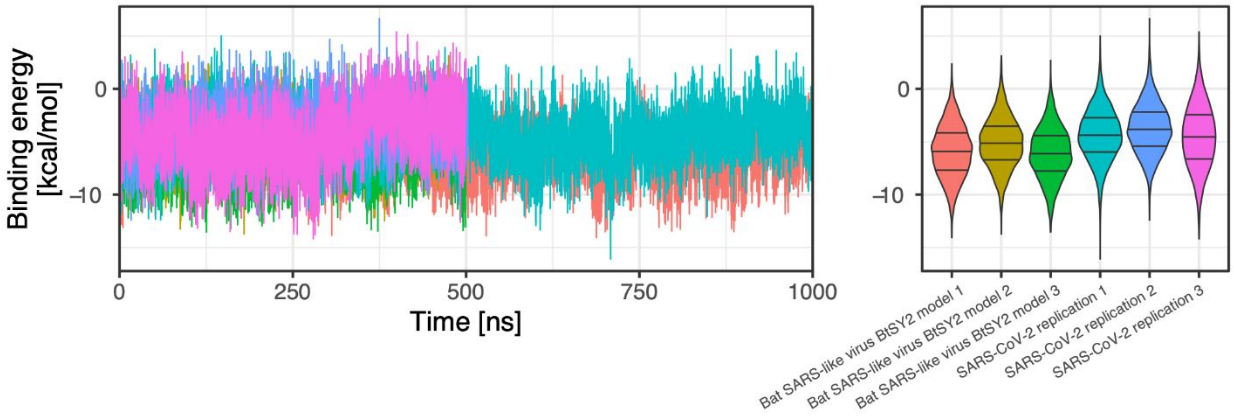

Fig. S3 | The predicted binding energy of the RBD-hACE2 complex in the duration of MD simulations. Two 1000-ns-long main simulations and four 500-ns-long replications were performed. These results showed that Bat SARS-like coronavirus BtSY2 RBD can consistently bind to hACE2, and the binding energy is slightly lower than human SARS-CoV-2, suggesting higher affinity.

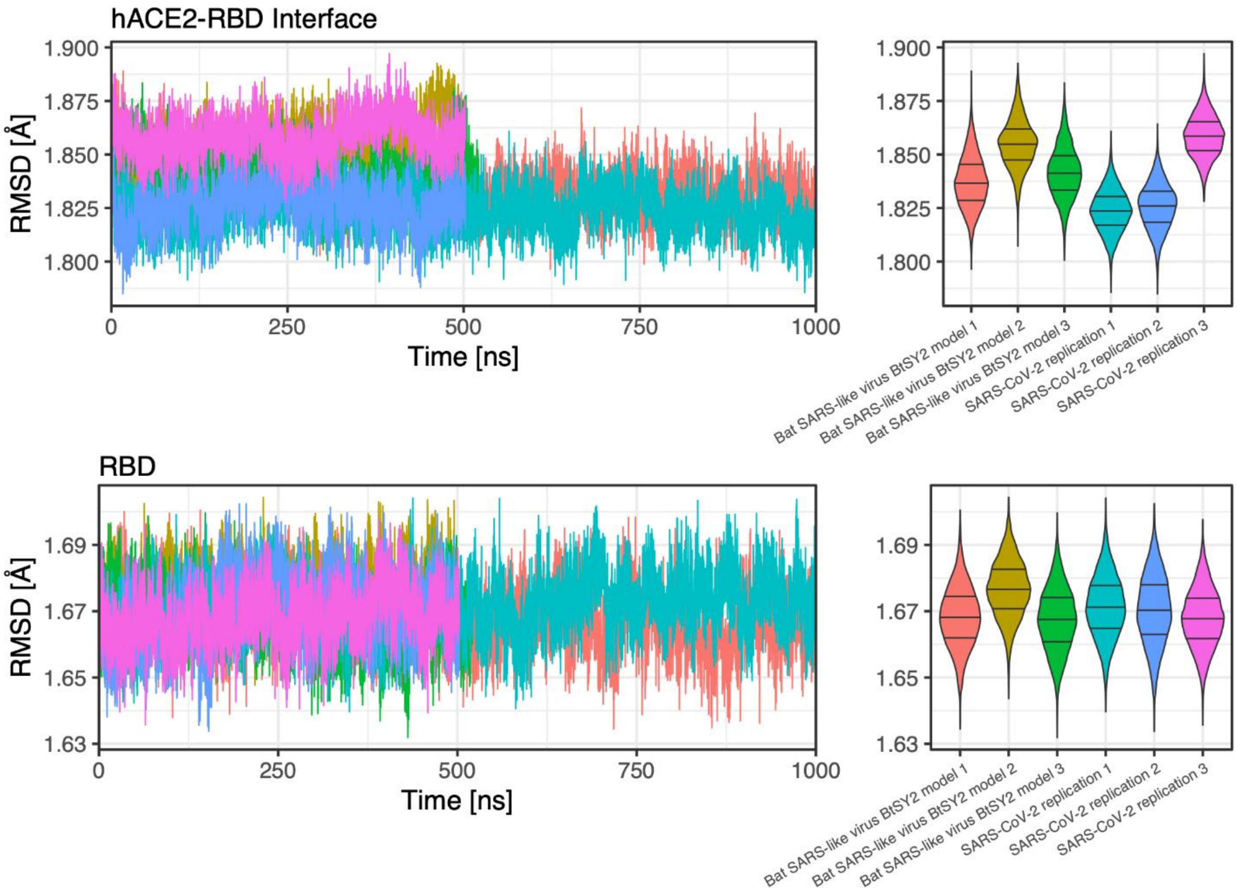

Fig. S4 | The deviation in protein backbone position during the MD simulations. RMSD is the abbreviation of root-mean-square deviation of atomic positions. We used backbone (C, N and O atoms in the main chain) RMSD to reflect the stability of RBD-hACE2 binding. Bat SARS-like coronavirus BtSY2 displayed similar binding stability with human SARS-CoV-2, regarding the RBD and RBD-hACE2 interface.

Supplementary tables

Table S1 ~ S3. Please refer to corresponding spreadsheet files (excel).

Table S4. Partial Mantel tests showing the effect of host phylogenetic distance, geographic distance and time interval on virome similarity.

Variable	Coefficient of correlation	P value
Phylogenetic distance	0.245	<0.001
Geographic distance	0.170	<0.001
Time interval	0.048	0.135

Table S5. Identification of five viruses of concern and their prevalence among bats.

Virus name	Closest known human or livestock pathogen (amino-acid identity%)	Bat host species	Prevalence (positive/total individuals)
Bat SARS-like virus BtSY1	SARS-CoV Tor2 (99.6%, RdRp)	*Rh. thomasi*	2 / 14
		Rh. macrotis	1 / 2
Bat SARS-like virus BtSY2	SARS-CoV Tor2 (99.1%, RdRp) SARS-CoV-2 Wuhan-Hu-1 (97.4%, RBD)	*Rh. marshalli*	1 / 7
		Rh. pusillus	1 / 16
Rhinolophus bat coronavirus HKU2-like	SADS-CoV GDWT-P83 (99.5%, RdRp)	*Rh. thomasi*	1 / 14
		Rh. pusillus	1 / 16
Mammalian orthoreovirus	Porcine reovirus SHR-A (99.1%, RdRp)	*As. stoliczkanus*	3 / 35
		Hi. armiger	3 / 11
		Hi. larvatus	1 / 13
		Rh. marcrotis	1 / 2
Rotavirus A type 1	Human rotavirus AU-1 (98.1%, RdRp)	*As. stoliczkanus*	9 / 35
		Rh. thomasi	1 / 14
		Rh. pusillus	1 / 16
		Rh. marshalli	1 / 7
		Rh. pearsonii	1 / 2