

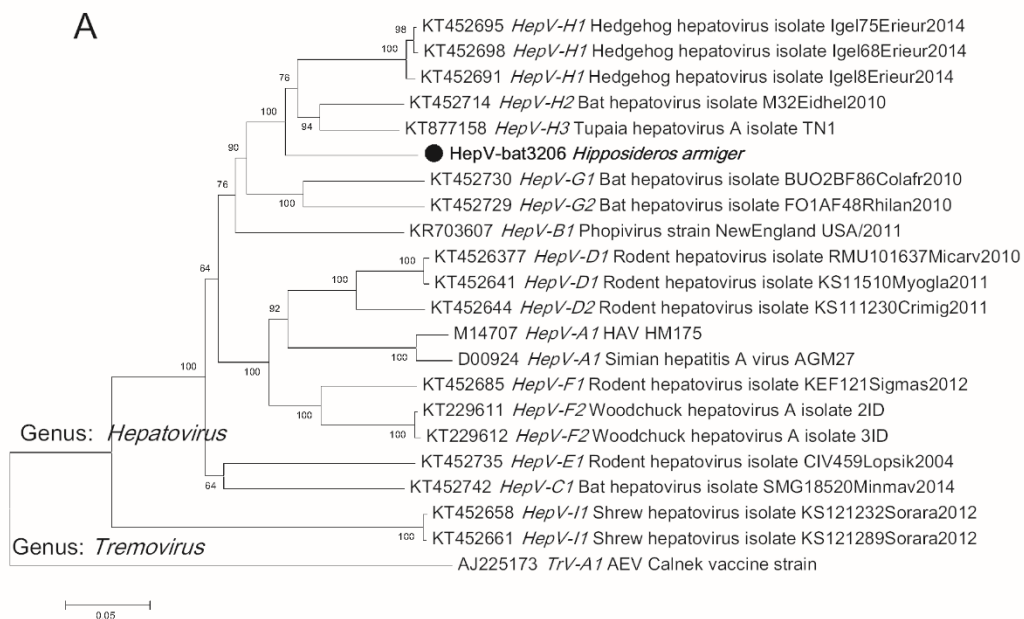
Electronic Supplementary Material

Genomic Characterization of a Novel Hepatovirus from Great Roundleaf Bats in China

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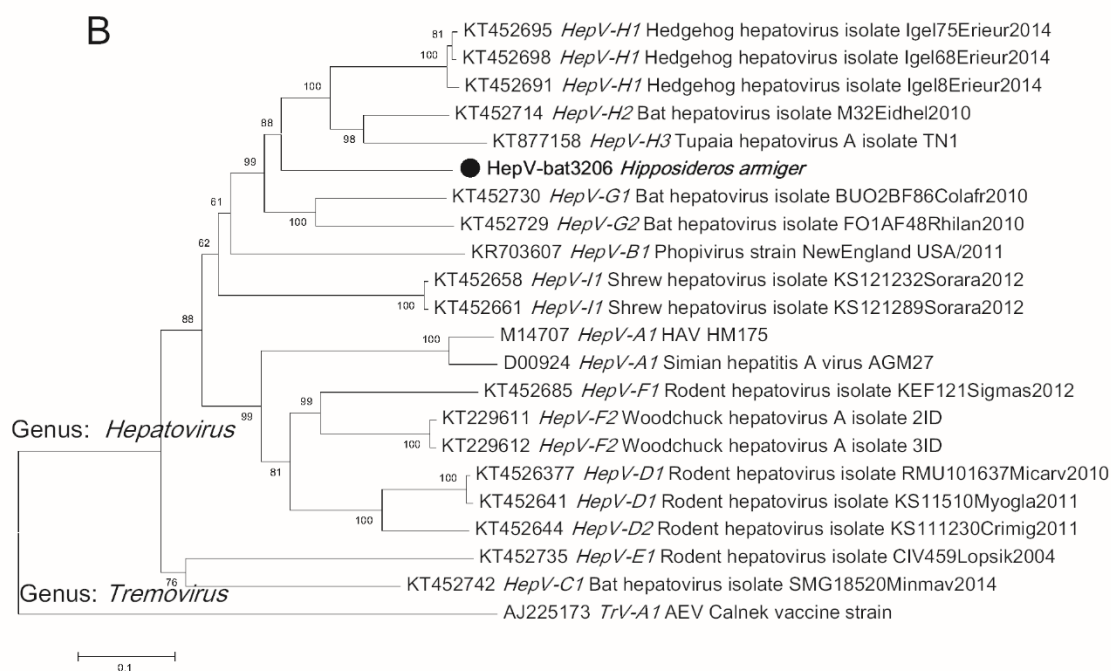


Figure S1. The phylogenetic tree of *Hepatovirus* based on amino acid sequences of P1 (capsid protein) (A) and P3CD (polymerase protein) (B). The neighbor-joining phylogenetic tree was constructed using the MEGA7 with 1000 bootstrap replicates. The virus sequence obtained in this study is indicated by the black solid circle.

Table S1 Hepatovirus detection in *Hipposideros* bat feces or fecal swab samples

Sampling Date	Positive rate of hepatovirus	Location City, Province
2011	0/52	E'mei, Sichuan
2011	6/311 (1.93%)	Xianning, Hubei
2012	1/276 (0.36%)	Xianning, Hubei
2013	0/89	Xianning, Hubei
2014	2/202 (0.99%)	Xianning, Hubei
2013	0/82	Mojiang, Yunnan
2013	0/40	Qingyang, Anhui
2013	0/8	Tonglu, Zhejiang
2013	0/13	Guilin, Guangxi
2013	0/105	Nanling, Guangdong
2013	0/88	Yibin, Sichuan
Total	9/1266(0.71%)	