Title	Isolation and characterization of a novel alphaherpesvirus in fruit bats.
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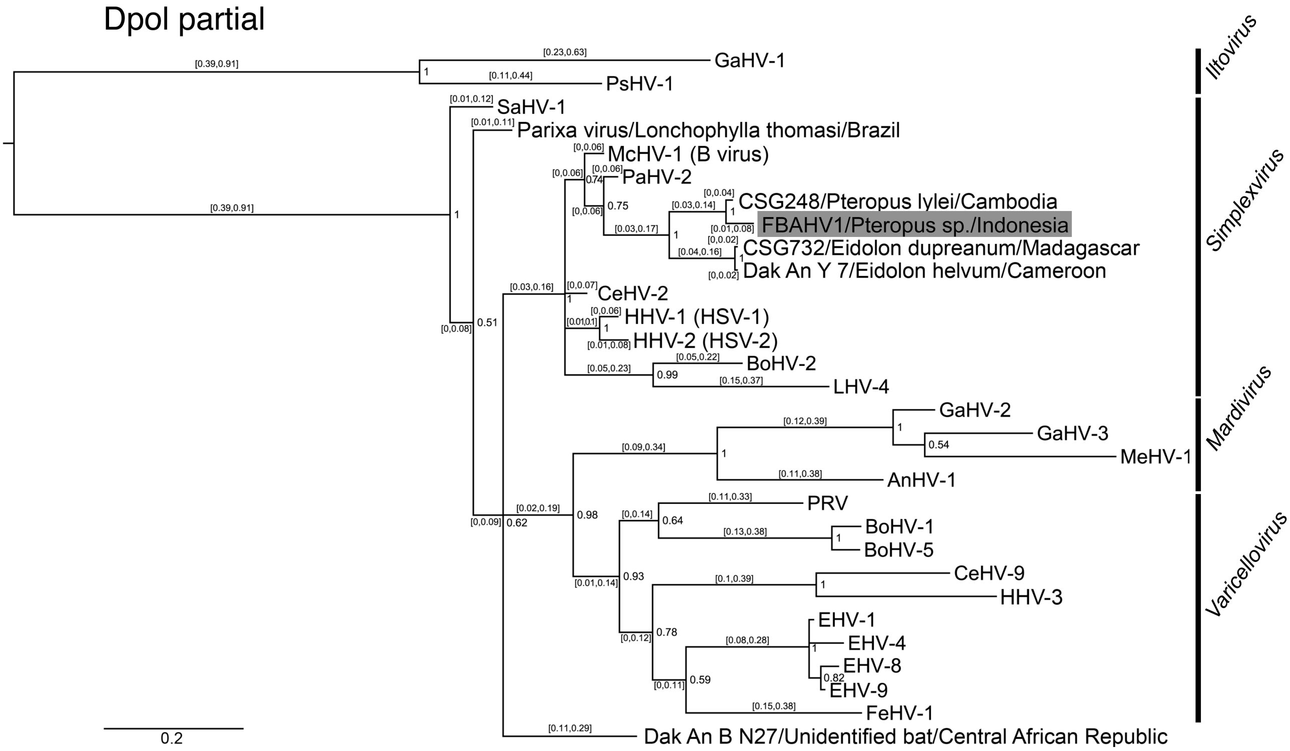

Fig. S1. Bayesian phylogenetic tree based on partial amino acid sequences of the *UL30* product.

Trees were constructed based on the deduced partial amino acid sequences (155 amino acids) of viral DNA polymerase (Dpol), which is encoded by *UL30* in simplex viruses. The WAG amino acid substitution model was used. Bayesian posterior probabilities are indicated at each tree root. The branch labels represent the 95% highest posterior density interval of the substitution rate. The scale bar represents a distance of 0.2 substitutions per site. FBAHV1 is shaded grey. The abbreviated virus names and the accession numbers of the sequences used for the analysis are shown in Table S1.

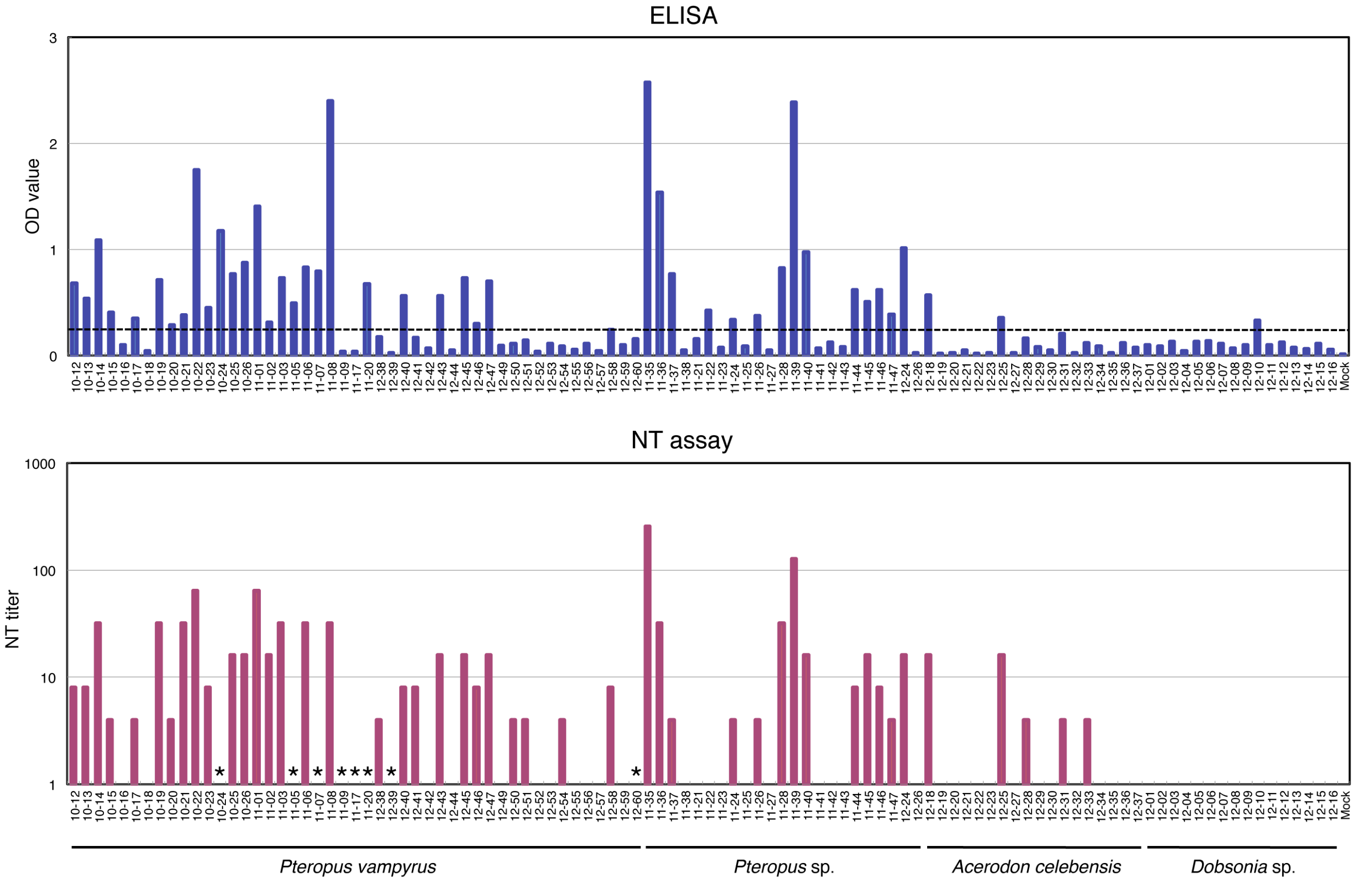

Fig. S2. FBAHV1-specific antibodies detected in sera collected from Indonesian fruit bats. The upper graph shows the result of the FBAHV1 ELISA. The horizontal dashed line indicates the cutoff value, which was set at an OD of 0.23. The lower graph shows the results of the virus neutralization test. Asterisks indicate samples removed from the analysis because they were either cytotoxic or of insufficient volume.

Table S1. Viruses used for phylogenetic analysis

Genus	Name	Abbreviation	Accession Number (Dpol / gG)
Simplexvirus	Cercopithecine herpesvirus 2	CeHV-2	YP_164473/YP_164506
	Herpes simplex virus type 1	HHV-1 (HSV-1)	NP_044632/NP_044666
	Herpes simplex virus type 2	HHV-2 (HSV-2)	NP_044500/NP_044534
	Macacine herpesvirus 1	McHV-1 (B virus)	NP_851890/NP_851923
	Papiine herpesvirus 2	PaHV-2	YP_443877/YP_443910
	Saimiriine herpesvirus 1	SaHV-1	YP_003933809/YP_003933846
	Bat simplexvirus 1	Dak An B N27	ACJ02393/―
	Eidolon dupraenum simplexvirus 1	CS732G	ACJ02384/―
	Eidolon helvum simplexvirus 1	Dak An Y 7	ACJ02395/―
	Lonchophylla thomasi simplexvirus 1	Parixa virus	ACJ02392/―
	Pteropus lylei simplexvirus 1	CSG248	ACJ02382/―
	Bovine herpesvirus 2	BoHV-2	AAD55134/AAD45608
	Leporid herpesvirus 4	LHV-4	AFR32472/AFR32506
	Macropodid herpesvirus 2	MaHV-2	―/AAL13142
Varicellovirus	Bovine herpesvirus 1	BoHV-1	NP_045328/NP_045369
	Bovine herpesvirus 5	BoHV-5	YP_003662494/YP_003662532
	Cercopithecine herpesvirus 9	CeHV-9	NP_077443/―
	Equid herpesvirus 1	EHV-1	YP_053075/YP_053114
	Equid herpesvirus 4	EHV-4	NP_045247/NP_045287
	Equid herpesvirus 8	EHV-8	YP_006273050/YP_006273009
	Equid herpesvirus 9	EHV-9	YP_002333511/YP_002333551
	Felid herpesvirus 1	FeHV-1	YP_003331549/YP_003331588
	Suid herpesvirus 1	SuHV-1	YP_068333/YP_068386
	Human herpesvirus 3	HHV-3	NP_040151/―
Mardivirus	Anatid herpesvirus 1	AnHV-1	YP_003084391/YP_003084432
	Gallid herpesvirus 2	GaHV-2	YP_001033959/―
	Gallid herpesvirus 3	GaHV-3	NP_066862/―
	Meleagrid herpesvirus 1	MeHV-1	NP_073324/―
Iltovirus	Gallid herpesvirus 1	GaHV-1	YP_182359/YP_182403
	Psittacid herpesvirus 1	PsHV-1	NP_944403/NP_944446

The Dpol ORF of MaHV-2 has not yet been sequenced. The gG ORF was absent from the genomes of HHV-3, CeHV-9, GaHV-2, GaHV-3, and MeHV-1. This ORF has not yet been sequenced in the Dak An B N27, CS732G, Dak An Y 7, Parixa virus, or CSG248 genomes.