

Identification numbers of sequences used in the work

Gene	Organism	Sequences of cDNA (NCBI Accession number)	Amino acid sequences (NCBI Accession number)
IL6	<i>Homo sapiens</i> <i>Pan troglodytes</i> <i>Gorilla gorilla</i> <i>Macaca mulatta</i> <i>Papio anubis</i> <i>Chlorocebus sabaeus</i> <i>Callithrix jacchus</i> <i>Saimiri boliviensis</i> <i>Otolemur garnettii</i> <i>Microcebus murinus</i> <i>Mus musculus</i> <i>Rattus norvegicus</i>	NM_000600.4 XM_518992.6 XM_004045160.1 NM_001042733.2 NM_001173536.1 FJ194486.1 NM_001267771.1 XM_003935111.2 NM_031168.2 NM_012589.2	NP_000591.1 XP_518992.2 XP_004045208.1 NP_001036198.2 NP_001167007.1 ACI28913.1 NP_001254700.1 XP_003935160.1 XP_012659779.1 XP_012628750.1 NP_112445.1 NP_036721.1
vIL6	human herpesvirus 8 (UNKNOWN-U73655) macacine herpesvirus 5 (17577) rhesus monkey rhadinovirus (H26-95) <i>Macaca nemestrina</i> rhadinovirus 2	U73655 NC_003401	AAB18244.1 NP_570753.1 AAC58690.1 AJE29651.1
IL17A	<i>Homo sapiens</i> <i>Pan troglodytes</i> <i>Gorilla gorilla</i> <i>Macaca mulatta</i> <i>Papio anubis</i> <i>Chlorocebus sabaeus</i> <i>Callithrix jacchus</i> <i>Saimiri boliviensis</i> <i>Aotus nancymae</i> <i>Mus musculus</i> <i>Rattus norvegicus</i>	NM_002190.2 XM_003833162.1 XM_004044183.1 XM_001106391.3 XM_003897728.2 XM_007972271.1 XM_002746684.2 XM_003923111.1 NM_010552.3 NM_001106897.1	NP_002181.1 XP_527408.2 XP_004044231.1 XP_001106391.1 XP_003897777.1 XP_007970462.1 XP_002746730.2 XP_003923160.1 XP_012296950.1 NP_034682.1 NP_001100367.1
vIL17	Saimiriine herpesvirus 2 (UNKNOWN-NC_001350)	NC_001350	NP_040215.1
IL17B	<i>Homo sapiens</i> <i>Pan troglodytes</i> <i>Mus musculus</i>		CAG33473.1 XP_001163413.1 XP_006526169.1
IL17C	<i>Homo sapiens</i> <i>Mus musculus</i>		AAQ88835.1 AAI45854.1
IL17D	<i>Homo sapiens</i> <i>Mus musculus</i>		AAQ89471.1 NP_665836.2
IL25	<i>Homo sapiens</i> <i>Mus musculus</i>		AAL57622.1 AAL57623.1
IL17F	<i>Homo sapiens</i> <i>Pan troglodytes</i> <i>Mus musculus</i>		XP_011512578.1 XP_527409.2 XP_006495586.1
IL17a/f	<i>Danio rerio</i>		XP_009291138.1
IL10	<i>Homo sapiens</i> <i>Pan troglodytes</i> <i>Gorilla</i> <i>Pongo abelii</i> <i>Macaca mulatta</i> <i>Papio anubis</i> <i>Callithrix jacchus</i> <i>Saimiri boliviensis</i> <i>Mus musculus</i> <i>Rattus norvegicus</i>	NM_000572.2 XM_016927617.1 XM_004028289.1 XM_002809541.2 XM_005540653.2 XM_003893197.2 XM_002760733.2 XM_003930436.2 NM_010548.2 NM_012854.2	NP_000563.1 NP_001129092.2 XP_004028338.1 XP_002809587.1 NP_001038192.1 XP_003893246.1 XP_002760779.1 XP_003930485.1 NP_034678.1 NP_036986.2
vIL10	human herpesvirus 4	AJ507799.2	CAD53385.1

Phylogenetic Trees Reconstructed by the Maximal Likelihood Method and Bayesian Analysis

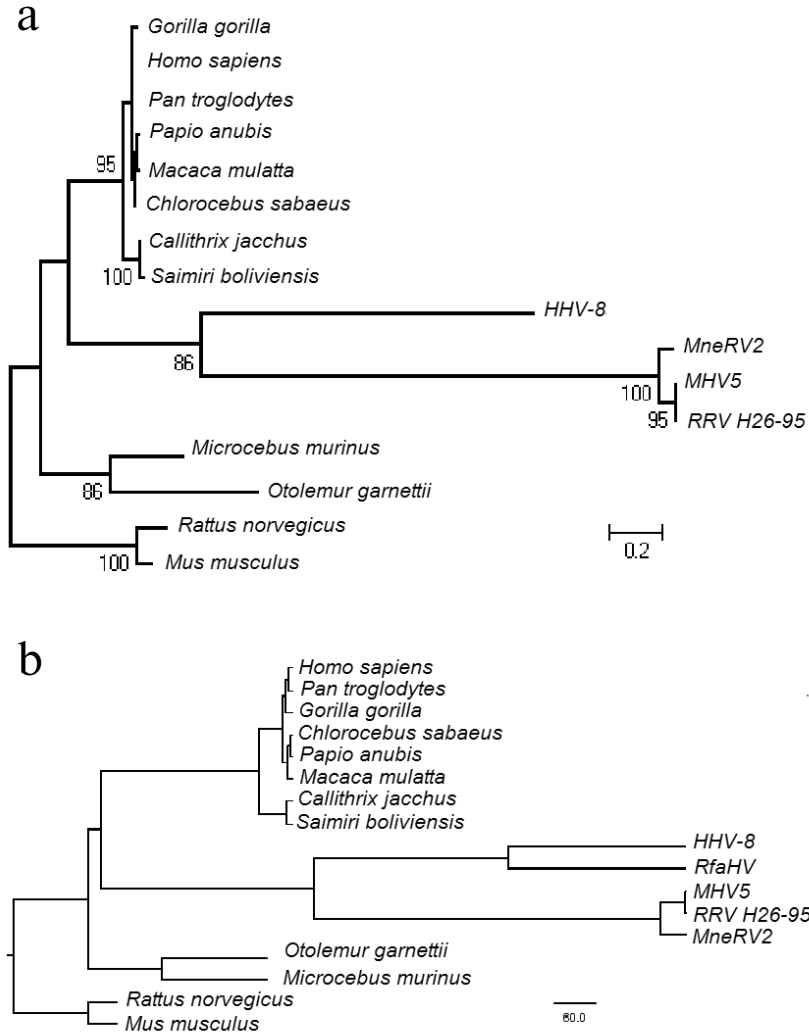


Fig. S1. Sequences of IL-6 of human herpesvirus 8 and of some macaque herpesviruses are related to sequences of IL-6 of dry-nosed monkeys (suborder *Haplorhini*). The tree is reconstructed based on multiple alignment of amino acid sequences of IL-6 homologs with an evolutionary model JTT [1] (a). At reconstructing the tree by the Bayesian method, a relaxed lognormal model of molecular clock is used (b). Topologies of the trees obtained by different methods are coincident.

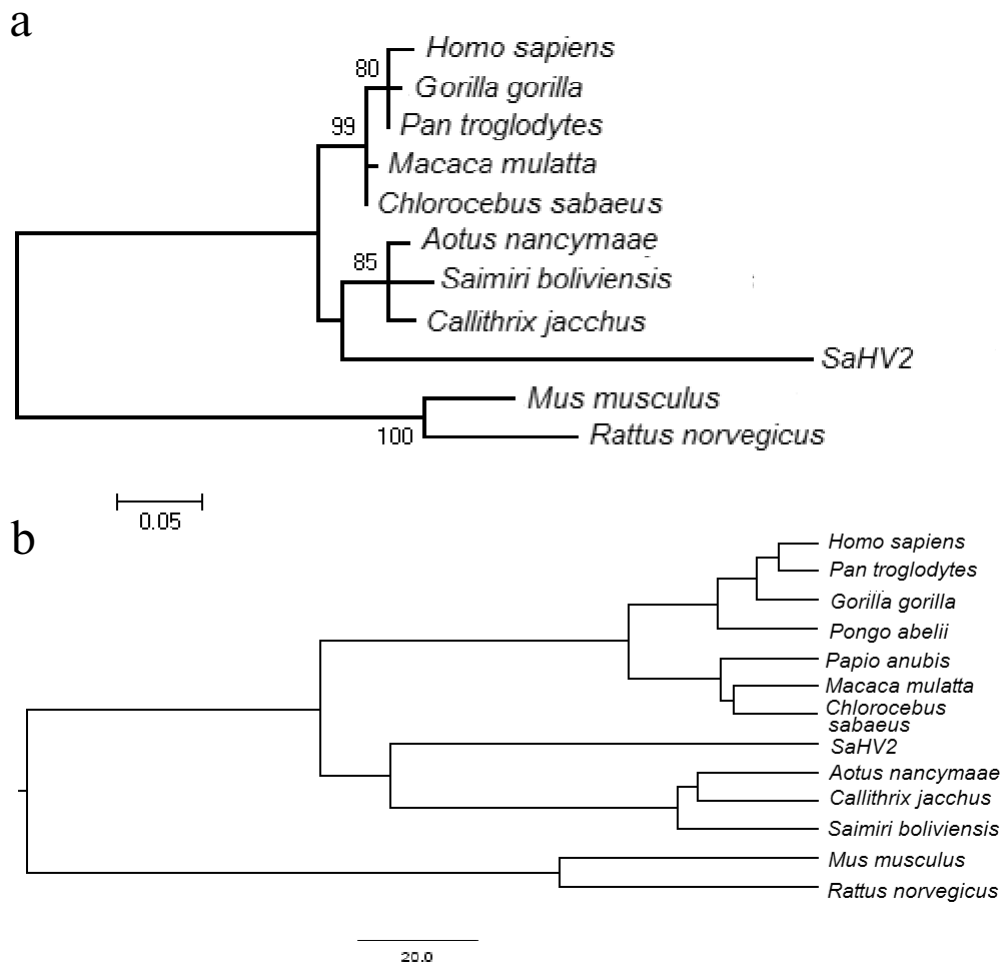


Fig. S2. Virokine of Saimiriine herpesvirus 2 (SaHV2) is homologous to IL-17A and clustered together with homologs IL-17A of the New World monkey. The tree is reconstructed based on multiple alignment of amino acid sequences of IL-17A homologs using an evolutionary model JTT+G [1] (a). At reconstructing the tree by the Bayesian method, the relaxed lognormal model of molecular clock is used [2] (b). Topologies of trees obtained by different methods are coincident.

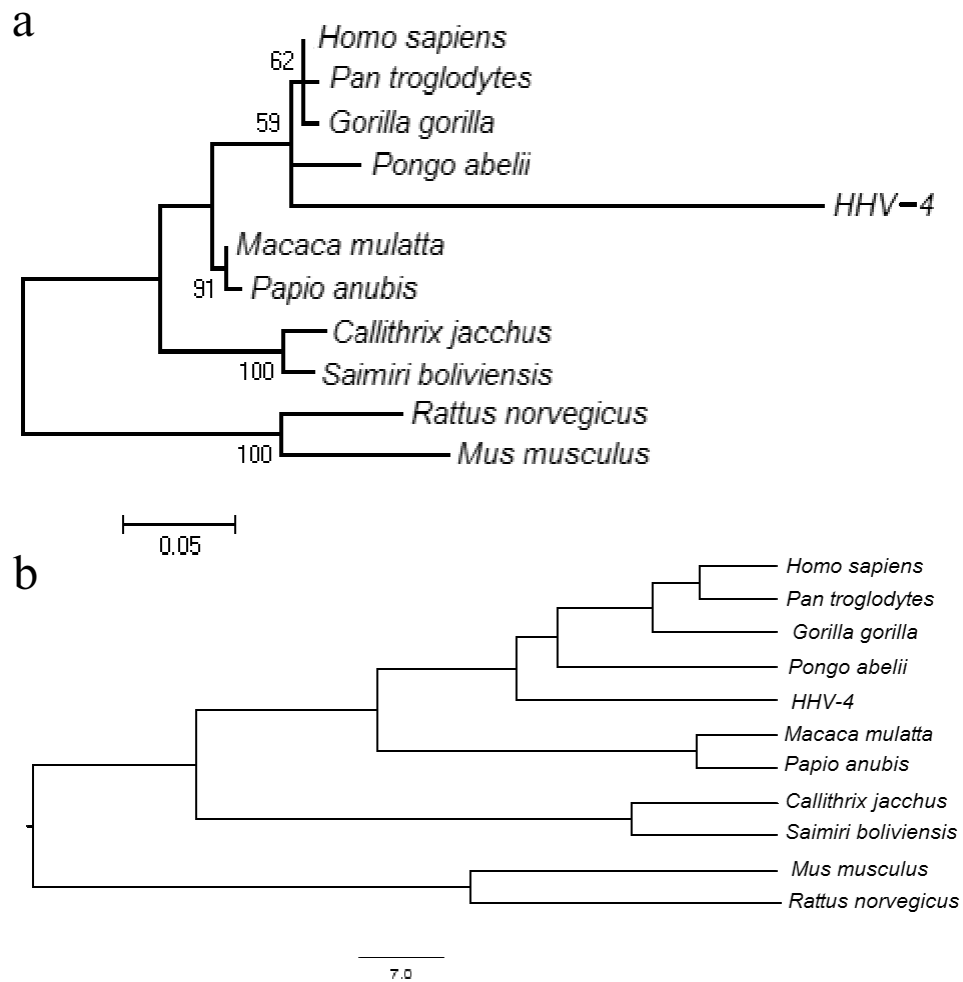


Fig. S3. Virokine of the Epstein–Barr virus (HHV-4) is related to IL-10 of anthropoid apes. The tree is reconstructed based on multiple alignment of amino acid sequences of IL-10 homologs by an evolutionary model JTT+I [1] (a). At reconstructing the tree by the Bayesian method, the relaxed lognormal model of molecular clock is used [2] (b). Topologies of trees obtained by different methods are coincident.

REFERENCES

1. Jones, D. T., Taylor, W. R., and Thornton, J. M. (1992) The rapid generation of mutation data matrices from protein sequences, *Comput. Appl. Biosci.: CABIOS*, **8**, 275-282.
2. Drummond, A. J., Ho, S. Y., Phillips, M. J., and Rambaut, A. (2006) Relaxed phylogenetics and dating with confidence, *PLoS Biol.*, **4**, e88.