

**Table S4 A. Genetic distance (Kimura) for gag-env portions**

	PTR	GGO	MMU	PAN
PTR	0.028 +/- 0.003			
GGO	0.038 +/- 0.003	0.041 +/- 0.003		
MMU	0.092 +/- 0.006	0.096 +/- 0.006	0.103 +/- 0.007	
PAN	0.097 +/- 0.007	0.101 +/- 0.007	0.106 +/- 0.007	0.090 +/- 0.006

\*Portions of the gag and env genes (X=823 bp) were resequenced for n PTERV1 elements from common chimpanzee (PTR), gorilla (GGO), rhesus macaque (MMU) and the olive baboon (PAN). The number of substitutions between and within groups is compared (Kimura 2-parameter model).

\*\*Overall substitution among all elements was 0.073 +/- 0.004

**Table S4 B. Genetic distance (Kimura) for LTR portions.**

	PTR	GGO	MMU	PAN
PTR	0.031 +/- 0.006			
GGO	0.039 +/- 0.006	0.037 +/- 0.006		
MMU	0.140 +/- 0.015	0.143 +/- 0.015	0.142 +/- 0.016	
PAN	0.250 +/- 0.023	0.245 +/- 0.023	0.181 +/- 0.018	0.242 +/- 0.020

\*The number of substitutions (K2M) for LTR (295 bp) sequence was compared between and within species.

\*\*Overall substitution among all elements was 0.157 +/- 0.013