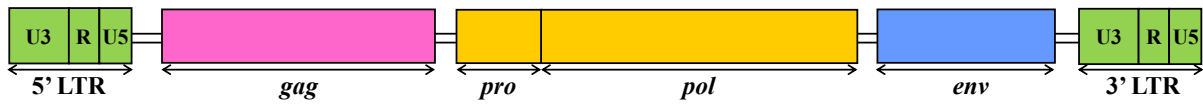
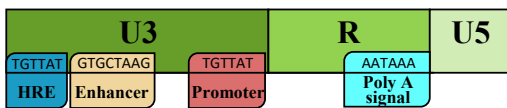




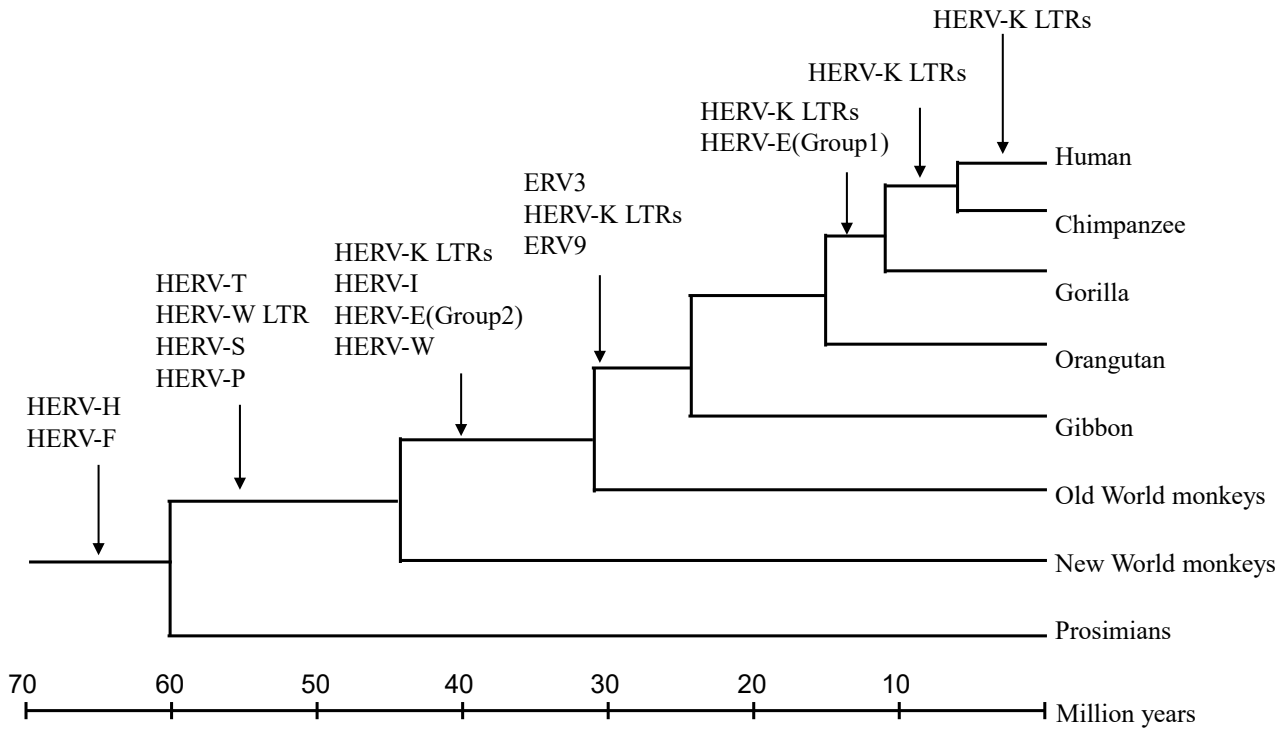
A General HERV structure



B Solitary LTR structure



Supplementary Fig. S1. The structure of human endogenous retroviruses (HERVs). (A) The general structure of HERVs. (B) The general structure of solitary long terminal repeat (LTR) elements derived from HERVs. LTR, long terminal repeat; *gag*, group-specific antigen; *pol*, reverse transcriptase; *pro*, protease; *env*, envelope protein.



Supplementary Fig. S2. The evolutionary tree of the human endogenous retrovirus (HERV) subfamily. Arrows indicate the approximate insertion times of several endogenous retroviruses during hominoid radiation.

Supplementary Table S1. The distribution of LTR containing ZFS by LTR class/family

Class/Family	The number of LTR fragments containing ZFS	The number of LTR fragments in the human genome	Composition	Density
LTR	49	2201	0.63%	2.23%
LTR?	0	122	0.00%	0.00%
LTR/ERV	3	579	0.04%	0.52%
LTR/ERV1	2686	172893	34.33%	1.55%
LTR/ERVK	618	10490	7.90%	5.89%
LTR/ERVL	1930	157992	24.67%	1.22%
LTR/ERVL?	4	1800	0.05%	0.22%
LTR/ERVL-MaLR	2400	343675	30.68%	0.70%
LTR/Gypsy	58	10764	0.74%	0.54%
LTR/Gypsy?	75	7816	0.96%	0.96%
Total LTR	7823	708332	100.00%	1.10%

※ A "?" at the end of the class/family signifies that the curator was unsure of the classification.