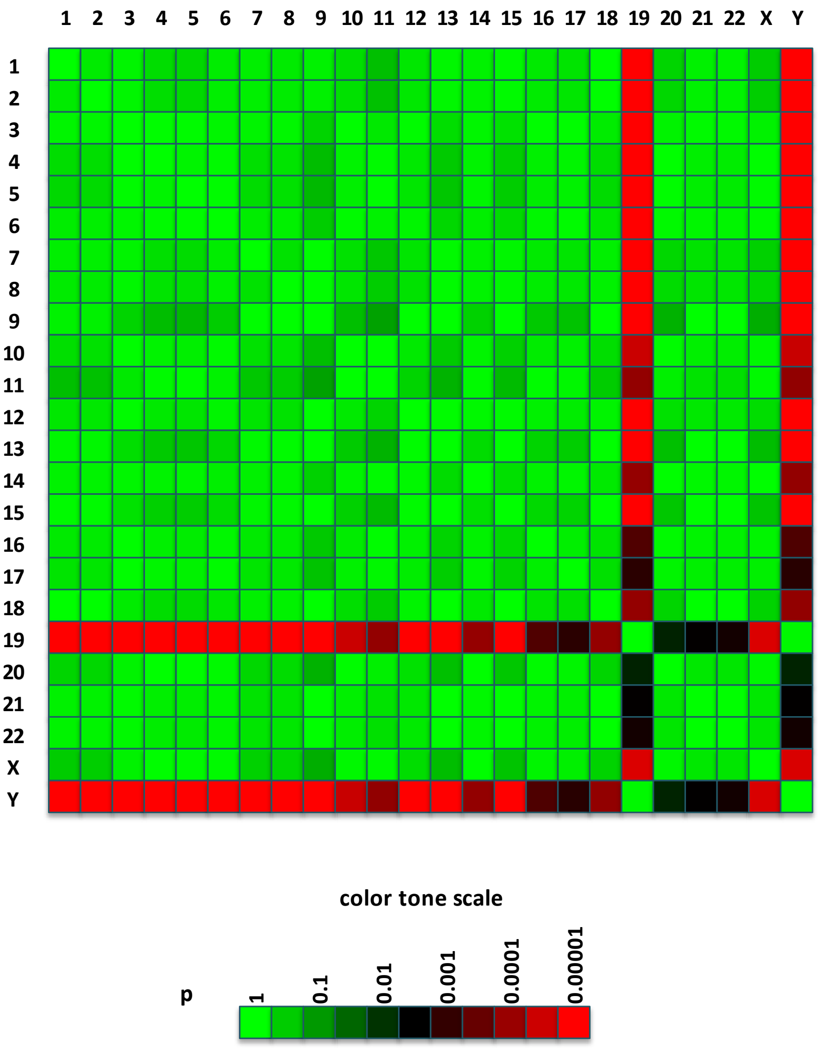

Fig. S1. Heatmap of p values obtained from the chi-square for the difference in the frequency of HML-6 proviruses insertions calculated between each pair of chromosomes. All p values obtained from the comparison of chromosome 19 and Y with all other chromosomes were statistically significant, with a cumulative probability of false discoveries less than 5%, as assessed by the Benjamini-Hockberg procedure. Conversely, all other comparisons were not statistically significant

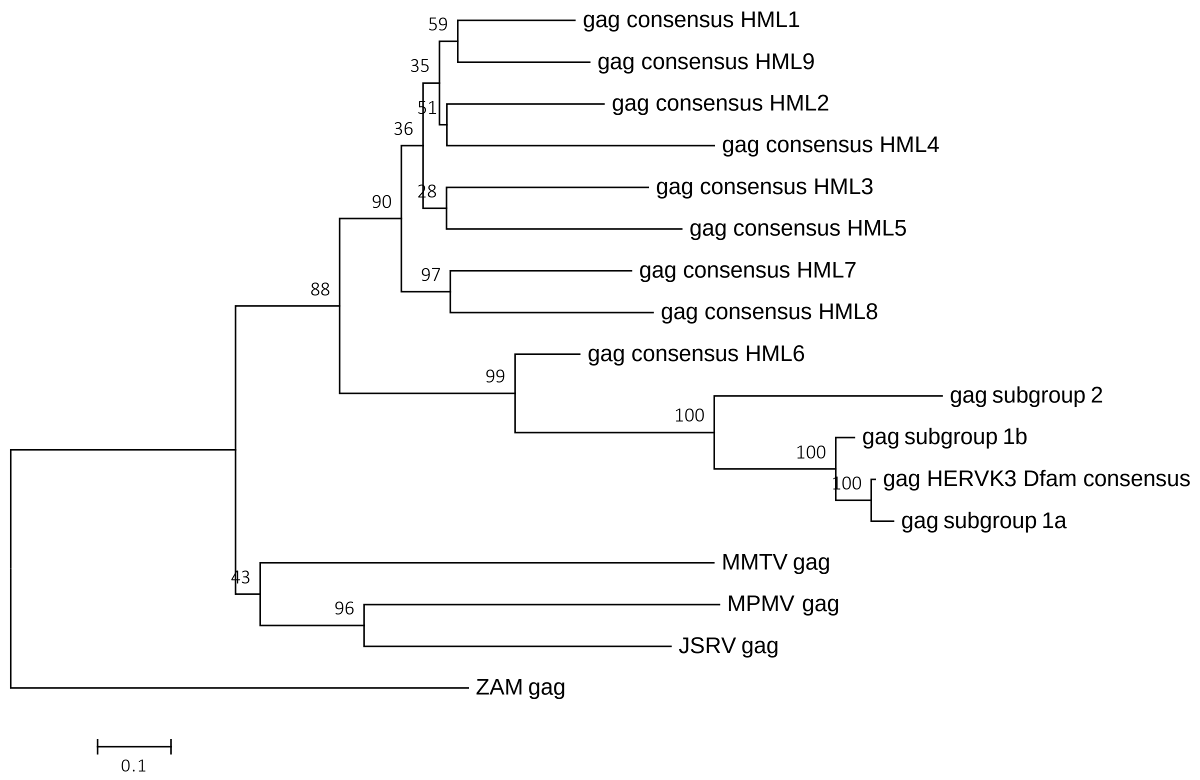

Fig. S2. Phylogenetic tree of the HML gag consensus sequences. The phylogeny of HML-6 group was investigated by performing a NJ analysis of amino acid sequences of gag. Our consensus sequences for the gag gene of each subgroup and the gag consensus sequences of the others HML groups are included in this tree. The gag sequences of the exogenous betaretroviruses MMTV, MPMV and JSRV, and gag sequence of ZAM, endogenous retrovirus in *drosophila* were used as out-groups. The phylogenetic tree has been built by using the Bootstrap method with 1000 replicates.

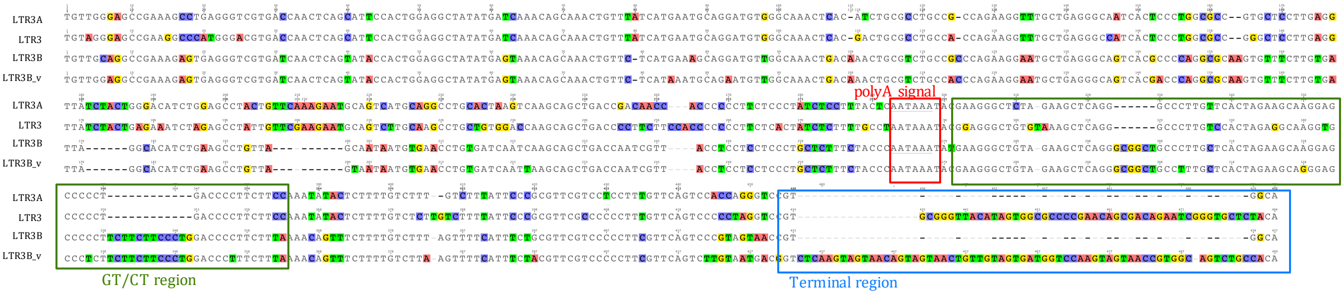

Fig. S3. Structural characterization of HML-6 LTRs. The alignments between the LTR3A, LTR3, LTR3B and LTR3B_v Dfam consensus sequences are showed as two-dimensional dot plots matrices, where the sequences were compared along the vertical and horizontal axes and the similarity between them are indicated by black dots composing a diagonal lines across the matrix. In particular, the dotplots showed differences in length between LTR3A and LTR3 consensus and between LTR3B and LTR3B_v consensus, caused by deletions in the LTR3A and LTR3B_v a 3'-ends.

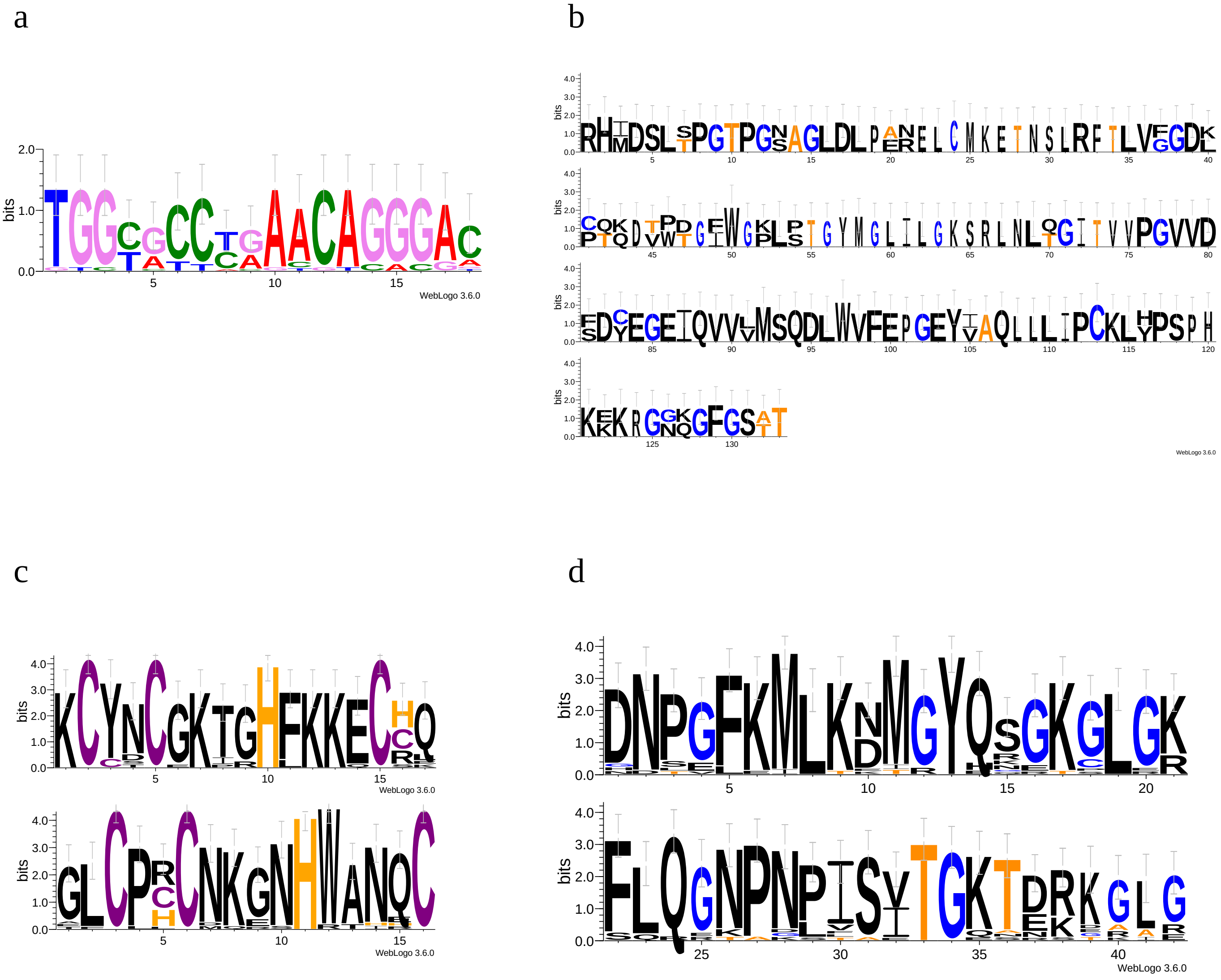

Fig. S4. Sequence logos of PBS and beta-retroviral conserved motifs. (a) PBS for lysine nucleotide sequence; (b) Type 1 and type2 Trimeric dUTPase consensus domains; (c) Gag nucleocapsid Zinc fingers and (d) G-patch domain. The height of symbols indicates the relative frequency of each nucleotide or amino acid. Logo created at http://weblogo.berkeley.edu/logo.cgiof.

File S.1 Coordinates of 66 HML-6 loci in genome assembly hg38 (A). Coordinates of HML-6 LTRs obtained by performing a BLAT search in genome assembly hg19 (B) and corresponding coordinates in genome assembly hg38 (C)

File S.1-A

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Supplemental file 1

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File S.1-B

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File S.1-C

#Coordinates of HML-6 LTRs in genome assembly hg38

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File S.2 Fasta alignment of HML-6 type 1 and type 2 consensus sequences generated by Geneious software (A) and collection of HML-6 Rec amino acid sequences and a Rec amino acid consensus also generated by Geneious software (B)

File S.2-A

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#Alignment of type 1 and type 2 generated consensus sequences
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File S.2-B

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# HML-6 Rec amino acid sequences and HML-6 Rec consensus sequence
>HML-6 Rec consensus
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