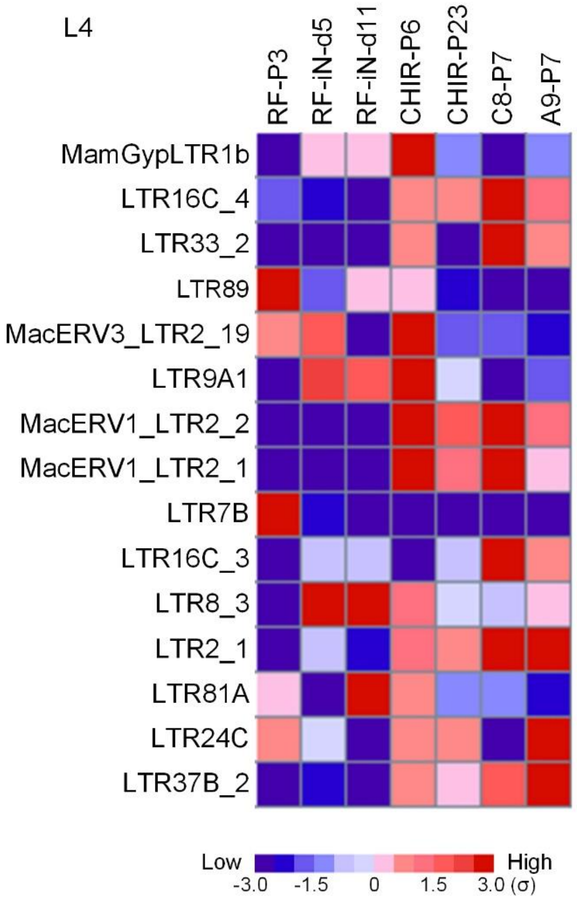

Figure S1. The expression levels of LTRs in the Cluster L4 of Figure 3A.

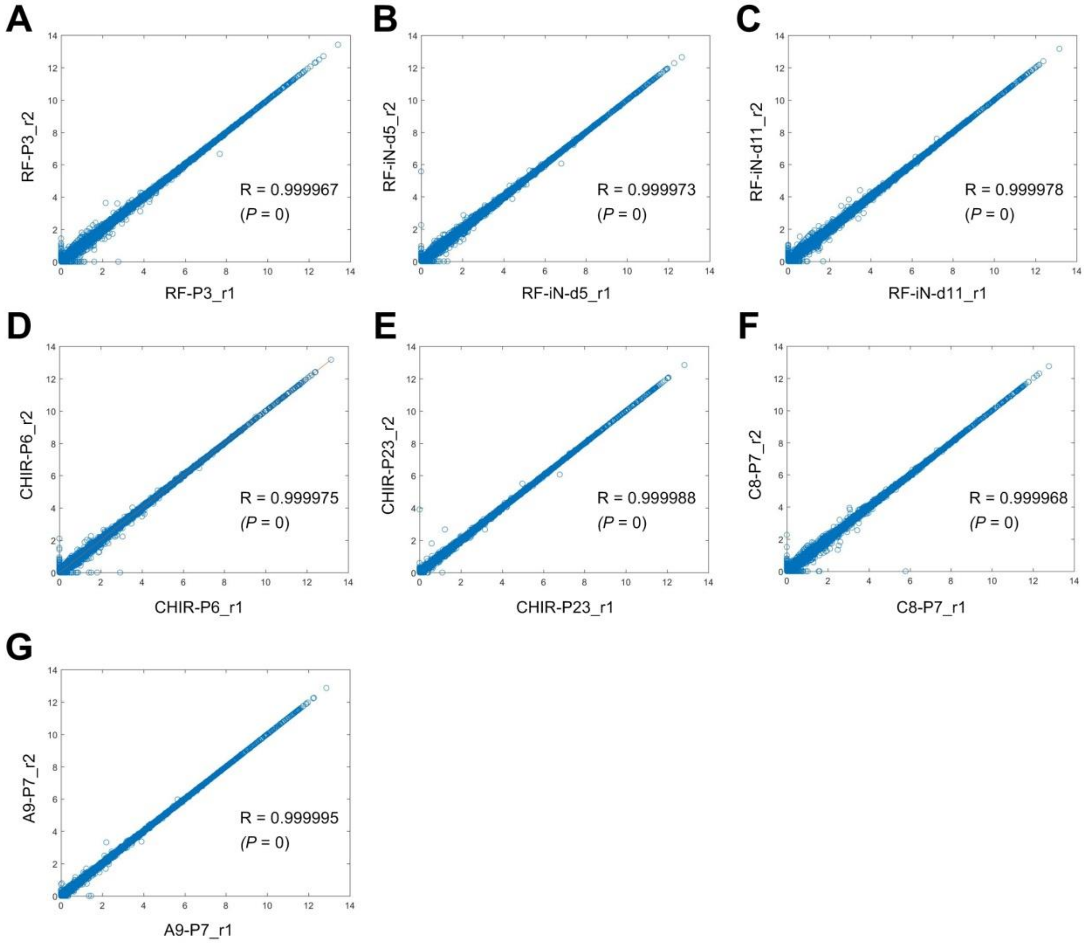

Figure S2. The scatter plots of log2 scaled abundances (FPKM + 1) of genes. The correlation values (R) and *P*-values (*P*) were calculated by using the corrcoef function in MatLab. (A) The scatter plot for the two biological replicates of the RF-P3 cell line. (B) The scatter plot for the two biological replicates of the RF-iN-d5 cell line. (C) The scatter plot for the two biological replicates of the RF-iN-d11 cell line. (D) The scatter plot for the two biological replicates of the CHIR-P6 cell line. (E) The scatter plot for the two biological replicates of the CHIR-P23 cell line. (F) The scatter plot for the two biological replicates of the C8-P7 cell line. (G) The scatter plot for the two biological replicates of the A9-P7 cell line.

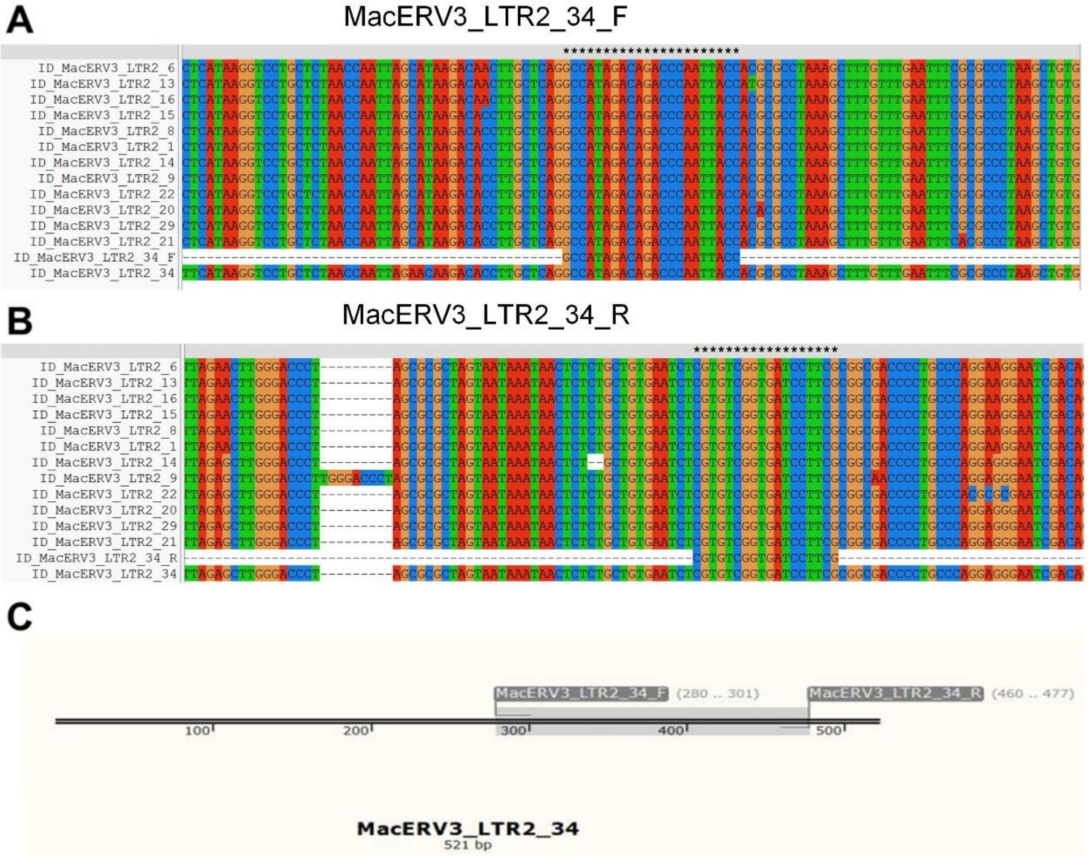

Figure S3. The primers used to validate the expression of 13 MacERV3 LTRs. (A) The alignment of the forward primer MacERV3_LTR2_34_F and the 13 MacERV3 LTRs. (B) The alignment of the reverse primer MacERV3_LTR2_34_R and the 13 MacERV3 LTRs. (C) The precise loci of the two primers on one of the selected MacERV3 LTRs, MacERV3_LTR2_34.