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Editing of the TRIM5 gene decreases the permissiveness of human T lymphocytic cells to HIV-1

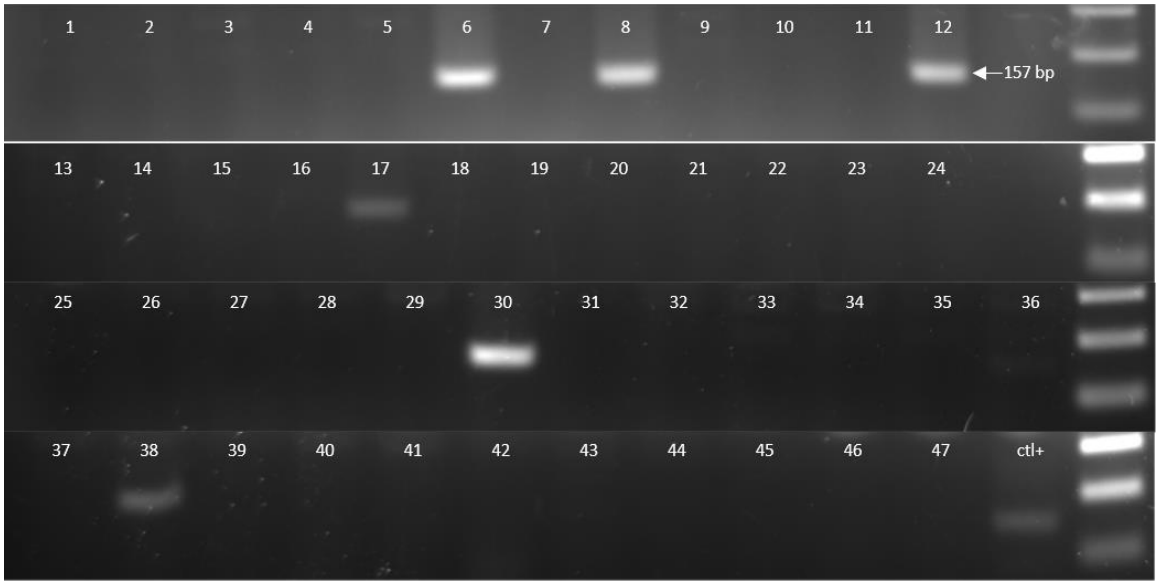

Figure S1. HDR editing-specific PCR screening of Jurkat cells transfected with CRISPR-Cas9 RNPs and donor ssDNA. 47 clonal cell populations were lysed and subjected to a PCR assay in which one of the primers is complementary to the correctly HDR-edited *TRIM5* region targeted for mutagenesis. A PCR product of the expected size was found in clones 6, 8, 12, 17, 30, 38. Ctl+ consisted of Jurkat cells following CRISPR components transfection but prior to the isolation of clones.

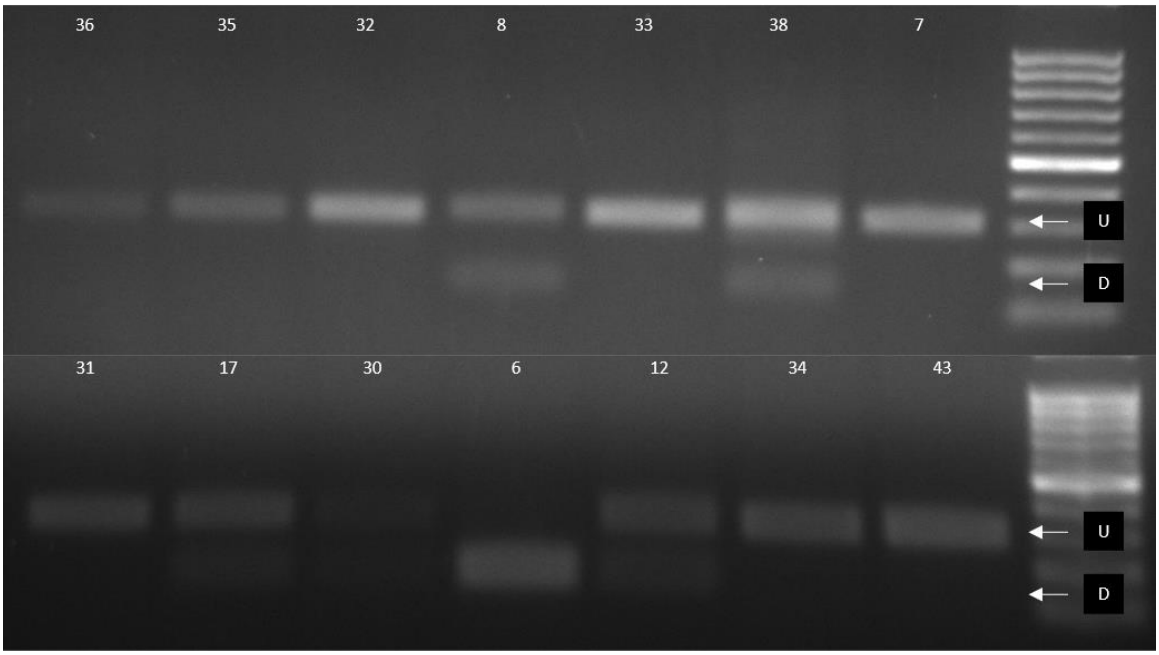

Figure S2. HaeIII screening of selected Jurkat clones. The 6 clones found to be positive in the HDR editing-specific PCR test, along with 8 randomly chosen negative clones, were subjected to a PCR assay using primers that bind outside of the genomic region complementary to the HDR donor DNA, followed by digestion with HaeIII. U and D indicates bands of the expected size for the undigested PCR product and the HaeIII digestion products, respectively.

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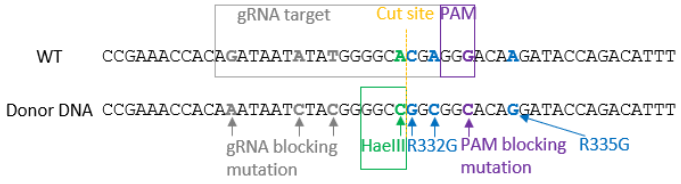

		N mutations	Indels	Subst.
Clone6	CCGAAACCACAGATAATATA**C**GGGGC**C**GG**C**GG**C**ACAAGATACCAGACATTT	5/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**C**ACAGGATACCAGACATTT	5/8	n	n
Clone 7	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 8	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**T**ACAGGATACCAGACATTT	4/8	n	y
Clone 12	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**T**ACAGGATACCAGACATTT	4/8	n	y
Clone 17	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**T**ACAGGATACCAGACATTT	4/8	n	y
Clone 30	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**T**ACAGGATACCAGACATTT	4/8	n	y
Clone 31	CCGAAACCACAGATAATATATGGG-CACGAGGGACAAGATACCAGACATTT	0/8	y	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 32	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 33	CCGAAACCACAGATAATATATGGG-CACGAGGGACAAGATACCAGACATTT	0/8	y	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 34	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 35	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 36	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
Clone 38	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGC**C**GG**C**GG**T**ACAGGATACCAGACATTT	4/8	n	y
	CCGAAACCA**T**A----------TGAATTTCAATTATT	0/8	y	y
Clone 43	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n
	CCGAAACCACAGATAATATATGGGGCACGAGGGACAAGATACCAGACATTT	0/8	n	n

Figure S3. MiSeq sequencing results for all clones analyzed. This is an extended version of Figure 1, showing sequencing results for the 8 randomly chosen clones negative for HDR editing in the specific PCR test, in addition to the 6 clones found to be positive.

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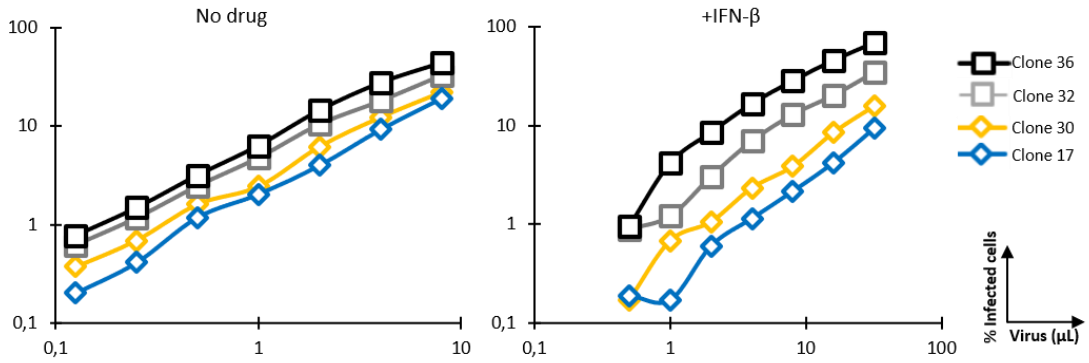

Figure S4. Permissiveness of HDR-edited clone 17 to HIV-1$_{NL\text{-}GFP}$ infection. Jurkat clonal cell populations were analyzed for permissiveness to HIV-1 infection. Clones 17 and 30 are monoallelically edited to express R332G-R335G TRIM5α whereas clones 32 and 36 are unedited. Cells were infected with increasing doses of HIV-1$_{NL\text{-}GFP}$ in the presence or not of IFN-β. The percentage of cells expressing GFP was determined by FACS two days later.