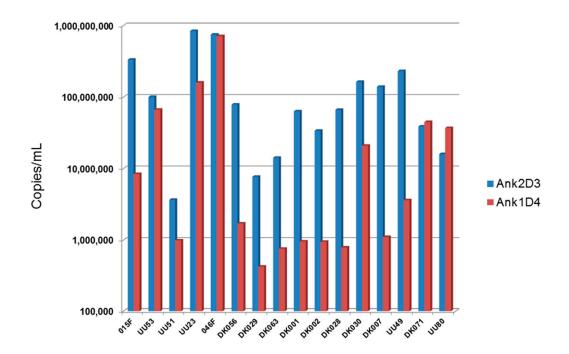
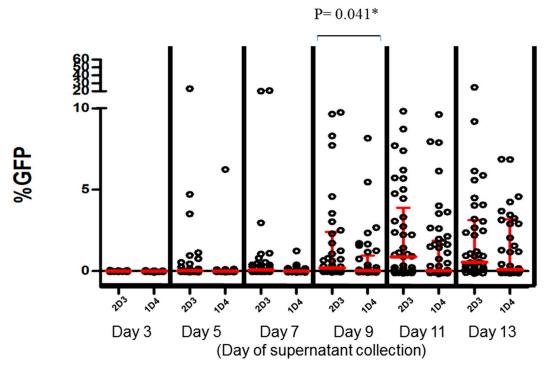


**Figure S1.** The intracellular levels of p24CA in SupT1/Ank<sup>GAG</sup>1D4, and SupT1/Ank<sup>A3</sup>2D3 cells on day 7 post-infection. The SupT1/Ank<sup>GAG</sup>1D4 and SupT1/Ank<sup>A3</sup>2D3 cells were collected on day 7 post-infection for this purpose. The representative 14 samples in each cluster (C1, C2, C3, and C4) and two samples (DK071 and UU80), for which Ank<sup>GAG</sup>1D4 did not show the inhibition effect, were selected. Cellular proteins were extracted by RIPA buffer. The total protein lysates were normalised to 10  $\mu$ g/mL to determine the intracellular levels of p24CA using Genscreen ULTRA HIV Ag-Ab Assay.



**Figure S2.** The viral load analysis from culture supernatants of SupT1/Ank<sup>GAG</sup>1D4 and SupT1/Ank<sup>A3</sup>2D3 infected with individual viruses. The representative 14 samples in each cluster (C1, C2, C3, and C4) and two samples (DK071 and UU80), which Ank<sup>GAG</sup>1D4 did not show the inhibition effect, were selected. The level of viral genomic RNA collected on day 7 post-infection was determined using COBAS AmpliPrep/COBAS TaqMan HIV-1 test V2.0.



**Figure S3.** The infectivity of released virion. The tat-driven GFP reporter Jurkat T-cells (kindly gifted by Dr. Toshiyuki Miura) were challenged with viral supernatants harvested from various days post

chimeric HIV-1 infection. After three days of infection, these cells were harvested for flow cytometry. The percentage of green fluorescent protein (GFP)-positive cell was statistically analysed by Mann-Whitney U test/ Wilcoxon W test.



B)

## Amino acid position 18Amino acid position 132Amino acid position 144ConsensusRRRDK071RRRUU80RRR

υ,						
1		10	20	30	40	. 50
pnl4 3P I V C	NLQG	QMVHQAI	SPRTLNAWV	KVVEEKAFSP	EVIPMESALS	EGATPQ
DK071 ·	A	P N	1 M	G - N -		
				G - N -		
UU01 M -	A H -	L - P L	S T	I G - G -	K S	A - P
		60	70	80	90	100
pnl4 3D L N T	TMLNT	VGGHQAA	MQMLKETIN	EEAAEWDRLH	IP V H A G P I A P C	GOMREPR
					P	
					P	
UU01 H N	4 I	M R R - P	V T	D V -	- L P Y P - F	2 K - K
		110	120	130	140	150
pnl4 3GSDI	AGTT	STLQEQI	GWMTHNPPI	PVGEIYKRWI	ILGLNKIVRN	1 Y S
DK071			G A -		- M	

Sample No.	Sequence identity to pNL4-3 (%)
DK071	90.4
UU80	91.7
UU01	66.4

**Figure S4.** The NTD<sup>p24CA</sup> residue comparison of the chimeric viruses DK071, UU80, and UU01. (**A**) The Arginine (R) residues 18, 132, and 143 of DK071 and UU80 were depicted. (**B**) The NTD<sup>p24CA</sup> sequence alignment of DK071, UU80, and UU01 against subtype B NL4-3 virus. The percentage of the sequence identity was shown.