

Supplementary Information

Antibody 10-1074 suppresses viremia in HIV-1-infected individuals

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a Pseudotyped viruses

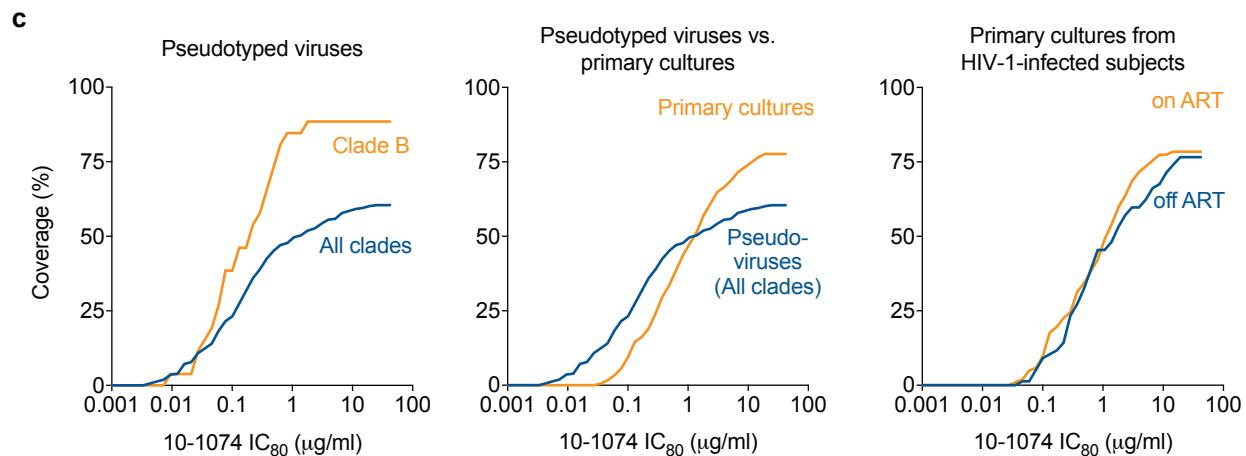
Subtype	Tested strains	Mean _{IC₈₀} *	Neutralized (%)**
A1	13	0.09	53.8
B	26	0.13	88.5
C	211	0.20	61.1
D	5	0.04	20.0
G	7	0.06	85.7
01_AE	16	n.d.	0.0
02_AG	9	0.79	77.8
07_BC	5	0.04	80.0
08_BC	2	0.97	100.0
A1C	4	n.d.	0.0
A1D	2	0.17	50.0
A1CD	1	0.06	100.0
CD	5	0.11	80.0
All	306	0.18	60.5

b Primary culture samples

ART	Tested samples	Mean _{IC₈₀} *	Neutralized (%)**
off	77	0.80	76.6
on	102	0.58	78.4
All	179	0.67	77.7

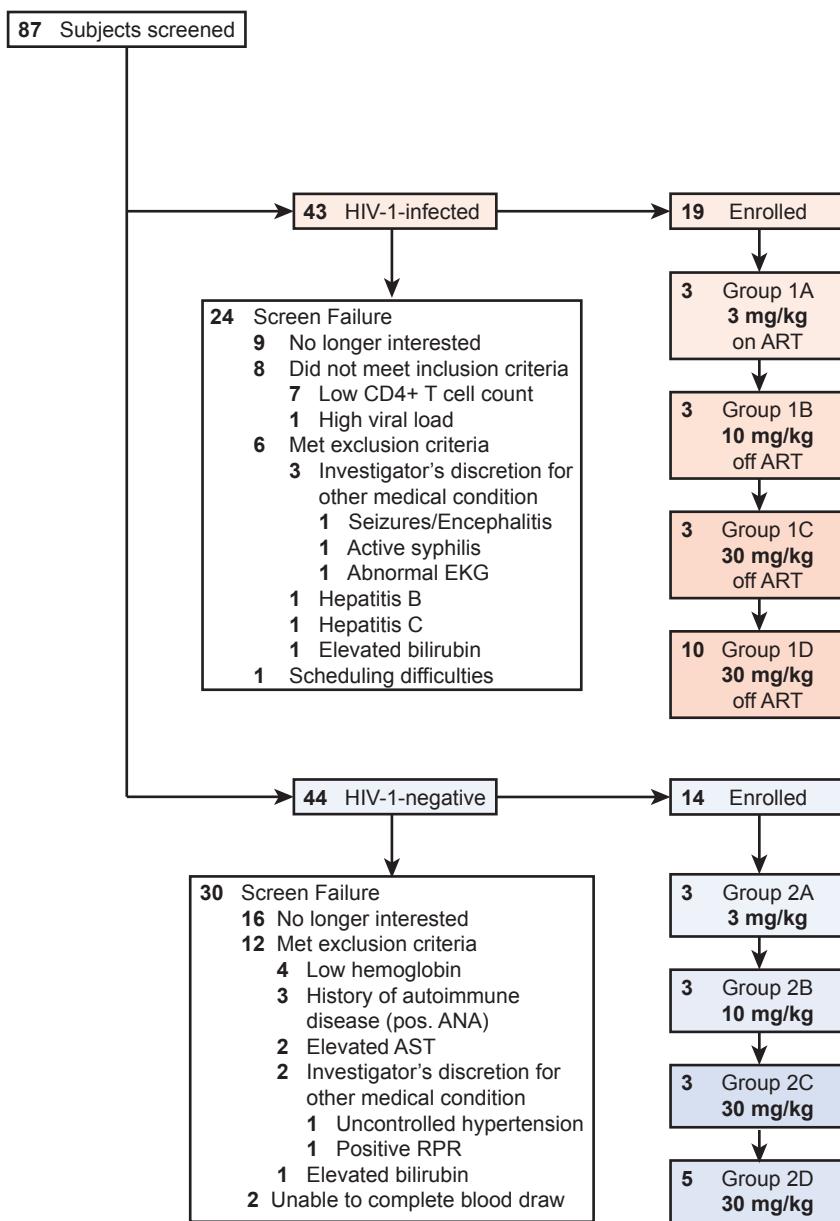
* Geometric mean of neutralized viruses.

** IC₈₀ < 20 µg/ml.



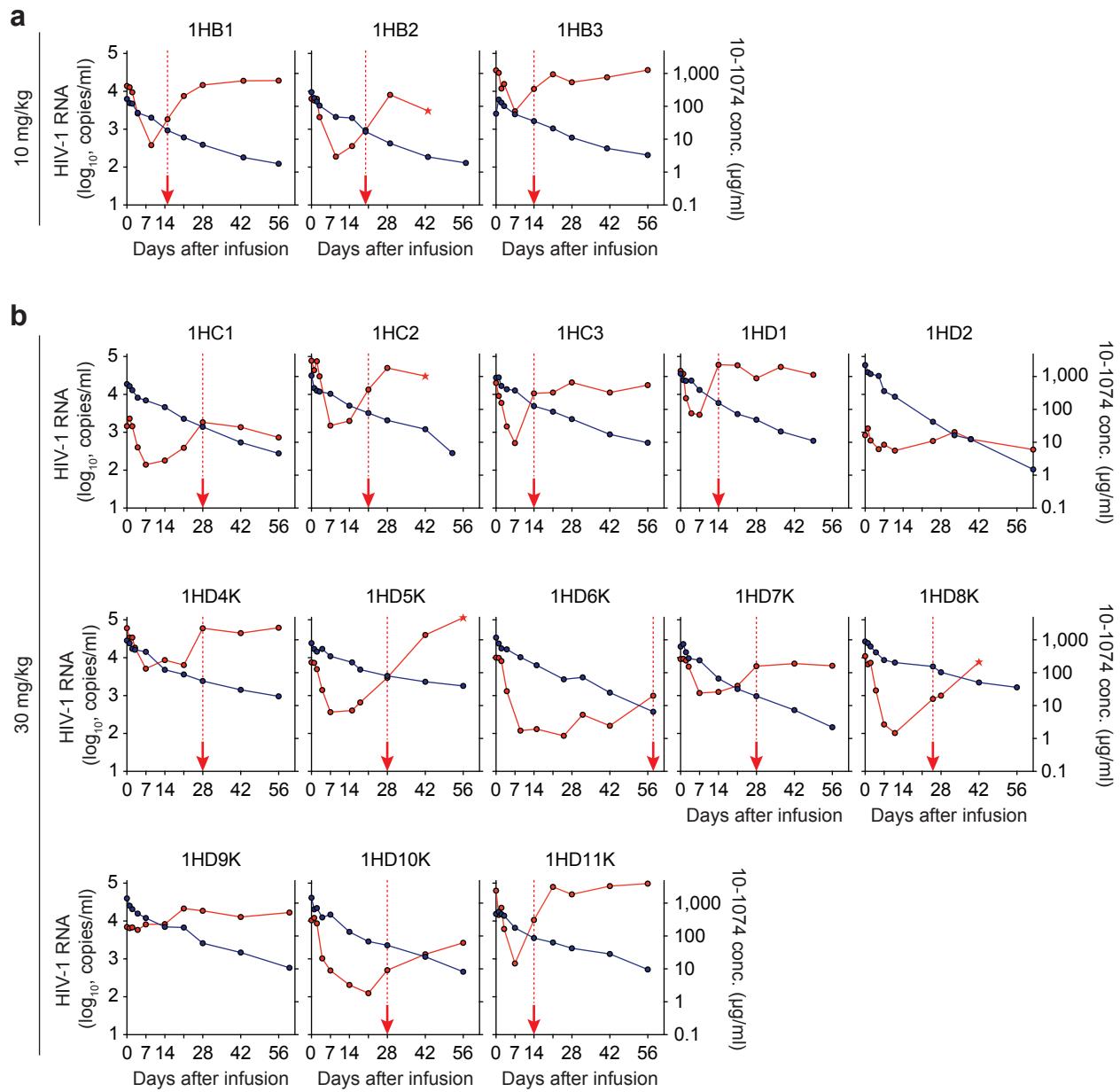
Supplementary Figure 1. HIV-1 neutralizing activity of 10-1074

(a) Summary of 10-1074 neutralizing *in vitro* activity based on 306 HIV-1 pseudotyped viruses comprising 13 subtypes and recombinant forms. Data were retrieved from the ‘CATNAP Database’ (Yoon *et al.*, Nucleic Acid Res 2015) and analyzed using ‘AntibodyDatabase’ by Anthony West (West *et al.*, PNAS 2013). Mean IC₈₀-values are color-coded (dark red: < 0.1 µg/ml; light red: 0.1 - 0.49 µg/ml, and orange: 0.5 - 1 µg/ml). n.d.: not determined. (b) 10-1074 neutralizing *in vitro* activity of 179 primary culture samples obtained by viral outgrowth assay from HIV-1-infected subjects living in the U.S. or Germany. 77 subjects were off and 102 were on antiretroviral therapy (ART; values partially obtained from previous measurements, Scheid and Horwitz *et al.*, Nature 2016). Neutralizing activity was determined by the TZM.bl neutralization assay. (c) Illustration of the fraction (i.e., % coverage; y-axis) of HIV-1 isolates/cultures that are neutralized at a given IC₈₀ (µg/ml; x-axis) using the data sets from (a) and (b).



Supplementary Figure 2. Subject enrollment and study design

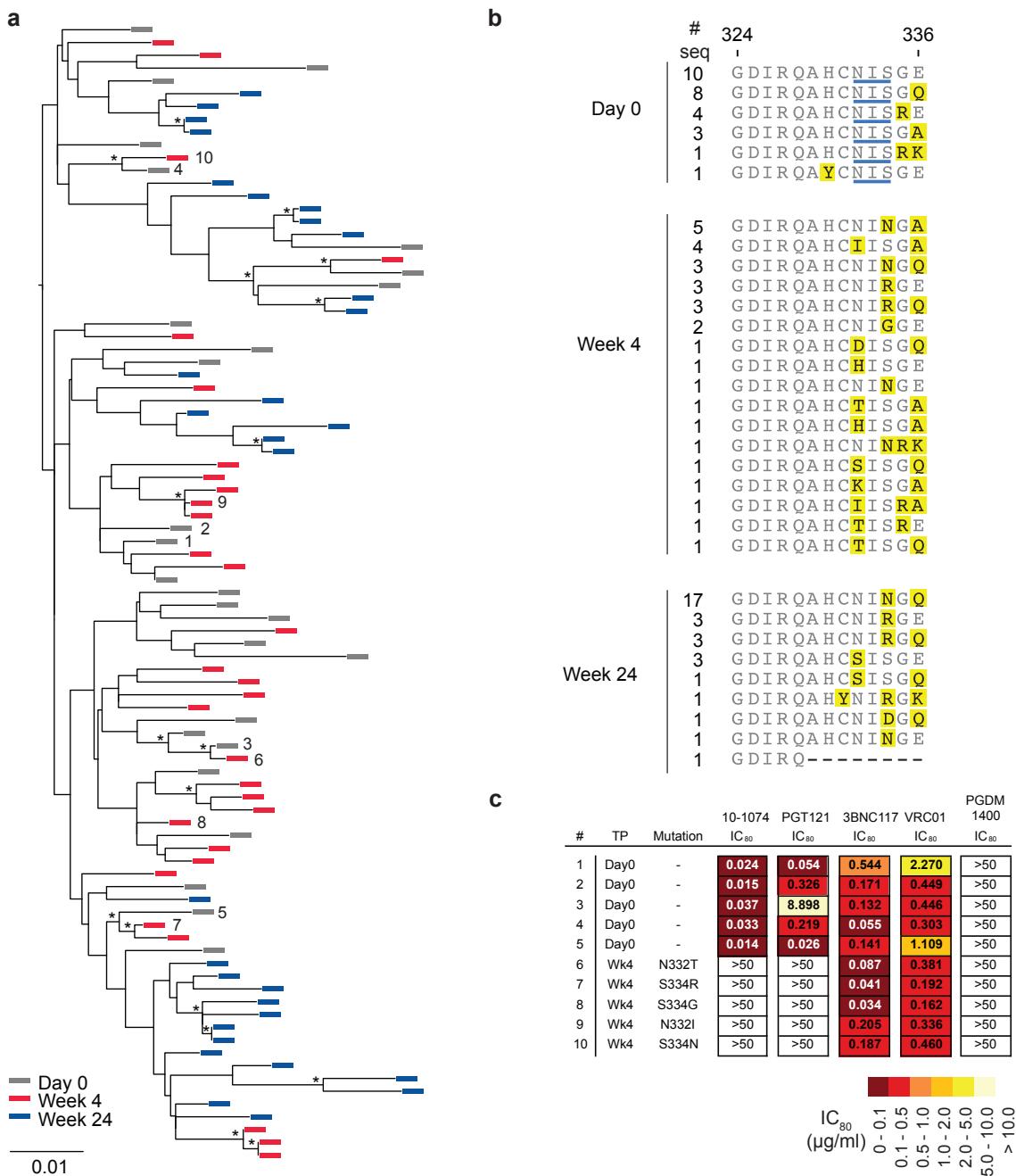
A total of 87 HIV-1-infected and -uninfected subjects were screened for study participation. In both cohorts, 10-1074 was sequentially administered at increasing doses of 3 mg/kg (groups 1A and 2A), 10 mg/kg (groups 1B and 2B), or 30 mg/kg (groups 1C-D and 2C-D) to HIV-1-infected (groups 1) and HIV-1-uninfected (groups 2) participants. Of a total of 87 subjects screened, 19 HIV-1-infected and 14 -uninfected participants were enrolled.



Supplementary Figure 3. Viremia and 10-1074 serum levels in HIV-1-infected subjects

(**a, b**) HIV-1 RNA plasma copies (solid red line) and 10-1074 serum concentration determined by TZM-bl assay (blue line) after a single intravenous infusion of 10-1074 at a dose of 10 mg/kg (**a**) or 30 mg/kg (**b**). Arrows and dashed red lines indicate time of viral rebound, defined as an increase of HIV-1 RNA of at least $0.5 \log_{10}$ that is confirmed at the next study visit. Stars indicate initiation of antiretroviral therapy.

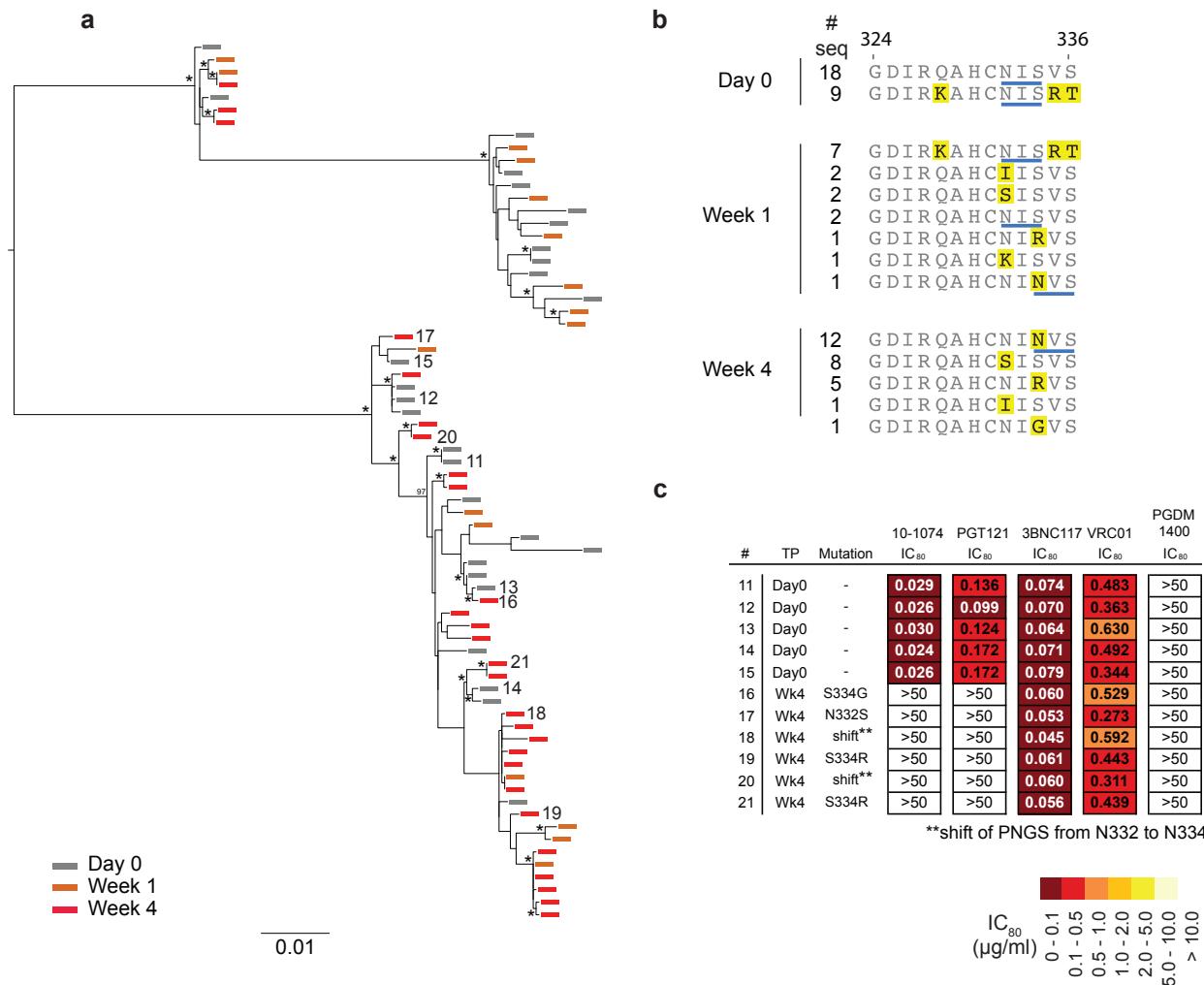
Supplementary Figure 4 (1HB1)



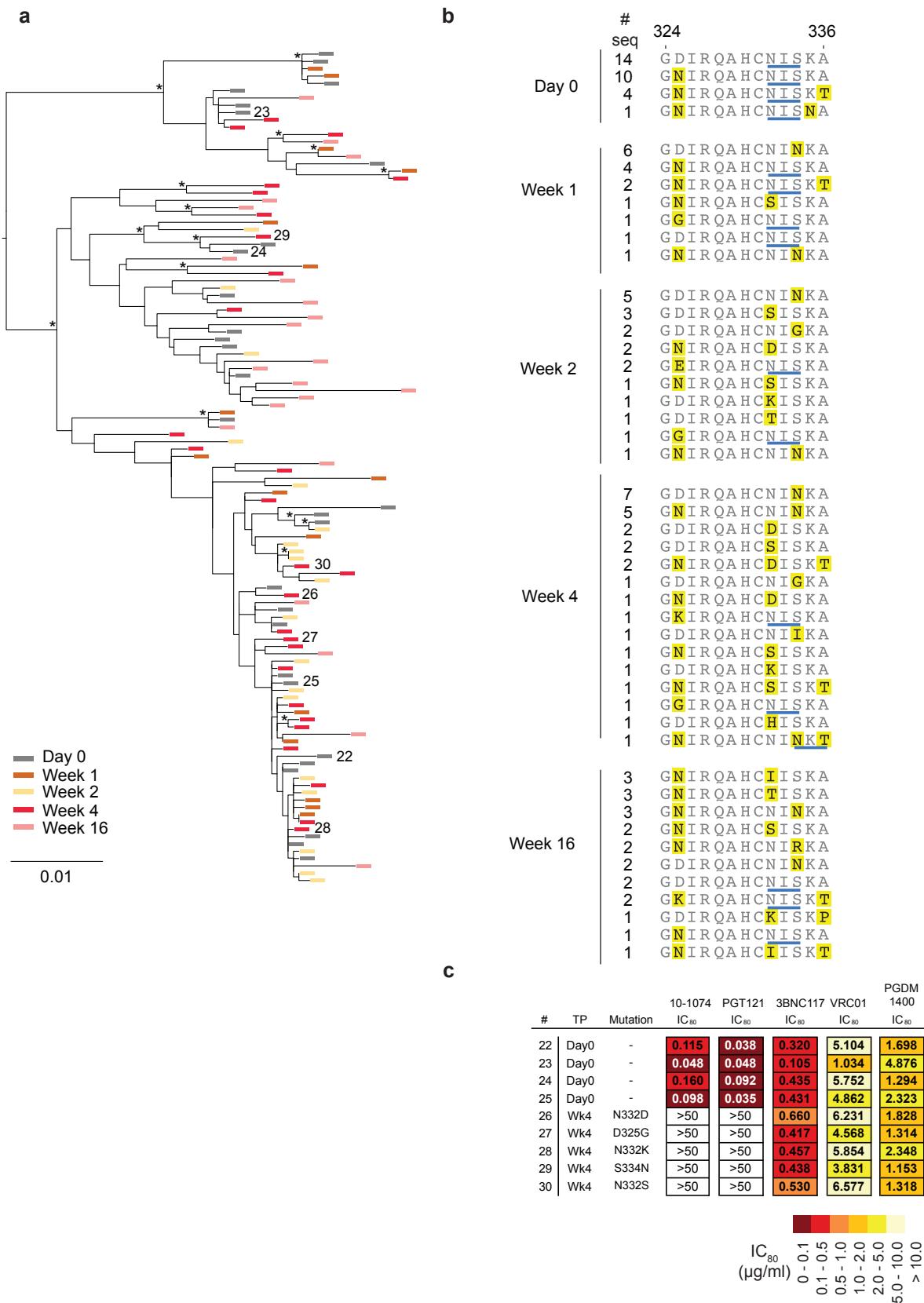
Supplementary Figure 4. Phylogenetic analysis of plasma env sequences obtained before and after 10-1074 infusion

(a) Maximum-likelihood phylogenetic trees of plasma-derived env sequences from subjects sampled before (Day 0/pre-infusion visit) and at different timepoints (Wk 1, Wk 2, Wk 4, Wk 8, Wk 12, Wk 16, Wk 20, Wk 24) after 10-1074 infusion. Black asterisks indicate nodes with bootstrap support $\geq 70\%$. (b) Amino acid alignment of HxB2 positions 324–336 of SGS sequences. Columns one and two indicate the time point sampled and number of sequences, respectively. Yellow boxes denote changes from day 0 majority variant. Light blue lines indicate intact potential N-linked glycosylation motifs at either N332 or N334 (when present). (c) Pseudovirus neutralization data of selected subjects' plasma envelope sequences. Shown are IC₅₀ values in (μ g/ml) of 5 different monoclonal antibodies that are currently in or planned for clinical testing.

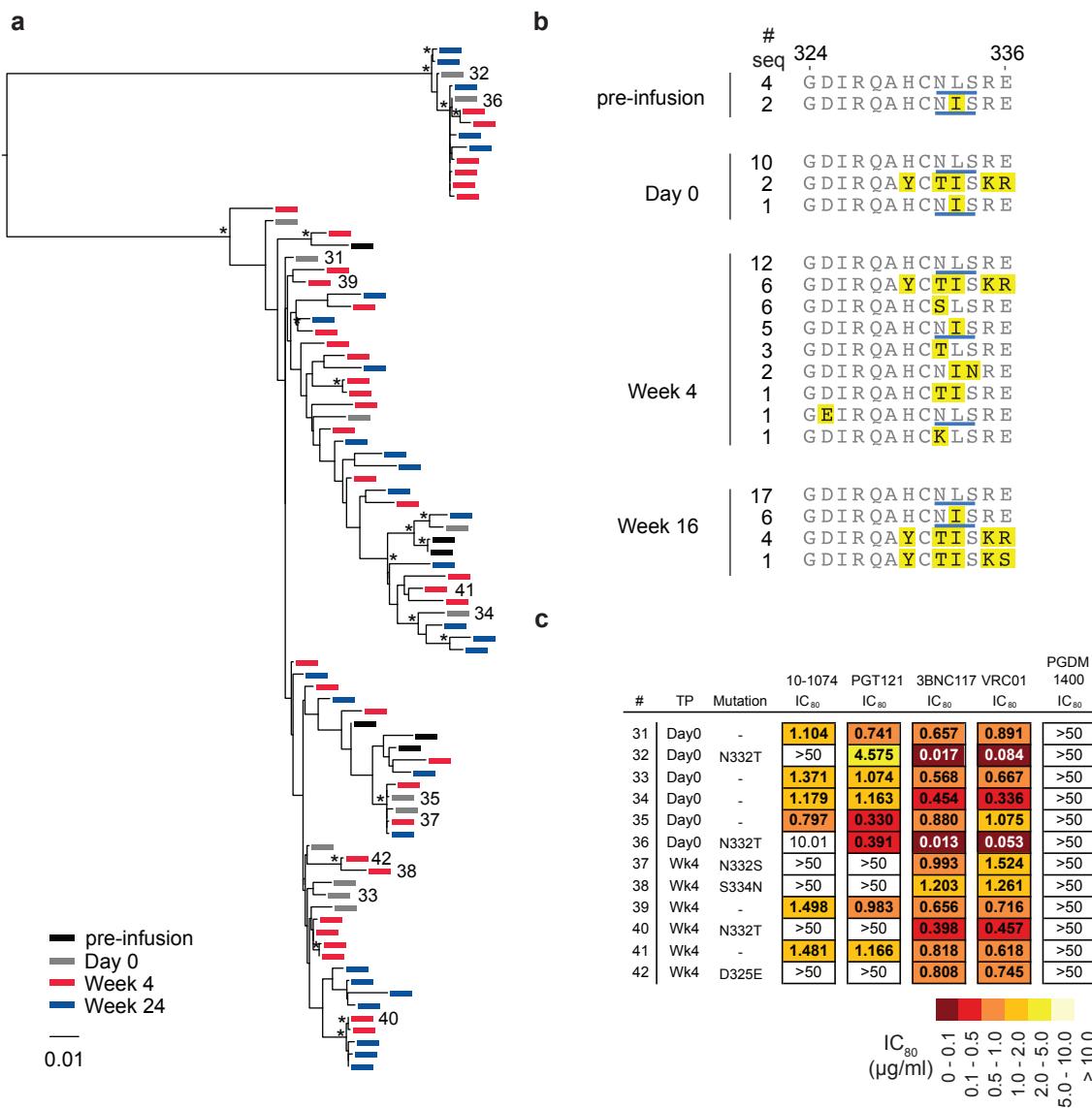
Supplementary Figure 4 continued (1HB2)



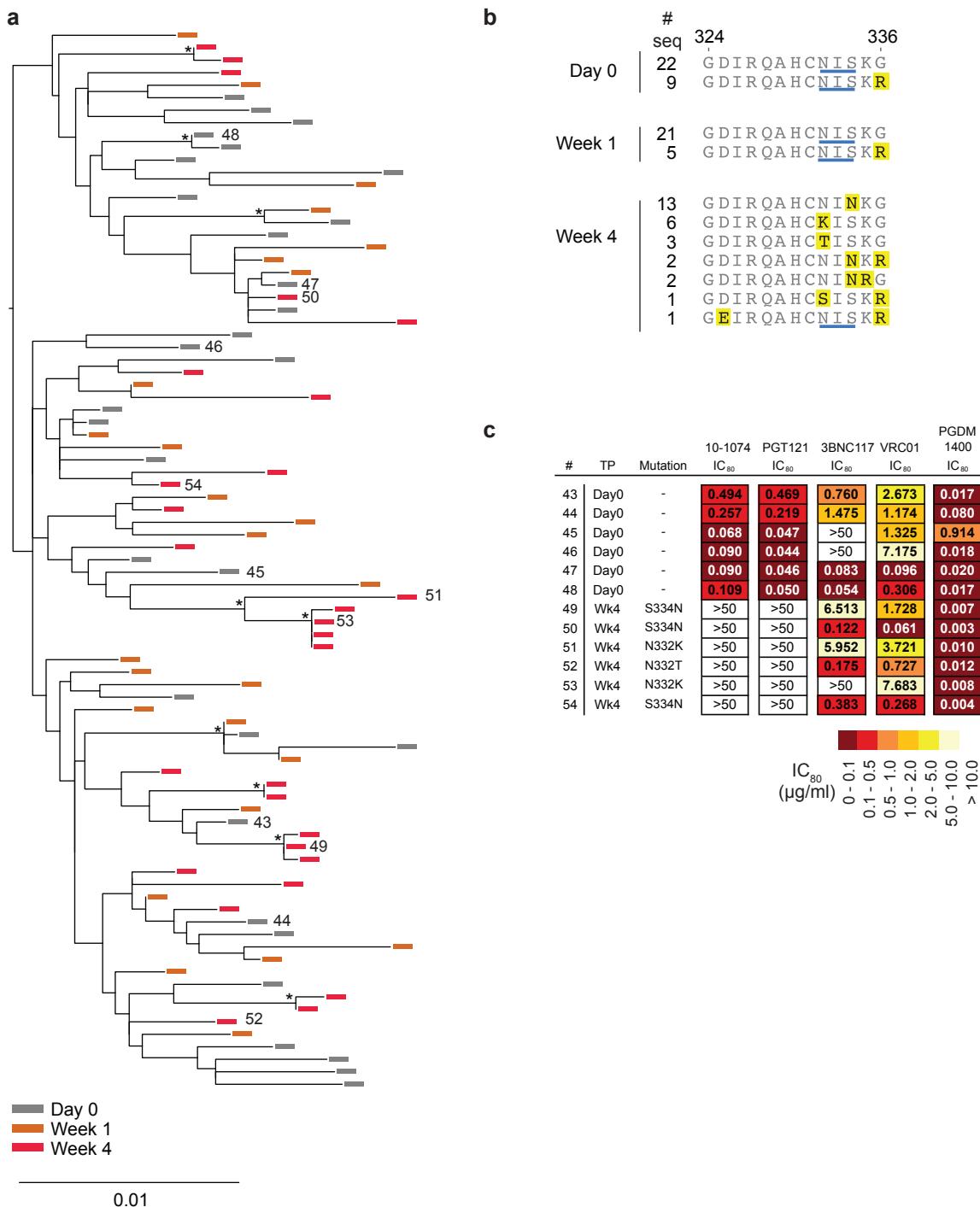
Supplementary Figure 4 continued (1HB3)



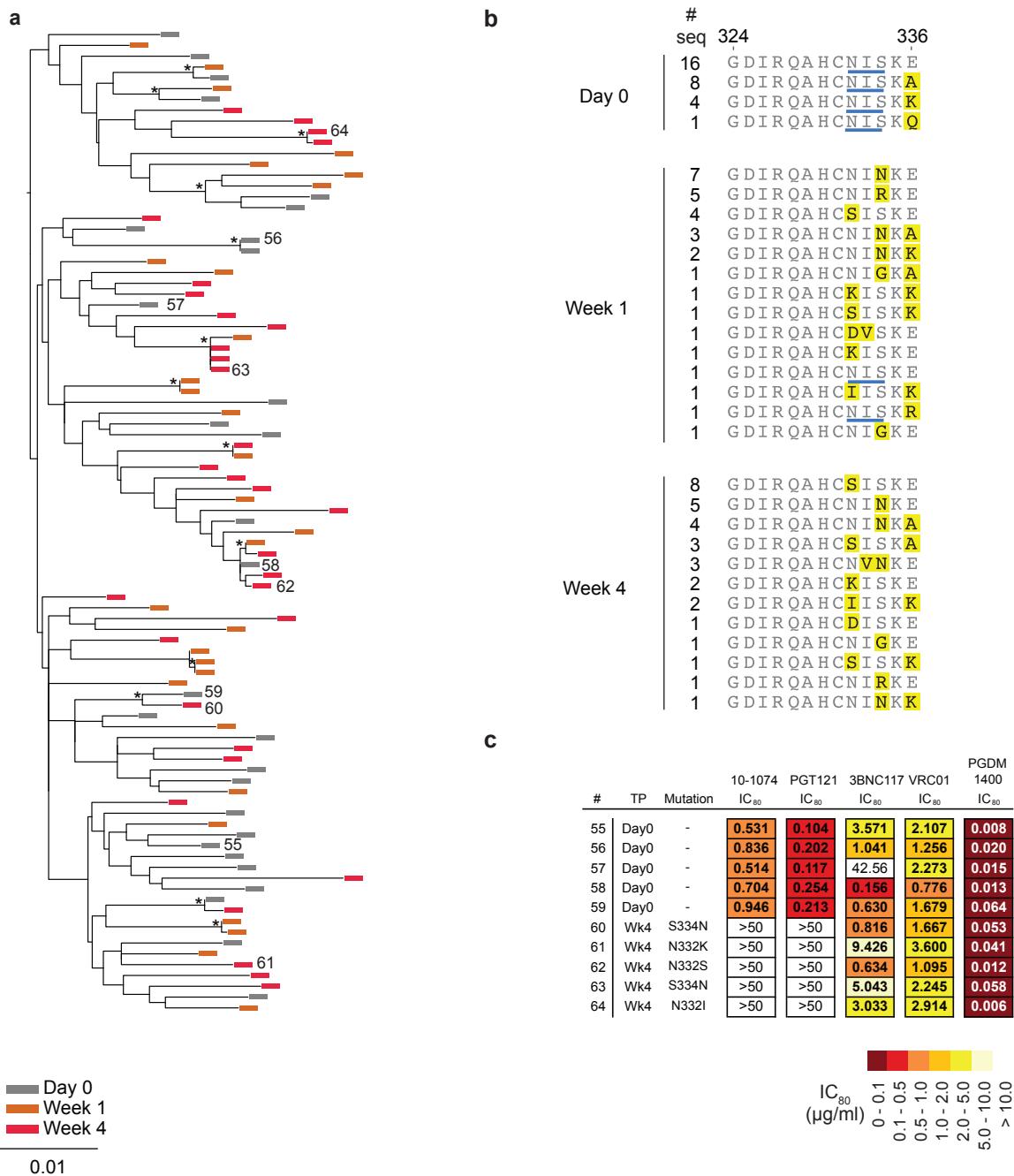
Supplementary Figure 4 continued (1HC1)



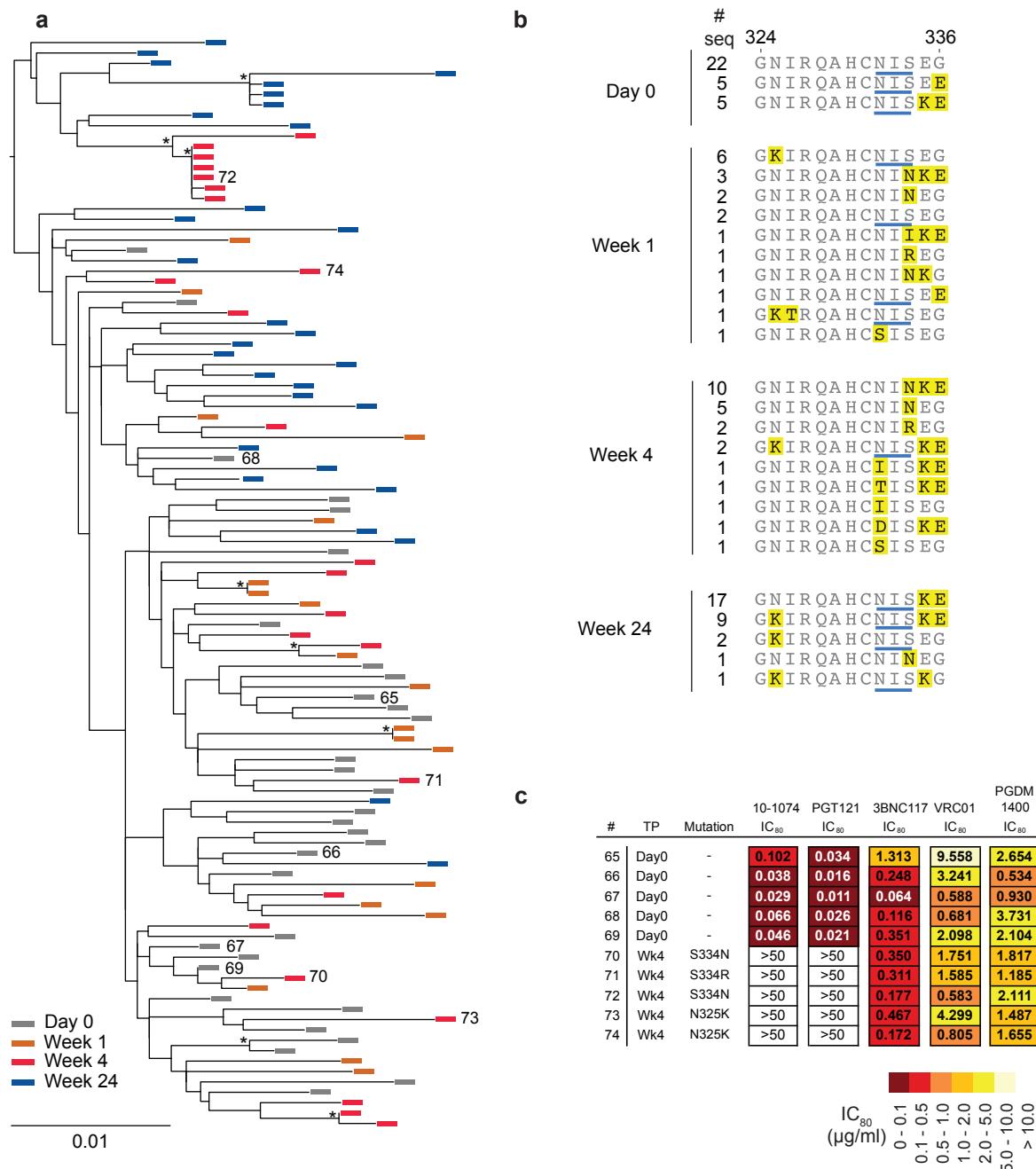
Supplementary Figure 4 continued (1HC2)



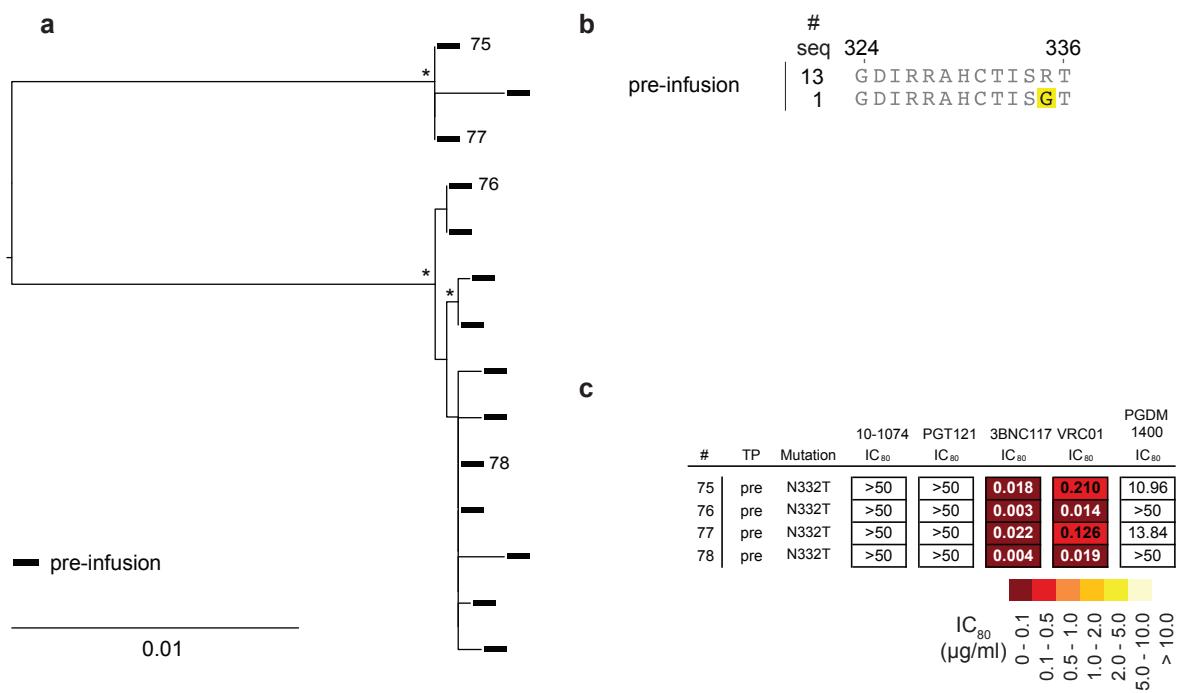
Supplementary Figure 4 continued (1HC3)



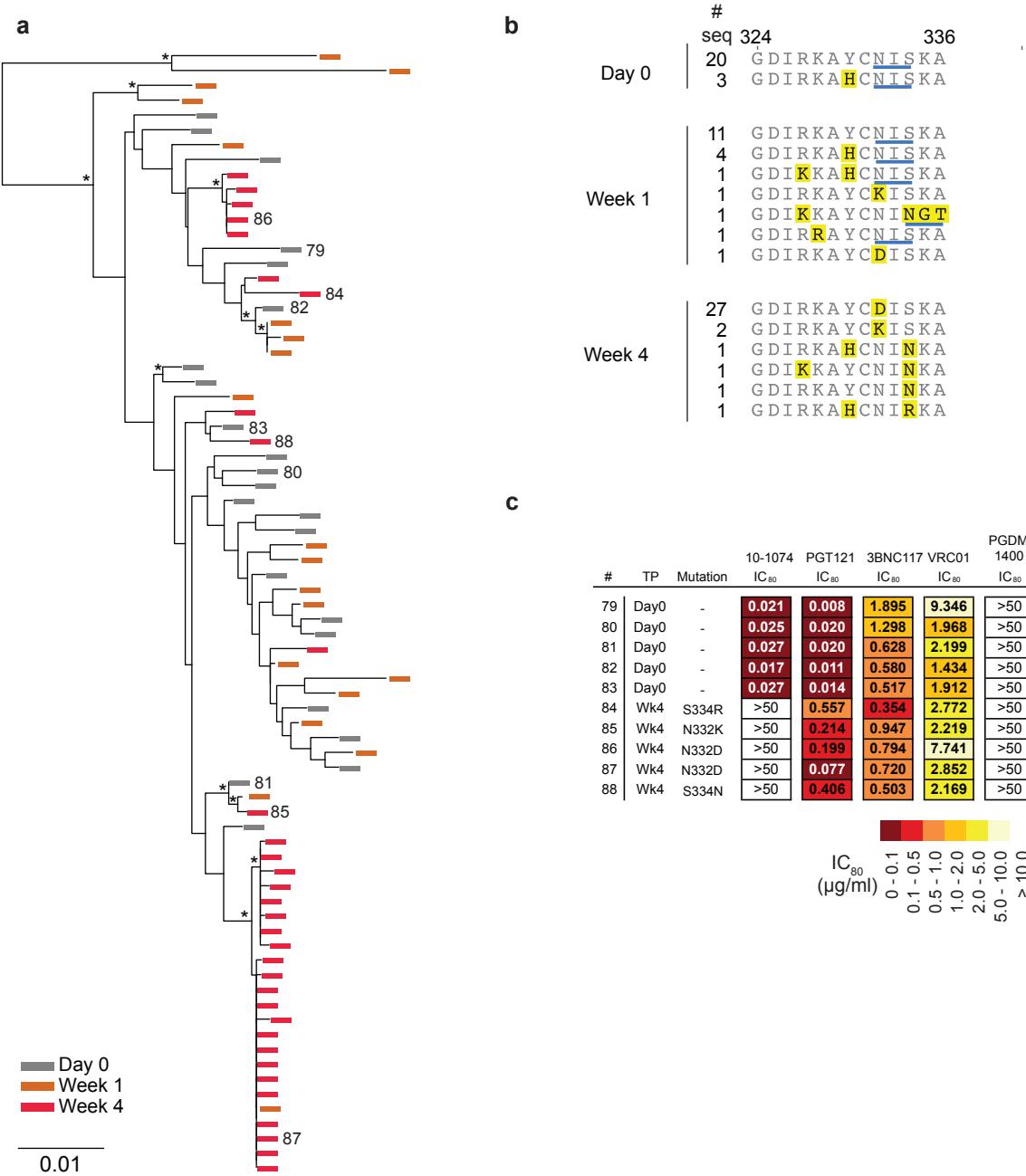
Supplementary Figure 4 continued (1HD1)



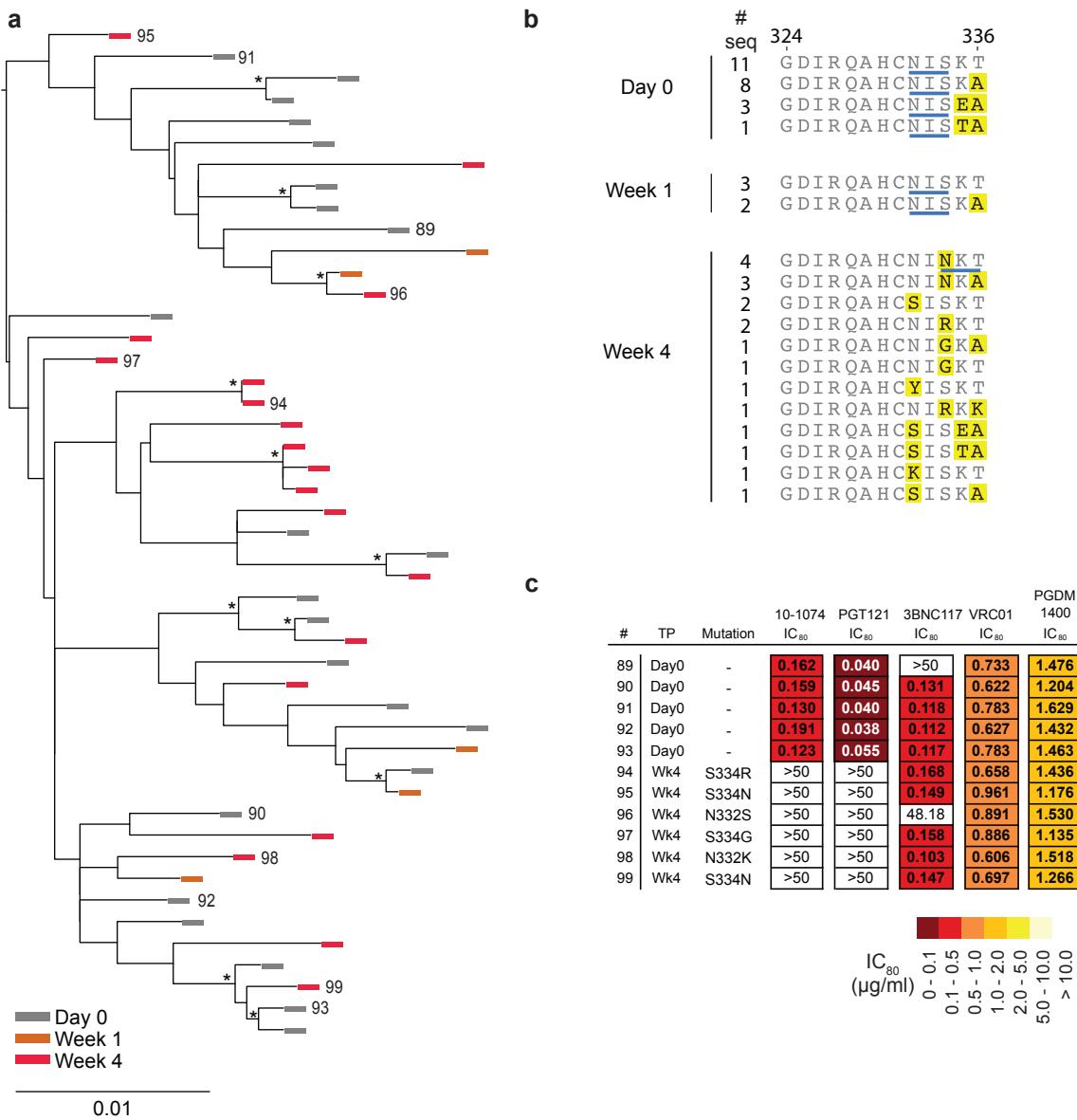
Supplementary Figure 4 continued (1HD2)



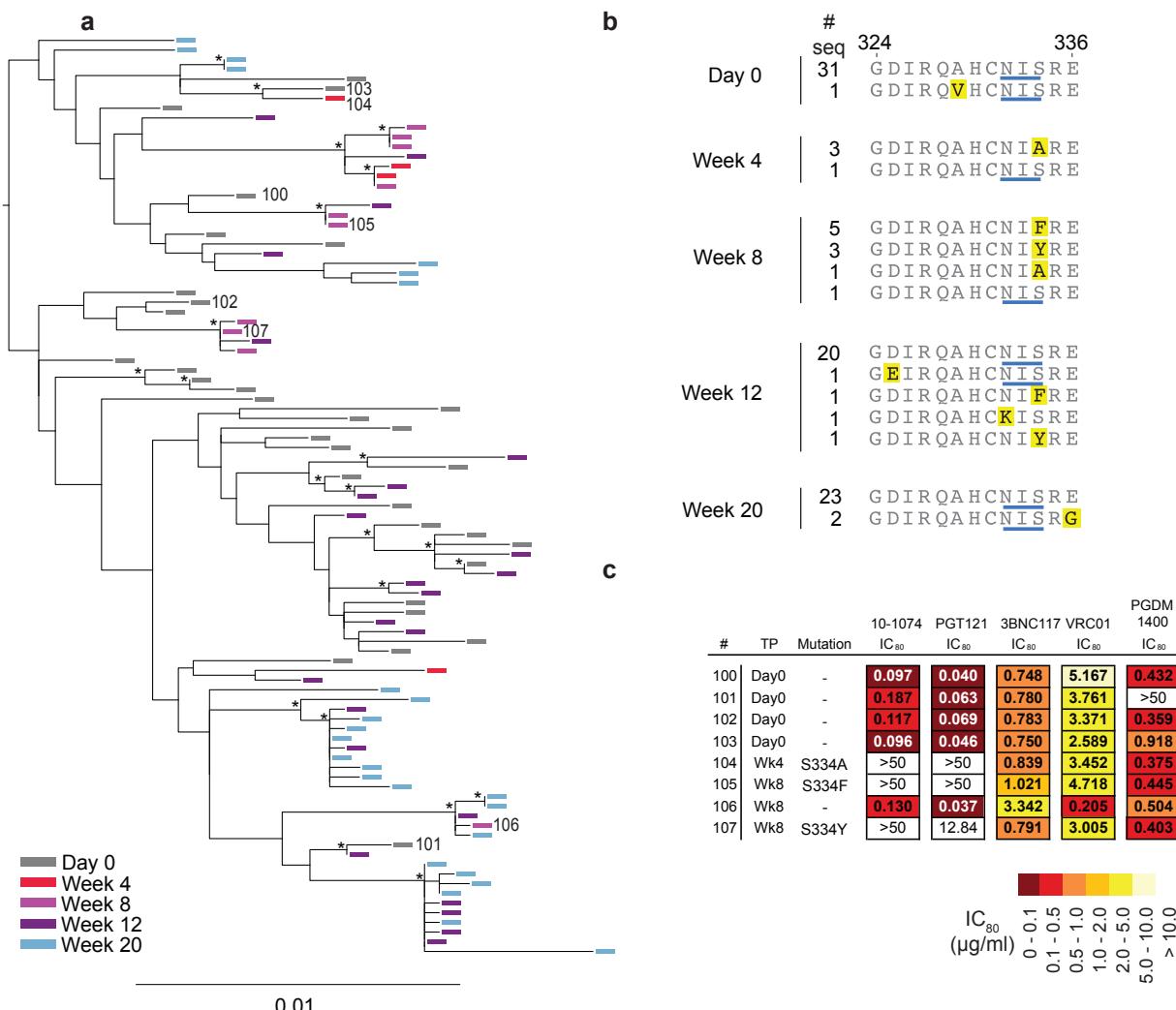
Supplementary Figure 4 continued (1HD4K)



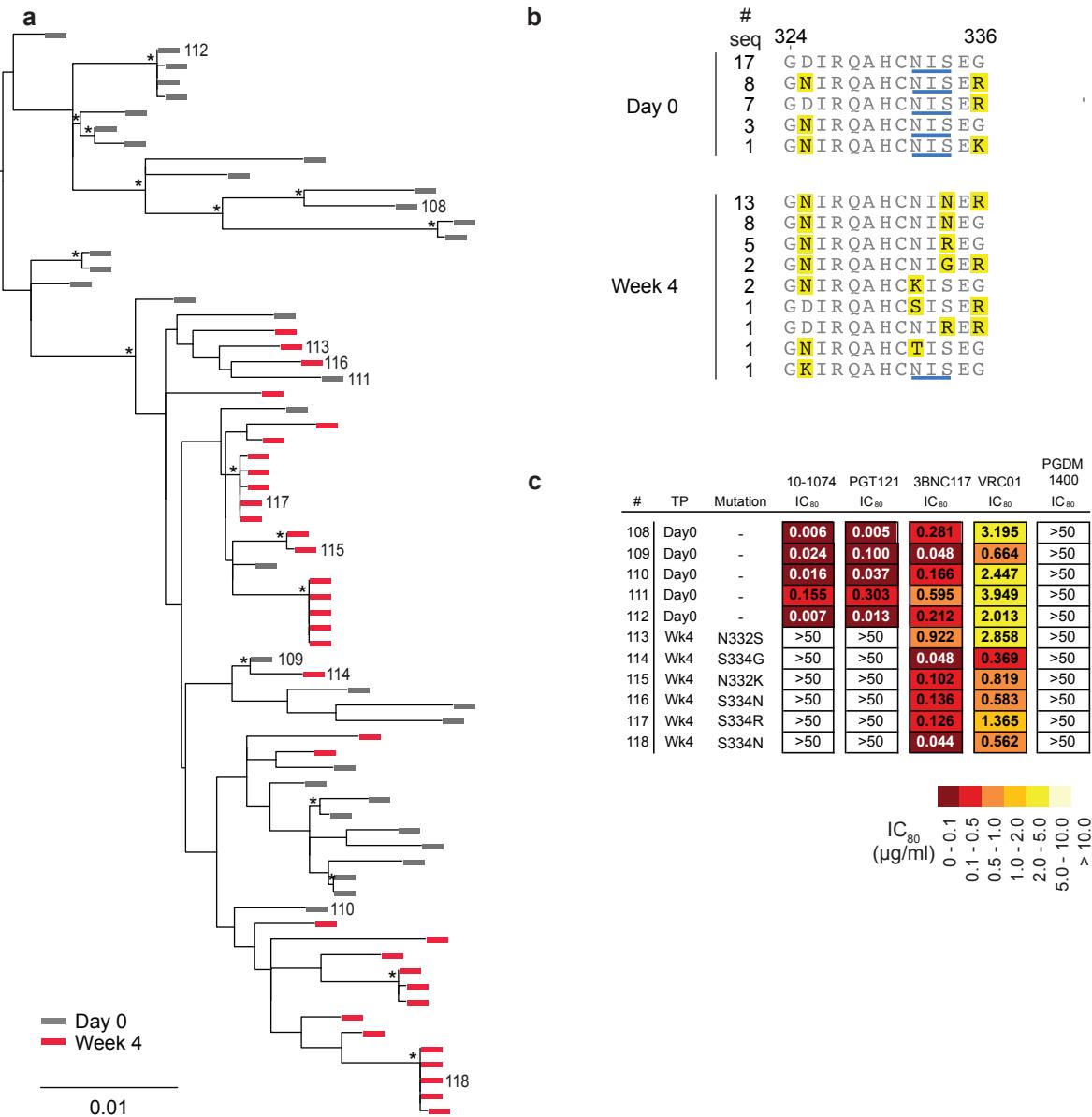
Supplementary Figure 4 continued (1HD5K)



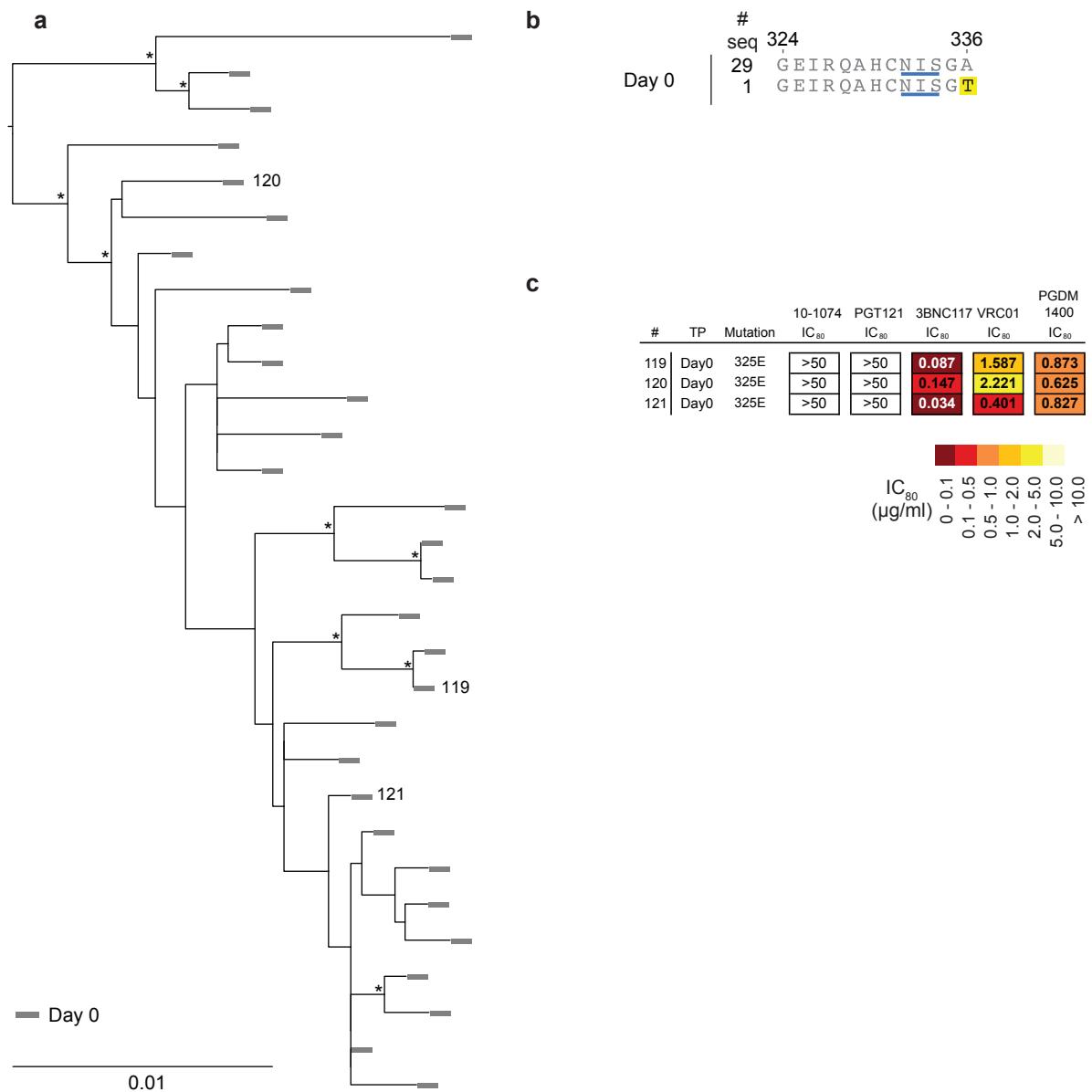
Supplementary Figure 4 continued (1HD6K)



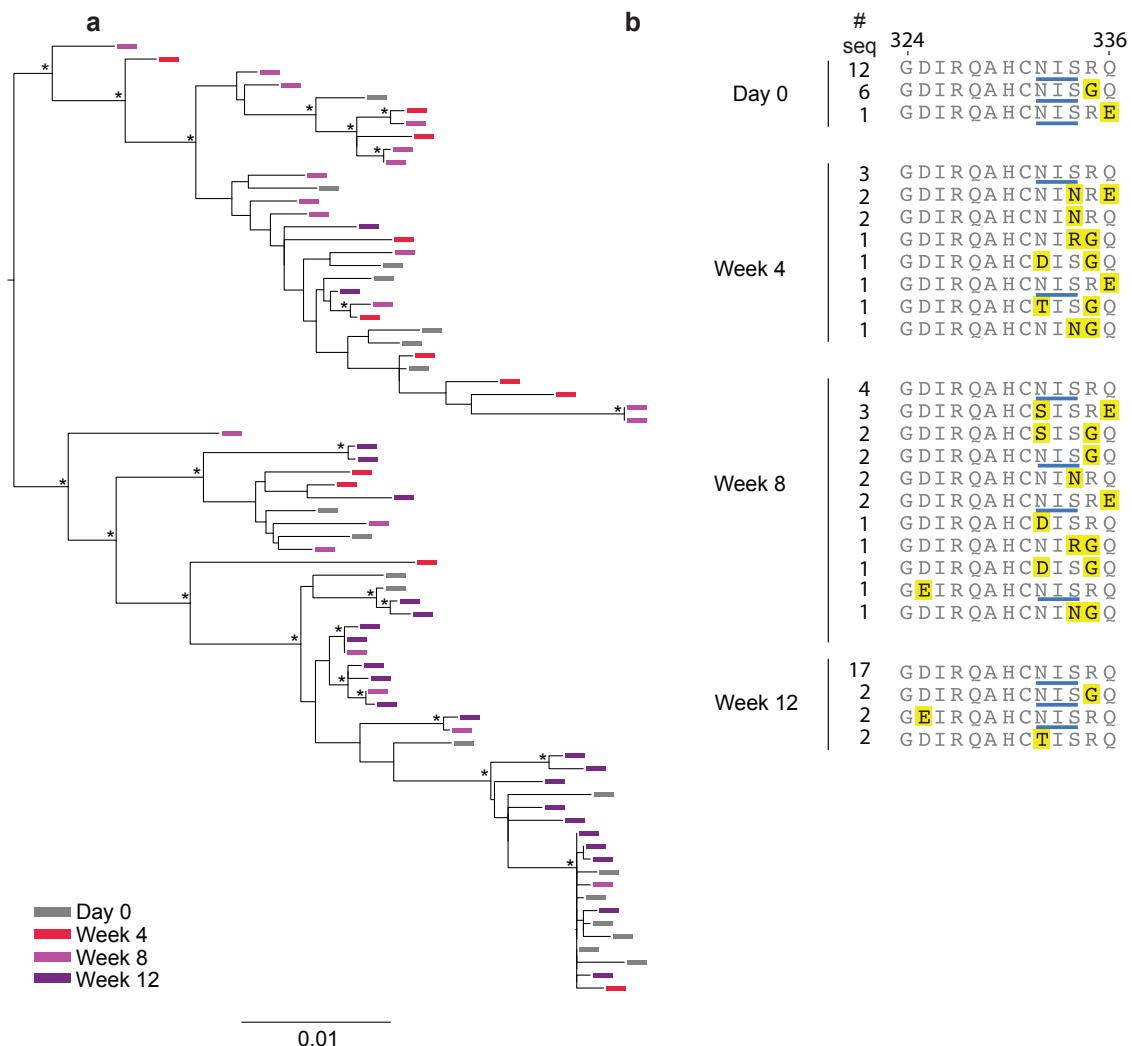
Supplementary Figure 4 continued (1HD8K)



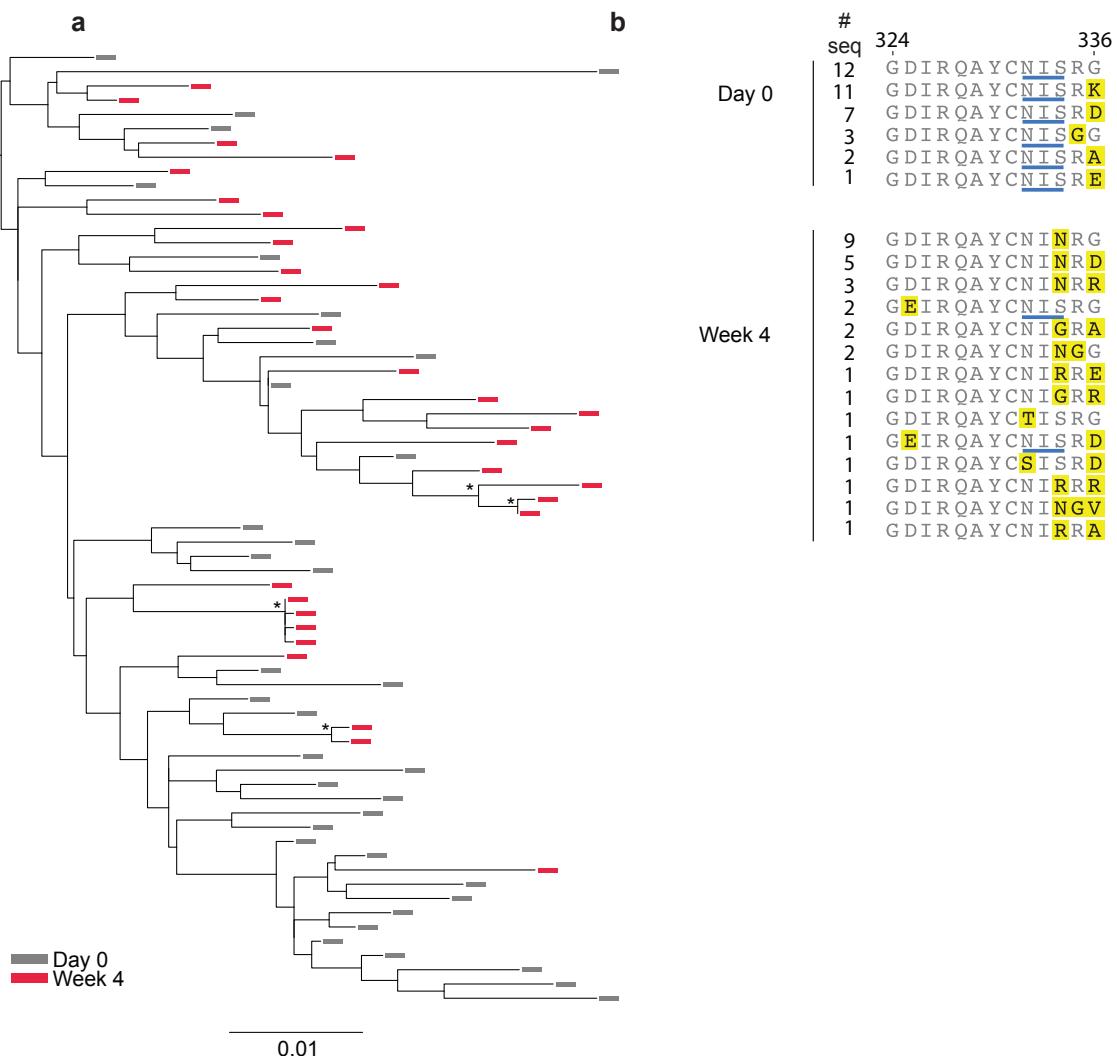
Supplementary Figure 4 continued (1HD9K)

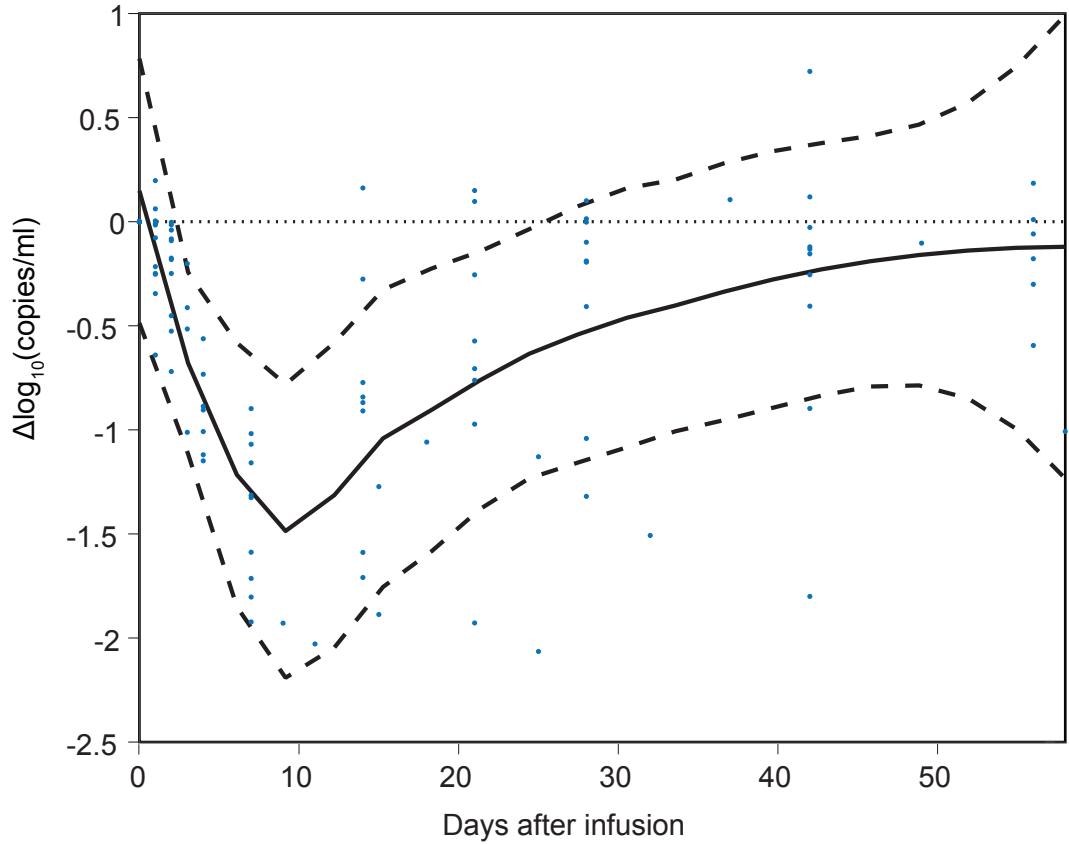


Supplementary Figure 4 continued (1HD10K)



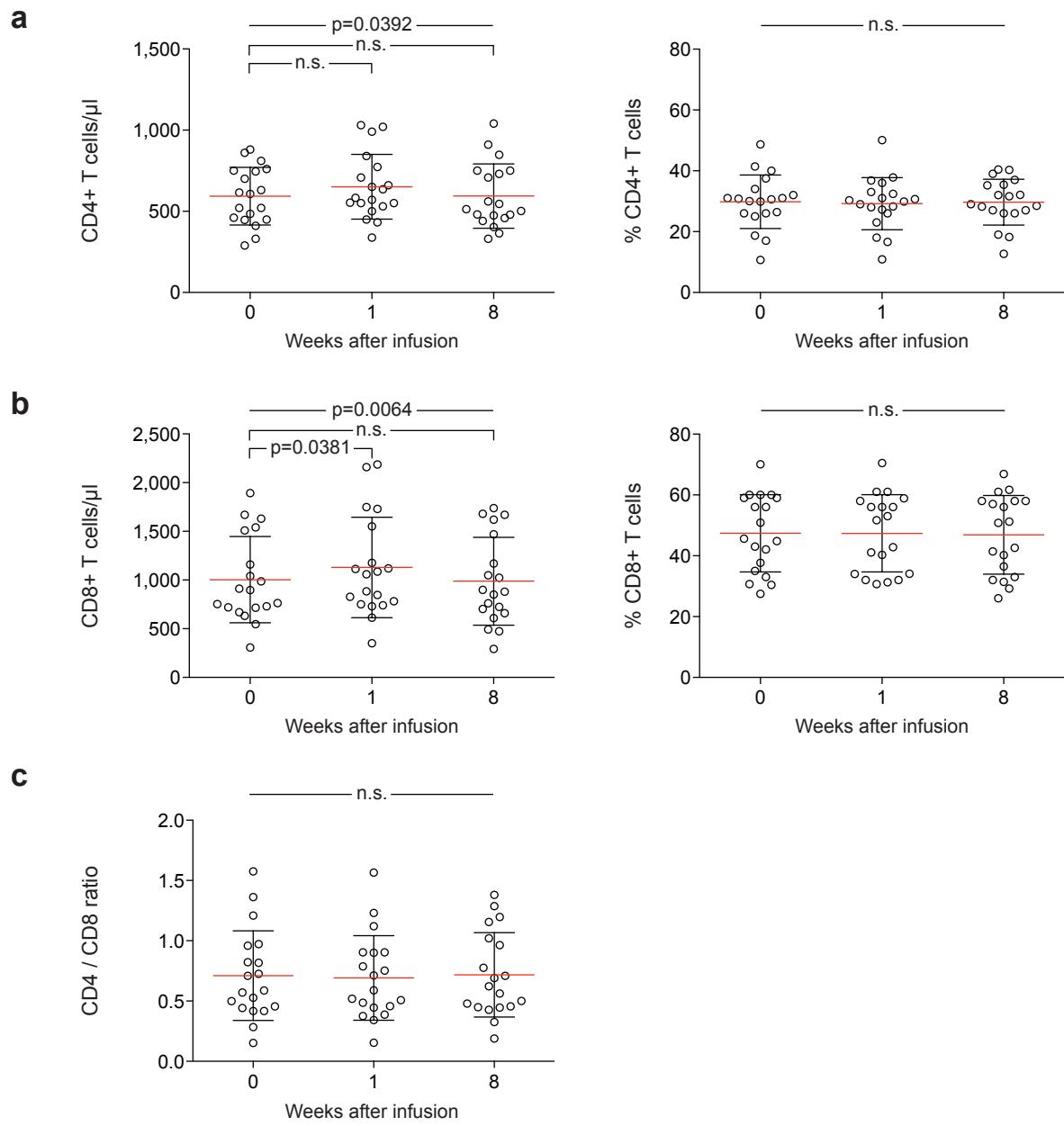
Supplementary Figure 4 continued (1HD11K)





Supplementary Figure 5. Statistical analysis of viral load changes in the 10-1074-sensitive HIV-1-infected 30 mg/kg dose group

The significance of viral load changes after 10-1074 infusion was analyzed using simultaneous confidence bands. Each blue dot represents a viral load measurement of a responder that received the 30 mg/kg dose. Simultaneous confidence bands were computed with the R package locfit (version 1.5-9.1) using the Gaussian family for the local likelihood function. The solid line represents the regression fit and the dashed lines show the simultaneous confidence bands at 95% certainty level. The simultaneous confidence bands exclude zero from about 3 days after infusion to about 27 days after infusion, demonstrating that there is a significant effect on viral load reduction during that time period.



Supplementary Figure 6. CD4+ and CD8+ T cell counts

(a-b) Absolute counts (left panels) and relative frequencies (right panels) of CD4+ T cells (**a**) and CD8+ T cells (**b**) before, and 1 and 8 weeks after 10-1074 infusion. **(c)** CD4/CD8 ratio before, and 1 and 8 weeks after 10-1074 infusion. Mean is indicated by the red line and bars represent standard deviation. Differences between time points were tested by repeated measures one-way ANOVA. If significant, Dunnett's test was performed post hoc to compare week 1 and week 8 to baseline, respectively.

Sensitive subjects

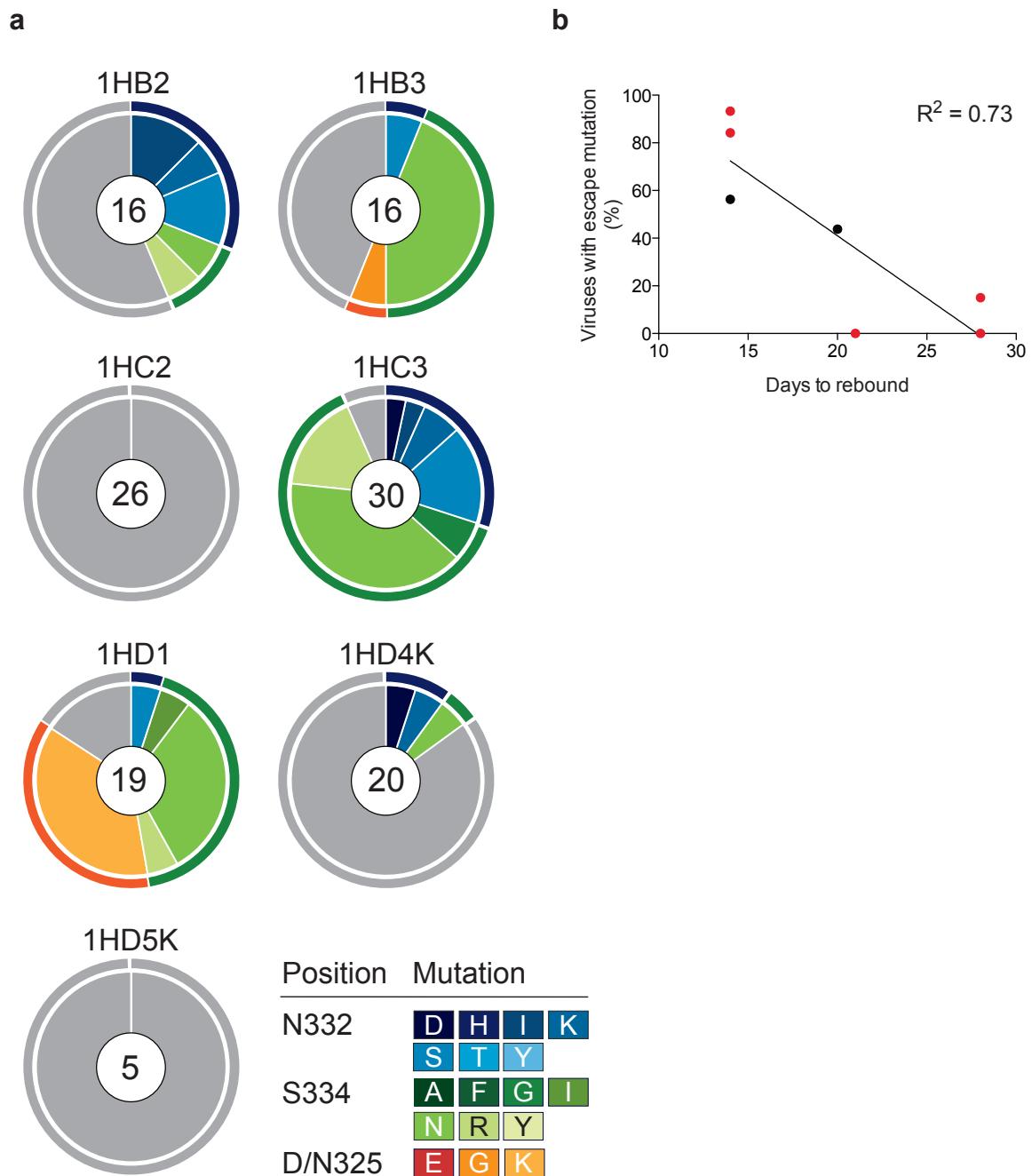
TP	# seqs	1HB1	# seqs	1HB2	# seqs	1HB3	# seqs	1HC1	# seqs	1HC2	# seqs	1HC3	# seqs	1HD1
Day 0	25	AAC ATT AGT N I S	27	AAC ATT AGT N I S	29	AAC ATT AGT N I S	5	AAC CTT AGT N L S	31	AAC ATT AGT N I S	27	AAC ATT AGT N I S	32	AAC ATT AGT N I S
	1	AAC ATT AGT N I S					5	AAT CTT AGT N L S			2	AAT ATT AGT N I S		
	1	AAT ATC AGT N I S					2	ACT ATT AGT T I S			1	AAC ATT AGT N I S		
Week 4	10	AAC ATT AAT N I N	12	AAC ATT AAT N I N	12	AAC ATT AAT N I N	7	AAC CTT AGT N L S	17	AAC ATT AAT N I N	12	AGC ATT AGT S I S	15	AAC ATT AAT N I N
	5	ATC ATT AGT I I S	8	AGC ATT AGT S I S	4	GAC ATT AGT D I S	6	AAT CTT AGT N L S	5	AAA ATT AGT K I S	10	AAC ATT AAT N I N	2	ATC ATT AGT I I S
	3	AAC ATT AGA N I R	5	AAC ATT AGG N I R	3	GAC ATT AGT S I S	6	ACT ATT AGT T I S	3	ACC ATT AGT T I S	3	AAC GTT AAT N V N	2	AAC ATT AGG N I R
	3	AAC ATT AGG N I R	1	AAC ATT GGT N I G	2	AAC ATT AGT N I S	5	AAC ATT AGT N I S	1	AAC ATT AGT N I S	2	AAATT AGT K I S	2	AAC ATT AGT N I S
	3	ACC ATT AGT T I S	1	ATC ATT AGT I I S	1	GAC ATT AGT H I S	4	AGT CTT AGT S L S	1	AAG ATT AGT K I S	2	ATC ATT AGT I I S	1	AGC ATT AGT S I S
	2	CAC ATT AGT H I S			1	AAC ATT AAT N I I	3	ACT CTT AGT T L S	1	AGC ATT AGT S I S	1	AAC ATT GGT N I G	1	GAC ATT AGT D I S
	2	AAC ATT GGT N I G			1	AGC ATT AGC S I S	2	AAC ATT AAT N I N	1	GAC ATT AGT D I S	1	GAC ATT AGT D I S	1	ACC ATT AGT T I S
	1	GAC ATT AGT D I S			1	AAA ATT AGT K I S	2	AGC CTT AGT S L S						
	1	AGC ATT AGT S I S			1	GAC ATT AGC D I S	1	AAA CCTT AGT K L S						
	1	AAA ATT AGT K I S			1	AAC ATT GGT N I G	1	AGC ATT AGT T I S						
Week 4*	23	AAC ATC AGT N I S	23	AAC ATT AGT N I S	32	AAT ATT TCT N I S	36	AAC ATT AGT N I S	19	AAC ATT AGT N I S	36	AAC ATT AGT N I S		
	27	GAC ATC AGT D I S	7	AAC ATT AAT N I N	5	AAT ATT TGT N I F	21	AAC ATT AAT N I N	13	AAC ATT AGT N I S	20	AAC ATT AAT N I N		
	3	AAC ATC ATT N I N	5	AGC ATT AGT S I S	4	AAT ATT GCT N I A	6	AAC ATT AGC N I R	8	AAC ATT AAT N I N	3	AAC ATT AGT N I S		
	2	AAA ATC AGT K I S	2	AAC ATT AGG N I R	3	AAT ATT TAT N I Y	2	AAA ATT AGT K I S	5	AGC ATT AGT S I S	3	AAC ATT AGG N I R		
	1	AAC ATC CGT N I R	2	AAC ATT GGT N I G	2	AAT ATT TCT N I S	2	AAC ATT GGT N I G	3	GAC ATT AGT D I S	3	AAC ATT GGT N I G		
			1	AAC ATT AGA N I R			1	AAC ATT AGT N I S	2	AAC ATT AGG N I R	1	AGC ATT AGT S I S		
			1	AAA ATT AGT K I S			1	AGC ATT AGT S I S	1	AGC ATT AGT T I S	1	AGC ATT AGT T I S		
			1	TAC ATT AGT Y I S			1	AGC ATT AGT T I S						

Resistant subjects

TP	# seqs	1HD2**	# seqs	1HD9K
Day 0	14	ACC ATT AGT T I S	30	AAT ATT AGT N I S

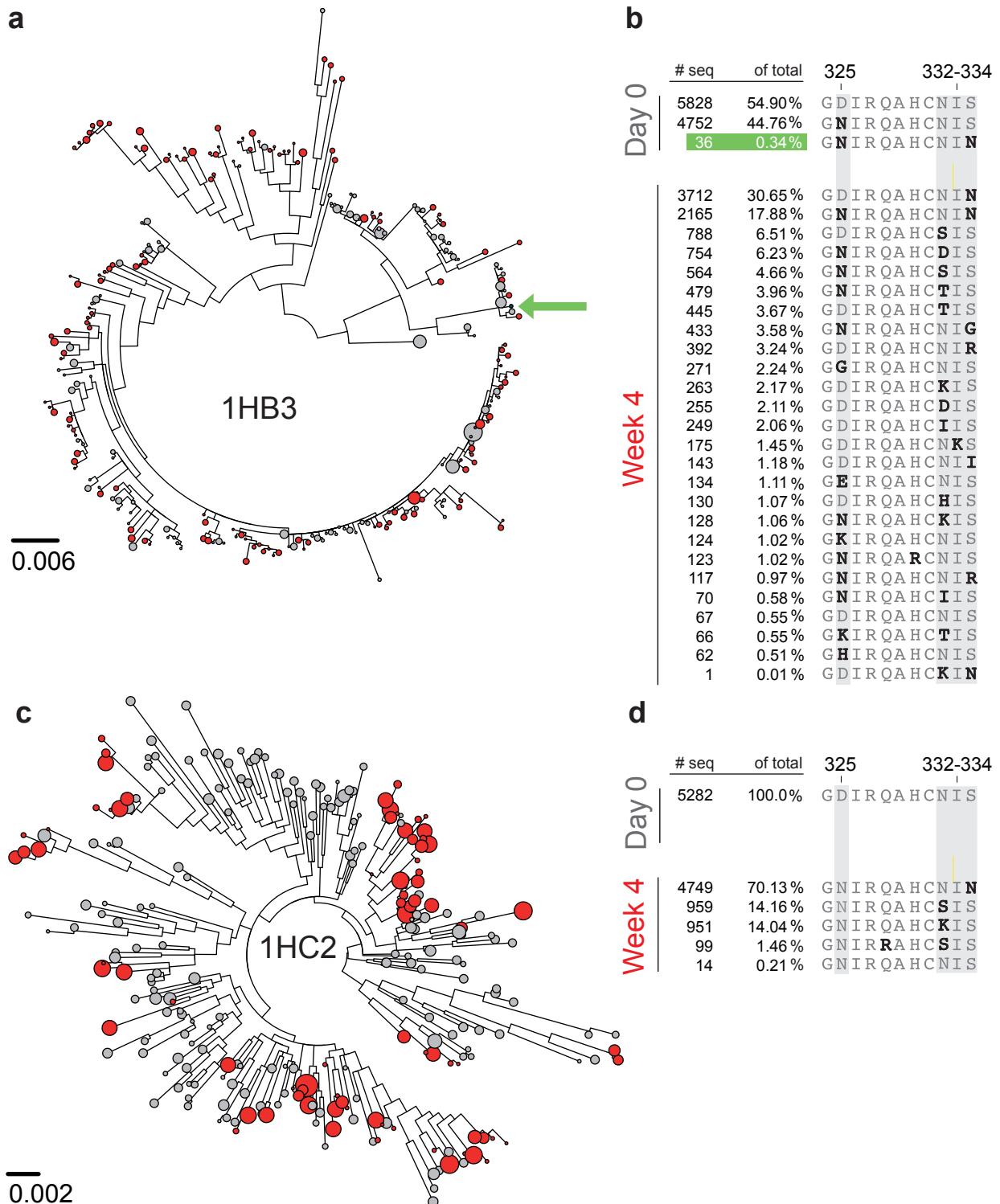
Supplementary Figure 7. Nucleotide alignment of N332 glycan region in study participants

Depicted are the different nucleotide motifs encoding the N332 glycan region (positions 332-334) in each subject at Day 0 (d0, **pre-infusion for 1HD2) and four weeks after infusion of 10-1074 (*wk4 and wk8 for 1HD6K, 1HD10K). To the left of each motif is the number of sequences matching a particular motif. Translation of the 9-nt span is shown below each nucleotide sequence. Yellow boxes highlight nucleotide changes away from the Day 0 majority variant. Red boxes highlight amino acid changes that disrupt the potential N-linked glycosylation site (PNGS) at position 332, while tourquoise boxes highlight non-synonymous changes that do not disrupt the PNGS. Subjects that harbored 10-1074-sensitive viruses on day 0 are shown on top, subjects that harbored resistant viruses at the bottom.



Supplementary Figure 8. Relative frequency of 10-1074 escape mutations in plasma envelope sequences 1 week after infusion

(a) Pie charts illustrate the relative abundance of particular amino acid mutations at envelope residues 325, 332, and 334 as analyzed by SGS. Type of escape mutation indicated by color code. (b) Correlation of time to viral rebound (x-axis) and the percentage of viruses mutated at 325, 332 or 334 (y-axis). Colors of dots indicate dose groups (10 mg/kg, black; 30 mg/kg, red).



Supplementary Figure 9. SMRT sequencing of subjects 1HB3 and 1HC2

Maximum-likelihood phylogenetic trees of full-length plasma envelope single molecule real time sequencing of subjects 1HB3 (a) and 1HC2 (c) obtained on Day 0 and Week 4 after 10-1074 infusion. Branches show high-quality consensus reads (HQCSs) with their respective copy number visualized by the size of the circle. Tables in (b) and (d) summarize obtained number of filtered reads (# seq) for sequence variants in envelope region 324-334 and the relative frequency of each variant (of total) for the two subjects, respectively. Arrow in (b) highlights Day 0 minor variant carrying a $^{332}\text{NIN}^{334}$ mutation.

Supplementary Table 1. Study participant demographics

a Demographics of HIV-1-infected participants enrolled in groups 1A-1D

Study ID	10-1074 dose	Age (years)	Gender	Race	Years since HIV-1 diagnosis	HIV-1 clade	ART regimen at enrollment**	HIV-1-RNA at day 0*** (copies/ml)	CD4+ T cell count at day 0 (cells/ μ l)
1HA1	3 mg/kg	47	Male	Black	26	ND	RPV/TDF/FTC	<20D	750
1HA2	3 mg/kg	36	Male	Black/Hispanic	3	ND	EVG/cobi/TDF/FTC	<20D	745
1HA3	3 mg/kg	49	Female	White/Hispanic	20	ND	EFV/TDF/FTC	<20	484
1HB1	10 mg/kg	32	Male	Black	15	B	-	13,920	449
1HB2	10 mg/kg	26	Male	Black	3	B	-	6,380	520
1HB3	10 mg/kg	53	Female	Black	19	B	-	35,810	616
1HC1	30 mg/kg	53	Male	Black	21	B	-	1,460	289*
1HC2	30 mg/kg	25	Male	Black	1	B	-	77,610	607
1HC3	30 mg/kg	33	Male	Black	6	B	-	20,140	411
1HD1	30 mg/kg	25	Male	Black	2	B	-	41,770	520
1HD2	30 mg/kg	51	Female	White	16	B	-	840	447
1HD4K	30 mg/kg	46	Male	White	6	B	-	60,300	330
1HD5K	30 mg/kg	42	Male	White	3	B	-	7,570	630
1HD6K	30 mg/kg	38	Male	White	2	B	-	10,100	700
1HD7K	30 mg/kg	53	Male	White	7	B	-	9,250	860
1HD8K	30 mg/kg	45	Male	White	2	B	-	11,000	880
1HD9K	30 mg/kg	27	Male	White	4	B	-	6,960	810
1HD10K	30 mg/kg	44	Male	White	11	B	-	10,500	760
1HD11K	30 mg/kg	24	Male	White	2	B	-	63,400	460

* Absolute CD4+ T cell count was 342 cells/ μ l at screening.

** RPV - rilpivirine, TDF - tenofovir disoproxil, FTC - emtricitabine, EVG - elvitegravir, cobi - cobicistat, EFV - efavirenz.

*** <20D - HIV-1-RNA detected but below limit of quantification (20 copies/ml). <20 - No HIV-1 RNA detected.

ND: Not determined.

b Demographics of HIV-1-negative participants enrolled in groups 2A-2D

Study ID	10-1074 dose	Age (years)	Gender	Race
2HA1	3 mg/kg	41	Male	Black
2HA2	3 mg/kg	58	Male	Black
2HA3	3 mg/kg	43	Female	White
2HB1	10 mg/kg	60	Male	Unknown
2HB2	10 mg/kg	34	Male	White
2HB3	10 mg/kg	34	Male	Black
2HC1	30 mg/kg	49	Male	White
2HC2	30 mg/kg	58	Female	Black
2HC3	30 mg/kg	52	Male	White
2HD1	30 mg/kg	28	Female	Black
2HD2	30 mg/kg	25	Male	Multiple
2HD3	30 mg/kg	39	Male	Black
2HD4	30 mg/kg	57	Male	White/Hispanic
2HD5	30 mg/kg	27	Female	White

Supplementary Table 2. Safety data*

Adverse Events	Reported AEs	% of AEs	% of participants	Possibly related	Mild	Moderate	Severe	Uninfected			HIV-1-infected		
								3 mg/kg (n=3) 10 mg/kg (n=3) 30 mg/kg (n=8)			3 mg/kg (n=3) 10 mg/kg (n=3) 30 mg/kg (n=13)		
								no. of adverse events			no. of adverse events		
Upper respiratory infection	15	26.32	39.4	-	15	-	-	1	1	9	-	1	3
Headache	6	10.53	18.2	5	5	1	-	-	2	1	-	1	2
Skin infection (folliculitis, furunculosis, tinea corporis)	4	7.02	12.1	-	4	-	-	-	-	1	2	-	1
Surgical and medical procedures (mammoplasty, hysterectomy, tooth extraction)	3	5.26	6.1	-	1	1	1	-	-	-	2	-	1
Arthralgia	2	3.51	6.1	-	2	-	-	-	1	1	-	-	-
Dyspepsia	2	3.51	6.1	-	1	1	-	1	-	1	-	-	-
Gastroenteritis	2	3.51	6.1	-	1	1	-	-	-	-	-	-	2
Localized musculoskeletal pain	2	3.51	6.1	-	2	-	-	-	-	-	-	1	1
Rash	2	3.51	6.1	-	1	1	-	-	-	-	-	-	2
Vomiting / Nausea	2	3.51	6.1	-	2	-	-	1	-	-	-	-	1
Abdominal pain	1	1.75	3.0	1	1	-	-	-	-	-	-	1	-
Diplopia	1	1.75	3.0	-	1	-	-	-	-	-	1	-	-
Dizziness	1	1.75	3.0	1	1	-	-	-	-	-	1	-	-
Depressive episode	1	1.75	3.0	-	1	-	-	-	-	-	-	-	1
Dry eyes	1	1.75	3.0	1	1	-	-	-	-	-	-	1	-
Elevated total bilirubin	1	1.75	3.0	1	1	-	-	-	-	-	-	-	1
Epistaxis	1	1.75	3.0	-	1	-	-	-	-	1	-	-	-
Head injury due to fall	1	1.75	3.0	-	1	-	-	-	-	-	-	1	-
Herpes zoster	1	1.75	3.0	-	1	-	-	-	-	-	-	-	1
Increased blood pressure	1	1.75	3.0	-	-	1	-	-	-	-	1	-	-
Malaise/Fatigue	1	1.75	3.0	1	1	-	-	-	-	-	-	1	-
Menorrhagia	1	1.75	3.0	-	1	-	-	-	-	-	1	-	-
Pruritus	1	1.75	3.0	1	1	-	-	-	-	-	-	-	1
Soft tissue hematoma	1	1.75	3.0	-	1	-	-	-	-	-	-	-	1
Toothache	1	1.75	3.0	-	1	-	-	-	-	-	1	-	-
Traumatic ear injury	1	1.75	3.0	-	1	-	-	-	-	-	-	-	1
Urinary tract infection	1	1.75	3.0	-	1	-	-	-	-	1	-	-	-

* Adverse events reported during 24 weeks of follow-up after 10-1074 infusion by 14/14 HIV-1-negative and 16/19 HIV-1-infected individuals (1HA1-1HD8K), and during 12 (1HD11K) and 20 (1HD9K, 1HD10K) weeks of follow up by the remaining 3 HIV-1 infected individuals.

Supplementary Table 4. Pharmacokinetics of 10-1074

a Pharmacokinetics by study subject

ID	HIV-1	10-1074 dose	Method (strain)	C _{max} (µg/ml)	Adjusted R ²	Estimated t _{1/2} (days)	Lambda (lower, days)	Lambda (upper, days)	AUC (INF_pred)	T _{last} (days)	C _{last} (µg/ml)	AUC_% Extrap_pred
2HA1	Negative	3 mg/kg	TZM.bl (Du422.1)	64.5	0.96	34.0	14	142	1,338.0	142	1.75	4.8
2HA2	Negative	3 mg/kg	TZM.bl (Du422.1)	130.1	0.97	16.8	7	56	1,281.1	56	5.41	8.7
2HA3	Negative	3 mg/kg	TZM.bl (Du422.1)	80.5	0.97	20.8	5	83	1,270.0	83	1.99	5.6
1HA1	Positive	3 mg/kg	TZM.bl (3103.v3.c10)	44.4	0.99	17.2	21	84	418.8	168	0.30	0.1
1HA2	Positive	3 mg/kg	TZM.bl (3103.v3.c10)	56.3	0.92	19.7	15	106	436.2	106	0.30	1.5
1HA3	Positive	3 mg/kg	TZM.bl (3103.v3.c10)	62.7	0.92	19.1	14	84	471.1	84	0.60	3.3
2HB1	Negative	10 mg/kg	TZM.bl (Du422.1)	358.3	0.97	21.0	7	137	3,924.7	137	1.67	1.0
2HB2	Negative	10 mg/kg	TZM.bl (Du422.1)	404.8	0.97	36.8	21	168	5,543.0	168	3.82	3.2
2HB3	Negative	10 mg/kg	TZM.bl (Du422.1)	331.0	0.99	22.8	7	133	3,862.5	133	1.83	1.5
1HB1	Positive	10 mg/kg	TZM.bl (3103.v3.c10)	167.4	0.97	12.1	15	56	1,193.1	56	1.80	2.3
1HB2	Positive	10 mg/kg	TZM.bl (3103.v3.c10)	270.6	0.93	9.5	9	57	1,619.0	57	1.90	1.2
1HB3	Positive	10 mg/kg	TZM.bl (3103.v3.c10)	160.3	0.96	11.5	7	56	1,535.7	56	3.30	2.8
2HC1	Negative	30 mg/kg	TZM.bl (Du422.1)	1,409.3	0.99	16.4	8	140	13,400.1	140	1.67	0.2
2HC2	Negative	30 mg/kg	TZM.bl (Du422.1)	1,761.6	0.97	27.8	14	176	21,427.5	176	5.72	1.0
2HC3	Negative	30 mg/kg	TZM.bl (Du422.1)	1,990.3	0.98	19.3	7	137	15,646.8	137	3.66	0.5
2HD1	Negative	30 mg/kg	TZM.bl (Du422.1)	1,318.2	0.97	24.3	21	141	13,689.5	141	4.45	1.1
2HD2	Negative	30 mg/kg	TZM.bl (Du422.1)	1,828.6	0.96	27.8	28	168	16,480.4	168	4.84	0.8
2HD3	Negative	30 mg/kg	TZM.bl (Du422.1)	1,403.3	0.98	13.8	14	85	10,173.9	85	5.72	1.0
2HD4	Negative	30 mg/kg	TZM.bl (Du422.1)	966.4	0.97	26.5	29	140	12,585.5	169	5.80	0.7
2HD5	Negative	30 mg/kg	TZM.bl (Du422.1)	659.1	0.98	27.9	14	144	9,679.9	144	6.92	2.3
1HC1	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	590.8	0.99	11.2	21	84	4,618.8	84	1.00	0.3
1HC2	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	1,069.9	0.98	8.9	7	84	6,201.0	84	0.70	0.1
1HC3	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	935.6	0.99	11.2	14	79	7,526.8	79	2.30	0.5
1HD1	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	1,226.2	1.00	8.9	14	84	8,785.8	84	0.60	0.1
1HD2	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	2,225.7	0.99	6.9	7	62	11,457.5	62	1.50	0.1
1HD4K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	947.9	0.99	16.1	14	147	8,431.3	147	0.40	0.1
1HD5K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	795.5	0.97	21.8	7	168	10,866.9	168	1.40	0.4
1HD6K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	1,171.9	0.99	8.6	9	84	8,543.5	84	0.60	0.1
1HD7K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	742.9	1.00	8.8	14	56	4,462.4	56	2.20	0.6
1HD8K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	892.7	0.99	21.8	7	168	10,441.9	168	1.40	0.4
1HD9K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	1,395.4	0.97	9.1	7	82	9,414.1	82	0.90	0.2
1HD10K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	1,452.2	0.97	8.7	14	84	8,031.9	84	0.40	0.1
1HD11K	Positive	30 mg/kg	TZM.bl (3103.v3.c10)	543.1	0.96	12.8	7	56	5,366.5	56	9.60	3.6

Supplementary Table 4. Pharmacokinetics of 10-1074 - continued

b Pharmacokinetics by study group

10-1074 dose	HIV-1	# of subjects	C _{max} (μg/ml)			t _{1/2} (days)		
			Mean	SD	Range	Mean	SD	Range
3 mg/kg	Negative	3	91.7	34.2	64.5 - 130.1	23.9	9.0	16.8 - 34.0
3 mg/kg	Positive	3	54.5	9.3	44.4 - 62.7	18.7	1.3	17.2 - 19.7
10 mg/kg	Negative	3	364.7	37.3	331 - 404.8	26.9	8.6	21.0 - 36.8
10 mg/kg	Positive	3	199.4	61.7	160.3 - 270.6	11.0	1.4	9.5 - 12.1
30 mg/kg	Negative	8	1,417	447.9	659.1 - 1,990	23.0	5.7	13.8 - 27.9
30 mg/kg	Positive	13	1,076	445.0	543.1 - 2,226	11.9	5.0	6.9 - 21.8
All	Negative	14				24.0	6.6	13.8 - 36.8
All	Positive	19				12.8	4.9	6.9 - 21.8

Supplementary Table 7. Primer-ID deep sequencing of V3 loop (HXB2 nt 6854 - 7356)

Subject	Day 0				Week 4			
	# IDs (total)	Sequence motif	# IDs	of total	# IDs (total)	# IDs	of total	
1HB1	344	G(N/D)IR - NxS	344	100%	286	0	0.00%	
		N332 mutation	0	0%		40	13.99%	
		S334 mutation	0	0%		246	86.01%	
		D/N325 mutation	0	0%		0	0%	
1HB3	370	G(N/D)IR - NxS	370	100%	223	0	0.00%	
		N332 mutation	0	0%		95	42.60%	
		S334 mutation	0	0%		127	56.95%	
		D/N325 mutation	0	0%		1	0.45%	
1HC2	622	G(N/D)IR - NxS	622	100%	504	2	0.40%	
		N332 mutation	0	0%		220	43.65%	
		S334 mutation	0	0%		279	55.35%	
		D/N325 mutation	0	0%		3	0.60%	
1HC3	125	G(N/D)IR - NxS	125	100%	241	0	0.00%	
		N332 mutation	0	0%		82	34.02%	
		S334 mutation	0	0%		159	65.98%	
		D/N325 mutation	0	0%		0	0%	
1HD1	616	G(N/D)IR - NxS	616	100%	590	1	0.17%	
		N332 mutation	0	0%		90	15.25%	
		S334 mutation	0	0%		389	65.93%	
		D/N325 mutation	0	0%		110	18.64%	

IDs: Number of distinct primer IDs (coverage > 10) that yielded an unambiguous majority consensus.

