

Supplemental Figure 1

	10	20	30	40	50	60	70	80	90	99
HIV _{NL4-3}	PQITLWQRPL	VTIKIGGQLK	EALLDTGADD	TVLEEMNLPG	RWKPKMIGGI	GGFIKVRQYD	QILIEICGHK	AIGTVLVGPT	PVNIIGRNLL	TQIGCTLNF
HIV _{SQV-5μM}ID...V..	...V.....	..P.....	..C.....	...V.....M
HIV _{APV-5μM}FI..VV.....
HIV _{LPV-5μM}FI.....IA...	V.....	...V.....
HIV _{IDV-5μM}FI.....I....	...V.....	..P.....	V.S.....	..T.....
HIV _{NFV-5μM}FTNI....	V..S.....
HIV _{ATV-5μM}I.....Q.....I..I..L	A.....	..P.....	V.....	..T.....
HIV _{TPV-15μM}II..I....I....	...VR.....	..VP.....	V.S.....	..T.....M	..L.....
HIV _{DRV^R_{P20}}I	...V...R	...I.....	..I..I....L....P.....A.....M
HIV _{DRV^R_{P30}}I	...V...R	...I.....	..I..I....L....P.....QA.V...M
HIV _{DRV^R_{P51}}I	...V...R	...I.....	..IF..I....L....	...M.....	..P.....QI.V...M
HIV _{F16}F	I.V...QMIV.AI....IV...	...M..K...	..VPV.....	..TA.....	...V...VM
HIV _{F39}V	I.VRV...TIF..I....	K...L....	...L..K..E	..P....E.T	IMS.....	...V...VM	..L.....
HIV _{V42}V	..VV.V...MIF.....	..T..IV...	...M....E	NVP...Y.K.	ILS...I...	..A.....VM
HIV _{T45}F	IPV.V...PTIF.GI....V.....	..VP.....T	I.S...A.	...V...VM	..L.....
HIV _{T48}I	..V.V...V.	...I.....	..IF.....	..E..L...V.	...L....E	..P.....	V.S.....	..A.V.....
HIV _{F71}I	IKV.....VIF.GID...LV...	...M..KE..	..PV.V....	V.S.....	...V...MM

Figure S1. Amino acid sequence of the PI-resistant HIV-1 variants. Amino acid substitutions identified in protease-encoding region of laboratory-selected FDA-approved HIV variants (HIV_{SQV-5μM}, HIV_{APV-5μM}, HIV_{LPV-5μM}, HIV_{IDV-5μM}, HIV_{NFV-5μM}, HIV_{ATV-5μM}, and HIV_{TPV-15μM}, and HIV_{DRV^R}S: HIV_{DRV^R_{P20}}, HIV_{DRV^R_{P30}}, and HIV_{DRV^R_{P51}}), and recombinant clinical HIV isolates (r_{CL}HIV_{F16}, r_{CL}HIV_{F39}, r_{CL}HIV_{V42}, r_{CL}HIV_{T45}, r_{CL}HIV_{T48}, and r_{CL}HIV_{F71}) compared to the wild-type HIV_{NL4-3} are illustrated. Identity with the sequence at individual amino acid positions is indicated by a dot.

Supplemental Figure 2

a.	HIV _{P30} ^{22wkDRV}	CCT CAA ATC ACT CTT TGG CAA CGA CCC ATC GTC ACA ATA AAG GTA GGG GGG CAA CTA AGG GAA GCT CTA ATA GAT ACA GGA 81	Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Val Gly Gly Gln Leu Arg Glu Ala Leu Ile Asp Thr Gly 27
		GCA GAT GAT ACA ATA TTT GAA GAA ATA AAT TTG CCA GGA AGA TGG AAA CCA AAA TTG ATA GGG GGA ATT GGA GGT TTT ATG 162	Ala Asp Asp Thr Ile Phe Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly Gly Ile Gly Gly Phe Met 54
		AAA GTA AGA CAG TAT GAT CAG ATA CCC ATA GAA ATC TGT GGG CAT CAA GCT ATA GGT ACA GTA TTA GTA GGA CCT ACA CCT 243	Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile Glu Ile Cys Gly His Gln Ala Ile Gly Thr Val Leu Val Gly Pro Thr Pro 81
		ATC AAC GTA ATT GGA AGA AAT ATG TTG ACT CAG ATT GGC TGC ACC TTA AAT TTC 297	Ile Asn Val Ile Gly Arg Asn Met Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe 99
b.	HIV _{P30} ^{45wk003-15}	CCT CAA ATC ACT CTT TGG CAA CGA CCC ATC GTC CCA ATA AAG GTA GGG GGG CAA CTA AGG GAA GCT CTA ATA GAT ACA GGA 81	Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Pro Ile Lys Val Gly Gly Gln Leu Arg Glu Ala Leu Ile Asp Thr Gly 27
		GCA GAT GAT ACA ACA TTA AAA GAA ATA AAT TTG CCA GGA AGA TGG AAA CCA AAA TTG ATA GGG GGA ATT GGA GGT TTT ATC 162	Ala Asp Asp Thr Thr Leu Lys Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly Gly Ile Gly Gly Phe Ile 54
		AAA GTA AGA CAG TAT GAT CAG ATA CCC ATA GAA ATC TGT GGG CAT CAA GCT ATA GGT ACA GTA TTA GTA GGA CCT ACA CCT 243	Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile Glu Ile Cys Gly His Gln Ala Ile Gly Thr Val Leu Val Gly Pro Thr Pro 81
		ATC AAC GTA ATT GGA AGA AAT ATG TTG ACT AAG ATT GGC TGC ACC TTA AAT TTC 297	Ile Asn Val Ile Gly Arg Asn Met Leu Thr Lys Ile Gly Cys Thr Leu Asn Phe 99
c.	HIV _{P30} ^{45wk001-15}	CCT CAA ATC ACT CTT TGG CAA CGA CCC ATC GTC ACA ATA AAG GTA GGG GGG CAA CTA AGG GAA GCT CTA ATA GAT ACA GGA 81	Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Val Gly Gly Gln Leu Arg Glu Ala Leu Ile Asp Thr Gly 27
		GCA GAT GAT ACA GTA TTA GAA GAA ATA AAT TTG CCA GGA AGA TGG AAA CCA AAA TTG ATA GGG GGA ATT GGA GGT TTT ATC 162	Ala Asp Asp Thr Val Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly Gly Ile Gly Gly Phe Ile 54
		AAA GTA AGA CAG TAT GAT CAG ATA CCC ATA GAA ATC TGT GGG CAT CAA GTT ATA GGT ACA GTA TTA GTA GGA CCT ACA CCT 243	Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile Glu Ile Cys Gly His Gln Val Ile Gly Thr Val Leu Val Gly Pro Thr Pro 81
		GTC AAC GTA ATT GGA AGA AAT ATG TTG ACT CAG ATT GGC TGC ACC TTA AAT TTC 297	Val Asn Val Ile Gly Arg Asn Met Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe 99

Figure S2. Nucleotide and amino acid sequences of HIV variants selected with DRV, GRL-003-15, and GRL-001-15. Nucleotide and amino acid sequences of the protease-encoding region of HIV variants obtained from selection of HIV_{DRV}^R_{P30} in the presence of DRV (a), GRL-003-15 (b), or GRL-001-15 (c) are shown. Note that only the major clones obtained on weeks 22, 45, and 45 with DRV (HIV_{P30}^{22wkDRV}), GRL-003-15 (HIV_{P30}^{45wk003-15}), and GRL-001-15 (HIV_{P30}^{45wk001-15}), respectively, are shown.

Table S1 Partition and distribution coefficient of DRV, GRL-003-15, GRL-001-15, GRL-121-13, and GRL-142-13

Compounds	Concentration (μM)				Log $P_{\text{octanol/partition}}$ *	Log $D_{\text{octanol/TBS}}$ *
	1-Octanol	Water	1-Octanol	TBS		
DRV	0.8	9.4	0.6	9.3	-1.08	-1.48
GRL-003-15	1.6	9.4	1.5	9.4	-0.76	-1.11
GRL-001-15	1.5	8.6	1.1	8.4	-0.76	-1.19
GRL-121-13	1.1	9.5	0.8	9.9	-0.92	-1.37
GRL-142-13	1.9	9.0	1.7	8.8	-0.67	-1.01

* The partition ($\log P$) and distribution ($\log D$) coefficients of GRL-003-15, GRL-001-15, GRL-121-13, and GRL-142-13 were determined. DRV was used as a control. 1-Octanol, an organic alcohol, and water were used for $\log P$ determination, while tris buffered saline (TBS) (pH 7.4) and octanol were utilized for the $\log D$ assay. Prior to the retrieval of actual values, a standard curve was generated as a reference. The drug concentrations for each compartment (octanol, water, and TBS) were measured at an absorbance of 230 using a light spectrophotometer. $\log P$ and $\log D$ values were calculated according to the formulas given in Materials and Methods.

Table S2 Antiviral effects of GRL-003-15, GRL-001-15, and GRL-121-13 against selected PI-resistant HIV-1 variants and recombinant clinical HIV-1 isolates compared to that of DRV

HIV strains	Fold change against DRV*			
	DRV	GRL-003-15	GRL-001-15	GRL-121-13
HIV _{NL4-3}	1	0.016	0.020	0.10
HIV _{SQV-5μM}	1	0.00011	0.013	0.00052
HIV _{APV-5μM}	1	0.000021	0.0000070	0.00069
HIV _{LPV-5μM}	1	0.00000043	0.000012	0.0000064
HIV _{IDV-5μM}	1	0.000017	0.0000091	0.00025
HIV _{NFV-5μM}	1	0.00017	0.000038	0.0047
HIV _{ATV-5μM}	1	0.000035	0.000083	0.0019
HIV _{TPV-15μM}	1	0.000017	0.0020	0.0030
HIV _{DRV^R P20}	1	0.027	0.0046	0.053
HIV _{DRV^R P30}	1	0.015	0.00079	0.11
HIV _{DRV^R P51}	1	0.014	0.013	0.037
rCLHIV _{F16}	1	0.00000025	0.00000018	0.00080
rCLHIV _{F39}	1	0.011	0.011	0.013
rCLHIV _{V42}	1	0.011	0.012	0.043
rCLHIV _{T45}	1	0.019	0.019	0.017
rCLHIV _{T48}	1	0.000010	0.0011	0.0019
rCLHIV _{F71}	1	0.012	0.012	0.051

*The values indicate fold change of EC₅₀ values of each HIV variant against those of DRV.