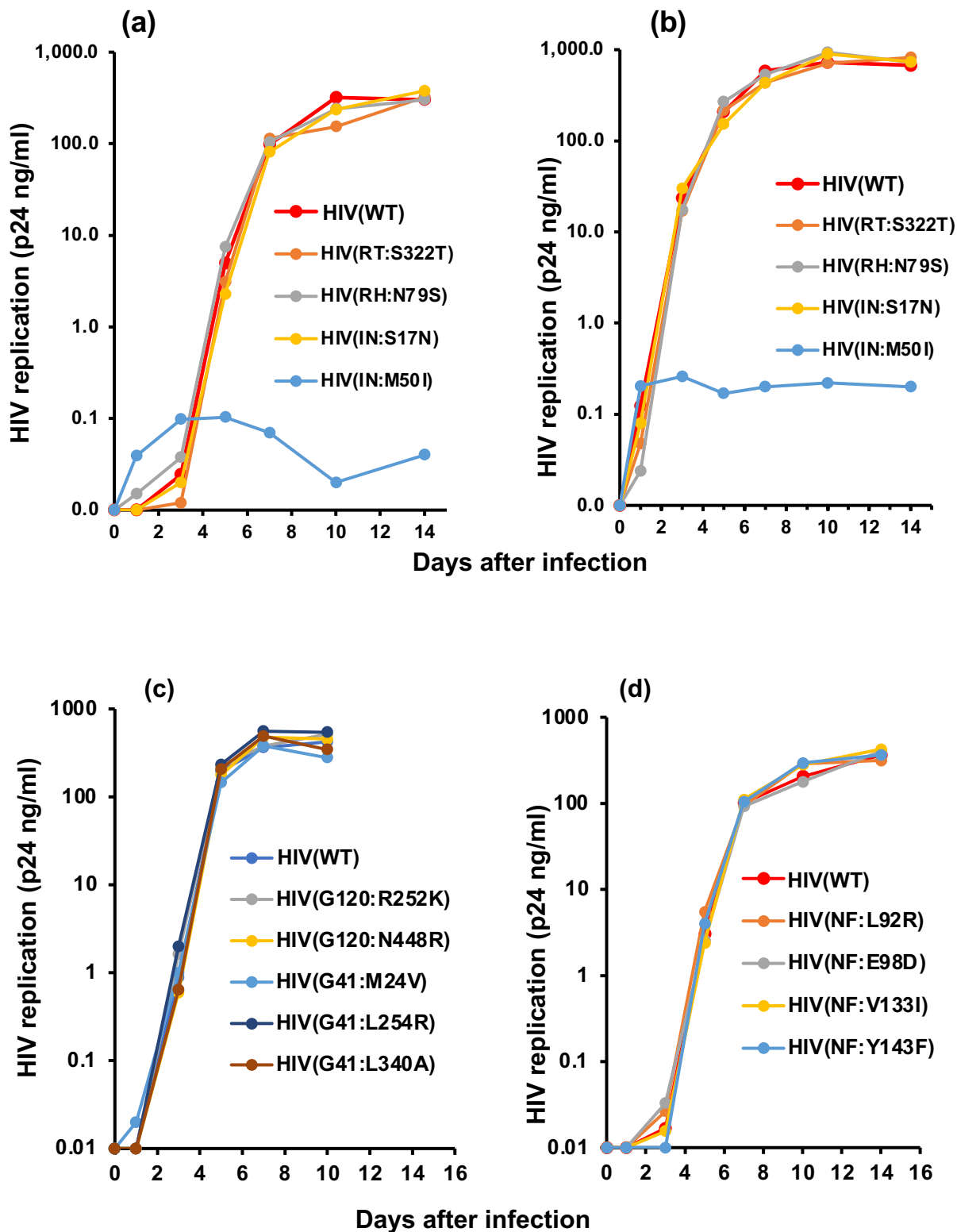


**Supplementary Information
(Figures and Tables)**

**Natural Occurring Polymorphisms in HIV-1
Integrase and RNase H Regulate Virus Release and
Autoprocessing**

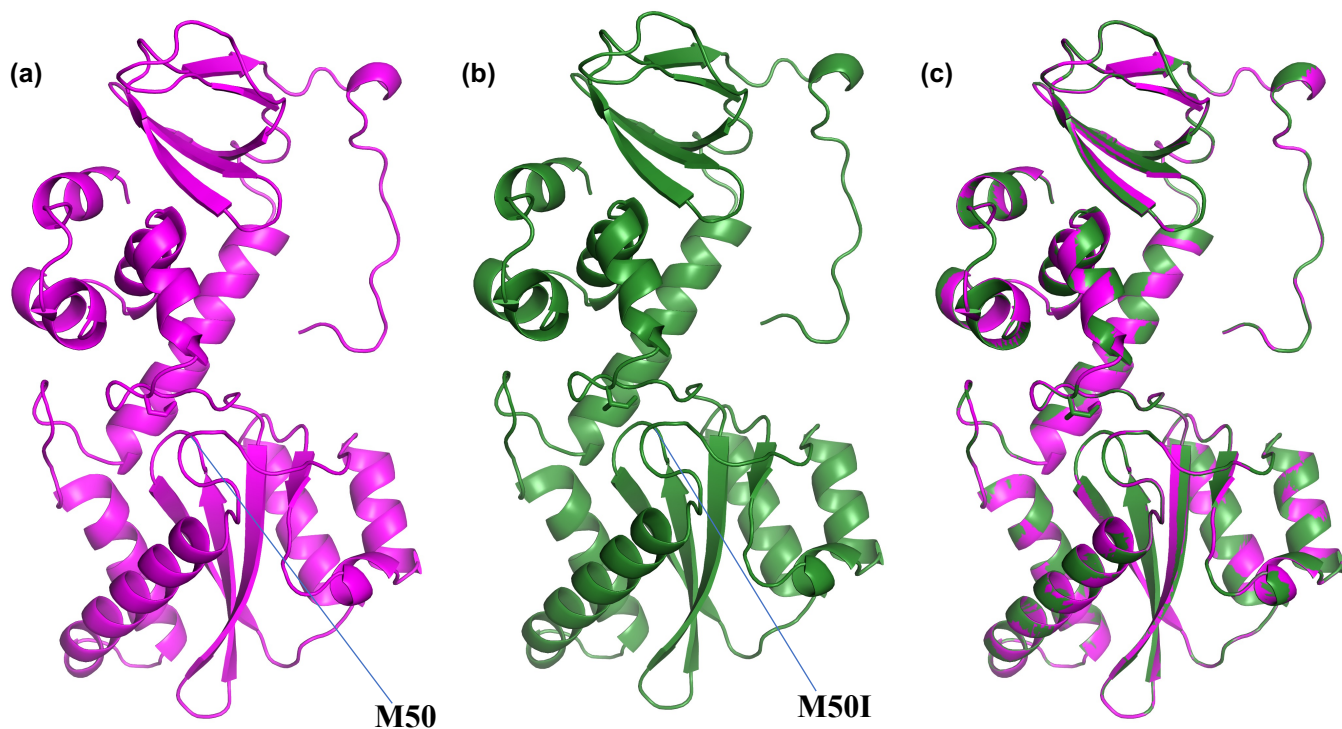
T. Imamichi, JG. Bernbaum, S. Laverdure, et al.,

Supplemental Fig. S1. Comparison of HIV replication activity between HIV(WT) and mutants



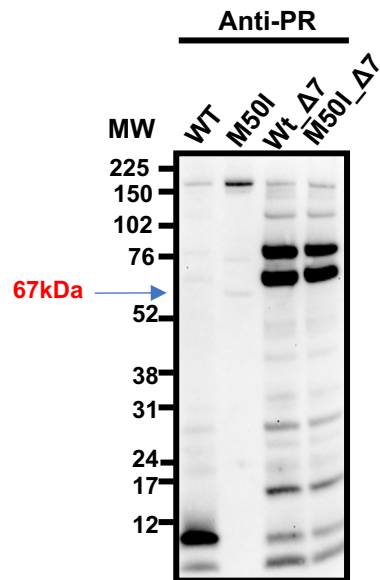
PHA-stimulated primary CD4 T cells from normal healthy donor were infected with HIV(WT) or variants containing mutation in GagPol as described in the materials and methods. The infected cells were cultured for 14 days with changing media on every 3-4 days. HIV replication was monitored using a p24 antigen capture kit. Data indicates means \pm SD.

Supplemental Fig. S2, Predicted structure analysis of IN protein.



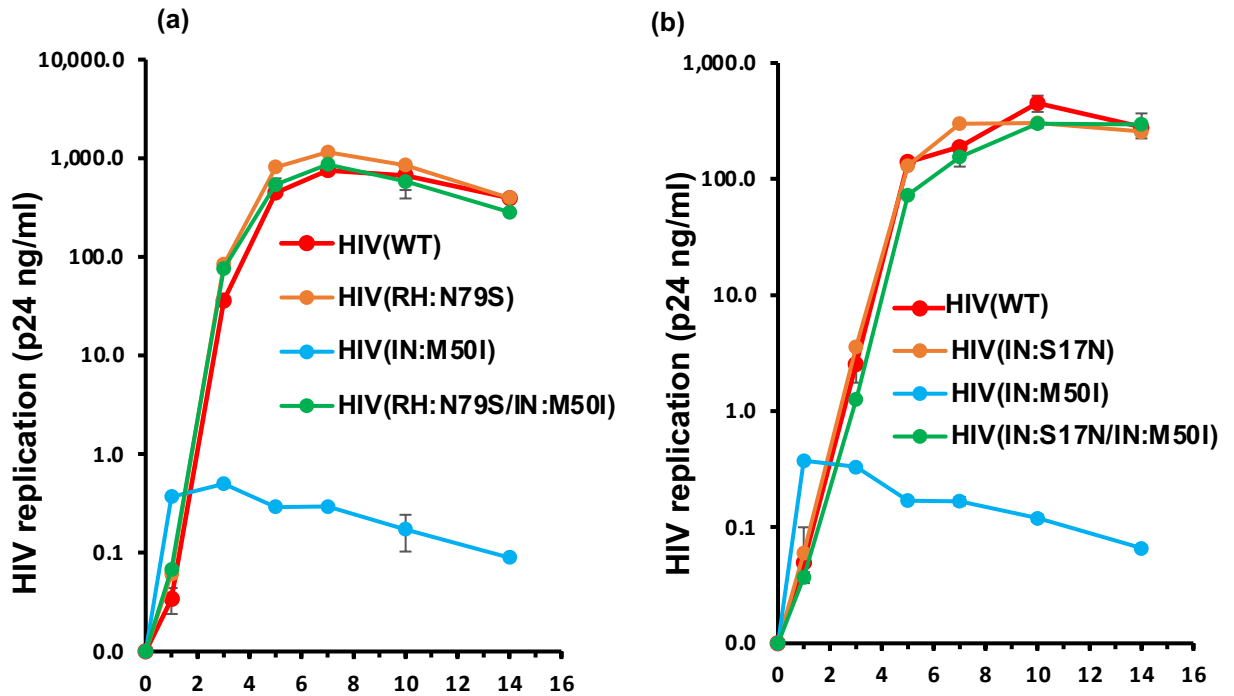
(a and b) *In Silico*, full-length IN structures were created as described in the materials and methods. (c) Alignment of homology models from Robetta between IN:WT (magenta) and IN:M50I (forest). The side chains in positions IN:50 are shown in lines.

Supplemental Fig. S3, Anti-PR antibody detects 67kDa band in HIV(M50I) lysate



Virus particles were isolated from transfection sup using ultracentrifugation as described in the Materials and Methods, and 5 μ g/ml of total viral proteins were subjected to WB. PR fragments were detected by polyclonal anti-PR antibody. Near 67kDa band is detected in M50I lysate.

Supplemental Fig. S4: Impact of RH:N79S and IN:N79S on HIV(INM50I) replication



PHA-stimulated primary CD4 T cells from a normal healthy donor were infected with HIV(WT), HIV(RH:N79S), HIV(IN:M50I), HIV(RH:N79S/IN:M50I), HIV(IN:S17N) or HIV(IN:S17N/M50I) as described in the Materials and Methods. The infected cells were cultured for 14 days with changing media on every 3-4 days. HIV replication was monitored using a p24 antigen capture kit. Data indicates means \pm SD.

Supplemental Table S1: p24 antigen concentration in HIV stocks

Denoted HIV	p24 $\mu\text{g/ml}$ * (%)
HIV(Wt)	89 \pm 12 (n=7) (100)
HIV(RT:S322T)	71 (n=2)
HIV(RH:N79S)	59 (n=2)
HIV(IN:S17N)	84 \pm 14 (n=2) (94)
HIV(IN:M50I)	0.30 \pm 0.087 (n=7) (0.34)
HIV(G120:R252K)	79 (n=2)
HIV(G120:N448R)	122 (n=2)
HIV(G41:M24V)	83 (n=2)
HIV(G41:M24L)	85 (n=2)
HIV(G41:L254R)	157 (n=2)
HIV(G41:L340A)	105 (n=2)
HIV(NF:K92R)	128 (n=2)
HIV(NF:E98D)	99 (n=2)
HIV(NF:V133I)	79 (n=2)
HIV(NF:Y143F)	122 (n=2)
HIV(IN:S17N/M50I)	160 (n=2)
HIV(RH:N79S/M50I)	136 \pm 28 (n=3)
HIV(WT) from HeLa	296 (n=2) (100)
HIV(M50I) from HeLa	0.825 (n=2) (0.3)

* Transfection supernatants from HEK293T cells or HeLa were collected and viral particles were pelleted using ultracentrifugation at 100,000 xg as described in the Materials and Methods.

Each viral pellet was resuspended in 1/100 volume of the transfection supernatants in complete culture media. Viral concentration was determined by measuring HIV p24 antigen by ELISA.

Supplemental Table S2: Population analysis of amino acid (aa) residue at Codon 50 in IN and Codon 79 in RH

		aa at Codon 50 in IN							Grand Total	
		Del *	I	L	M	R	T	V		?
aa at Codon 79 in RH	Del				2 **					2
	C				5					5
	D				2					2
	G		2		4					6
	H				1					1
	M				1					1
	N	1	203	5	1441	3	14	1	9	1677
	R		1		2					3
	S		194 *** (3.8%)	11	3128	7	21	6	12	3379
	T				8					8
	?		1		13		1		1	16
Grand Total	1	401	16	4607	10	36	7	22	5100 (100%)	

*: "Del " and " ? " indicate "deletion of the codon" and " unsure aa", respectively. I: Ile, L: leu,

M: Met, R: Arg, T: Thr, V: Val, C: Cys, D: Asp, G: Gly, H: His, N: Asn, S: Ser.

Yellow font letters show aa of the subtype B sequence at each codon.

Green letters show mutations of the interest.

** : Number of clinical isolate containing the sequence.

*** : Number of clinical isolates containing a combination of IN:M50I and RH:N79S mutations.

The numbers in the parentheses indicates the percentages of population in a total 5100 sequence data.

Supplemental Table S3: Population analysis of amino acid (aa) residues at Codons 17 and 50 and in IN

		aa at Codon 50 in IN								
		Del *	I	L	M	R	T	V	?	Grand Total
aa at Codon 17 in IN	Del				1 **					1
	C		7		60	1				68
	G		1							1
	N	1	58 *** (1.1%)	4	822		10		5	900
	R		1							1
	S		323	11	3607	9	24	6	15	3995
	T		9	1	106		2	1	1	120
	?		2		11				1	14
	Grand Total	1	401	16	4607	10	36	7	22	5100 (100)

*: "Del" and "?" indicate "deletion of the codon" and "unsure aa", respectively.

I: Ile, L: leu, M: Met, R: Arg, T: Thr, V: Val, C: Cys, G: Gly, N: Asn, R: Arg, S: Ser, T; Thr.

Yellow font letters show aa of the subtype B sequence at each codon.

Green letters show mutations of the interest.

** : Number of clinical isolates containing the sequence.

***: Numbers of clinical isolates containing a combination of IN:M50I and IN:S17N mutation.

The numbers in the parentheses indicates the percentages of population in a total 5100 sequence data.

Supplemental Table S4: Population analysis of IN:M50I in CRF

IN codon50										
CRFs ¹	IN:M50 ²	IN:M50I ³	Total ⁴	%of IN:M50I		CRFs ¹	IN:M50 ²	IN:M50I ³	Total ⁴	%of IN:M50I
01_AE	1991	90	2115	4.26%		58_01B	6	0	6	0.00%
02_AG	501	35	592	5.91%		59_01B	8	0	8	0.00%
03_AB	6	0	6	0.00%		60_BC	2	0	6	0.00%
04_cpx	8	0	8	0.00%		61_BC	2	0	3	0.00%
05_DF	3	0	4	0.00%		62_BC	3	0	3	0.00%
06_cpx	121	7	129	5.43%		63_02A	15	116	175	66.29%
07_BC	398	12	411	2.92%		64_BC	8	0	8	0.00%
08_BC	309	14	331	4.23%		65_cpx	7	0	7	0.00%
09_cpx	5	0	6	0.00%		66_BF1	2	1	3	33.33%
10_CD		0	3	0.00%		67_01B	1	0	2	0.00%
11_cpx	21	7	30	23.33%		68_01B	4	0	4	0.00%
12_BF	15	0	16	0.00%		69_01B	7	0	7	0.00%
13_cpx	22	2	27	7.41%		70_BF1	3	0	3	0.00%
14_BG	15	0	15	0.00%		71_BF1	11	3	14	21.43%
15_01B	8	0	8	0.00%		72_BF1	5	0	5	0.00%
16_A2D	2	2	4	50.00%		73_BG	3	0	3	0.00%
17_BF	7	0	7	0.00%		74_01B	3	0	3	0.00%
18_cpx	11	0	11	0.00%		75_BF	3	0	3	0.00%
19_cpx	5	1	6	16.67%		76_01B	2	0	2	0.00%
20_BG	5	0	5	0.00%		77_cpx	4	0	4	0.00%
21_A2D	3	0	3	0.00%		78_cpx	2	1	3	33.33%
22_01A1	3	20	27	74.07%		79_0107	3	0	3	0.00%
23_BG	2	0	2	0.00%		80_0107	3	0	3	0.00%
24_BG	7	1	9	11.11%		81_cpx	2	0	2	0.00%
25_cpx	2	1	6	16.67%		82_cpx	6	0	6	0.00%
26_A5U	1	3	4	75.00%		83_cpx	10	0	11	0.00%
27_cpx	3	1	4	25.00%		84_A1D	0	0	3	0.00%
28_BF	5	0	5	0.00%		85_BC	10	0	11	0.00%
29_BF	8	0	8	0.00%		86_BC	3	0	3	0.00%
31_BC	0	0	3	0.00%		87_cpx	3	0	3	0.00%
32_06A6	3	0	4	0.00%		88_BC	3	0	3	0.00%
33_01B	7	0	7	0.00%		89_BF	8	0	8	0.00%
34_01B	3	0	3	0.00%		90_BF1	6	3	9	33.33%
35_AD	22	0	23	0.00%		92_C2U	5	0	5	0.00%
36_cpx	4	0	4	0.00%		93_cpx	2	0	3	0.00%
37_cpx	13	0	13	0.00%		95_02B	5	0	5	0.00%
38_BF	1	0	1	0.00%		96_cpx	3	0	3	0.00%
39_BF	2	1	3	33.33%		97_01B	5	0	5	0.00%
40_BF	3	0	4	0.00%		98_06B	1	0	1	0.00%
41_CD	0	0	3	0.00%		99_BF	3	0	3	0.00%
42_BF	14	2	17	11.76%		100_01C	3	0	3	0.00%
43_02G	5	0	5	0.00%		101_01B	3	0	3	0.00%
44_BF	2	1	3	33.33%		102_0107	2	0	2	0.00%
45_cpx	7	1	8	12.50%		103_01B	4	0	4	0.00%
46_BF	8	0	8	0.00%		104_0107	3	0	3	0.00%
47_BF	3	0	3	0.00%		105_0108	5	0	5	0.00%
48_01B	3	0	3	0.00%		106_cpx	10	0	10	0.00%
49_cpx	1	3	4	75.00%		107_01B	4	0	4	0.00%
50_A1D	5	0	5	0.00%		108_BC	5	0	5	0.00%
51_01B	0	0	7	0.00%		109_0107	3	0	3	0.00%
52_01B	3	0	3	0.00%		110_BC	3	0	3	0.00%
53_01B	4	0	4	0.00%		111_0108	4	0	4	0.00%
54_01B	3	0	3	0.00%		112_01B	0	0	4	0.00%
55_01B	12	0	12	0.00%		113_0107	4	0	4	0.00%
56_cpx	4	0	4	0.00%		114_0155	8	0	8	0.00%
57_BC	7	0	7	0.00%		115_01C	2	0	2	0.00%
						117_0107	7	0	7	0.00%
						118_BC	1	0	1	0.00%
						Grand Total	3879	328	4403	7.45%

1: Name of CRF, 2: Sequence numbers containing IN:M50

3: Sequence numbers containing IN:M50I, 4: Analyzed total sequence number

Supplemental Table S5: Population analysis of RH:N79S in CRF

CRFs ¹	RH:N79 ²	RH:N79S ³	Total ⁴	% of RH:N79S	CRFs ¹	RH:N79 ²	RH:N79S ³	Total ⁴	% of RH:N79S
01_AE	1843	95	1946	4.88%	56_cpx	0	4	4	100.00%
02_AG	171	6	179	3.35%	57_BC	7	0	7	0.00%
03_AB	1	4	5	80.00%	58_01B	6	0	6	0.00%
04_cpx	8	0	8	0.00%	59_01B	8	0	8	0.00%
05_DF	4	0	4	0.00%	60_BC	6	0	6	0.00%
06_cpx	15	2	17	11.76%	61_BC	3	0	3	0.00%
07_BC	400	7	411	1.70%	62_BC	3	0	3	0.00%
08_BC	317	8	331	2.42%	63_02A	9	4	13	30.77%
09_cpx	5	0	5	0.00%	64_BC	8	0	8	0.00%
10_CD	3	0	3	0.00%	65_cpx	7	0	7	0.00%
11_cpx	6	18	24	75.00%	66_BF1	3	0	3	0.00%
12_BF	12	2	15	13.33%	67_01B	0	2	2	100.00%
13_cpx	10	0	10	0.00%	68_01B	4	0	4	0.00%
14_BG	12	0	12	0.00%	69_01B	0	7	7	100.00%
15_01B	7	1	8	12.50%	70_BF1	0	3	3	100.00%
16_A2D	4	0	4	0.00%	71_BF1	1	13	14	92.86%
17_BF	7	0	7	0.00%	72_BF1	5	0	5	0.00%
18_cpx	8	0	8	0.00%	73_BG	3	0	3	0.00%
19_cpx	0	5	5	100.00%	74_01B	3	0	3	0.00%
20_BG	0	5	5	100.00%	75_BF	3	0	3	0.00%
21_A2D	3	0	3	0.00%	76_01B	0	2	2	100.00%
22_01A1	14	0	14	0.00%	77_cpx	4	0	4	0.00%
23_BG	0	2	2	100.00%	78_cpx	3	0	3	0.00%
24_BG	0	9	9	100.00%	79_0107	3	0	3	0.00%
25_cpx	3	0	3	0.00%	80_0107	3	0	3	0.00%
26_A5U	4	0	4	0.00%	81_cpx	2	0	2	0.00%
27_cpx	4	0	4	0.00%	82_cpx	0	6	6	100.00%
28_BF	0	5	5	100.00%	83_cpx	0	11	11	100.00%
29_BF	7	1	8	12.50%	84_A1D	3	0	3	0.00%
31_BC	3	0	3	0.00%	85_BC	11	0	11	0.00%
32_06A6	4	0	4	0.00%	86_BC	0	3	3	100.00%
33_01B	7	0	7	0.00%	87_cpx	3	0	3	0.00%
34_01B	3	0	3	0.00%	88_BC	3	0	3	0.00%
35_AD	21	0	22	0.00%	89_BF	8	0	8	0.00%
36_cpx	3	0	3	0.00%	90_BF1	3	6	9	66.67%
37_cpx	4	0	4	0.00%	92_C2U	5	0	5	0.00%
38_BF	1	0	1	0.00%	93_cpx	3	0	3	0.00%
39_BF	1	2	3	66.67%	95_02B	3	2	5	40.00%
40_BF	1	3	4	75.00%	96_cpx	0	3	3	100.00%
41_CD	3	0	3	0.00%	97_01B	5	0	5	0.00%
42_BF	17	0	17	0.00%	98_06B	0	1	1	100.00%
43_02G	3	0	3	0.00%	99_BF	0	3	3	100.00%
44_BF	3	0	3	0.00%	100_01C	3	0	3	0.00%
45_cpx	6	0	6	0.00%	101_01B	3	0	3	0.00%
46_BF	8	0	8	0.00%	102_0107	2	0	2	0.00%
47_BF	3	0	3	0.00%	103_01B	0	4	4	100.00%
48_01B	3	0	3	0.00%	104_0107	3	0	3	0.00%
49_cpx	3	1	4	25.00%	105_0108	5	0	5	0.00%
50_A1D	5	0	5	0.00%	106_cpx	9	0	10	0.00%
51_01B	7	0	7	0.00%	107_01B	0	4	4	100.00%
52_01B	3	0	3	0.00%	108_BC	5	0	5	0.00%
53_01B	4	0	4	0.00%	109_0107	3	0	3	0.00%
54_01B	0	3	3	100.00%	110_BC	0	3	3	100.00%
55_01B	12		12	0.00%	111_0108	4	0	4	0.00%
					112_01B	4	0	4	0.00%
					113_0107	4	0	4	0.00%
					114_0155	8	0	8	0.00%
					115_01C	2	0	2	0.00%
					117_0107	7	0	7	0.00%
					118_BC	1	0	1	0.00%
					Grand Total	3200	260	3483	7.46%

1: Name of CRF, 2: Sequence numbers containing RH:N79

3: Sequence numbers containing RH:N79S, 4: Analyzed total sequence number

Supplemental Table S6: Population analysis of IN:S17N in CRF

CRFs ¹	IN:S17 ²	IN:S17N ³	Total ⁴	% of IN:S17N	CRFs ¹	IN:S17 ²	IN:S17N ³	Total ⁴	% of IN:S17N
01_AE	2087	19	2116	0.90%	58_01B	6	0	6	0.00%
02_AG	559	16	592	2.70%	59_01B	8	0	8	0.00%
03_AB	5	0	6	0.00%	60_BC	6	0	6	0.00%
04_cpx	2	6	8	75.00%	61_BC	3	0	3	0.00%
05_DF	3	1	4	25.00%	62_BC	3	0	3	0.00%
06_cpx	106	23	129	17.83%	63_02A	174	0	175	0.00%
07_BC	408	3	411	0.73%	64_BC	8	0	8	0.00%
08_BC	322	6	331	1.81%	65_cpx	1	6	7	85.71%
09_cpx	6	0	6	0.00%	66_BF1	1	0	3	0.00%
10_CD	1	2	3	66.67%	67_01B	2	0	2	0.00%
11_cpx	28	1	30	3.33%	68_01B	3	1	4	25.00%
12_BF	3	13	16	81.25%	69_01B	7	0	7	0.00%
13_cpx	19	8	27	29.63%	70_BF1	3	0	3	0.00%
14_BG	10	4	15	26.67%	71_BF1	4	6	14	42.86%
15_01B	8	0	8	0.00%	72_BF1	1	3	5	60.00%
16_A2D	4	0	4	0.00%	73_BG	3	0	3	0.00%
17_BF		7	7	100.00%	74_01B	2	1	3	33.33%
18_cpx	2	8	11	72.73%	75_BF		2	3	66.67%
19_cpx	3	2	6	33.33%	76_01B	2	0	2	0.00%
20_BG	5	0	5	0.00%	77_cpx	4	0	4	0.00%
21_A2D	3	0	3	0.00%	78_cpx	3	0	3	0.00%
22_01A1	26	0	27	0.00%	79_0107	3	0	3	0.00%
23_BG	2	0	2	0.00%	80_0107	3	0	3	0.00%
24_BG	8	1	9	11.11%	81_cpx	1	1	2	50.00%
25_cpx	5	1	6	16.67%	82_cpx	6	0	6	0.00%
26_A5U	4	0	4	0.00%	83_cpx	11	0	11	0.00%
27_cpx	1	2	4	50.00%	84_A1D	3	0	3	0.00%
28_BF	4	1	5	20.00%	85_BC	10	1	11	9.09%
29_BF	1	5	8	62.50%	86_BC		3	3	100.00%
31_BC	3	0	3	0.00%	87_cpx	1	2	3	66.67%
32_06A6	3	1	4	25.00%	88_BC	3	0	3	0.00%
33_01B	5	1	7	14.29%	89_BF	6	2	8	25.00%
34_01B	3	0	3	0.00%	90_BF1	3	5	9	55.56%
35_AD	22	1	23	4.35%	92_C2U	2	3	5	60.00%
36_cpx	4	0	4	0.00%	93_cpx		2	3	66.67%
37_cpx	12	0	13	0.00%	95_02B	5	0	5	0.00%
38_BF	1	0	1	0.00%	96_cpx		3	3	100.00%
39_BF	1	2	3	66.67%	97_01B	5	0	5	0.00%
40_BF	2	2	4	50.00%	98_06B	1	0	1	0.00%
41_CD	3	0	3	0.00%	99_BF	2	0	3	0.00%
42_BF	17	0	17	0.00%	100_01C	3	0	3	0.00%
43_02G	5	0	5	0.00%	101_01B	3	0	3	0.00%
44_BF	3	0	3	0.00%	102_0107		2	2	100.00%
45_cpx	8	0	8	0.00%	103_01B	3	1	4	25.00%
46_BF	1	7	8	87.50%	104_0107	3	0	3	0.00%
47_BF		2	3	66.67%	105_0108	5	0	5	0.00%
48_01B	3	0	3	0.00%	106_cpx	10	0	10	0.00%
49_cpx	4	0	4	0.00%	107_01B	4	0	4	0.00%
50_A1D	5	0	5	0.00%	108_BC	2	3	5	60.00%
51_01B	7	0	7	0.00%	109_0107	3	0	3	0.00%
52_01B	3	0	3	0.00%	110_BC	3	0	3	0.00%
53_01B	4	0	4	0.00%	111_0108	4	0	4	0.00%
54_01B	1	1	3	33.33%	112_01B		0	4	0.00%
55_01B	12	0	12	0.00%	113_0107	4	0	4	0.00%
56_cpx	4	0	4	0.00%	114_0155	8	0	8	0.00%
57_BC	6	1	7	14.29%	115_01C	2	0	2	0.00%
					117_0107	7	0	7	0.00%
					118_BC	1	0	1	0.00%
					Grand Total	4151	194	4404	4.41%

1: Name of CRF, 2: Sequence numbers containing IN:S17

3: Sequence numbers containing IN:S17N, 4: Analyzed total sequence number

Supplemental Table S7: Population analysis of RH:N79/IN:M50I in CRF

IN:M50/RH:N79				
CRF ¹	RH:N79S/IN:M50I ²	Total	IN:M50I ³	% of RH:N79S/IN:M50I
01_AE		1	77	1.30%
02_AG		0	17	0.00%
06_cpx		0	2	0.00%
07_BC		0	12	0.00%
08_BC		1	14	7.14%
11_cpx		5	6	83.33%
13_cpx		0	2	0.00%
16_A2D		0	2	0.00%
22_01A1		0	12	0.00%
24_BG		1	1	100.00%
26_A5U		0	3	0.00%
27_cpx		0	1	0.00%
39_BF		0	1	0.00%
42_BF		0	2	0.00%
44_BF		0	1	0.00%
45_cpx		0	1	0.00%
49_cpx		0	3	0.00%
63_02A		3	12	25.00%
66_BF1		0	1	0.00%
71_BF1		3	3	100.00%
78_cpx		0	1	0.00%
90_BF1		2	3	66.67%
Grand Total		16	177	9.04%

1: Name of CRF

2: Sequence numbers containing RH:N79S and IN:M50I.

3: Total analyzed sequence number containing IN:M50I with RH sequence

Supplemental Table S8: Population analysis of IN:S17N/IN:M50I in CRF

IN:M50/IN:S17				
CRF ¹	IN:17N/IN:M50I ²	Total IN:M50I ³	% of IN:N17S/M50I	
01_AE	0	89	0.00%	
02_AG	1	35	2.86%	
06_cpx	0	7	0.00%	
07_BC	0	12	0.00%	
08_BC	0	14	0.00%	
11_cpx	1	7	14.29%	
13_cpx	1	2	50.00%	
16_A2D	0	2	0.00%	
19_cpx	0	1	0.00%	
22_01A1	0	20	0.00%	
24_BG	0	1	0.00%	
25_cpx	1	1	100.00%	
26_A5U	0	3	0.00%	
27_cpx	1	1	100.00%	
39_BF	0	1	0.00%	
42_BF	0	2	0.00%	
44_BF	0	1	0.00%	
45_cpx	0	1	0.00%	
49_cpx	0	3	0.00%	
63_02A	0	116	0.00%	
66_BF1	0	1	0.00%	
71_BF1	1	3	33.33%	
78_cpx	0	1	0.00%	
90_BF1	1	3	33.33%	
Grand Total	7	327	2.14%	

1: Name of CRF

2: Sequence numbers containing IN:S17N and IN:M50I.

3: Total analyzed sequence number containing IN:M50I.

Supplementary Table S9: Primer sequences for site-directed mutagenesis (Sense strands)

RT:S322T	5'-GGAGTGTATTATGACCCAACAAAAGACTTAATAGCAGAA-3'
RH:N79S	5'-GTGAATCAGAGTTAGTCAATCAAATAATAGAGCAGT-3'
IN:S17N	5'-GAACATGAGAAATATCACAATAATTGGAGAGCAATGGCT-3
IN:M50I	5'-CTAAAAGGGGAAGCCATACATGGACAAGTAGAC-3'
G120:R252K	5'-CAATGTACACATGGAATCAAACCAGTAGTATCAACTCAACTG-3'
G120:N448R	5'-GGACAAATTAGATGTTTCATCAAGGATTACTGGGCTGCTATTAAC-3'
G41:M24L	5'-AGCACTATGGGCTGCACGTCCTGACGCTGACGGTACAGGCC-3'
G41:L254R	5'-GGAGCCTGTGCCGCTTCAGCTACCACCG-3'
G41:L340A	5'-CTAGAAGAATAAGACAGGGCGCGGAAAGGATTTTGCTA-3'
G41:M24V	5'-ACTATGGGCGCAGCGTCGGTGACGCTGACGGTACAGGC-3'
NF:L92R	5'-TTAGCCACTTTTTAAGAGAAAAGGGGGGACTGG-3'
NF:E98D	5'-AAAAGGGGGGACTGGATGGGCTAATCACTCCCA-3'
NF:V133I	5'-ACACACCAGGGCCAGGGATCAGATATCCACTGA-3'
NF:Y143F	5'-GACCTTTGGATGGTGCTTCAAGCTAGTACCAGT-3'
PR:D25N	5'-CAATTAAGGAAGCTCTATTAATAACAGGAGCAGATGATACAG-3'.
IN:DCTD	5'-GTGATGATTGTGTGGCAAGTAGACAGTGATGAGGATTAACACATG-3'
IN: DIN	5'-GCTGGAATCAGGAAAGTACTATTTTAGATGGAATAGATAAGG-3'
IN: D14aa	5'-CATCAGGGATTATGGATAAACAGATGGCAGGTG-3'
IN:D288G	5'-GTGGCAAGTAGACAGGATGAGGGTTAACACATGGAAAAGATTAG-3'
IN:M50V	5'-CTAAAAGGGGAAGCCGTGCATGGACAAGTAGAC-3'
IN:M50R	5'-CTAAAAGGGGAAGCCAGGCATGGACAAGTAGAC-3'
IN:M50L	5'-CTAAAAGGGGAAGCCCTGCATGGACAAGTAGAC-3'
IN:M50T	5'-CTAAAAGGGGAAGCCACACATGGACAAGTAGAC-3'
SITE7:FP>VP	5'-CAGATTGGCTGCACTTTAAATGTTCCATTAGTCCTATTGAG-3'