

PI Major Mutations:None

PI Accessory Mutations:None

PR Other Mutations:K14KR 4/17% 16/24% • **I15SV** 1/10% 16/17% • **M36I** 14% 16/13/10% • **R41K** 14% 16/13/10% • **I62V** 100% 16/12/10% • **L63P** 100% 16/12/10% • **V75I** 100% 16/13/10% • **V82I** 14% 16/13/10% • **I93L** 100% 16/14%

Protease Inhibitors	
atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
fosamprenavir/r (FPV/r)	Susceptible
indinavir/r (IDV/r)	Susceptible
lopinavir/r (LPV/r)	Susceptible
nelfinavir (NFV)	Susceptible
saquinavir/r (SQV/r)	Susceptible
tipranavir/r (TPV/r)	Susceptible

PR comments

- Other
- V82I** is a highly polymorphic mutation that is not selected by PIs. It is the consensus amino acid in subtype G viruses.

No drug resistance mutations were found for PI.

NRTI Mutations:**M41ML** 16/10% 1/17% • **S685N** 1/14% 16/12% • **L74V** 14% 16/13/10% • **Y115F** 14% 16/13/10% • **M184V** 100% 16/13/10%

NNRTI Mutations:**Y181C** 100% 16/13/10% • **H221Y** 100% 16/13/10%

RT Other Mutations:V8I 14% 16/13/10% • V35T 14% 16/13/10% • S48T 100% 16/13/10% • K49R 100% 16/13/10% • V60I 100% 16/13/10% • K104KR 1/10% 16/12% • K122E 100% 16/13/10% • D123E 14% 16/13/10% • I135T 100% 16/13/10% • S162C 100% 16/13/10% • D177E 14% 16/13/10% • V179I 14% 16/13/10% • T200A 100% 16/13/10% • Q207E 14% 16/13/10% • R211K 14% 16/13/10% • D237DE 1/10% 12/10% • V245Q 100% 16/13/10% • D250E 14% 16/13/10% • Q524K 100% 16/13/10% • K527E 100% 16/13/10% • E529D 100% 16/13/10% • A534S 100% 16/13/10% • I542IV 1/10% 12/10% • A554S 100% 16/13/10%

Nucleoside Reverse Transcriptase Inhibitors		Non-nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance	doravirine (DOR)	Intermediate Resistance
zidovudine (AZT)	Susceptible	efavirenz (EFV)	Intermediate Resistance
stavudine (D4T)	Susceptible	etravirine (ETR)	Intermediate Resistance
didanosine (DDI)	High-Level Resistance	nevirapine (NVP)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance	rilpivirine (RPV)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance		
tenofovir (TDF)	Low-Level Resistance		

RT comments

NRTI

- M41L** is a TAM that usually occurs with T215Y. In combination, **M41L** plus T215Y confer intermediate / high-level resistance to AZT and d4T and contribute to reduced ddi, ABC and TDF susceptibility.
- L74V** causes intermediate ABC resistance. L74I causes low-level ABC resistance.
- Y115F** causes intermediate resistance to ABC and low-level resistance to TDF.
- M184V/I** cause high-level in vitro resistance to 3TC and FTC and low/intermediate resistance to ABC (3-fold reduced susceptibility). **M184V/I** are not contraindications to continued treatment with 3TC or FTC because they increase susceptibility to AZT and TDF and are associated with clinically significant reductions in HIV-1 replication.

NNRTI

- Y181C** is a non-polymorphic mutation selected in persons receiving NVP, ETR and RPV. It confers high-level resistance to NVP, intermediate resistance to ETR and RPV, and low-level resistance to EFV. It does not significantly reduce DOR susceptibility.
- H221Y** is a non-polymorphic accessory mutation selected primarily by NVP, RPV, and DOR. It frequently occurs in combination with Y181C.

Other

- V179I** is a polymorphic mutation that is frequently selected in persons receiving ETR and RPV. However, it has little, if any, direct effect on NNRTI susceptibility.

Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
<u>M41ML</u>	5	15	15	10	0	0	5
<u>L74V</u>	30	0	0	60	0	0	0
<u>L74V + M184V</u>	15	0	0	0	0	0	0
<u>Y115F</u>	30	0	0	0	0	0	15
<u>Y115F + M184V</u>	15	0	0	0	0	0	5
<u>M184V</u>	15	-10	-10	10	60	60	-10
Total	110	5	5	80	60	60	15

Rule	DOR ⚡	EFV ⚡	ETR ⚡	NVP ⚡	RPV ⚡
<u>Y181C</u>	10	30	30	60	45
<u>Y181C + H221Y</u>	10	0	0	0	10
<u>H221Y</u>	10	10	10	15	15
Total	30	40	40	75	70

Drug resistance interpretation: IN

HVDB 9.5.1 (2023-11-05)

INSTI Major Mutations:

None

INSTI Accessory Mutations:

None

IN Other Mutations:

K14R 100%
n=123 • M50L 10%
n=124 • I72V 90%
n=122 • E96ED D: 43%, S: 57%
n=129 • T112A 17%
n=120 • S119T 100%
n=121 • T124AG D: 93%, A: 11%
n=120 • T125A 100%
n=120 • G193R 99%
n=121 • V201I 17%
n=124 • T206S 100%
n=122 • I208L 91%
n=121 • L234I 99%
n=121 • S283G 98%
n=120

Integrase Strand Transfer Inhibitors

bictegravir (BIC)

Susceptible

cabotegravir (CAB)

Susceptible

dolutegravir (DTG)

Susceptible

elvitegravir (EVG)

Susceptible

raltegravir (RAL)

Susceptible

Mutation scoring: IN

HVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for INSTI.