

PI Major Mutations:None

PI Accessory Mutations:None

PR Other Mutations:

I13V100%

from:32,000

 •

K14R10%

from:31,812

 •

L33V100%

from:38,775

 •

M36I100%

from:38,810

 •

N37D10%

from:38,001

 •

P39Q100%

from:38,012

 •

R41K100%

from:38,700

 •

R37K10%

from:31,817

 •

D60E10%

from:31,838

 •

I62V100%

from:31,880

 •

L63P100%

from:31,238

 •

I64V100%

from:31,200

Protease Inhibitors	
atazanavir/r (ATV/r)	Susceptible
darunavir/r (DRV/r)	Susceptible
lopinavir/r (LPV/r)	Susceptible

PR comments

Other

- L33I/V are minimally polymorphic mutations that do not appear to be selected by PIs or to reduce their susceptibility.

No drug resistance mutations were found for PI.

NRTI Mutations:

K70KEQ0.40%

from:17,352

G100%

from:32,000

D100%

from:32,000

 •

L74LI0.70%

from:38,827

 •

M184V100%

from:32,500

NNRTI Mutations:

K103N100%

from:38,300

 •

E138EG0.70%

from:38,848

 •

V179L100%

from:32,620

 •

Y181YC0.70%

from:32,600

 •

H221HY0.40%

from:32,004

RT Other Mutations:

K20R100%

from:37,307

 •

V35I100%

from:17,221

 •

K49R100%

from:17,878

 •

V60I100%

from:38,102

 •

K102HY14.10%

from:34,861

 •

D121HY0.40%

from:32,076

 •

K122E100%

from:14,007

 •

D123DG0.40%

from:32,706

 •

I135T100%

from:17,800

 •

I142IL1.10%

from:32,002

 •

S162C100%

from:32,758

 •

D177E100%

from:32,816

 •

I178FL1.10%

from:32,817

 •

T200A100%

from:31,881

 •

Q207EG0.40%

from:31,838

 •

R211K100%

from:38,801

 •

D237E100%

from:32,500

 •

V245Q100%

from:38,177

 •

D250E100%

from:38,776

 •

A272P100%

from:31,817

 •

K277R100%

from:31,800

 •

L282C100%

from:32,170

 •

L283I100%

from:32,500

 •

V292VI0.40%

from:32,004

 •

I293V100%

from:32,500

 •

E297A100%

from:32,007

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

RT comments

NRTI

- K70(E/Q)/M/T/S/G cause low-level resistance to ABC and TDF.
- L74V causes intermediate ABC resistance. L74I causes low-level ABC resistance.
- 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

- K103N is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- E138Q/G are non-polymorphic accessory mutations selected by ETR occasionally NVP and EFV. They cause low-level reductions in susceptibility to NVP, RPV, and ETR.
- V179L is a rare non-polymorphic mutation listed as a RPV-associated resistance mutation by the FDA package insert. Its effects on NNRTI susceptibility have not been well studied.
- 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.

Drug resistance mutation scores of NRTI:

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Rule	ABC	AZT	FTC	3TC	TDF
K70KEQ	15	0	10	10	15
L74LI	15	0	0	0	5
M184V	15	-10	60	60	-10
K70KEQ + M184V	0	0	0	0	10
Total	45	-10	70	70	20

Drug resistance mutation scores of NNRTI:

Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + Y181YC	5	0	0	0	0
Y181YC	10	30	30	60	45
Y181YC + H221HY	10	0	0	0	10
H221HY	10	10	10	15	15
K103N	0	60	0	60	0
E138EG	0	10	10	10	15
V179L	0	10	10	10	15
Total	35	120	60	155	100