Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	P9X • L10C • V11Y • T12G • I13P • K14E • I15E • G16K • L19P • E35D • M36I • N37K • R41K • M46R • R57K • L63T • H69K • L89M

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

- L10F is a common non-polymorphic, PI-selected accessory mutation associated with reduced in vitro susceptibility to LPV and DRV. L10I/V are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations. L10R/Y are rare, non-polymorphic PI-selected mutations. Their effects on PI susceptibility have not been well studied. **L10C** is a highly unusual mutation at this position.
- M46I/L are relatively non-polymorphic PI-selected mutations. In combination with other PI-resistance mutations, they are associated with reduced susceptibility to each of the PIs except DRV. **M46R** is a highly unusual mutation at this position.

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations:	M184V • T215F
NNRTI Mutations:	A98G • V108I • Y188H • G190A
RT Other Mutations:	K11T • K20R • V21I • V35T • T39N • K43R • P52L • V60I • W88C • K101Q • K122E • D123N • I135T • K166* • K173A • D177E • V179I • Q182X • V189I • T200A • I202* • E203R • Q207A • R211S • K220N • Δ221 • Q222I • K223R • E224R • H235I • P236* • D237Q • K238M • W239T • T240Y • V241S • Q242Y

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Low-Level Resistance
zidovudine (AZT)	Intermediate Resistance
stavudine (D4T)	Intermediate Resistance
didanosine (DDI)	Low-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Intermediate Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Low-Level Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	Intermediate Resistance

RT comments

NRTI

- **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.
- **T215Y/F** are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.

NNRTI

- **A98G** is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- **V108I** is a relatively non-polymorphic accessory mutation selected in vitro and/or in vivo with each of the NNRTIs. It appears to contribute to reduced susceptibility to most NNRTIs only in combination with other NNRTI-resistance mutations.
- **Y188H** is a non-polymorphic mutation selected in persons receiving NVP and EFV. It causes about 5 to 10-fold reduced susceptibility to NVP and EFV. It appears to cause little if any reduction in susceptibility to RPV, ETR, or DOR.
- **G190A** is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. It does not significantly reduce susceptibility to RPV, ETR, or DOR.

Other

- **K101Q** is a relatively non-polymorphic mutation that is weakly selected in persons receiving NVP and EFV. It is of uncertain phenotypic and clinical significance.
- **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.
- K238T/N are uncommon non-polymorphic mutations selected in persons receiving NVP and EFV usually in combination with K103N. Alone, K238T/N appear to have minimal effects on NNRTI susceptibility. **K238M** is a highly unusual mutation at this position.

- This virus is predicted to have intermediate-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be contraindicated.

Mutation scoring: RT — HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M184V	15	-10	-10	10	60	60	-10
T215F	10	60	40	15	0	0	10
Total	25	50	30	25	60	60	0

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
A98G	15	15	10	30	15
V108I	10	10	0	15	0
Y188H	5	30	0	60	0
G190A	0	45	10	60	15
Total	30	100	20	165	30

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	V11M • T12L • I13V • L19I • R41K • L63P • H69Q • V75I • V77I • I93L

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

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations:	M184V • T215L
NNRTI Mutations:	A98G • K101E • V108I • Y181C • G190A
RT Other Mutations:	P4T • V35T • K49R • V60I • D121Y • K122E • I135T • S162C • D177E • V179I • T200I • Q207E • R211K • F214L • P217L • K219H • M230D • V241L • V245K • L246C • Δ247 • E248Q • D250E • D256* • I257F • Q258T • K259E • L260V

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Low-Level Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Potential Low-Level Resistance
didanosine (DDI)	Low-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Susceptible

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	High-Level Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	High-Level Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	High-Level Resistance

RT comments

NRTI

- **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.
- T215Y/F are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF. **T215S/C/D/E/I/V/N/A/L** do not reduce NRTI susceptibility but arise from viruses that once contained T215Y/F. The presence of one of these revertant mutations suggests that the patient may have once been infected with a virus containing T215Y/F.

NNRTI

- **A98G** is a non-polymorphic accessory mutation associated with low-level reduced susceptibility to each of the NNRTIs.
- **K101E** is a non-polymorphic accessory mutation that confers intermediate resistance to NVP and RPV and low-level reductions in susceptibility to EFV, ETR, and DOR when it occurs with other NNRTI-resistance mutations.
- **V108I** is a relatively non-polymorphic accessory mutation selected in vitro and/or in vivo with each of the NNRTIs. It appears to contribute to reduced susceptibility to most NNRTIs only in combination with other NNRTI-resistance mutations.
- **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.
- **G190A** is a non-polymorphic mutation that causes high-level resistance to NVP and intermediate resistance to EFV. It does not significantly reduce susceptibility to RPV, ETR, or DOR.

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.
- K219E/Q/N/R are accessory TAMS that usually occur in combination with multiple other TAMs. K219W is an uncommon NRTI-selected mutation. **K219H** is an unusual mutation at this position.
- M230L is an uncommon non-polymorphic mutation selected in persons receiving EFV, NVP, and RPV. It causes intermediate to high-level resistance to each of the NNRTIs. M230I is a rare mutation selected by RPV. Its effects on NNRTI susceptibility have not been well studied. It also often occurs as a result of APOBEC-mediated G-to-A hypermutation resulting in viruses that are likely to be noninfectious. **M230D** is a highly unusual mutation at this position.

Mutation scoring: RT — HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M184V	15	-10	-10	10	60	60	-10
T215L	0	10	20	10	0	0	0
Total	15	0	10	20	60	60	-10

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
A98G	15	15	10	30	15
A98G + Y181C	5	5	5	5	5
K101E	15	15	15	30	45
K101E + G190A	5	0	5	0	0
V108I	10	10	0	15	0
V108I + Y181C	5	0	0	0	0
Y181C	10	30	30	60	45
Y181C + G190A	10	0	10	0	10
K101E + Y181C	0	5	5	5	0
G190A	0	45	10	60	15
Total	75	125	90	205	135

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	V11R • T12D • I13S • K14T • I15G • K20S • L23Y • L24* • D25I • T26R • G27S • A28D • D30H • T31Q • V32R • Δ34 • E35X • M36S • N37P • L38M • R41K • R57K • I62V • L63V • E65D • H69K • T74S • L89M

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

- D30N is a non-polymorphic mutation NFV-selected mutation that causes high-level resistance to NFV but not to other PIs. **D30H** is a highly unusual mutation at this position.
- V32I is a non-polymorphic mutation selected by LPV, ATV, and DRV which is associated with reduced susceptibility to each of these PIs. **V32R** is a highly unusual mutation at this position.
- **T74S** is a PI-selected accessory mutation that is polymorphic in most non-B subtypes.

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations:	L74V • Y115F • M184V
NNRTI Mutations:	K103N • V108I • Y181C • H221Y • F227L • P236L
RT Other Mutations:	E6D • V35T • T39A • V60I • K101R • D123E • I135T • I142V • T165L • K173A • Q174K • D177E • I178M • E194D • T200A • Q207A • R211S • F214S • P217S • K219X • P225X • P226S • H235I • D237T • K238V • W239D • T240S • V241Q • Q242L • P243L • I244Q • V245L • Δ247 • D250E • Δ255 • I257* • Q258Y • K259T • L260E • V261I • G262V • K263R • L264N • N265L • W266T • A267G • I274T • K275E • K277N • K281Q

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Potential Low-Level Resistance

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	High-Level Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Intermediate Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	High-Level Resistance

RT comments

NRTI

- **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

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- **V108I** is a relatively non-polymorphic accessory mutation selected in vitro and/or in vivo with each of the NNRTIs. It appears to contribute to reduced susceptibility to most NNRTIs only in combination with other NNRTI-resistance mutations.
- **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.
- **F227L** is a non-polymorphic mutation that usually occurs in combination with V106A. It is selected in vivo and in vitro with both NVP and DOR. In this context it is associated with high-level reductions in NVP and DOR susceptibility and intermediate reductions in EFV susceptibility. F227I/V are extremely rare mutations that have been selected in vitro by DOR.
- **P236L** is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs.

Other

- K238T/N are uncommon non-polymorphic mutations selected in persons receiving NVP and EFV usually in combination with K103N. Alone, K238T/N appear to have minimal effects on NNRTI susceptibility. **K238V** is a highly unusual mutation at this position.

Mutation scoring: RT — HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
L74V	30	0	0	60	0	0	0
L74V + M184V	15	0	0	0	0	0	0
Y115F	30	0	0	0	0	0	15
Y115F + M184V	15	0	0	0	0	0	5
M184V	15	-10	-10	10	60	60	-10
Total	105	-10	-10	70	60	60	10

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + Y181C	5	0	0	0	0
V108I	10	10	0	15	0
V108I + Y181C	5	0	0	0	0
Y181C	10	30	30	60	45
Y181C + H221Y	10	0	0	0	10
H221Y	10	10	10	15	15
F227L	60	15	0	30	0
P236L	10	0	0	0	0
K103N	0	60	0	60	0
Total	120	125	40	180	70

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: V11X · T12C · I13Q · K14* · G16A · L23Y · L24* · E35D · M36I · N37K · R41K · H69K · L89M

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

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: M41L · M184V · L210W · T215Y
NNRTI Mutations: K103N
RT Other Mutations: E28K · K32E · V35T · K49R · V60I · K122E · D123S · I135T · E169A · K173S · Q174K · D177E · T200A · I202V · Q207A · K219X · E224D · P226S · L228R · E233D · L234S · H235S · P236D · D237S · K238D · W239S · T240H · V241Y · Q242K · P243L · I244Q · V245K · L246R · P247E · E248L · K249T · D250V · S251M

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance
zidovudine (AZT)	High-Level Resistance
stavudine (D4T)	High-Level Resistance
didanosine (DDI)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Intermediate Resistance

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Susceptible
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Susceptible
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	Susceptible

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.
- **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.
- **L210W** is a TAM that usually occurs in combination with M41L and T215Y. The combination of M41, **L210W** and T215Y causes high-level resistance to AZT and intermediate resistance to ABC and TDF.
- **T215Y/F** are TAMs that causes intermediate/high-level resistance to AZT and potentially low-level resistance to ABC and TDF.

NNRTI

- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.

Other

- L234I is a nonpolymorphic mutation selected in persons receiving NVP and EFV. It is also selected in vitro by ETR and DOR. In combination with V106A, it is associated with high-level DOR resistance. Its effect on susceptibility when it occurs alone has not been well characterized. **L234S** is a highly unusual mutation at this position.
- P236L is a rare mutation selected commonly by DLV, which appears to have little if any effect on current NNRTIs. **P236D** is a highly unusual mutation at this position.
- K238T/N are uncommon non-polymorphic mutations selected in persons receiving NVP and EFV usually in combination with K103N. Alone, K238T/N appear to have minimal effects on NNRTI susceptibility. **K238D** is a highly unusual mutation at this position.

Mutation scoring: RT HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
M41L	5	15	15	10	0	0	5
M41L + M184V + T215Y	10	0	0	0	0	0	0
M41L + L210W	10	10	10	10	0	0	10
M41L + L210W + T215Y	10	0	0	0	15	15	10
M41L + T215Y	10	10	10	10	5	5	10
M184V	15	-10	-10	10	60	60	-10
L210W	5	15	15	10	0	0	5
L210W + T215Y	10	10	10	10	0	0	10
T215Y	10	60	40	15	0	0	10
Total	85	110	90	75	80	80	50

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N	0	60	0	60	0

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: M46I • I47A
PI Accessory Mutations: F53L
PR Other Mutations: V11X • T12I • I13S • K14* • K20R • E35D • M36I • R41K • K45R • R57K • L63P • I64L • A71V • I72V

Protease Inhibitors	
atazanavir/r (ATV/r)	Low-Level Resistance
darunavir/r (DRV/r)	Potential Low-Level Resistance
fosamprenavir/r (FPV/r)	High-Level Resistance
indinavir/r (IDV/r)	Low-Level Resistance
lopinavir/r (LPV/r)	High-Level Resistance
nelfinavir (NFV)	High-Level Resistance
saquinavir/r (SQV/r)	Low-Level Resistance
tipranavir/r (TPV/r)	Intermediate Resistance

PR comments

Major

- **M46I/L** are relatively non-polymorphic PI-selected mutations. In combination with other PI-resistance mutations, they are associated with reduced susceptibility to each of the PIs except DRV.
- **I47A** is a non-polymorphic mutation selected by LPV. It usually occurs in combination with V32I and in this context it confers high-level resistance to LPV and low-level resistance to DRV.

Accessory

- **F53L** is a nonpolymorphic accessory mutation selected primarily by SQV, IDV, ATV and LPV. In combination with other mutations, It is associated with reduced susceptibility to ATV and possibly LPV. F53Y is an uncommon nonpolymorphic accessory PI-selected mutation that has not been well studied.

Other

- **K20R** is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.
- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR

HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of PI: Download CSV

Rule	ATV/r	DRV/r	FPV/r	IDV/r	LPV/r	NFV	SQV/r	TPV/r
M46I	10	0	10	10	10	30	10	5
F53L	10	0	0	0	0	10	15	0
I47A	0	10	60	15	60	30	0	30
Total	20	10	70	25	70	70	25	35

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: L74V • Y115F • M184V • K219E
NNRTI Mutations: L100I • K103N
RT Other Mutations: E6K • K32R • V35T • E40L • K43E • S48L • V60I • K70* • K122E • D123S • T139A • K173S • Q174K • T200A • Q207A • R211S • L228Q • V245H • L246C • P247R • Δ250 • L260* • V261W • G262E • Δ263 • L264X • N265* • W266L • A272K • I274L • K275R

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	High-Level Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	High-Level Resistance
emtricitabine (FTC)	High-Level Resistance
lamivudine (3TC)	High-Level Resistance
tenofovir (TDF)	Low-Level Resistance

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Intermediate Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Intermediate Resistance
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	High-Level Resistance

RT comments

NRTI

- **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.
- **K219E/Q/N/R** are accessory TAMS that usually occur in combination with multiple other TAMs.

NNRTI

- **L100I** is a non-polymorphic mutation that usually occurs in combination with K103N. In this setting it confers high-level resistance to NVP, EFV, and RPV and intermediate resistance to ETR and DOR.
- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.

Mutation scoring: RT HIVDB 9.5.1 (2023-11-05)

Drug resistance mutation scores of NRTI: Download CSV

Rule	ABC	AZT	D4T	DDI	FTC	3TC	TDF
L74V	30	0	0	60	0	0	0
L74V + M184V	15	0	0	0	0	0	0
Y115F	30	0	0	0	0	0	15
Y115F + M184V	15	0	0	0	0	0	5
M184V	15	-10	-10	10	60	60	-10
K219E	5	10	10	5	0	0	5
Total	110	0	0	75	60	60	15

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
L100I	15	60	30	60	60
L100I + K103N	15	0	0	0	0
K103N	0	60	0	60	0
Total	30	120	30	120	60