Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: L10G • V11E • T12V • I13S • G16E • L33V • N37T • R41K • R57K • L63T • I64V • E65D

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. **L10G** is a highly unusual mutation at this position.
- **L33I/V** are minimally polymorphic mutations that do not appear to be selected by PIs or to reduce their susceptibility.

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: K65R • S68N • Y115F • M184V
NNRTI Mutations: K103N • Y181C • G190A
RT Other Mutations: V35T • T39A • K46Q • K49R • V60I • K101Q • D123E • I135T • I142V • D177E • T200X • Q207R • R211K • P217S • P225L • E233D • Δ234 • H235S • P236S • D237* • K238* • V245N • L246A • P247E • E248K • D250* • S251L • W252Y • T253D • V254L • N255Q • D256S • I257S • Q258R • K259N • L260T • V261G • G262Q • K263S • L264I • N265Y • W266Q • K275* • V276I • L279I • K281N • L282A • Δ284 • T286S • K287* • V292* • I293* • P294L

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

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

RT comments

NRTI

- **K65R** confers intermediate reductions in susceptibility to TDF, ABC, and 3TC/FTC. It increases AZT susceptibility. In NRTI-experienced, INSTI-naive patients with **K65R**, TDF+3TC+DTG is usually highly effective and more effective than AZT/3TC/DTG. However, in patients receiving TDF+3TC+DTG, there is a risk of emergent DTG resistance that does not arise in NRTI-naive patients receiving TDF+3TC+DTG.
- **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.
- **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

- **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.
- P225H is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of P225H and K103N synergistically reduces NVP, EFV and DOR susceptibility. **P225L** is a highly unusual mutation at this position.
- 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. **L234del** 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. **P236S** 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
K65R	45	-10	60	60	30	30	50
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
K65R + S68N	0	0	0	0	0	0	5
Total	105	-20	50	70	90	90	65

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + Y181C	5	0	0	0	0
Y181C	10	30	30	60	45
Y181C + G190A	10	0	10	0	10
K103N	0	60	0	60	0
G190A	0	45	10	60	15
Total	25	135	50	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 • T12A • I13S • K14S • G16E • E35D • M36I • 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: K65R • S68G • Δ69
NNRTI Mutations: Y181C • G190S
RT Other Mutations: E6D • V35T • V60I • K101Q • K122E • D123N • I135T • P170L • K173S • Q174K • D177E • V179I • T200A • Q207A • R211S • K219X • L228S • W229L • M230D • E233D • Δ234 • H235S • P236S • D237* • K238Q • V245E • P247Q • N255M • D256I • I257Y • Q258R • K259I

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

- **K65R** confers intermediate reductions in susceptibility to TDF, ABC, and 3TC/FTC. It increases AZT susceptibility. In NRTI-experienced, INSTI-naive patients with **K65R**, TDF+3TC+DTG is usually highly effective and more effective than AZT/3TC/DTG. However, in patients receiving TDF+3TC+DTG, there is a risk of emergent DTG resistance that does not arise in NRTI-naive patients receiving TDF+3TC+DTG.
- **S68G** is a polymorphic mutation that is often selected in combination with K65R. It partially restores the replication defect associated with K65R.
- Amino acid deletions between codons 67 and 70 are rare and usually occur in combination with multiple TAMs, K65R, or the Q151M mutation complex. Deletions at position 67 are more often associated with multiple TAMs. Deletions at positions 69 and 70 are more often associated with K65R or the Q151M mutation complex. Deletions at codon 68 are extremely rare and less well characterized.

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.
- **G190S** is a non-polymorphic mutation that confers high-level resistance to NVP and EFV. It may also be associated low-levels reductions in DOR susceptibility. It does not appear to be selected by ETR or RPV or to reduce their in vitro susceptibility.

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.
- 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.
- 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. **L234del** 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. **P236S** 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. **K238Q** 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
K65R	45	-10	60	60	30	30	50
T69del	15	0	30	30	15	15	15
K65R + S68G	0	0	0	0	0	0	5
Total	60	-10	90	90	45	45	70

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
Y181C	10	30	30	60	45
Y181C + G190S	10	0	10	0	10
G190S	20	60	10	60	15
Total	40	90	50	120	70

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	T12I • I13* • K14* • K20X • M36I • R41K • L63C • I64V • V82I

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.

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:	K65R
NNRTI Mutations:	L100I • K103N
RT Other Mutations:	V35T • K49R • E53D • V60I • T84P • K122E • D177E • I178M • M184* • T200I • Q207N • H208I • R211K • T216I • P217L • P225L • P226Y • P236S • L246T • P247A • D250E • A272L • C280L

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

- **K65R** confers intermediate reductions in susceptibility to TDF, ABC, and 3TC/FTC. It increases AZT susceptibility. In NRTI-experienced, INSTI-naive patients with **K65R**, TDF+3TC+DTG is usually highly effective and more effective than AZT/3TC/DTG. However, in patients receiving TDF+3TC+DTG, there is a risk of emergent DTG resistance that does not arise in NRTI-naive patients receiving TDF+3TC+DTG.

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.

Other

- P225H is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of P225H and K103N synergistically reduces NVP, EFV and DOR susceptibility. **P225L** 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. **P236S** 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
K65R	45	-10	60	60	30	30	50

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

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	T12N • I13* • K14S • E21X • E35D • M36I • G40V • R41K • R57K • H69K • V82I • 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

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

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 • M184V
NNRTI Mutations:	K103N • G190A
RT Other Mutations:	E6K • K11T • K20R • V21I • V35T • T39R • E40K • K43E • E44K • G45V • V60I • D67K • R72K • G93R • K101Q • K122E • D123N • P170L • K173A • D177E • I178M • V179I • I195L • T200A • I202V • Q207N • R211K • P226S • L246T • P247A • E248R • K249Q • N255M • Δ256 • I257X • Q258I • K259Q • L260K • V261* • G262W • K263E • L264N • N265K • A267G • V276* • C280V • K281* • L282T • L283P • R284S • G285R • T286E • K287P • A288S • L289T

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)	Susceptible

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

RT comments

NRTI

- **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.
- **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

- D67N is a non-polymorphic TAM associated with low-level resistance to AZT. D67G/E/S/T/H are non-polymorphic NRTI-selected mutations that generally occur in viruses with multiple TAMs. **D67K** is a highly unusual mutation at this position.
- **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.

- This virus is predicted to have low-level reduced susceptibility to **RPV**. The use of the combination of CAB/**RPV** should be considered to be relatively 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
L74V	30	0	0	60	0	0	0
L74V + M184V	15	0	0	0	0	0	0
M184V	15	-10	-10	10	60	60	-10
Total	60	-10	-10	70	60	60	-10

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N	0	60	0	60	0
G190A	0	45	10	60	15
Total	0	105	10	120	15

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: V11X • T12V • I13S • L19I • N37A • R41K • L63P • I64L

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: L74I • M184V
NNRTI Mutations: K103N • P225H • F227C • M230L
RT Other Mutations: K32N • V35T • T39K • I47L • V60I • Q85R • K122E • D123S • S162C • P170L • K173L • Q174K • D177E • I178L • T200A • Q207E • R211K • T216I • K223X • Δ243 • I244L • V245* • L246T • P247A • N255M • D256I • I257Y • Q258R • K259V • L260V

Nucleoside Reverse Transcriptase Inhibitors	
abacavir (ABC)	Intermediate Resistance
zidovudine (AZT)	Susceptible
stavudine (D4T)	Susceptible
didanosine (DDI)	High-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

- 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.
- **P225H** is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of **P225H** and K103N synergistically reduces NVP, EFV and DOR susceptibility.
- **F227C** is a nonpolymorphic mutation selected in persons receiving DOR and rarely in persons receiving ETR and RPV. It usually occurs in combination with other DRMs and in this setting has consistently been associated with the highest possible levels of DOR resistance. It is also usually associated with intermediate or high-level reductions in susceptibility to NVP, EFV, ETR, and RPV.
- **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.

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
L74I	15	0	0	60	0	0	5
M184V	15	-10	-10	10	60	60	-10
Total	30	-10	-10	70	60	60	-5

Drug resistance mutation scores of NNRTI: Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K103N + P225H	10	0	0	0	0
P225H	20	45	0	45	0
F227C	60	45	30	45	45
M230L	60	45	30	60	60
K103N	0	60	0	60	0
Total	150	195	60	210	105

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	V11X • T12R • I13V • K14S • I15Q • G16* • G17R • Q18T • K20R • E35D • M36I • R41K • R57K • L63V • H69K • I72V • 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

- **K20R** is a highly polymorphic PI-selected accessory mutation that increases replication fitness in viruses with PI-resistance mutations.

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
NNRTI Mutations:	L100I • K103N
RT Other Mutations:	K11T • K20R • V35T • T39R • K49R • V60I • K122E • D123N • M164L • E169A • K173S • Q174K • D177E • V179I • M184G • R199F • T200I • I202G • E204* • Q207A • R211K • K219T • K220S • Δ221 • Q222I • K223R • E224W • P225T • P226V • F227M • L228S • K238E • I244M • V245Q • E248* • K249Q • S251W • N255M • D256I • I257A • Q258E • K259I • L260V • V261G • G262D • K263E • L264V • N265G • W266L • A267S • Q269H • I270T • Y271D • A272E • G273* • I274D • K275S • V276W • K277L • Q278L • C280R • K281R

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

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.

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.
- 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. **M184G** is a highly unusual mutation at this position.
- K219E/Q/N/R are accessory TAMS that usually occur in combination with multiple other TAMs. K219W is an uncommon NRTI-selected mutation. **K219T** is an unusual mutation at this position.
- P225H is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of P225H and K103N synergistically reduces NVP, EFV and DOR susceptibility. **P225T** is a highly unusual mutation at this position.
- 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. F227C is a nonpolymorphic mutation selected in persons receiving DOR and rarely in persons receiving ETR and RPV. It usually occurs in combination with other DRMs and in this setting has consistently been associated with the highest possible levels of DOR resistance. It is also usually associated with intermediate or high-level reductions in susceptibility to NVP, EFV, ETR, and RPV. **F227M** 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. **K238E** 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
Y115F	30	0	0	0	0	0	15
Total	60	0	0	60	0	0	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

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: None
PR Other Mutations: V11M • T12L • I13A • K14N • I15V • R41K • L63P • I64V • V77I

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: **S68N** • **L74I** • **M184I**
NNRTI Mutations: **K101E** • **K103N** • **E138A**
RT Other Mutations: V35T • V60I • V90I • D121H • K122E • T139S • I142V • P150S • I178L • T200A • Q207G • R211K • K219X • E224N • P225I • P226H • L234X • V245K • P247X • D250E • N255M • D256I • I257* • L260* • V261W • G262E • Δ263-264 • W266K • A267W • S268A • Q269V • I270R • Y271F • A272I • G273R • Q278S • K281N • L282A • T286V • K287* • V292G • I293S

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

Non-nucleoside Reverse Transcriptase Inhibitors	
doravirine (DOR)	Low-Level Resistance
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Low-Level 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.
- **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

- **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.
- **K103N** is a non-polymorphic mutation that confers high-level reductions in NVP and EFV susceptibility. It is the most commonly transmitted DRM.
- **E138A** is a common polymorphic accessory mutation weakly selected in persons receiving ETR and RPV. It reduces ETR and RPV susceptibility ~2-fold. Its effect on ETR- and RPV-containing regimens is likely to be minimal.

Other

- **V90I** is a polymorphic accessory mutation weakly selected by each of the NNRTIs. It is associated with minimal, if any, detectable reduction in NNRTI susceptibility.
- P225H is a non-polymorphic EFV-selected mutation that usually occurs in combination with K103N. The combination of P225H and K103N synergistically reduces NVP, EFV and DOR susceptibility. **P225I** 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
L74I	15	0	0	60	0	0	5
M184I	15	-10	-10	10	60	60	-10
Total	30	-10	-10	70	60	60	-5

Drug resistance mutation scores of NNRTI:

Download CSV

Rule	DOR	EFV	ETR	NVP	RPV
K101E	15	15	15	30	45
K103N	0	60	0	60	0
E138A	0	0	10	0	15
K101E + M184I	0	0	0	0	15
Total	15	75	25	90	75

Drug resistance interpretation: PR

HIVDB 9.5.1 (2023-11-05)

PI Major Mutations: None
PI Accessory Mutations: K20T
PR Other Mutations: V11X • T12C • I13Q • K14* • I15N • G16R • G17R • Q18K • E35D • M36I • 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)	Low-Level Resistance
saquinavir/r (SQV/r)	Susceptible
tipranavir/r (TPV/r)	Susceptible

PR comments

Accessory

- **K20T** is a non-polymorphic accessory PI-selected mutation associated with reduced susceptibility to ATV and LPV.

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
K20T	5	0	5	5	0	15	5	0

Drug resistance interpretation: RT

HIVDB 9.5.1 (2023-11-05)

NRTI Mutations: M184V • T215L
NNRTI Mutations: K103N
RT Other Mutations: K20R • V21I • V35T • T39K • K104I • K122E • D123N • I135V • I167X • K173S • Q174K • D177E • V179M • I180X • I195X • G196E • R199S • T200I • Δ202 • E203* • E204R • L205T • R206K • Q207S • R211S • F214L • T216L • P217R • D218Q • K220H • H221Q • Q222K • Δ223 • W229C • Y232D • P236S • D237* • K238H • P243X • V245L • P247L • E248V • D250T • S251A • W252D • T253C • V254H • N255E • D256L • I257T • Q258E • K259T • L260S • V261A • G262K • K263L • L264T • N265* • W266V • A267S • S268Q • Q269N

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)	Susceptible
efavirenz (EFV)	High-Level Resistance
etravirine (ETR)	Susceptible
nevirapine (NVP)	High-Level Resistance
rilpivirine (RPV)	Susceptible

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

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

Other

- V179D/E are somewhat polymorphic accessory NNRTI-selected mutation. In combination with other NNRTI DRMs, they appear to contribute low-levels of reduced susceptibility to each of the NNRTIs. In particular, the combinations of K103R/V179D and V106I/V179D act synergistically to reduce NVP and EFV susceptibility. V179F is a non-polymorphic mutation selected in combination with Y181C in persons receiving ETR. Alone it has little effect on NNRTI susceptibility, however in combination with Y181C it is associated with high-level reductions in ETR and RPV susceptibility. V179T is a rare non-polymorphic mutation occasionally selected in persons receiving NNRTIs. It is associated with minimal, if any, reduction in ETR and RPV susceptibility. 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. **V179M** is an 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. **P236S** 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. **K238H** 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
K103N	0	60	0	60	0