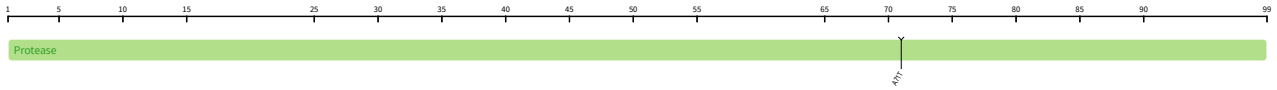
1. Y181C-H01

Sequence summary

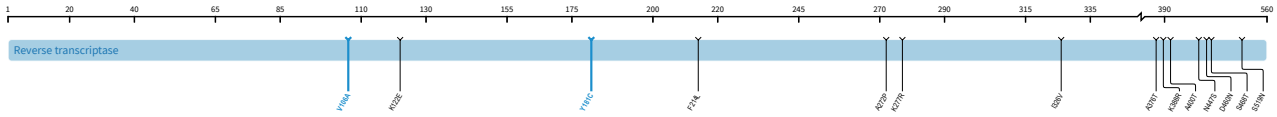
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.16%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

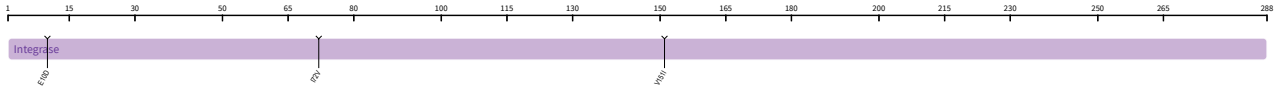
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

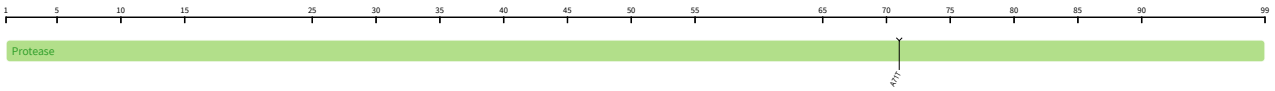
2. Y181C-H02

Sequence summary

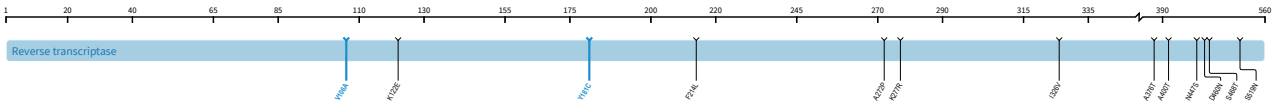
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.23%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

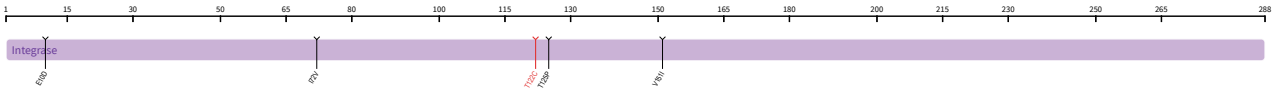
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • A400T • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T122C • T125P • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

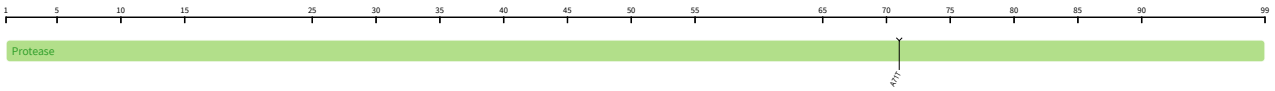
3. Y181C-H03

Sequence summary

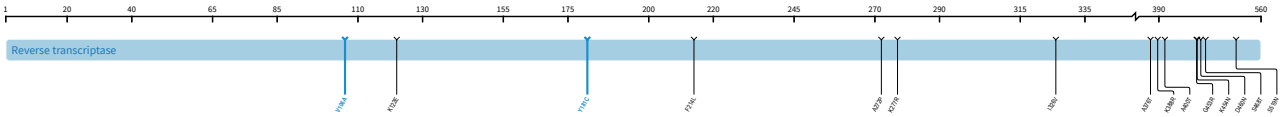
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.30%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

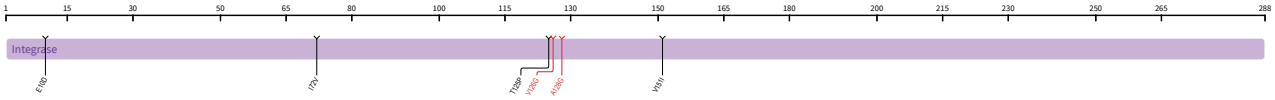
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • G453R • K454N • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T125P • V126G • A128G • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

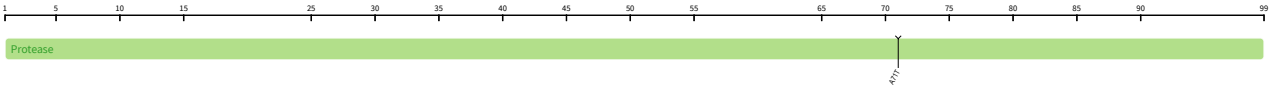
4. Y181C-H04

Sequence summary

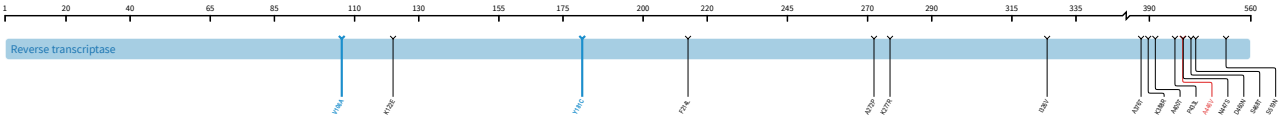
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.37%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

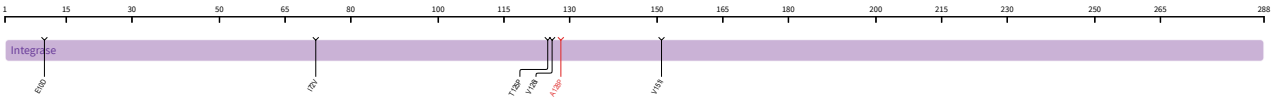
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • P433L • A446V • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T125P • V126I • A128P • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

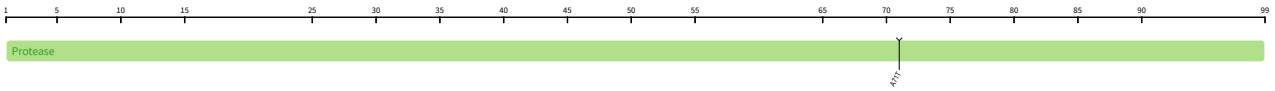
5. Y181C-H05

Sequence summary

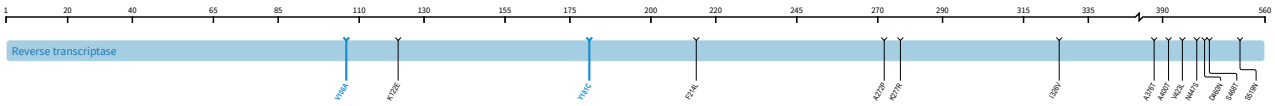
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288 (missing: 129)
Subtype:	⊞ B (1.34%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

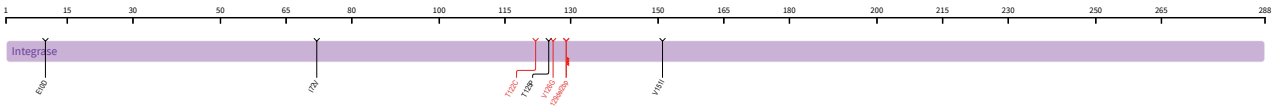
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Warning**: The IN gene has a frameshift: 129del2bp.
- **Note**: One non-drug-resistance position was not sequenced or aligned: IN 129.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • A400T • V423L • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T122C • T125P • V126G • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

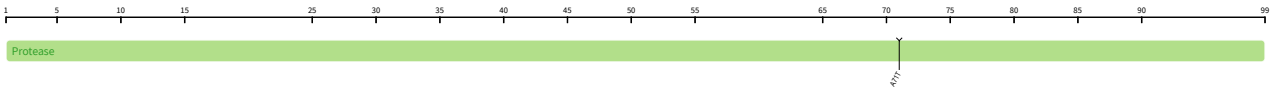
6. Y181C-H06

Sequence summary

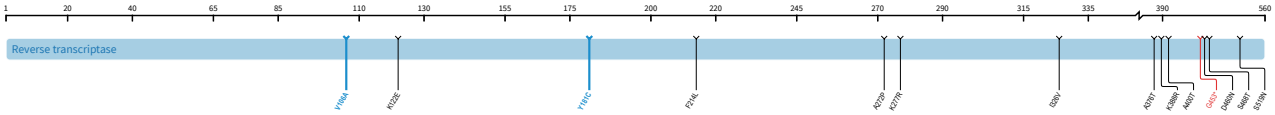
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288 (missing: 47)
Subtype:	⊞ B (1.44%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

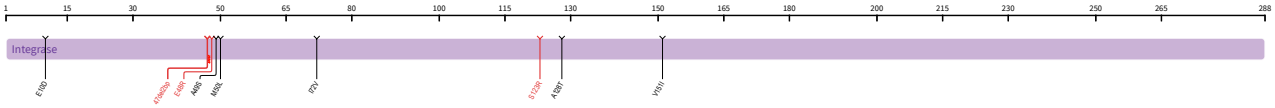
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Warning**: The IN gene has a frameshift: 47del2bp.
- **Note**: One non-drug-resistance position was not sequenced or aligned: IN 47.
- **Note**: There is one stop codon in RT: RT:G453*.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations: None
NNRTI Mutations: V106A • Y181C
RT Other Mutations: K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • G453* • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations: None
INSTI Accessory Mutations: A128T
IN Other Mutations: E10D • E48R • A49S • M50L • I72V • S123R • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Accessory

- **A128T** is a relatively nonpolymorphic possible INSTI-selected mutation, which does not appear to reduce INSTI susceptibility.

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

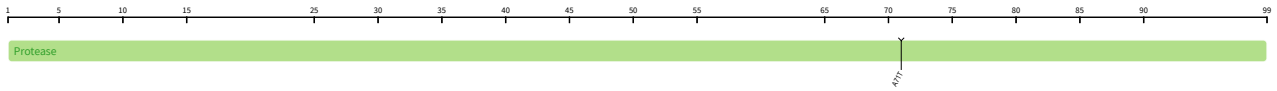
7. Y181C-H07

Sequence summary

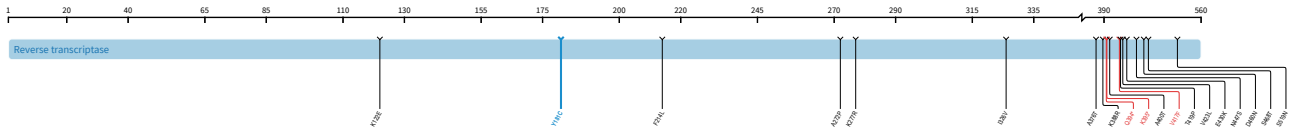
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.37%)
PR SDRMs:	None
RT SDRMs:	Y181C
IN SDRMs:	None

Sequence quality assessment

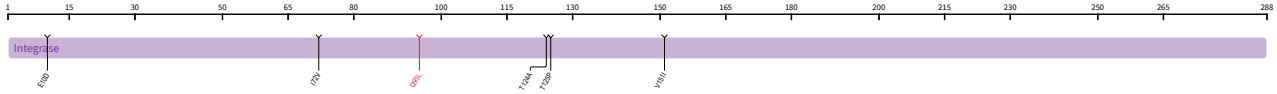
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Severe warning**: There are 2 stop codons in RT: RT:Q394*, RT:K395*.
- **Note**: There are 3 unusual mutations in RT: Q394*, K395*, V417F.
- **Note**: There is one unusual mutation at a drug-resistance position in IN: Q95L.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • Q394* • K395* • A400T • V417F • T419P • V423L • E430K • N447S • D460N • S468T • S519N

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

RT comments

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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
Y181C	10	30	30	60	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • Q95L • T124A • T125P • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

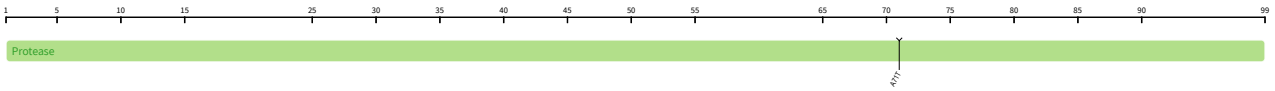
8. Y181C-H08

Sequence summary

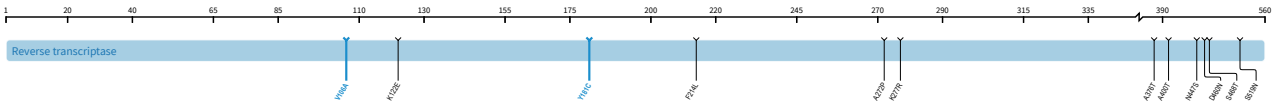
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.27%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

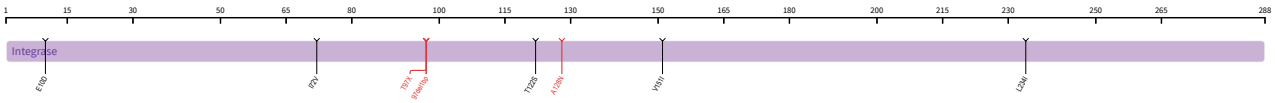
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Warning**: The IN gene has a frameshift: 97del1bp.
- **Note**: There is one unusual mutation at a drug-resistance position in IN: T97X.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • A376T • A400T • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T97X • T122S • A128N • V151I • L234I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

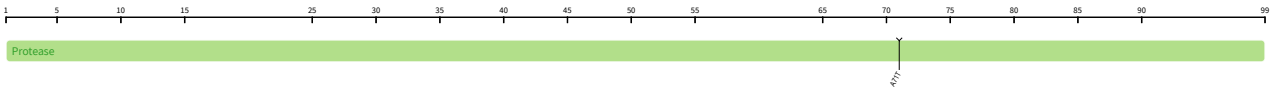
9. Y181C-H09

Sequence summary

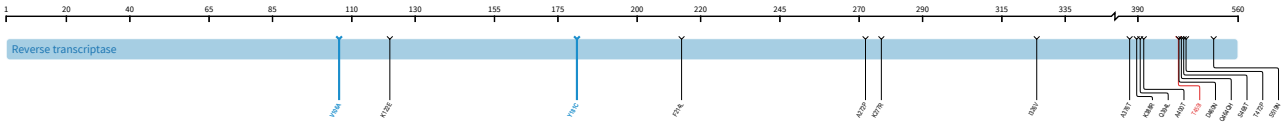
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.34%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

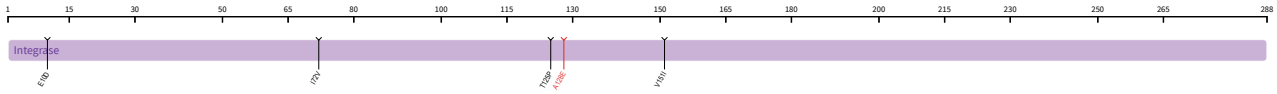
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations: None
NNRTI Mutations: V106A • Y181C
RT Other Mutations: K122E • F214L • A272P • K277R • I326V • A376T • K388R • Q394L • A400T • T459I • D460N • Q464QH • S468T • T472P • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations: None
INSTI Accessory Mutations: None
IN Other Mutations: E10D • I72V • T125P • A128E • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

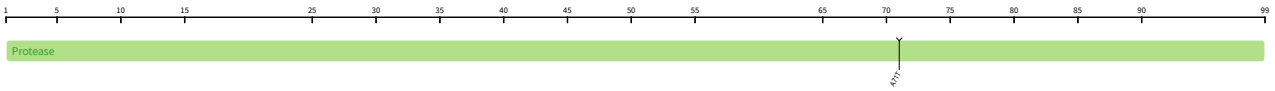
10. Y181C-H10

Sequence summary

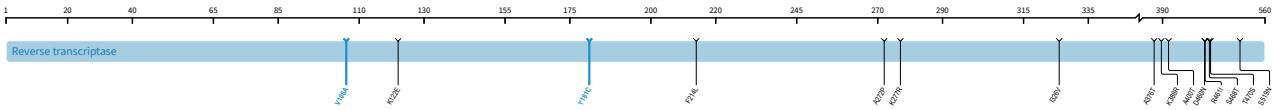
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.34%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

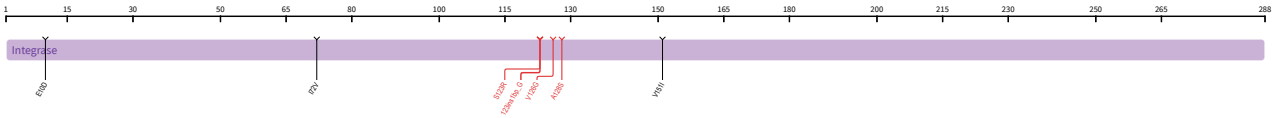
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Warning**: The IN gene has a frameshift: 123ins1bp_G.
- **Note**: There are 3 unusual mutations in IN: S123R, V126G, A128S.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • D460N • R461I • S468T • T470S • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • S123R • V126G • A128S • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

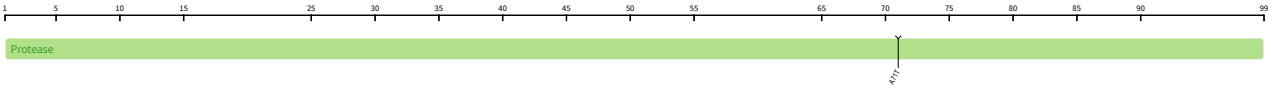
11. Y181C-H11

Sequence summary

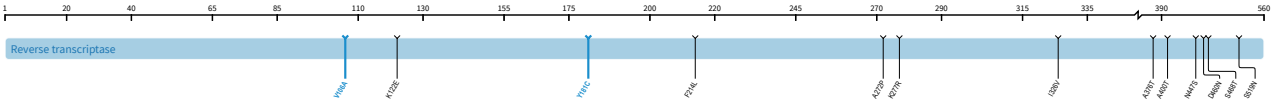
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.16%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

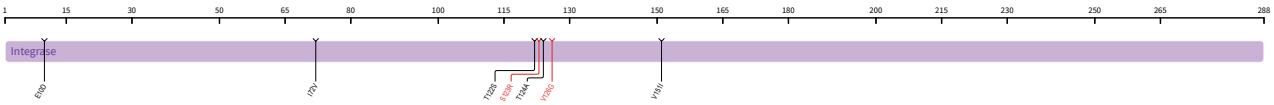
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



There are no known sequence quality issues.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • A400T • N447S • D460N • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T122S • S123R • T124A • V126G • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible
raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.

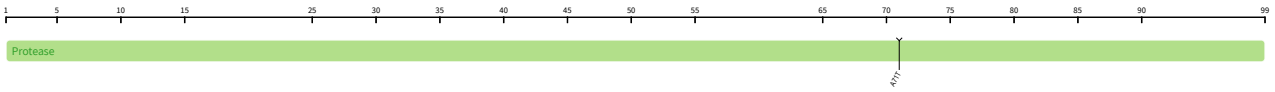
12. Y181C-H12

Sequence summary

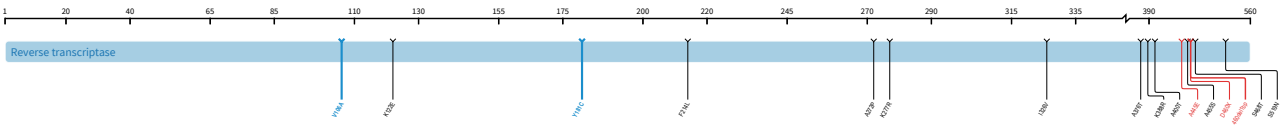
Sequence includes PR:	codons 1 - 99
Sequence includes RT:	codons 1 - 560
Sequence includes IN:	codons 1 - 288
Subtype:	⊞ B (1.48%)
PR SDRMs:	None
RT SDRMs:	V106A, Y181C
IN SDRMs:	None

Sequence quality assessment

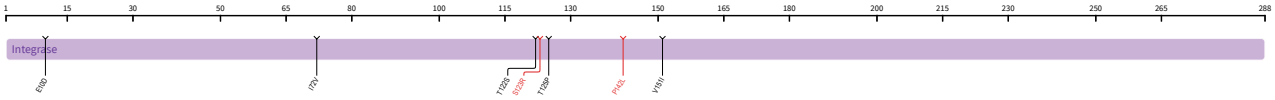
Protease (PR)



Reverse transcriptase (RT)



Integrase (IN)



- **Warning**: The RT gene has a frameshift: 460del1bp.

Drug resistance interpretation: PR

HIVDB 9.4 (2022-12-07)

PI Major Mutations:	None
PI Accessory Mutations:	None
PR Other Mutations:	A71T

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

PR comments

Other

- **A71V/T** are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Mutation scoring: PR — HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for PI.

Drug resistance interpretation: RT — HIVDB 9.4 (2022-12-07)

NRTI Mutations:	None
NNRTI Mutations:	V106A • Y181C
RT Other Mutations:	K122E • F214L • A272P • K277R • I326V • A376T • K388R • A400T • A445E • A455S • D460X • S468T • S519N

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

RT comments

NNRTI

- **V106A** is a non-polymorphic mutation that confers high-level resistance to NVP and DOR, and intermediate resistance to EFV. It is commonly selected in vitro and in vivo by DOR.
- **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.
- 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 9.4 (2022-12-07)

No drug resistance mutations were found for NRTI.

Drug resistance mutation scores of NNRTI:

Rule	DOR	EFV	ETR	NVP	RPV
V106A	60	45	0	60	0
Y181C	10	30	30	60	45
Total	70	75	30	120	45

Drug resistance interpretation: IN — HIVDB 9.4 (2022-12-07)

INSTI Major Mutations:	None
INSTI Accessory Mutations:	None
IN Other Mutations:	E10D • I72V • T122S • S123R • T125P • P142L • V151I

Integrase Strand Transfer Inhibitors	
bictegravir (BIC)	Susceptible
cabotegravir (CAB)	Susceptible
dolutegravir (DTG)	Susceptible
elvitegravir (EVG)	Susceptible

raltegravir (RAL)	Susceptible

IN comments

Other

- **V151I** is an accessory INSTI selected mutation that occurs in 1% to 3% of viruses from ART-naive persons depending on subtype. Alone, it appears to have little or no effect on INSTI susceptibility.

Mutation scoring: IN HIVDB 9.4 (2022-12-07)

No drug resistance mutations were found for INSTI.