

# Genotypic ARV Resistance Report

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## Patient Information

Our Ref. ID: VCI-21246

Name:	♂ 11	Your Ref. ID:	P21-09773
Hospital/Site:	PRIBTA	Study/Visit:	
Risk Factor:	No Information	Collection Date:	05-Mar-2022
Clinical Staging:	No Information	CDC Staging:	No Information
		Genotyping Date:	16-Mar-2022

## Lab Information

Current CD4:	No Information	Current Antiretroviral:	Unknown
Current VL:	151000 copies/ml (11-Mar-2022)		

## Summary Data

Subtype and % similarity to closest reference isolate:	CRF01_AE (97%)
Sequence includes RT: condons:	20 - 244

## Resistance Report ( RT )

RT TAMs:	-
RT NRTIs:	-
RT NNRTIs:	-
RT Other:	V35T, T39K, K43E, V60I, K122E, D123N, I135T, K173I, Q174K, D177E, I178M, V179I, I202V, Q207A, R211S, K238R

Antiretroviral	High-level resistance	Intermediate resistance	Low-level resistance	Potential low-level resistance	Susceptible
<b>NRTI</b>					
zidovudine (AZT)					
tenofovir (TDF)					
stavudine (D4T)					
lamivudine (3TC)					
emtricitabine (FTC)					
didanosine (DDI)					
abacavir (ABC)					
<b>NNRTI</b>					
rilpivirine (RPV)					
nevirapine (NVP)					
etravirine (ETR)					
efavirenz (EFV)					
doravirine (DOR)					

ConsensusR#21246RT.txt

Remark: 1. Although the mutation is not found, it does not mean that one is fully susceptible to the treatment since the resistant virus may be minor population which cannot be detected by the assay (detectable limit = viral load 1,000 copies/ml).  
2. The accumulation of TAMs (M41L, D67N, K70R, L210W, T215Y/F, K219Q/E) increases resistance to tenofovir. Mutations M41L and L210W, contribute more than others  
3. References: Stanford dBase system (<http://hivdb.stanford.edu/>)

Reported by:  Date: 16/3/2022

## Vaccine and Cellular Immunology Laboratory

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## RT Comments

- Other
- K238R is a common polymorphism that does not reduce NNRTI susceptibility.
  - V179I is a polymorphic mutation that is frequently selected in patients receiving ETR and RPV. But it has little, if any, direct effect on NNRTI susceptibility.

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