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ANRS - AC 11 : RESISTANCE GROUP
GENOTYPE INTERPRETATION: NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS

	Mutations associated to resistance	Mutations associated to « possible resistance »
ZDV	• T215Y/F • At least 3 mutations among : M41L, D67N, K70R, L210W, T215A/C/D/E/G/H/I/L/N/S/V, K219Q/E [1, 2, 3, 4] • Q151M • Insertion at codon 69	• T215A/C/D/E/G/H/I/L/N/S/V [1, 2, 3, 4]
3TC/FTC	• M184V/I • Insertion at codon 69	• K65R [11, 12, 16] • Q151M
ddI	• At least a score of + 2 among: M41L + T69D + L74V/I + 215Y/F + K219Q/E – K70R – M184 V/I [5, 14, 15, 17, 18] • L74V/I without any mutations among M41L, T69D, K70R, M184 V/I, T215Y/F, K219Q/E [19] • Q151M • Insertion at codon 69	• K65R [11, 12]
d4T	• V75A/M/S/T • T215Y/F [6] • At least 3 mutations among : M41L, D67N, K70R, L210W, T215A/C/D/E/G/H/I/L/N/S/V, K219Q/E [4, 7, 14, 15] • Q151M • Insertion at codon 69	• T215A/C/D/E/G/H/I/L/N/S/V [4, 7]
ABC	• At least 5 mutations among : M41L, D67N, L74V/I, M184V/I, L210W, T215Y/F [8, 19, 29] • No TAMs and at least 2 mutations among: K65R, L74V/I, Y115F and M184V/I [24, 25, 26, 27, 28, 29] • Q151M • Insertion at codon 69	• 4 mutations among : M41L, D67N, L74V/I, M184V/I, L210W, T215Y/F [8, 19, 29] • K65R [9, 11, 12]
TDF	• At least 6 mutations among: M41L, E44D, D67N, T69D/N/S, L74V, L210W, T215Y/F [13, 20] • K65R [9, 10, 11, 12] • Insertion at codon 69	• 3, 4 or 5 mutations among: M41L, E44D, D67N, T69D/N/S, L74V, L210W, T215Y/F [13] • K70E [21, 22, 23]

TAMs = M41L, D67N, K70R, L210W, T215Y/F, K219Q/E

ZDV: zidovudine, 3TC: lamivudine, FTC: emtricitabine, ddI: didanosine, d4T: stavudine, ABC: abacavir, TDF: tenofovir

Mutations associated to antiretroviral regimen but with uncertain signification: E44A, D67E/G, T69A, K219N/R

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GENOTYPE INTERPRETATION: NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS

	Mutations associated to resistance	Mutations associated to « possible resistance »
EFV	• L100I • K101E • K103H/N/S/T [1] • V106M [2] • Y181C/I • Y188C/L • G190A/C/E/Q/S/T/V • P225H • M230L	
NVP	• A98S (for HIV-1 subtype C only) [3] • L100I • K101E • K103H/N/S/T [1] • V106A/M [2] • Y181C/I • Y188C/H/L • G190A/C/E/Q/S/T/V • M230L	• A98S (for other subtypes than HIV-1 subtype C) [3]
ETV TMC125	• At least 4 among: V90I, A98G, L100I, K101E/P, V106I, V179D/F, Y181C/I/V, G190A/S [4]	• 3 mutations among: V90I, A98G, L100I, K101E/P V106I, V179D/F, Y181C/I/V, G190A/S [4]

EFV: efavirenz, NVP: nevirapine, ETV (TMC125): etravirine

Mutations associated to antiretroviral regimen but with uncertain signification: K101H/N/Q

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GENOTYPE INTERPRETATION: PROTEASE INHIBITORS

	Mutations associated to resistance	Mutations associated to « possible resistance »
IDV	• M46I/L • V82A/F/M/S/T [11] • I84A/V [8] • L90M and at least 2 among : K20M/R, L24I, V32I, M36I, I54V/L/M/T, A71V/T, G73S/A, V77I	• L90M
SQV/RTV 1000/100 mg BID	• G48V • At least 4 mutations among: L10F/I/M/R/V, I15A/V, K20I/M/R/T, L24I, I62V, G73S/T, V82A/F/S/T, I84V, L90M [9]	• 3 mutations among: L10F/I/M/R/V, I15A/V, K20I/M/R/T, L24I, I62V, G73S/T, V82A/F/S/T, I84V, L90M [9]
NFV	• D30N • I84A/V [8] • N88S/D • L90M	• V82A/F/S/T and at least 2 among: L10I, M36I, M46I/L, I54V/L/M/T, A71V/T, V77I [1]
fosAPV/RTV 700/100 mg BID	• I50V • V32I and I47A/V [2, 13, 14] • At least 4 mutations among: L10F/I/V, L33F, M36I, I54A/L/M/S/T/V, I62V, V82A/C/F/G, I84V, L90M [2]	
LPV/r	• At least 8 mutations among : L10F/I/R/V, K20M/R, L24I, L33F, M46I/L, I50V, F53L, I54M/L/T/V, L63P, A71I/L/V/T, V82A/F/S/T, I84V, L90M [3, 4, 5] • I47A [15, 16] • L76V [18, 19]	• 6 or 7 mutations among: L10F/I/R/V, K20M/R, L24I, L33F, M46I/L, I50V, F53L, I54M/L/T/V, L63P, A71I/L/V/T, V82A/F/S/T, I84V, L90M [3, 4, 5]
ATV/RTV 300/100 mg QD	• I50L [6] • At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, I84V, I85V, L90M [7, 12]	
TPV/RTV 500/200 mg BID	For HIV-1 subtype B only: At least a score of 3 : 36I/L/V – 53L/W/Y + 58E + 69I/K/N/Q/R/Y + 89I/M/R/T/V [10]	For HIV-1 subtype B only: a score of 2 : 36I/L/V – 53L/W/Y + 58E + 69I/K/N/Q/R/Y + 89I/M/R/T/V [10]
DRV/RTV	• At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, G73S, L76V, I84V, L89V [17]	• 3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, G73S, L76V, I84V, L89V [17]

TMC114/rtv 600/100 mg BID		

IDV: indinavir, SQV: saquinavir, NFV: nelfinavir, RTV: ritonavir, fosAPV: fosamprenavir, LPV: lopinavir, ATV:atazanavir, TPV: tipranavir, DRV (TMC114) : darunavir

Mutations associated to antiretroviral regimen but with uncertain signification: K20T, M46V

N88S mutation is associated to better virological response to fosamprenavir [2]

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GENOTYPE INTERPRETATION: FUSION INHIBITOR

	Mutations associated to resistance
ENF **T20**	• **G36A/D/E/S/V [1, 2, 3, 4, 5, 6, 7]** • **V38A/E/K/M** • **Q40H/K/P/T** • **N42D/T** • **N43D/H/K/S** • **L44M** • **L45Q/M**

ENF (T20): enfuvirtide

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GENOTYPE INTERPRETATION: INTEGRASE INHIBITORS

	Mutations associated to resistance
RAL	• **Q148H/G/K/R/E [1, 2]** • **N155H [1, 2]** • **E157Q [2]** • **E92Q [1, 2]**

RAL: raltegravir

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GENOTYPE INTERPRETATION FOR HIV-2

NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS
• **Q151M : Resistance to d4T, ABC [1]** • **Q151M + M184V : Resistance to all NRTI except TDF [2]** • **M184V : Resistance to 3TC/FTC [2]**
NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS
• **Naturally resistant to all NNRTI [3, 4]**
PROTEASE INHIBITORS
• **Naturally resistant to APV and fosAPV [3, 4]** • **Contradictory data for ATV [5]**
FUSION INHIBITOR
• **Naturally resistant to T20 [3, 4]**

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