

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

	Mutations associated with resistance	Mutations associated with « possible resistance »
ZDV	<ul style="list-style-type: none"> • 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 	<ul style="list-style-type: none"> • T215A/C/D/E/G/H/I/L/N/S/V [1, 2, 3, 4]
3TC/FTC	<ul style="list-style-type: none"> • M184V/I • Insertion at codon 69 	<ul style="list-style-type: none"> • K65R [11, 12, 16] • Q151M
ddl	<ul style="list-style-type: none"> • At least a score of + 2 among: M41L + T69D + 215Y/F + K219Q/E – K70R – M184 V/I [5, 14, 15, 17, 18] • L74V/I [19] • Q151M • Insertion at codon 69 	<ul style="list-style-type: none"> • K65R [11, 12]
d4T	<ul style="list-style-type: none"> • 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] • K65R [30, 31, 32] • Q151M • Insertion at codon 69 	<ul style="list-style-type: none"> • T215A/C/D/E/G/H/I/L/N/S/V [4, 7]
ABC	<ul style="list-style-type: none"> • At least 4 mutations among: M41L, D67N, M184V/I, L210W, T215Y/F [8, 19, 29] • K65R [9, 11, 12] • L74V/I [24, 25, 26, 27, 28, 29] • Y115F • Q151M • Insertion at codon 69 	<ul style="list-style-type: none"> • 3 mutations among: M41L, D67N, M184V/I, L210W, T215Y/F [8, 19, 29]
TDF	<ul style="list-style-type: none"> • At least 6 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215Y/F [13, 20, 33] • K65R/E/N [9, 10, 11, 12, 34, 35] • Insertion at codon 69 • K70E [21, 22, 23] 	<ul style="list-style-type: none"> • 3, 4 or 5 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215Y/F [13, 33]

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

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GENOTYPE INTERPRETATION: NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS**

	Mutations associated with resistance	Mutations associated with « possible resistance »
EFV	<ul style="list-style-type: none"> • L100I • K101E • K103H/N/S/T [1] • V106M [2] • E138K [12, 13] • Y181C/I • Y188C/L • G190A/C/E/Q/S/T/V • P225H • M230L 	
NVP	<ul style="list-style-type: none"> • 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 	<ul style="list-style-type: none"> • E138K [13]
ETR	<ul style="list-style-type: none"> • At least 4 among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, Y181C/I, G190A/S, M230L [4, 7, 8, 9, 10, 11] • E138K [12, 13] • Y181V [5, 6] • Y181C+H221Y [7] 	<ul style="list-style-type: none"> • 3 mutations among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, Y181C/I, G190A/S, M230L [4, 7, 8, 9, 10, 11] • E138A/G/Q/R [5, 6, 7, 8]
RPV	<ul style="list-style-type: none"> • K101E/P [9, 13] • E138A/G/K/Q/R/S [12, 13, 14] • V179L [9] • Y181C/I/V [13] • Y188L [9] • H221Y [13] • M230I/L/V [9] • L100I + K103N/S [9, 15] • L100I + K103R + V179D [15] 	

EFV: efavirenz, NVP: nevirapine, ETR: etravirine, RPV : rilpivirine

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GENOTYPE INTERPRETATION: PROTEASE INHIBITORS**

	Mutations associated with resistance	Mutations associated with « possible resistance »
IDV	<ul style="list-style-type: none"> • 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 	<ul style="list-style-type: none"> • L90M
SQV/RTV 1000/100 mg BID	<ul style="list-style-type: none"> • 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] 	<ul style="list-style-type: none"> • 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	<ul style="list-style-type: none"> • D30N • I84A/V [8] • N88S/D • L90M 	<ul style="list-style-type: none"> • V82A/F/S/T and at least 2 among: L10I, M36I, M46I/L, I54V/L/M/T, A71V/T, V77I [1]
FPV/RTV 700/100 mg BID	<ul style="list-style-type: none"> • 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, 20] 	
LPV/r	<ul style="list-style-type: none"> • At least 6 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, 21] • I47A [15, 16] • L76V [18, 19] 	<ul style="list-style-type: none"> • 4 or 5 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, 21]
ATV/RTV 300/100 mg QD	<ul style="list-style-type: none"> • I50L [6] • N88S [28,29,30] • At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, I84V, I85V, L90M [7, 12, 22] 	
TPV/RTV 500/200 mg BID	<ul style="list-style-type: none"> • 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, 23] 	<ul style="list-style-type: none"> • A score of + 2*: 36I/L/V – 53L/W/Y + 58E + 69I/K/N/Q/R/Y + 89I/M/R/T/V [10, 23]
DRV/RTV 600/100 mg BID	<ul style="list-style-type: none"> • At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [17, 24, 25, 26] 	<ul style="list-style-type: none"> • 3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [17, 24, 25, 26]

IDV: indinavir, SQV: saquinavir, NFV: nelfinavir, RTV: ritonavir, FPV: fosamprenavir, LPV: lopinavir, ATV:atazanavir, TPV: tipranavir, DRV : darunavir

* Insufficient data for HIV-1 subtype non-B

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GENOTYPE INTERPRETATION: FUSION INHIBITOR

	Mutations associated with resistance
ENF	<ul style="list-style-type: none">• 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
T20	

ENF (T20): enfuvirtide

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GENOTYPE INTERPRETATION: INTEGRASE INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
RAL	<ul style="list-style-type: none"> • T66K [10] • E92Q [1, 2] • G118R [10, 17] • F121Y [10,17] • G140A/S [7] • Y143A/C/G/H/R/S [1, 3, 4, 5, 8, 14] • Q148E/G/H/K/R [1, 2] • V151L [9] • N155H/S/T [1, 2, 9] • E157Q [2] 	
EVG	<ul style="list-style-type: none"> • T66I/A/K [6] • E92Q [6] • G118R [17] • F121Y [9,17] • E138K • G140C/S • Y143A/C/G/H/R/S [14] • P145S [9] • S147G • Q148H/R/K [6] • V151L [9] • N155H/S/T [6,9] • E157Q [11] 	
DTG	<ul style="list-style-type: none"> • G118R [12,13] • F121Y [17] • V151L [9] • S153Y • T66K + L74M • E92Q + N155H • Q148H/K/R + at least 2 mutations among: L74I or E138A/K/T or G140A/C/S [15] • Q148R + N155H • R263K [16] 	<ul style="list-style-type: none"> • T66K [9] • S153F • Q148H/K/R + 1 mutation among: L74I or E138A/K/T or G140A/C/S [15]

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RAL: raltegravir, EVG: elvitegravir, DTG: dolutegravir

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