ANRS – MIE VIROLOGY NETWORK : RESISTANCE GROUP
GENOTYPE INTERPRETATION: NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
ZDV	• T215A/C/D/E/G/H/I/L/N/S/V/Y/F [1, 2, 3, 4] • At least 3 mutations among: M41L, D67N, K70R, L210W, K219Q/E [1, 2, 3, 4] • Q151M • Insertion at codon 69	
3TC/FTC	• K65R [8, 9, 11] • M184V/I • Insertion at codon 69	• Q151M
ABC	• At least 3 mutations among: M41L, D67N, M184V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [5, 20] • K65R [6, 8, 9, 24] • L74V/I [16, 17, 18, 19, 20, 24] • Y115F [24] • Q151M • Insertion at codon 69	• 2 mutations among: M41L, D67N, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [5, 20] • M184V/I [24]
TDF/TAF	• At least 4 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [10, 12, 21, 25, 26] • K65R/E/N [6, 7, 8, 9, 22, 23, 25, 26] • Insertion at codon 69 • K70E [13, 14, 15]	• 3 mutations among: M41L, E44D, D67N, T69D/N/S, L74V/I, L210W, T215A/C/D/E/G/H/I/L/N/S/V/Y/F [10, 21, 25, 26]
ISL	• M184V/I [27, 28, 29]	• A114S [29]

ZDV: zidovudine, 3TC: lamivudine, FTC: emtricitabine, ABC: abacavir, TDF: tenofovir disoproxil fumarate, TAF: tenofovir alafenamide , ISL: islatravir

For didanosine and stavudine refer to previous rules (See Archives, September 2017, version 27)

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

ANRS – MIE VITOLOGY NETWORK: RESISTANCE GROUP
GENOTYPE INTERPRETATION: NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
EFV	• 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	• 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	• E138K [13]
ETR	• At least 3 among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, G190A/S, M230L [4, 7, 8, 9, 10, 11] • E138K [12, 13] • Y181C/I/V [5, 6] • H221Y [12,16]	• 2 mutations among: V90I, A98G, L100I, K101E/H/I/P/R, V106I, V179D/F/I/L/M/T, G190A/S, M230L [4, 7, 8, 9, 10, 11] • E138A/G/Q/R/S [5, 6, 7, 8]
RPV	• K101E/P [9, 13] • E138A/G/K/Q/R/S [12, 13, 14] • V179L [9] • Y181C/I/V [13] • Y188L [9] • F227C [9] • H221Y [13] • M230I/L/V [9] • L100I + K103N/S [9, 15] • L100I + K103R + V179D [15]	• A98G [22]

DOR	• **V106A/M [17, 18, 19, 20 ,21]** • **Y188L** • **G190E/S [21]** • **M230L** • **L100I + K103N [17, 19]** • **K103N + Y181C** • **K103N + P225H** • **F227C [21]** • **At least 4 among: A98G, L100I, K101E, V106I, E138K, , Y181C/V, G190A or H221Y [23]**	• **At least 2 among: A98G, L100I, K101E, V106I, E138K, Y181C/V, G190A or H221Y [23]** • **F227L/R [18,24]**

EFV: efavirenz, NVP: nevirapine, ETR: etravirine, RPV : rilpivirine, DOR : doravirine.

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

ANRS – MIE VIROLOGY NETWORK: RESISTANCE GROUP
GENOTYPE INTERPRETATION: PROTEASE INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
LPV/r	• At least 4 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 [1, 2, 3, 12] • I47A [7, 8] • L76V [10, 11]	• 3 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 [1, 2, 3, 12]
ATV/RTV 300/100 mg QD	• I50L [4] • N88S [18,19,20] • At least 3 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 6, 13, 21]	• 2 mutations among: L10F/I/V, G16E, L33F/I/V, M46I/L, D60E, A71V/T, I84V, I85V, L90M [5, 6, 13, 21]
DRV/RTV* 600/100 mg BID 800/100 mg QD	• At least 4 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17] • At least 2 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17]	• 3 mutations among: V11I, V32I, L33F, I47V, I50V, I54L/M, T74P, L76V, I84V, L89V [9, 14, 15, 16, 17]

LPV: lopinavir, ATV: atazanavir, DRV: darunavir, RTV: ritonavir

For indinavir, saquinavir, nelfinavir and fosamprenavir refer to previous rules (See Archives, September 2017, version 27)

* Please note that rules are different for DRV/RTV 600/100 mg BID and 800/100 mg QD
For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

ANRS – MIE VIROLOGY NETWORK: RESISTANCE GROUP
GENOTYPE INTERPRETATION: FUSION INHIBITOR

	Mutations associated with 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

GENOTYPE INTERPRETATION: ATTACHMENT INHIBITOR

	Mutations associated with “possible resistance” (gp120)
FTR*	• At least one mutation among: S375H/I/M/N/T, M426L/P, M434I/K, M475I [5]

FTR: fostemsavir

***HIV-1 CRF01_AE and HIV-1 group non-M strains are naturally resistant to Fostemsavir [1, 2, 3, 4]**

ANRS – MIE VIROLOGY NETWORK: RESISTANCE GROUP

GENOTYPE INTERPRETATION: INTEGRASE STRAND TRANSFER INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
RAL	• T66A/K [10, 40] • E92Q [1, 2] • G118R [10, 17] • F121Y [10,17] • G140A/S [7] • Y143A/C/G/H/R/S [1, 3, 4, 5, 8, 14] • N144D [42] • Q148E/G/H/K/R [1, 2] • V151L [9] • N155H/S/T [1, 2, 9] • E157Q [2] • S230R [18, 31, 32, 33] • R263K [16, 18] • L74 F/I + V75I [36]	
EVG	• T66A/I/K [6] • E92Q [6] • T97A [19,20] • G118R [17] • F121Y [9,17] • E138K • G140A/C/S [34, 41] • Y143A/C/G/H/R/S [14] • N144D [42] • P145S [9] • S147G [19] • Q148E/G/H/K/R [6] • V151L [9] • N155H/S/T [6, 9] • E157Q [11, 35] • S230R [18, 31, 32, 33] • R263K [18] • L74F/I + V75I [36]	

DTG* 50mg BID	• G118R [12,13] • F121Y [17] • N144D [42] • V151L [9,23] • S153F/Y [9, 23, 26, 34] • R263K [16] • T66K + L74M [9] • E92Q + N155H [9, 21, 22] • Q148H/K/R + at least 2 mutations among: L74I or T97A or E138A/K/T or G140A/C/S [15, 38, 39] • Q148H/K/R + N155H [9, 27, 28]	• T66K [9] • Q148H/K/R + 1 mutation among: L74I or E138A/K/T or G140A/C/S [15] • At least 4 mutations among: L74I/M, T97A, E138K, S147G, N155H [43]
DTG* 50mg QD	• G118R [12, 13] • F121Y [17] • E138A/K/T • G140A/C/S • N144D [42] • Q148H/K/R • V151L [9, 23] • S153F/Y [9, 23, 26, 34] • N155H [18] • S230R [29] • R263K [16] • T66K + L74M [9] • L74I + E92Q [30]	• T66K [9] • At least 3 mutations among: L74M, E92Q, T97A, S147G [43]

CAB**	• G118R [12, 13] • F121Y [17] • E138A/K/T • G140A/C/R/S [37] • N144D [42] • Q148H/K/R • V151L [9, 23] • S153F/Y [9, 23, 26, 34] • N155H [18] • S230R [29] • R263K [16] • T66K + L74M [9] • L74I + E92Q [30]	• T66K [9] • At least 3 mutations among: L74M, E92Q, T97A, S147G [43]
BIC**	• G118R [12, 13] • F121Y [17] • E138A/K/T • G140A/C/S • N144D [42] • Q148H/K/R • V151L [9, 23] • S153F/Y [9, 23, 26, 34] • N155H [18] • S230R [29] • R263K [16] • T66K + L74M [9] • L74I + E92Q [30]	• T66K [9] • At least 3 mutations among: L74M, E92Q, T97A, S147G [43]

RAL: raltegravir, EVG: elvitegravir, DTG: dolutegravir, CAB: cabotegravir, BIC: bictegravir

* Please note that rules are different for DTG 50 mg BID and DTG 50 mg QD
**Due to few data and to the very close structures of dolutegravir, cabotegravir and bictegravir some rules for dolutegravir QD are transposed to cabotegravir and bictegravir

For DNA provirus, Impact of stop codons and G to A mutations on ARV resistance is unknown

ANRS – MIE VIROLOGY NETWORK: RESISTANCE GROUP

GENOTYPE INTERPRETATION: CAPSID INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
LEN	• L56I [1] • M66I [1] • Q67H/K/N [1,3,4, 5] • K70H/N/R/S [1,2,3,4,5] • N74D/H/K/S [1,4,6] • A105T/S [4,6] • T107C/N [1,3,4,6]	

LEN: lenacapavir

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