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] • T107A/C/N/S [1,3,4,6]	

LEN: lenacapavir

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