

ANRS – MIE VIROLOGY NETWORK RESISTANCE GROUP  
GENOTYPE INTERPRETATION FOR HIV-2

GENOTYPE INTERPRETATION: NUCLEOSIDE AND NUCLEOTIDE REVERSE TRANSCRIPTASE INHIBITORS [1]

	Mutations associated with resistance	Mutations associated with « possible resistance »
ZDV	<ul style="list-style-type: none"><li>• Q151M</li><li>• S215A/C/F/L/Y + 1 mutation among K65R, N69S/T, K70R, Y115F, K223R</li></ul>	<ul style="list-style-type: none"><li>• S215A/C/F/L/Y</li></ul>
3TC/FTC	<ul style="list-style-type: none"><li>• M184I/V</li></ul>	<ul style="list-style-type: none"><li>• K65R</li></ul>
ABC	<ul style="list-style-type: none"><li>• K65R</li><li>• Q151M</li><li>• M184I/V + 1 mutation among: L74V, Y115F</li></ul>	<ul style="list-style-type: none"><li>• 2 mutations among: D67N, K70N/R, M184V/I, S215A/C/F/L/Y</li></ul>
TDF/TAF	<ul style="list-style-type: none"><li>• K65R</li><li>• Q151M + V111I</li></ul>	

ZDV: zidovudine, 3TC: lamivudine, FTC: emtricitabine, ABC: abacavir, TDF: tenofovir, TAF: tenofovir alafenamide

Didanosine and stavudine are not recommended

**GENOTYPE INTERPRETATION: PROTEASE INHIBITORS [1]**

	<b>Mutations associated with resistance</b>	<b>Mutations associated with « possible resistance »</b>
LPV	<ul style="list-style-type: none"><li>• 2 mutations among: I82F, I84V, L90M</li><li>• I54M</li><li>• V47A</li></ul>	<ul style="list-style-type: none"><li>• V62A + L99F</li><li>• 1 mutation among: I82F, I84V, L90M</li></ul>
DRV	<ul style="list-style-type: none"><li>• I50V</li><li>• I54M</li><li>• I84V + L90M</li></ul>	<ul style="list-style-type: none"><li>• 1 mutation among: I84V, L90M</li></ul>

LPV: lopinavir, DRV: darunavir

For indinavir and saquinavir refer to previous rules (See Archives, Version 27, September 2017)  
Atazanavir and tipranavir are not recommended

## GENOTYPE INTERPRETATION: INTEGRASE STRAND TRANSFER INHIBITORS [1-6]

	Mutations associated with resistance	Mutations associated with « possible resistance »
RAL	<ul style="list-style-type: none"> <li>• N155H/R</li> <li>• Q148K/R/H [3,4,5]</li> <li>• E92Q + T97A</li> <li>• Y143C/G/R + 1 mutation among: E92Q, T97A</li> <li>• Insertion at codon 231 [5]</li> <li>• G118R [6]</li> <li>• R263K [6,7]</li> </ul>	<ul style="list-style-type: none"> <li>• E92Q</li> <li>• Y143C/G/R</li> </ul>
EVG	<ul style="list-style-type: none"> <li>• E92G/Q</li> <li>• Q148K/R/H [3,4,5]</li> <li>• N155H</li> <li>• T97A + Y143C</li> <li>• Insertion at codon 231 [5]</li> <li>• G118R [6]</li> <li>• R263K [6,7]</li> </ul>	<ul style="list-style-type: none"> <li>• Y143C</li> </ul>
DTG	<ul style="list-style-type: none"> <li>• Q148K</li> <li>• G140S + Q148R/H [3,4,5]</li> <li>• E92Q + N155H</li> <li>• T97A + N155H</li> <li>• Insertion at codon 231 [5]</li> <li>• G118R [6]</li> <li>• R263K [6,7]</li> </ul>	<ul style="list-style-type: none"> <li>• Q148R/H [3]</li> <li>• N155H</li> <li>• E92Q</li> <li>• T97A + Y143C</li> </ul>
CAB*	<ul style="list-style-type: none"> <li>• Q148K</li> <li>• G140S + Q148R/H [3,4,5]</li> <li>• E92Q + N155H</li> <li>• T97A + N155H</li> <li>• Insertion at codon 231 [5]</li> <li>• G118R [6]</li> <li>• R263K [6,7]</li> </ul>	<ul style="list-style-type: none"> <li>• Q148R/H [3]</li> <li>• N155H</li> <li>• E92Q</li> <li>• T97A + Y143C</li> </ul>
BIC*	<ul style="list-style-type: none"> <li>• Q148K</li> <li>• G140S + Q148R/H [5]</li> <li>• E92Q + N155H</li> <li>• T97A + N155H</li> <li>• G118R [6]</li> <li>• R263K [6,7]</li> </ul>	<ul style="list-style-type: none"> <li>• Q148R/H</li> <li>• N155H</li> <li>• E92Q</li> <li>• T97A + Y143C</li> <li>• Insertion at codon 231 [5]</li> </ul>

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

\*Due to the very close structures of dolutegravir and cabotegravir, rules for dolutegravir are transposed to cabotegravir with the exception of the insertion at codon 231 for bictegravir

NON-NUCLEOSIDE REVERSE TRANSCRIPTASE INHIBITORS
• Naturally resistant to all NNRTI [2]
FUSION INHIBITOR
• Naturally resistant to enfuvirtide [2]
ATTACHEMENT INHIBITOR
• Naturally resistant to fostemsavir [8]

ANRS – MIE VIROLOGY NETWORK: RESISTANCE GROUP

GENOTYPE INTERPRETATION: CAPSID INHIBITORS

	Mutations associated with resistance	Mutations associated with « possible resistance »
LEN	• N73D [9]	• Q66H [9] • R69K [9] • A76V [9]

LEN: lenacapavir

## REFERENCES

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