

# Resistance to integrase inhibitors: a national study in HIV -1-infected treatment-naive and -experienced patients

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#### **Resistance to integrase inhibitors:** A National Study 1 in HIV-1-Infected Naïve and Experienced Patients 2

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- 33 Key words: integrase, inhibitors, mutations, patterns, resistance
- 34 **Summary**: This work described the resistance patterns in a large population of patients failing an
- 35 integrase inhibitor-based regimen. We showed that dolutegravir exhibited the highest robustness
- regarding resistance selection in case of virological failure in real world clinical setting. 36
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### 41 Synopsis

Introduction: It is of importance to describe integrase strand transfer inhibitors (INSTIs)
resistance profiles and factors associated with, in naïve- and experienced-patients failing an
INSTI-based regimen in clinical practice.

45 Methods: Data were collected from patients failing an INSTI-containing regimen in a 46 multicentre french study between 2014 and 2017. Failure was defined by 2 consecutive 47 plasma viral load (VL) > 50 copies/mL. Reverse transcriptase, protease and integrase genes 48 were sequenced at baseline and failure. INSTIs resistance-associated mutations (RAMs) 49 included in the ANRS genotypic algorithm were investigated.

Results: Among the 674 patients, 359 were failing raltegravir, 154 elvitegravir and 161 50 dolutegravir. Overall, 389 (58%) patients showed no INSTI RAMs at failure. At failure, 36% 51 of patients failing raltegravir exhibited viruses considered genotypically resistant to 52 53 raltegravir, 44% of patients failing elvitegravir exhibited viruses resistant to elvitegravir, 14% 54 and 7% of patients failing dolutegravir exhibited viruses resistant to dolutegravir once per day and twice daily, respectively. Patients with high VL at failure and low Genotypic Sensitivity 55 56 Score had a higher risk to select at least one INSTI RAM. Patients failing dolutegravir had significantly less INSTI RAMs at failure than patients failing raltegravir (OR=0.57, p = 0.02) 57 or elvitegravir (OR=0.45, p = 0.005). Among the sixty eight patients failing a first-line 58 regimen: 11/41 (27%) patients failing raltegravir had at failure viruses with emergent INSTI 59 RAMs, 7/18 (39%) with elvitegravir and 0/9 with dolutegravir. 60

61 Conclusions: These results confirmed the robustness of dolutegravir regarding resistance
62 selection in case of virological failure in routine clinical care.

## 64 Introduction

Integrase strand transfer inhibitors (INSTIs), which actively block the integration of the HIV 65 genome into the host DNA, represent the latest antiretroviral (ARV) class to be approved for 66 treatment of HIV-infected individuals<sup>1</sup>. There are currently four INSTIs approved for the 67 treatment of HIV infection: raltegravir, elvitegravir, dolutegravir and more recently 68 bictegravir. Although highly efficacious in the management of HIV, both raltegravir and 69 elvitegravir are susceptible to the development of resistance mutations in case of virological 70 failure. The main resistance pathways that have been reported as selected both in vitro and in 71 vivo with raltegravir are Y143, Q148 and N155.<sup>2</sup> It is evident now that raltegravir and 72 elvitegravir share both the O148 and N155 major resistance pathways.<sup>3</sup> However, T66 and 73 E92 pathways are predominantly selected by elvitegravir.<sup>4</sup> In contrast to raltegravir and 74 elvitegravir that share a common resistance profile, dolutegravir has a markedly distinct 75 resistance profile and appears to have a higher genetic barrier to resistance. Indeed, in clinical 76 trials it has not been shown to select for any resistance-associated mutations in treatment 77 naïve patients when used in triple therapy. <sup>567</sup> However, one case of emergence of integrase 78 resistance mutation (Q148K + M184V) during virologic failure in a treatment-naïve man who 79 initiated tenofovir disoproxil fumarate/emtricitabine plus dolutegravir has been recently 80 published.<sup>8</sup> In addition, there have been some cases of treatment failure with resistance 81 mutations in treatment-experienced but INSTI-naïve patients, in particular with the emergence 82 of the R263K mutation.<sup>9</sup> Finally, in the particular setting of dolutegravir monotherapy in 83 treatment-experienced patients, the selection of other substitutions at positions E92, Q148, 84 N155 and S230 have been reported. <sup>10</sup> Bictegravir is the most recent INSTI and there is few 85 information available in regard to resistance against this drug. Given its similar chemical 86 structure with dolutegravir and the fact that bictegravir selected for 263K during in vitro 87 passages, we can assume that bictegravir share similar resistance profile as dolutegravir.<sup>11</sup> 88

Although INSTIs mutation pathways have extensively been studied, most of existing data arises from *in vitro* experiments or clinical trials with a limited number of patients and specific inclusion criteria. In this study, we focused on integrase genotypic resistance tests performed in real world clinical setting by the French national ANRS network in order to better characterize the profile of INSTI resistance among specimens obtained for clinical decision making and to identify factors associated with the selection of integrase resistance mutations.

#### 97 **Patients and methods**

Patients and antiretroviral regimens. HIV-1-infected patients who experienced virologic 98 failure to an INSTI-containing regimen between 2014 and 2017 were allowed to be included 99 in the study. Patients were treated with raltegravir, elvitegravir or dolutegravir with a 100 background regimen comprising mainly NRTIs, NNRTIs, and/or PIs. Virological failure was 101 102 defined as two consecutive HIV-1 viral loads (VL) > 50 copies/mL. Clinical data and treatment histories were collected for all patients recruited. Inclusion criteria and all data were 103 checked by the study monitor. The 21 participating laboratories belong to the Agence 104 Nationale de Recherches sur le SIDA et les hépatites virales (ANRS) AC43 network and 105 participate in the annual ANRS quality control assessment of HIV-1 drug resistance 106 sequencing.<sup>12</sup> The study was approved by the scientific committee of the ANRS AC43. 107

Genotypic resistance testing. The sequences of the protease (PR), reverse transcriptase (RT) 108 and integrase (IN) genes were determined at baseline and failure (on confirmation plasma 109 failure) laboratory ANRS 110 in each using the consensus technique (http://www.hivfrenchresistance.org/), the Abbott ViroSeq kit, or an in-house method. For 111 resistance interpretation, we used RT, PR and IN mutations present in the ANRS algorithm 112 (Version 28) to determine whether patients receiving a particular NRTI, NNRTI or PI, had 113 resistant, intermediate or susceptible virus strains. (www.hivfrenchresistance.org). List of 114 INSTIs associated mutations used in the study is: T66AIK, L74FIM, V75I, E92Q, T97A, 115 G118R, F121Y, E138AKT, G140ACS, Y143ACGHRS, P145S, S147G, Q148EGHKR, 116 V151L, S153FY, N155HST, E157Q, S230R, R263K. 117

The genotypic sensitivity score (GSS) of the current regimen (without INSTI) was calculated according to the ANRS resistance algorithm. For each antiretroviral drug, patients with drugsusceptible viruses were assigned a GSS of 1, and those with intermediate-level and highlevel resistance were assigned scores of 0.5 and 0, respectively. 122 <u>Statistical analysis</u>.

Quantitative variables are described by use of median and Interquartil Range (IQR) while 123 categorical variables are described in percent. HIV-1 RNA at failure, viral subtype (B versus 124 CRF02\_AG and other non-B), baseline CD4 cell count, CD4 cell count at failure, nadir CD4, 125 126 age, duration of infection, duration of INSTI treatment, the ongoing treatment (dual therapy, triple therapy and four and more therapy) and GSS were investigated as potential factors of 127 occurrence of INSTIs mutations by the use of Cochran-Armitage test. A logistic regression 128 129 model was also used to investigate whether previous variables were independent predictors of occurrence of INSTIs resistance associated mutations (RAMs). All variables tested with a P-130 value <0.10 in the univariate analysis were retained for the construction of the multivariate 131 model. The latter only keeps the variables significantly associated with the occurrence of 132 INSTIS mutation with a p-value <0.05. 133

#### 135 **Results**

Overall 674 patients failing an INSTI-containing regimen were included in the study from 21 136 French centres of the ANRS network. Patients were failing while receiving raltegravir (n = 137 138 359), elvitegravir (n = 154) or dolutegravir (n = 161) containing regimen and 10% of them were failing their first-line treatment. The main characteristics of the global study population 139 140 are presented in Table 1. The average age was 48.5 years (IQR: 39.9-55.4 years) and the majority (65%) of patients were male. Regarding HIV-1 subtypes, 55.8% harboured subtype 141 B and the most frequent non-B subtype was CRF02 AG (18%). The most prescribed 142 combinations with INSTI were 2 NRTIs (55%) and 1 NRTI + 1 PI (13%). Patients were 143 receiving 1, 2, 3 and more than 3 antiretrovirals including the INSTI in 1%, 17%, 66% and 144 145 15%, respectively.

Virologic failure occurred after a median time of 10.7 months (IQR: 5.7-30) following administration of INSTI-containing regimen. At failure, median viral load was 2.9  $log_{10}$ copies/mL (IQR: 2.3-4). Overall, viruses harboured no known INSTIs RAMs and were thus considered as fully genotypically susceptible to all INSTIs in 58% (n = 389) of cases. Thus, 42% of viruses harboured at least 1 INSTI RAM: 1, 2 and at least 3 mutations in 25% (n = 170), 10% (n = 71) and 6.5% (n = 44) of cases, respectively.

Regarding INSTIs RAMs in our dataset, the most frequent observed integrase mutations were 152 N155H/S/T (n = 112; 16.6%), L74F/I/M (n = 82; 11.9%), Q148H/K/R (n = 54; 8.0%) and 153 T97A (n = 53; 7.9%). The other detected INSTIs mutations were in less that 5% of cases: 154 T66A/I/K (n =15 ; 2.1%), V75I (n = 6 ; 0.9%), E92Q (n = 26 ; 3.9%), E138A/K/T (n = 22 ; 155 3.3%), G140A/C/S (n = 33 ; 4.9%), Y143A/C/G/H/R/S (n = 25 ; 3%), P145S (n = 3 ; 0.5%); 156 S147G (n = 10; 1.5%), V151L (n = 1; 0.2%), S153F/Y (n = 2; 0.3%), E157Q (n = 22; (n = 2)157 3.3%), S230G/R (n = 7; 0.6%) and R263K (n = 2; 0.3%). Q148H/K/R mutations were 158 selected significantly more frequently in B subtypes versus non-B subtypes (p = 0.0135). In 159

patients harboring viruses with 2 or 3 INSTIs RAMs, the most common combinations were
G140S/Q148H (12%), T97A/G140S/Q148H (6%) and L74I/E92Q (5%).

Interpretation of resistance to the different INSTIs is described in Figure 1. At failure, 36% of patients failing raltegravir exhibited plasma viruses considered genotypically resistant to raltegravir, 44% of patients failing elvitegravir exhibited plasma viruses considered resistant to elvitegravir, 14% and 7% of patients failing dolutegravir exhibited plasma viruses considered resistant to dolutegravir once per day (OD) and twice daily (BID), respectively.

We aimed to characterize clinical and virological factors associated with the emergence of 167 INSTIS RAMs (Table 2). The final multivariate model shows a higher risk of occurrence of at 168 169 least one INSTI RAM associated with a higher level of VL at failure (Odd Ratio (OR) = 1.2per 1  $\log_{10}$  copies/mL increase) (Figure 2) and a lower risk of occurrence of at least one 170 INSTI RAM with a higher level of GSS (OR = 0.29 for GSS = 1-1.5, OR = 0.12 for GSS = 2-171 2.5 and OR = 0.08 for GSS>3 versus GSS = 0-0.5). In addition, patients failing dolutegravir 172 had viruses with significantly less INSTIs RAMs at failure than patients failing raltegravir 173 (OR = 0.57, p = 0.02) and patients failing elvitegravir (OR = 0.45, p = 0.005). 174

Among the 674 patients, 68 were failing a first-line INSTI-based regimen: 41 containing 175 raltegravir, 18 elvitegravir and 9 dolutegravir. Among the 41 patients failing to a raltegravir-176 based regimen, 11 (27%) harboured INSTI RAMs on their genotypic resistance test at failure: 177 4 with emergent mutations (1 L74I/M, 1 T97A, 1 Y143R, 1 V75I) and 7 for whom no 178 179 baseline test was available: 3 L74I, 1 T97A, 1 E138K, 1 N155H, 1 E92Q + N155H, 1 T97A 180 + N155H + E157Q. Among the 18 patients failing to an elvitegravir-based regimen, 7 (39%) harboured INSTI RAMs on their genotypic resistance test at failure: 5 with emergent 181 182 mutations (1 T66I, 2 N155H, 1 E92Q + E157Q, 1 E92Q + S153Y + N155H) and 2 for whom 183 no baseline test was available: 1 L74I + P145S, 1 N155H + S230R. Among the 9 patients

failing to a dolutegravir-based regimen, 3 harboured INSTI RAMs on genotypic resistance 184 test at failure but none were considered as emergent: 2 mutations were already present at 185 baseline (1 L74I and 1 E157Q) and 1 E138K for which no baseline test was available. 186 Interestingly, 7/41 (17%) of the patients failing a first-line raltegravir-based regimen had 187 plasma viruses with M184V (4 M184V alone and 3 with INSTI mutation). Among the 18 188 patients failing of a first-line elvitegravir-based regimen, 7 (39%) had INSTI RAMs and all of 189 them also displayed a M184V mutation, while it was 0/9 in patients failing a dolutegravir fist-190 191 line regimen. However, the Fisher test did not show a significant association between the emergence of the M184V mutation and INSTI treatment (p = 0.07). 192

193

# 195 **Discussion**

The development and expanding use of integrase inhibitors in ARV-naïve and ARVexperienced patients makes it increasingly important to survey INSTIs resistance in the context of large clinical settings. <sup>13</sup> Here, we provide one of the largest data that characterizes INSTI resistance among INSTI failing patients obtained for clinical indications and in which collection of clinical and virological parameters were available.

Overall, our results show that 42% of patientsø viruses experiencing failure to INSTI harbor 201 viruses with at least one INSTI RAM. This rate is higher compared to a study that aimed to 202 characterize INSTI resistance among integrase resistance testing obtained for clinical 203 indications in the United States in which the investigators found that only 15.6% of viruses 204 harbored INSTI major mutations. <sup>14</sup> However, our results are similar to a more recent study 205 showing that 39% of patientsø viruses at time of failure to raltegravir harbor at least one 206 INSTI resistance mutation.<sup>15</sup> Methodological differences between studies can be noticed, as 207 the predefined list of INSTI RAMs has evolved with the inclusion of new mutations over 208 time. In addition, in the present study, we have analyzed failures to 3 different INSTIs and not 209 only to raltegravir, as compared in the French study <sup>15</sup> and in another study where the 210 laboratory did not obtain data on the patient's treatment status (naïve or experienced) or 211 history of prior ARV exposures. <sup>14</sup> This point is crucial as INSTIs have different resistance 212 profile and genetic barrier. Indeed, second-generation INSTIs, including dolutegravir display 213 214 a more robust resistance profile than either raltegravir or elvitegravir and offer a higher barrier to resistance compared to the first-generation class. <sup>16</sup> The resistance profile of dolutegravir 215 has been extensively characterized during the past few years and high-level dolutegravir 216 resistance requires multiple INSTI first-generation resistance mutations.<sup>3</sup> This is supported 217 by our results showing that at failure, only 14% and 7% of patients failing dolutegravir 218 exhibited viruses considered genotypically resistant to dolutegravir OD and BID, respectively, 219

whereas 36% of patients failing raltegravir exhibited viruses considered resistant to raltegravir 220 and 44% of patients failing elvitegravir exhibited viruses considered resistant to elvitegravir. 221 Indeed, dolutegravir efficacy has been initially investigated in the VIKING Phase IIb study 222 where antiretroviral-experienced patients, with raltegravir and/or elvitegravir resistant viruses, 223 received DTG 50 mg either OD (Cohort I) or BID (Cohort II).<sup>17</sup> In spite of the positive 224 results, the VIKING-3 study also highlighted how the dolutegravir response was most reduced 225 in subjects carrying viruses with resistance-associated mutations at position G140 and Q148. 226 <sup>18</sup> This mutation complex is known to cause up to a 10620-fold reduced susceptibility to 227 dolutegravir and, furthermore, subjects harboring viruses with Q148 +  $\times$  2 mutations have 228 96% lower odds of achieving VL <50 copies/mL at week 24 if compared with those with no 229 Q148 mutations.<sup>19,20</sup> In addition, our results reinforce the robustness of dolutegravir 230 regarding selection of resistance in clinical practice as patients failing dolutegravir had 231 232 significantly less INSTI resistance mutations at failure as compared to patients failing raltegravir or elvitegravir. 233

234 The most common resistance pathways identified in the present study were N155H/S/T, 235 L74F/I/M, Q148A/C/G/H/R/S and T97A. In addition, our findings corroborate previous observations, indicating the unique propensity of subtype B to the development of the 236 Q148+G140 mutation pathway.<sup>21</sup> A glycine to serine substitution at integrase position 140 237 requires only one nucleotide change in subtype B and two nucleotide changes in all non-B 238 clades, thus raising the genetic barrier to the emergence of G140 mutants. As mutations at 239 codon 140 play a key role in restoring the fitness of Q148 mutants, their occurrence can also 240 241 influence the emergence of Q148H/R/K, thus explaining the reduced prevalence of Q148 mutants observed in non-B subtypes. In the present study, some rare mutations have been also 242 evidenced, as the R263K mutation in two cases. The R263K mutation was the first mutation 243 rarely found selected at time of virological failure in experienced patients failing a first-line 244

dolutegravir -based treatment. <sup>9</sup> Further *in vitro* studies on R263K mutants showed a moderate
increase in phenotypic resistance level and a drastic reduction in viral replicative capacity.
More recently, it has been shown that in both single and multiple rounds of HIV-1 infections,
bictegravir and cabotegravir, two more recent INSTIs remained active against R263K mutant.
<sup>22</sup> Other mutations (i.e G118R and F121Y), rarely described in patients failing on raltegravir,
<sup>23</sup> have been also shown to induce broad cross-resistance to dolutegravir *in vitro*. <sup>24</sup> However,
we did not see evidence of either G118R or F121Y in this study.

Another interesting mutation is the E157Q mutation that is polymorphic, found between 1.7% 252 and 5.6% of viral sequences issued from ART-naïve patients depending on the viral subtype; 253 as well as acquired resistance emerging at failure of a raltegravir-based regimen in two case 254 reports.<sup>25</sup> Data on phenotypic resistance level of E157Q mutants and virological response of 255 patients harboring an E157Q virus initiating an INSTI-based regimen, showed that 256 dolutegravir might be the most recommended INSTI in such patients. <sup>26,27</sup> However, in the 257 present study, 1/9 patients who failed DTG had a virus already harbouring a E157Q at 258 baseline, thus it is difficult to give strong recommendations. 259

In clinical practice, it has been shown that after previous exposure to first-generation INSTIs, 260 treatment with dolutegravir showed long durability and that subjects infected with a non-B 261 HIV-1 subtype had a greater risk of having detectable VL at the last observation.<sup>28</sup> It is also 262 important to determine, in case of virological failure, which factors are associated with the 263 development of resistance mutations. In a previous study, we showed that a low GSS was 264 associated with the presence of raltegravir-associated mutations and that a high HIV-1 VL 265 level at failure (>1000 copies/mL) was associated with the presence of raltegravir-associated 266 mutations. <sup>15</sup> Here we reinforce this message showing that patients with high VL (> 3 log 267 cp/mL) at failure and low GSS have a higher risk to select at least one INSTI RAM. This has 268

clinical consequences suggesting that careful attention should be paid to patients withdetectable viral load under an INSTI regimen.

In this study we have made a special focus on failures in treatment-naïve patients. At failure, 271 27% of patients receiving raltegravir had emergent or not previously evidenced INSTI RAMs. 272 39% with elvitegravir and none with dolutegravir. In addition, 17% of patients failing 273 274 raltegravir had plasma viruses with a M184V mutation (4 alone and 3 with INSTI mutation), 39% of patients failing elvitegravir (always associated with INSTI mutation) and none in 275 patients failing dolutegravir. Our results corroborate data from clinical trials showing that 276 raltegravir and elvitegravir have relatively low genetic barrier to the development of 277 resistance with an overlapping resistance profile and do not protect NRTI backbone.<sup>29</sup> In 278 279 treatment-naïve patients, data from clinical trial showed neither resistance mutation to INSTIs nor to NRTIs in the rare patients experiencing virological failure in the dolutegravir arm up to 280 96 weeks. <sup>6</sup> Thus our data corroborate that the use of dolutegravir as first-line therapy in 281 282 clinical practice should also prevent the development of INSTI and associated-NRTI drug resistance. However, this should be carefully monitored because despite a high barrier to 283 resistance, no ARV agent is impervious to resistance and even it is extremely rare to date, 284 dolutegravir failure and resistance in treatment naïve patients is possible.<sup>8</sup> 285

Overall, this paper describes one of the largest studies characterizing INSTI resistance among resistance testing obtained for clinical indications from naïve and experienced patients failing to raltegravir, elvitegravir and dolutegravir and reveals factors associated with resistance to INSTIs that should be taken into consideration in clinical management. The results confirmed the robustness of dolutegravir regarding resistance selection in case of virological failure in routine clinical care.

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Amiens, C. Roussel; Angers, H. Le Guillou-Guillemette, A. Ducancelle ; Argenteuil, L. 298 Courdavault; Avicenne, C. Alloui, P. Honore; Besançon, Q. Lepiller, D. Bettinger; Bordeaux, 299 P. Bellecave, P. Pinson-Recordon, C. Tumiotto, S. Reigadas; Brest, S. Vallet, C Payan, JC. 300 Duthe; Caen, M. Leroux, J. Dina, A. Vabret; Clermont-Ferrand, A. Mirand, C. Henquell; 301 Créteil-Henri Mondor, M. Bouvier-Alias; Dijon, A. Simohamed ; Fort de France, G. Dos 302 Santos; Genève, S. Yerly, C. Gaille, W. Caveng, S. Chapalay, A. Calmy; Grenoble, A. 303 Signori-Schmuck, P Morand; HU Paris Sud, C. Pallier, M. Raho-Moussa, M. Mole, M-J. 304 Dulucq; LilleóTourcoing, L. Bocket, K.Alidjinou; Limoges, S. Ranger-Rogez; Lyon, M. A. 305 Trabaud, V Icard, J.C. Tardy; Marseille, C. Tamalet; Metz/Thionville, C. Delamare; 306 Montpellier, B. Montes; Nancy, E. Schvoerer, H. Fenaux; Nantes, A. Rodallec, E. André-307 Garnier, V. Ferré; Nice, A. De Monte, J. Dufayard; Orléans, A. Guigon, J. Guinard; Paris-308 Bichat Claude Bernard, D. Descamps, C. Charpentier, B Visseaux, G. Peytavin; Paris-Necker, 309 M. Fillion; Paris-Pitié-Salpêtrière, C. Soulié, I. Malet, M. Wirden, A. G. Marcelin, V. Calvez, 310 311 P. Flandre, L. Assoumou, D. Costagliola; Paris-Saint Antoine, L. Morand-Joubert, S. Lambert-Niclot, D. Fofana; Paris-Saint Louis, C. Delaugerre, ML Chaix, N. Mahjoub; Paris-312 Tenon, V. Schneider, C. Amiel; Poitiers, G. Giraudeau, A. Beby-Defaux, D. Plainchamp; 313 314 Rennes, A. Maillard; Rouen, E. Alessandri-Gradt, M. Leoz, J. C. Plantier; Strasbourg, P. Gantner S. Fafi-Kremer, P. Fischer; Toulouse, S. Raymond, J. Izopet, J Chiabrando; Tours, 315 F. Barin, G. Fajole, O. Burgault; Versailles, S. Marque Juillet. 316

### 317 <u>Members of the ANRS Clinical Centres by location</u>

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- 341

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- 427

429	Table 1. Baseline characteristics of the study population $(n = 674)$
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2 0-0.5 16.11% 3 1-1.5 27.22% 4 2-2.5 44.07% 5 >=3 12.59% 1 QR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score. 1 2 3 4 5 6 7 8 9 9	+50		
Median time since HIV-1 diagnosis, years (IQR)       15.7 (6.74-22.4)         Median duration of current INSTI regimen, months (IQR)       10.7 (5.7-30)         Median baselice plasma HIV-1 RNA log <sub>10</sub> copies/mL (IQR)       3.1 (1.9-4.9)         Median baselice DOA cell count/mm <sup>3</sup> (IQR)       2.9 (2.3.4)         Median failure plasma HIV-1 RNA log <sub>10</sub> copies/mL (IQR)       3.1 (1.9-4.9)         Median failure plasma HIV-1 RNA log <sub>10</sub> copies/mL (IQR)       3.1 (1.9-4.9)         Median baselice CDA cell count/mm <sup>3</sup> (IQR)       418 (223-670)         NRTIs       55.3 %         NRTIs       55.3 %         NRTIs       55.3 %         NRTIs       55.3 %         NRTIs       7 %         Pls       5.6 %         NRTIs + Pls       13.2 %         NRTIs + NRTIS       7 %         Q.0.5       16.11%         1-1.5       27.22%         2.2.5       44.07%         2.2.5       44.07%         2.2.5       44.07%         2.2.6       44.07%         2.2.7       12.59%         100, ki interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.         11       10.10 (0.10 (0.10 (0.10 (0.10 (0.10 (0.10 (0.10 (0.10 (0.		Male	65 %
Median duration of current INSTI regimen, months (IQR)       10.7 (5.7-30)         Median bascline plasma HIV-1 RNA log <sub>10</sub> copies/mL (IQR)       2.9 (2.3-4)         Median bascline CD4 cell count/mm <sup>3</sup> (IQR)       2.9 (2.3-4)         Median failure CD4 cell count/mm <sup>3</sup> (IQR)       418 (223-670)         INSTI co-treatment (%):       55.3 %         NRTIs       55.3 %         NRTIs       55.3 %         NRTIs       7 %         Pls       5.6 %         NNRTIs + PIs       13.2 %         NNRTIs + NRTIs       7 %         Pls       5.6 %         NNRTIs + NRTIs       3.8 %         Ohter       8.7 %         GSS Score (%):       2         Q.0.5       16.11%         1-1.5       27.22%         2.2.5       44.07%         >=3       12.59%         IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; NGSS, genotypic sensitivity score.         IQR       10.7 (5.7-30)         IQR       10.7 (5.7-30)         IQR       10.7 (5.7-30)         IQR       10.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5		Subtype B	56 %
Median duration of current INSTI regimen, months (IQR)       10.7 (5.7-30)         Median bascline plasma HIV-1 RNA log <sub>10</sub> copies/mL (IQR)       2.9 (2.3-4)         Median bascline CD4 cell count/mm <sup>3</sup> (IQR)       2.9 (2.3-4)         Median failure CD4 cell count/mm <sup>3</sup> (IQR)       418 (223-670)         INSTI co-treatment (%):       55.3 %         NRTIs       55.3 %         NRTIs       55.3 %         NRTIs       7 %         Pls       5.6 %         NNRTIs + PIs       13.2 %         NNRTIs + NRTIs       7 %         Pls       5.6 %         NNRTIs + NRTIs       3.8 %         Ohter       8.7 %         GSS Score (%):       2         Q.0.5       16.11%         1-1.5       27.22%         2.2.5       44.07%         >=3       12.59%         IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; NGSS, genotypic sensitivity score.         IQR       10.7 (5.7-30)         IQR       10.7 (5.7-30)         IQR       10.7 (5.7-30)         IQR       10.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5.7 (5		Median time since HIV-1 diagnosis, years (IOR)	15.7 (6.74-22.4)
Median failure plasma HIV-I RNA log <sub>10</sub> copies/mL (IQR)2.9 (2.3.4) 371 (173-649) Median failure CD4 cell count/mm² (IQR)371 (173-649) 4118 (223-670)NRTI of the CD4 cell count/mm² (IQR)418 (223-670)NRTI s5.5.3 % NRTIsNRTI s7 % PI NRTIsNRTI s7 % NRTIsPits5.6 % NRTIs + NRTIsOther8.7 %GSS Score (%):000.0.511.1.520-0.511.1.522.2.542.2.542.2.55>=312.59%6710711771213141515161718191910101112131415151617171819191910101112131415151617181919191910111213141515161718191919 <t< td=""><td></td><td>Median duration of current INSTI regimen, months (IQR)</td><td></td></t<>		Median duration of current INSTI regimen, months (IQR)	
Median failure plasma HIV-I RNA log <sub>10</sub> copies/mL (IQR)2.9 (2.3.4) 371 (173-649) Median failure CD4 cell count/mm² (IQR)371 (173-649) 4118 (223-670)NRTI of the CD4 cell count/mm² (IQR)418 (223-670)NRTI s5.5.3 % NRTIsNRTI s7 % PI NRTIsNRTI s7 % NRTIsPits5.6 % NRTIs + NRTIsOther8.7 %GSS Score (%):000.0.511.1.520-0.511.1.522.2.542.2.542.2.55>=312.59%6710711771213141515161718191910101112131415151617171819191910101112131415151617181919191910111213141515161718191919 <t< td=""><td></td><td>Madian baseling plasma HIV 1 PNA log _ appias/mL (IOP)</td><td>21(1040)</td></t<>		Madian baseling plasma HIV 1 PNA log _ appias/mL (IOP)	21(1040)
Median baseline CD4 cell count/mm <sup>3</sup> (IQR)       371 (173-649)         Median failure CD4 cell count/mm <sup>3</sup> (IQR)       418 (223-670)         INSTI co-treatment (%):       55.3 %         NRTIs       55.3 %         NRTIs       7%         NRTIs       7%         Pis       5.6 %         NNRTIs       7%         Pis       5.6 %         NNRTIs + Pis       4.9 %         NRTIs + NNRTIs       3.8 %         Other       8.7 %         GSS Score (%):       16.11%         1.1.5       27.22%         2.2.5       44.07%         >=3       12.59%         IQR, interquartile range: NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         IQR, interquartile range: NRTIs, nucleoside reverse transcriptase strand transfer inhibitors, GSS, genotypic sensitivity score.         IQR       9			
Median failure CD4 cell count/mm <sup>3</sup> (IQR)         418 (223-670)           NNT1 co-treatment (%):         55.3 %           NRT1s         13.2 %           NNT1s + Pls         13.2 %           NNRTIs         7 %           Pls         5.6 %           NNRTIs + Pls         4.9 %           NNRTIs + Pls         4.9 %           NNRTIs + NRTIs         3.8 %           Other         8.7 %           GSS Score (%):         0.0.5           0 0.0.5         16.11%           1 -1.5         27.22%           2 -2.5         44.07%           >=3         12.59%           1 IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; Pls, protease inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.           1         2           3         4           5         6           7         8           9         9		Median hasoling CD4 coll count/mm <sup>3</sup> (IOP)	
INSTI co-treatment (%):         55.3 %           NRTIs         FIS           NRTIS         55.3 %           NRTIS         7 %           PIS         7 %           PIS         5.6 %           NNRTIS + PIS         4.9 %           NRTIS + NINTIS         3.8 %           Other         3.8 %           Other         8.7 %           QR         0.0.5         16.11%           1.1.5         27.22%           2.2.5         44.07%           >=3         12.59%           IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.           IQR, interquartile range; NRTIs, nucleoside reverse transcriptase strand transfer inhibitors, GSS, genotypic sensitivity score.			
NRTIs       55.3 %         NRTIs       7%         Pis       5.6 %         NNRTIS       7%         Pis       5.6 %         NRTIS       4.9 %         NRTIS       3.8 %         Other       8.7 %         GSS Score (%):       0         0       0.5         1       1.1.5         2       0.2.5         4       2.2.5         4       2.2.5         4       2.2.5         4       2.2.5         9       10R, interquartile range: NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.         1       10R, interquartile range: NRTIs, nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         1       10R, interquartile range: NRTIs, nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         1       10R         1       10R     <			418 (223-070)
NRTIs + PIs       13.2 %         NRTIs       7 %         PIs       5.6 %         NNRTIs + NNRTIs       4.9 %         NRTIs + NNRTIs       3.8 %         Other       8.7 %         Image: Interquentile content of the state			55 3 %
NNRTIs       7 %         PIs       5.6 %         NNRTIs + PIs       4.9 %         NRTIs + NNRTIs       3.8 %         Other       8.7 %         GSS Score (%):       16.11%         1.1.5       27.22%         2.2.5       44.07%         >=3       12.59%         IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         IQR       interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         IQR       interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.			
Pls       5.6 %         NNRTIs + PIs       4.9 %         NRTIs + NNRTIS       3.8 %         Other       8.7 %         GSS Score (%):       16.11%         1.1.5       27.22%         2.2.5       44.07%         >=3       12.59%         IVRR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; SS, genotypic sensitivity score.         IVR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; SS, genotypic sensitivity score.         IVR         IVR     <			
NNRTIs + PIs       4.9 %         NNRTIs + NNRTIS       3.8 %         Other       8.7 %         GSS Score (%):			
NRTIs + NNRTIs       3.8 % Other         0       0.0.5         1       0.0.5         1.1.5       27.22%         2.2.5       44.07%         5       >=3         10R, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         10R, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         11         12         13         14         15         16         17         10R, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.         11         12         13         14         15         16         17         18         19         19         10         10         11         12         13         14         15         16         17         18         19         19         10         10         10 </td <td></td> <td></td> <td></td>			
Other         8.7 %           GSS Score (%):         1           0.0.5         16.11%           3         1-1.5         27.22%           4         2-2.5         44.07%           5         >=3         12.59%           6         1         1QR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; OSS, genotypic sensitivity score.           1         1           2         3           4         5           6         7           8         9			
2       0-0.5       16.11%         3       1-1.5       27.22%         4       2-2.5       44.07%         5       >=3       12.59%         6       7       1000000000000000000000000000000000000		Other	
3       1-1.5       27.22%         4       2-2.5       44.07%         5       >=3       12.59%         6       7       10, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.         1       2         3       4         5       6         6       7         8       9	31	GSS Score (%):	
4 2-2.5 44.07% >=3 12.59% QR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; PIs, protease inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.	32	0-0.5	16.11%
5 >=3 12.5%          IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; GSS, genotypic sensitivity score.         IQR         IQR <td>33</td> <td>1-1.5</td> <td>27.22%</td>	33	1-1.5	27.22%
6         7         1QR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors, GSS, genotypic sensitivity score.         1         2         3         4         5         6         7         8         9	34	2-2.5	44.07%
<ul> <li>IQR, interquartile range; NRTIs, nucleoside reverse transcriptase inhibitors; NNRTIs, non-nucleoside reverse transcriptase inhibitors; PIs, protease inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.</li> <li>Interquartile range; NRTIs, protease inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.</li> <li>Interquartile range; NRTIs, protease inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.</li> <li>Integrase strand transfer inhibitors; INSTI, integrase strand transfer inhibitors, GSS, genotypic sensitivity score.</li> </ul>	35	>=3	12.59%
2 3 4 5 6 7 8 9	40	Sensitivity score.	
3 4 5 6 7 8 9	41		
4 5 6 7 8 9	42		
5 6 7 8 9	43		
6 7 8 9	14		
7 8 9	15		
8 9	16		
9	17		
	18		
0	19		
	50		
1	51		

#### Table 2. Factors associated with the occurrence of INSTIs resistance associated

#### mutations

		Univariate Analysis		Multivariate Analysis		
		OR	95% IC	P-value	OR 95% IC	P-value
Age (per 10 years increase)		1.115	0.977-1.273	0.1065		
CD4 baseline (per 100 cells/mm3 increase)		1.007	0.960-1.056	0.7764		
CD4 Failure (per 100 cells/mn	CD4 Failure (per 100 cells/mm3 increase)		0.941-1.038	0.6387		
Nadir CD4 (per 100 cells/mm3 increase)		0.99	0.902-1.087	0.8338		
Duration of Infection (per yea	rs increase)	1.018	1.001-1.035	0.0393		
Duration of INSTI treatment (	per years increase)	1.052	0.982-1.126	0.1519		
LOG HIV RNA baseline (per 1 l	og10 copies/ml increase)	0.956	0.850-1.074	0.4478		
LOG HIV RNA Failure (per 1 log10 copies/ml increase)		1.345	1.165-1.553	<0.0001	1.223 1.027-1.456	0.0242
Vinal automotion a	CFR02 VS B	0.869	0.572-1.319	0.5425		
Viral subtype	NON B VS B	0.971	0.677-1.394	0.8239		
	1 or 1.5 VS 0 or 0.5	0.29	0.156-0.540	0.0715	0.293 0.156-0.551	0.1326
GSS	2 or 2.5 VS 0 or 0.5	0.101	0.056-0.184	<0.0001	0.116 0.063-0.213	<0.0001
	>=3 VS 0 or 0.5	0.075	0.035-0.162	<0.0001	0.079 0.036-0.174	<0.0001
Dual Therapy VS Triple Therapy		0.545	0.361-0.822	0.2545		
Dual Therapy VS Four and more Therapy		0.437	0.253-0.754	0.0235		
DTG VS RAL		0.406	0.270-0.610	<0.0001	0.567 0.345-0.931	0.0251
DTG VS EVG		0.362	0.226-0.581	<0.0001	0.448 0.254-0.789	0.0055

INSTI, integrase strand transfer inhibitors; OR, odds ratio; GSS, genotypic sensitivity score; DTG, dolutegravir; RAL, raltegravir; EVG, elvitegravir

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461	Figure 1. Genotypic interpretation of resistance to different integrase strand transfer
462	inhibitors (INSTIs) among the 674 patients failing an INSTI-containing regimen.
463	Predicted resistance to raltegravir (RAL), elvitegravir (EVG) and dolutegravir (DTG) once
464	per day (OD) or twice daily (BID) according to the ANRS algorithm.
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- 479 Figure 2. Association between level of HIV viral load at failure and the selection of
- 480 integrase strand transfer inhibitors (INSTIs) resistance associated mutations (RAMs).