

Pharmacological resistance profile and the most frequent mutations in patients of the Instituto Guatemalteco de Seguridad Social



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We studied 286 patients with virological failure to the first line of antiretroviral treatment (ART) admitted to the Infectology Service of the Hospital General de Enfermedades del Instituto Guatemalteco de Seguridad Social (IGSS) from 2015 to 2017. We included all the patients with virological failure to the first line of treatment and in which poor adherence was ruled out.

OBJECTIVE:

To determine the pharmacological resistance profile and the most frequent mutations for HIV-1 in patients admitted for virologic failure.

METHODOLOGY:

This was an observational, retrospective and transversal study. Mutations are reported in frequencies and percentages, the platform hivdb.stanford.edu/hivdb/by-mutations/ was used for the interpretation of mutations and they were reported in frequencies and percentages.

RESULTS:

Combined resistance for non-nucleotide reverse transcriptase inhibitors (NNRTIs) and nucleoside reverse transcriptase inhibitors (NRTIs) accounted for 25% of cases, followed by NNRTIs with 10%, the combination of NNRTIs and NRTIs and protease inhibitors (PIs) 9.1%, NRTIs 6% and finally for the IP 5%. The most frequent mutations for NNRTIs were K103N, L100I, V108I, G190A and E138G that confers high level of resistance to efavirenz (EFV) nevirapine (NVP), and intermediate resistance to Etravirine (ETR). The most frequent mutations for NRTIs were M184V/I, T215Y, Y115F and K65R conferring high level of resistance to lamivudine (3TC), emtricitabine (FTC), abacavir (ABC) and tenofovir (TDF) and for PIs The V11I, I54V, L76V and M46I mutation that confers high level of resistance to Atazanavir/ritonavir (ATV/r), Lopinavir/ritonavir (LPV/r) and darunavir/ritonavir (DRV/r).

CONCLUSIONS:

To our knowledge this is the largest report of mutations performed in Guatemala which provides valuable information on the behavior of HIV-1 in our population. The combined mutation to NNRTIs and NRTIs was the most common, which occurred in 1 in 4 patients. Mutations to NNRTIs and NRTIs together with PIs were the third most frequent.

Fig. 1. Resistance-conferring mutations for the Nucleoside Reverse Transcriptase Inhibitors

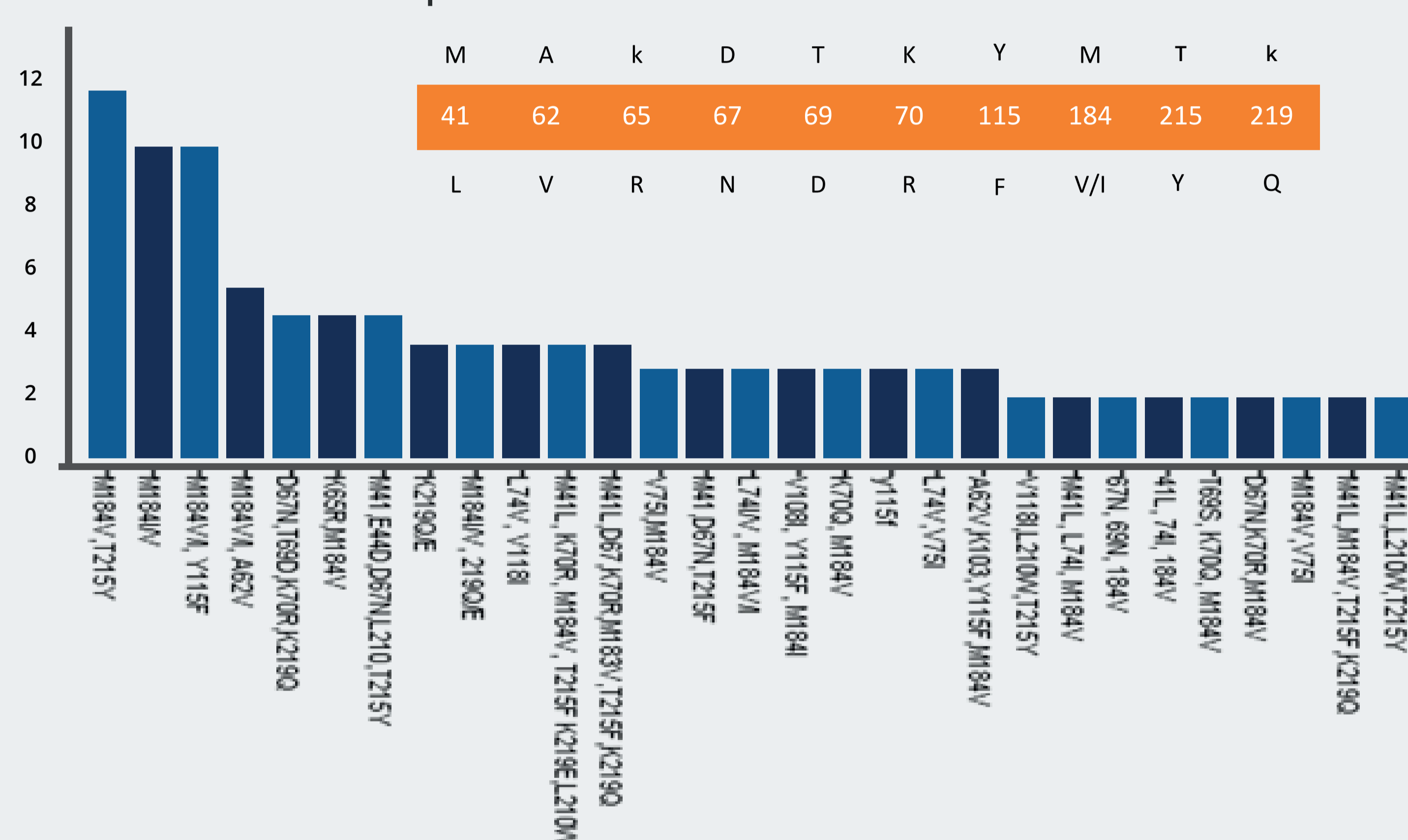


Fig. 2. Resistance-conferring mutations for the Non-Nucleoside Reverse Transcriptase Inhibitors

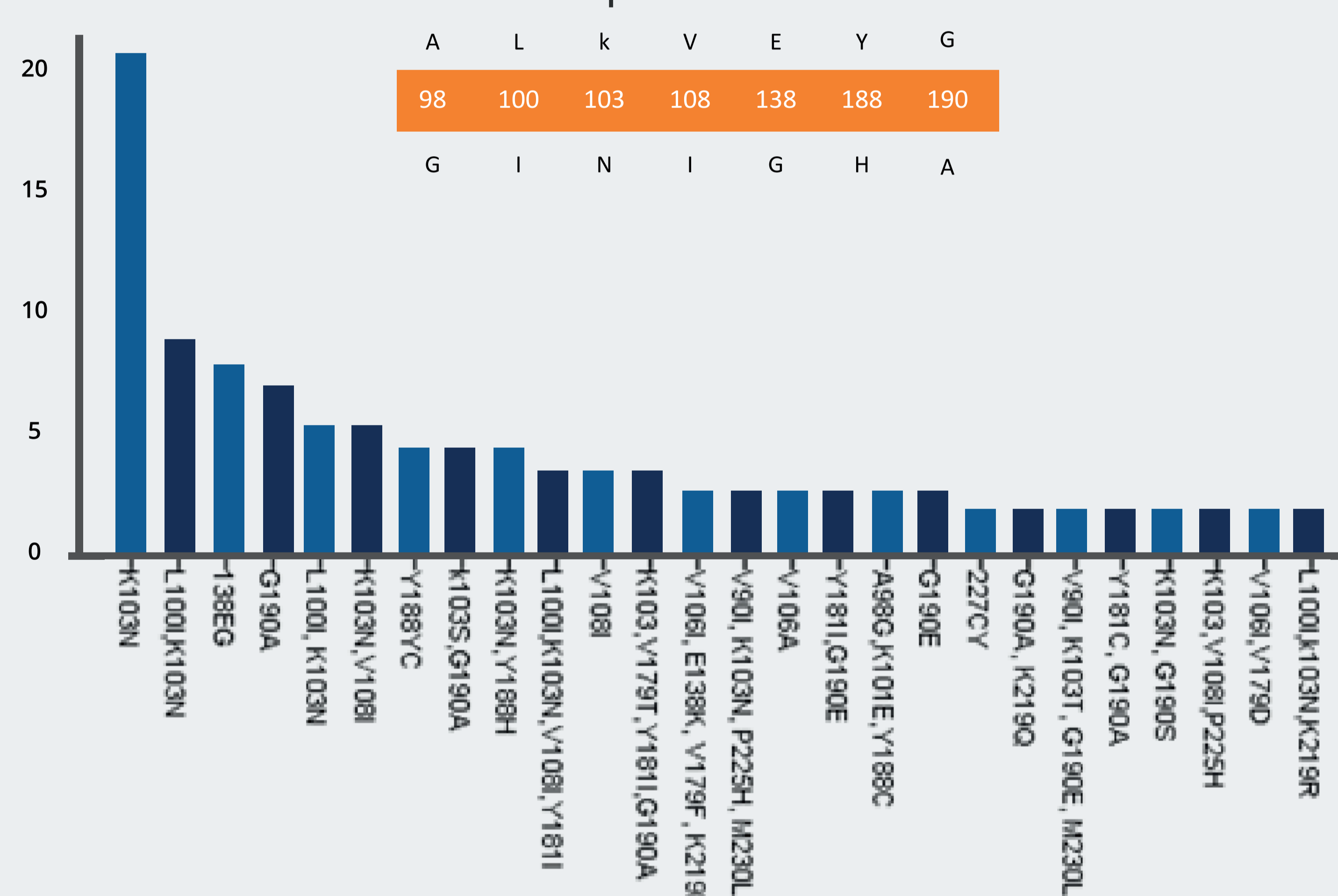


Fig. 3. Resistance-conferring mutations for the Protease Inhibitors

