

Use of DeepChek® v1.1 and VisibleChek® for the analysis and integration of 454 GS Junior data from the RT and Protease of HIV-1

N. Chueca¹, R. Camacho-Luque¹, M. Alvarez¹, J Lopez-Bueno¹, M.D. Merida¹, C Pérez-Pinar¹, R. Boulme², D. Gonzalez³, F. Garcia¹.
¹Hospital Universitario San Cecilio, Microbiology, Granada, Spain. ²Advanced Biological Laboratories SA, RDI, Luxembourg, Luxembourg.
³Advanced Biological Laboratories SA, RDI, Barcelona, Spain.



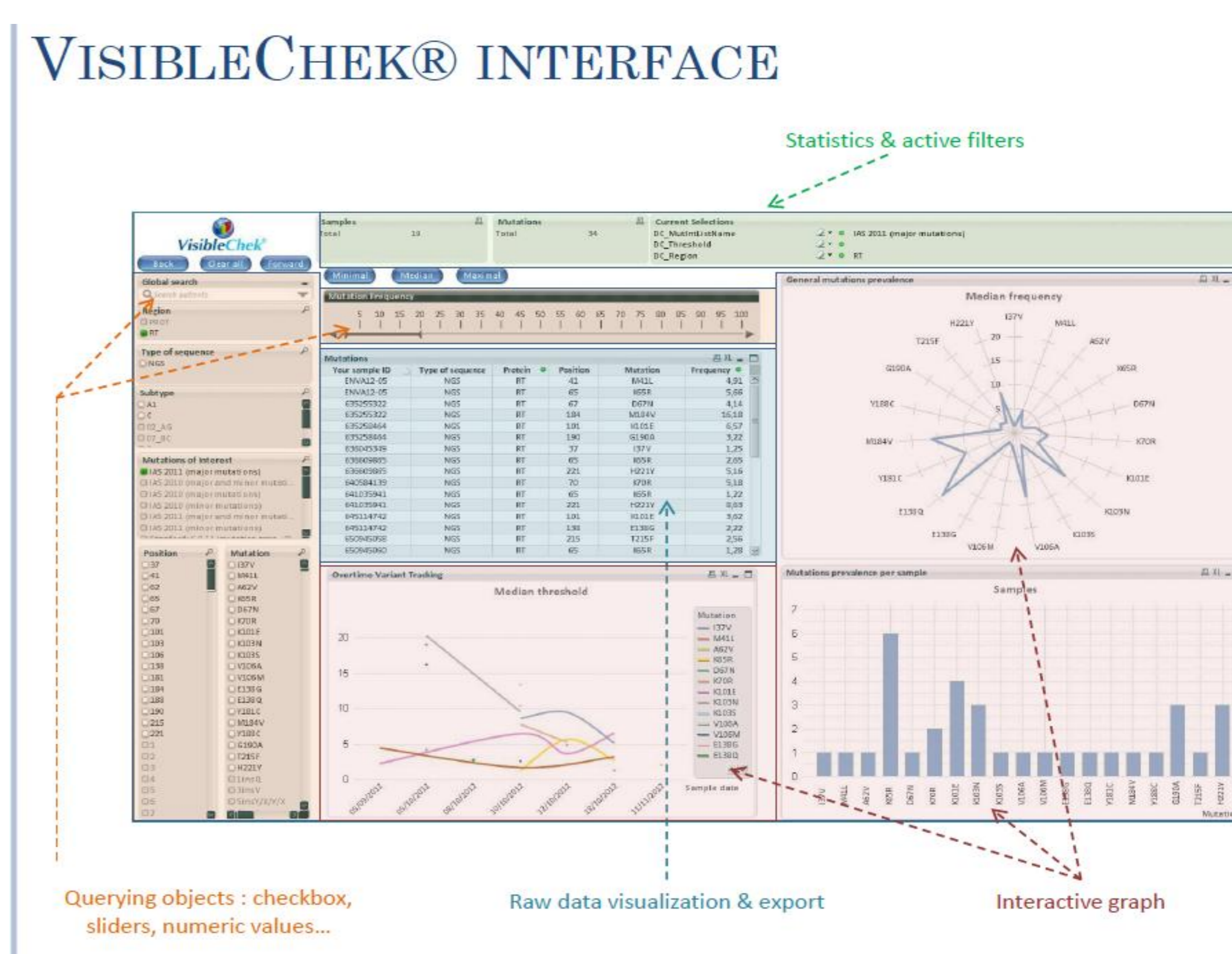
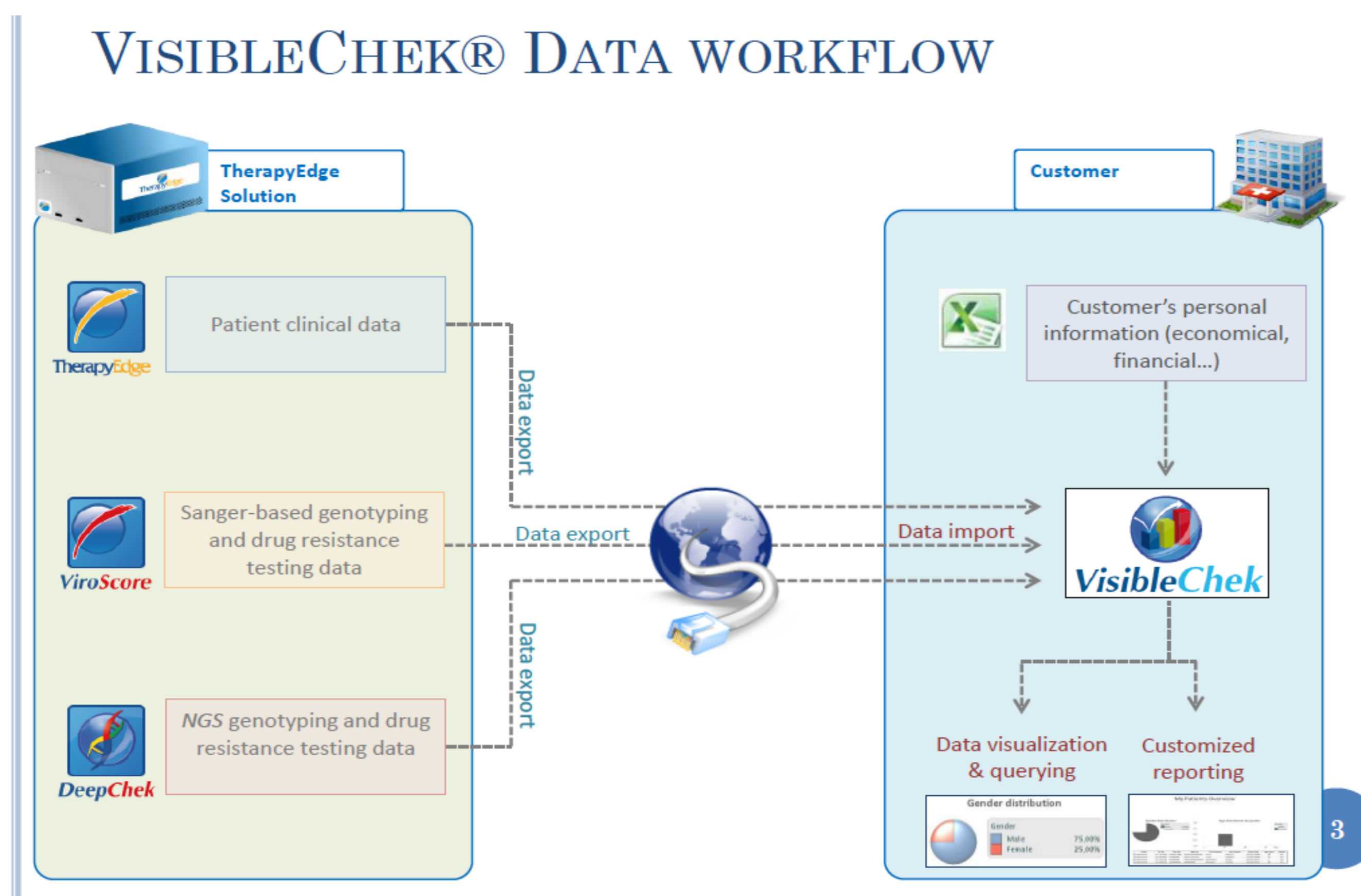
Background and Aim

Analysis of 454 derived sequences from the RT and the PRO of HIV-1 has traditionally required a profound bioinformatic analysis. Here we present the use of DeepChek® v1.1 for RT & PRO sequence analysis, and VisibleChek® for their integration with virological and clinical data.

Patients and Methods

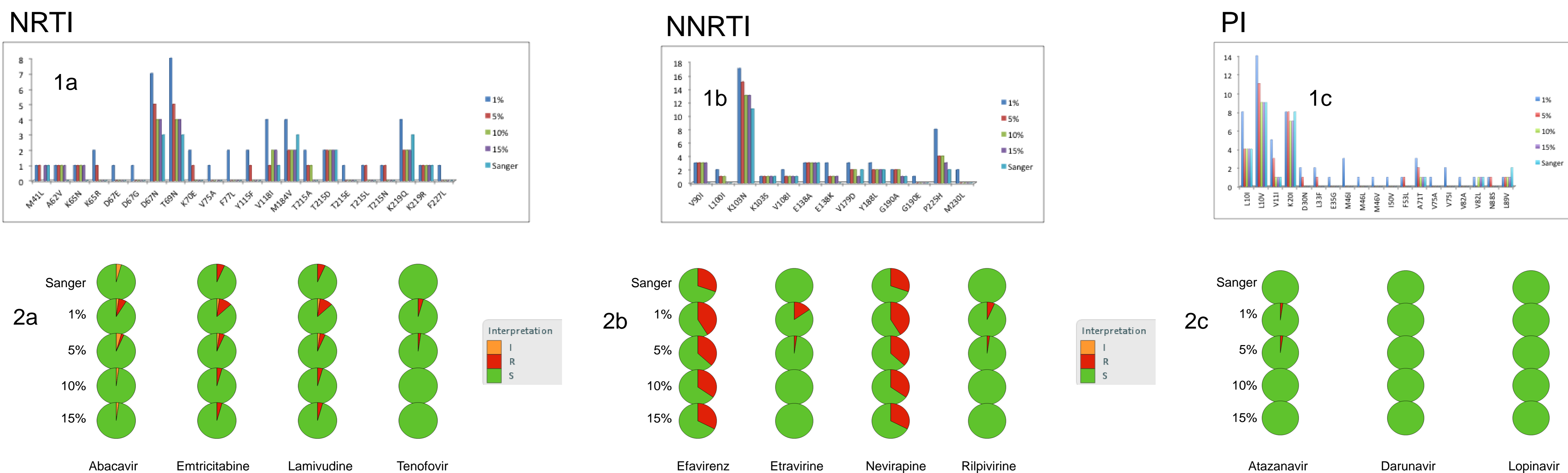
- ❖ 46 HIV-1 infected patients.
- ❖ UDS generated sequences were preprocessed in the GS Junior system;
- ❖ Aligned fasta UDS sequences were uploaded into the DeepChek® v1.1 module (Therapy Edge, ABL SA).
- ❖ Sanger sequences, obtained through Trugene HIV-1 genotypic kit, were uploaded in parallel.
- ❖ Stanford 6.2.0 version mutations scored as ≥ 5 were considered for analysis.
- ❖ Spanish HIV Research Network (RIS) algorithm
- ❖ Sanger and UDS data with different mutations thresholds (1%, 5%, 10% and 15%) were evaluated
- ❖ VisibleChek® was used for the integration of Clinical, Virological, Sanger and 454 molecular data in one single database

n=46	
median age (IQR)	36, 5 (32,75-44,25)
median CD4 (IQR)	551 (211,75-777,50)
Naïve	95%
Experienced	5%
Males	93%



Results

- ❖ Any mutation using Sanger sequencing in 29/46 patients, with a total number of 79 Stanford ≥ 5 mutation
- ❖ Any mutation using UDS 1% cutoff in 40/46 patients had at least one mutation, with a total number of 140 Stanford ≥ 5 mutation.
- ❖ The number of patients with NRTI, NNRTI and PI mutations is shown in Figures 1a, 1b & 1c
- ❖ Sanger Resistance data, 3/46 (6.5%) patients showed any resistance to NRTIs, 14/46 (30%) to NNRTIs; no resistance to PIs.
- ❖ UDS NRTI resistance data: 4/46 (8.6%) using 15% and 10% as thresholds, 5/46 (10.8%) using 5% as threshold, and 10/46 (21.7%) using 1% as threshold.
- ❖ UDS NNRTI resistance data: 15/46 (8.6%) using 15%, 16/46 (8.6%) using 10% as threshold, 17/46 (10.8%) using 5% as threshold, and 19/46 (21.7%) using 1%.
- ❖ UDS PI resistance data: 1/46 (2,1%) using 5% & 1% threshold.
- ❖ The number of patients with resistance to NRTI, NNRTI and PIs is shown in Figures 2a, 2b & 2c



Conclusions

- ❖ DeepChek® and VisibleChek® allow for an easy, reliable and rapid analysis of UDS data from HIV-1 reverse transcriptase and protease, and also integrase and envelope.
- ❖ Compared to Sanger data, UDS resulted in an increase of the number of resistance mutations, and the number of patients with any degree of resistance to NRTI and NNRTIs.
- ❖ No increase in resistance to Protease Inhibitors was observed.