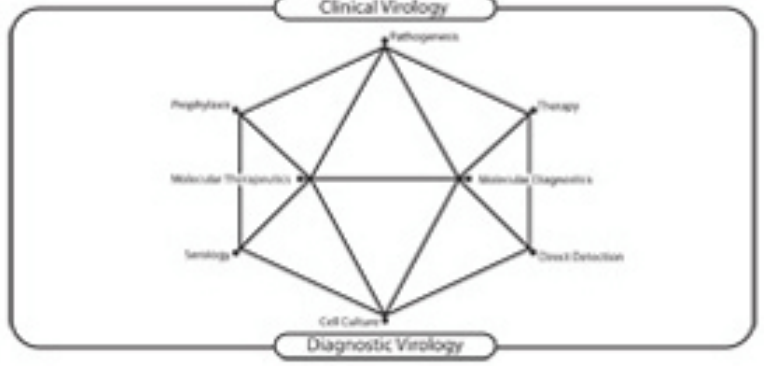# Use of Innovative Information Systems Combining HIV-1 Genotypic and Phenotypic Drug Resistance Interpretations For Routine and Research Applications

30th Annual Clinical Virology Symposium
April 27 – 30, 2014 | Daytona Beach, Florida

Isabelle Hardy[1], Daniela Moisi[2], Hugues Charest[3], Régis Cantin[3], Michel Roger[1], Mark A. Wainberg[2], Cécile Tremblay[1,3], Matthieu Barralon[4], Ronan Boulmé[4], Chalom Sayada[4], Dimitri Gonzalez[5], Bluma Brenner[2]

[1]Centre Hospitalier de l'Université de Montréal, Montreal, Quebec
[2]Jewish General Hospital, Montreal, Quebec
[3]Laboratoire de santé publique du Québec/INSPQ, Montreal, Quebec
[4]ABL SA, Luxembourg, Luxembourg
[5]ABL TherapyEdge Spain SL, Barcelona, Spain

Background

- Long-term management of HIV-1 infection requires individualized strategies tailored to each patient profile.

- The selection of antiretroviral (ARV) regimens needs to take into account the drug resistance patterns harbored by the individual.

- We have evaluated the ViroScore-HIV drug resistance algorithmic platform for routine clinical and research activities.

- This platform integrates genotypic analysis with multiple interpretative genotypic and phenotypic algorithms (*Fig. 1A*) to effectively track emergent resistance profiles that confer resistance to the 6 possible drug classes (*Fig. 1B*).

Fig. 1: Genotypic and phenotypic drug resistance algorithms (A), drug-classes and type of analyses (B) part of ViroScore-HIV.
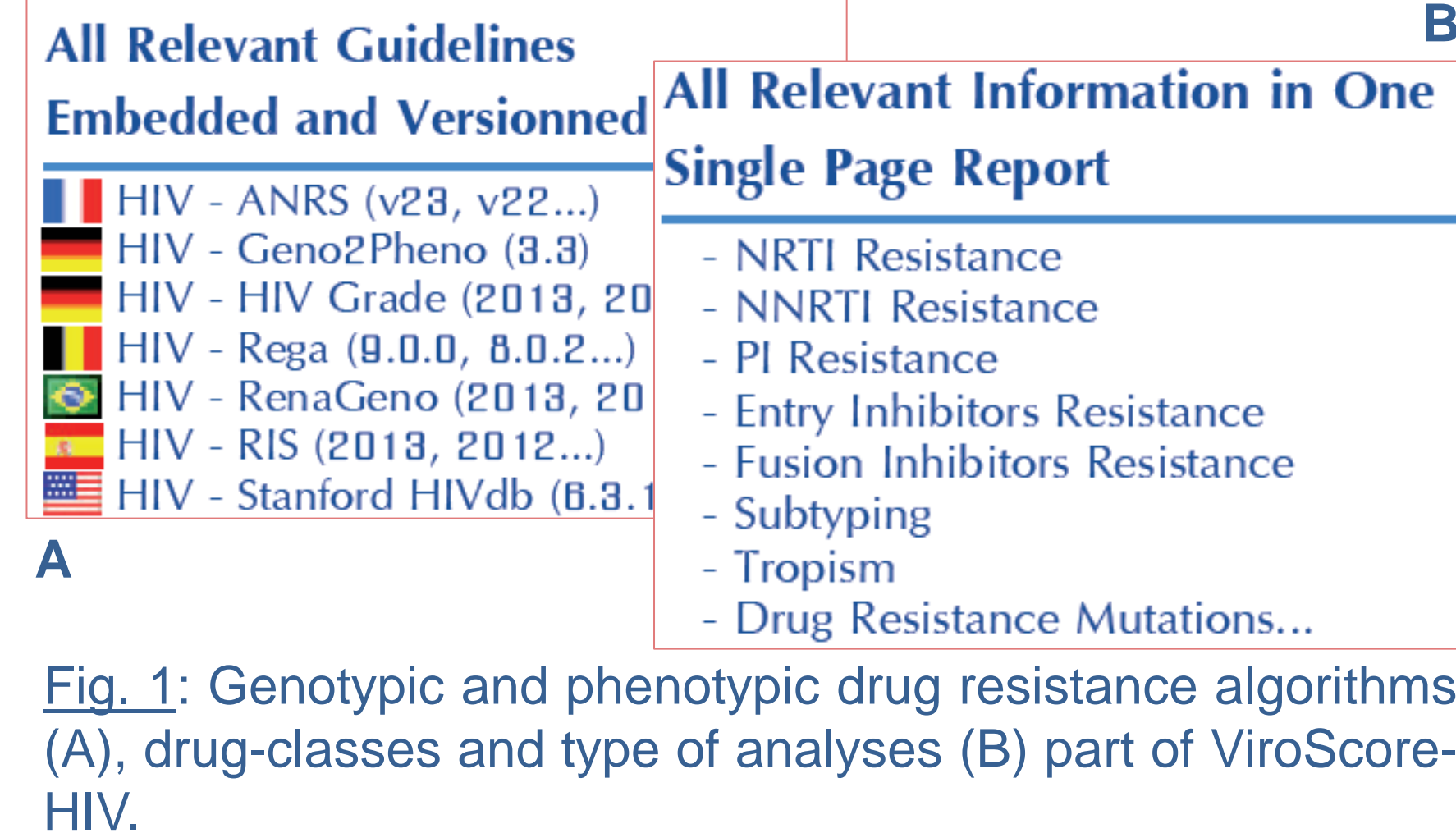
Methods

- ViroScore-HIV is a standardized and secured web solution, certified for In-Vitro Diagnostics (IVD) use which was installed and evaluated for the management of the routine clinical and research activities of 3 genotyping laboratories in Quebec, Canada (*Fig. 2*).

- Preliminary analyses on 50 sequences from our clinical database evaluated ViroScore-HIV on samples previously tested by the discontinued VircoType platform.

- The ViroScore-HIV platform was very flexible, providing algorithms for up to 8 different drug resistance guidelines spanning every protein of interest (protease, reverse transcriptase, integrase, GP41 and GP120 including tropism determination).

- Results (subtyping, variants calling and drug resistance) were compared to VircoType to assess the reliability and the user-friendliness of the application for diagnostics use.

- In addition, software was combined with VisibleChek, a data mining application tailored for the management of Sanger and Next Generation Sequencing (NGS) data, to assess usability for future research and clinical applications (*Fig. 4*).
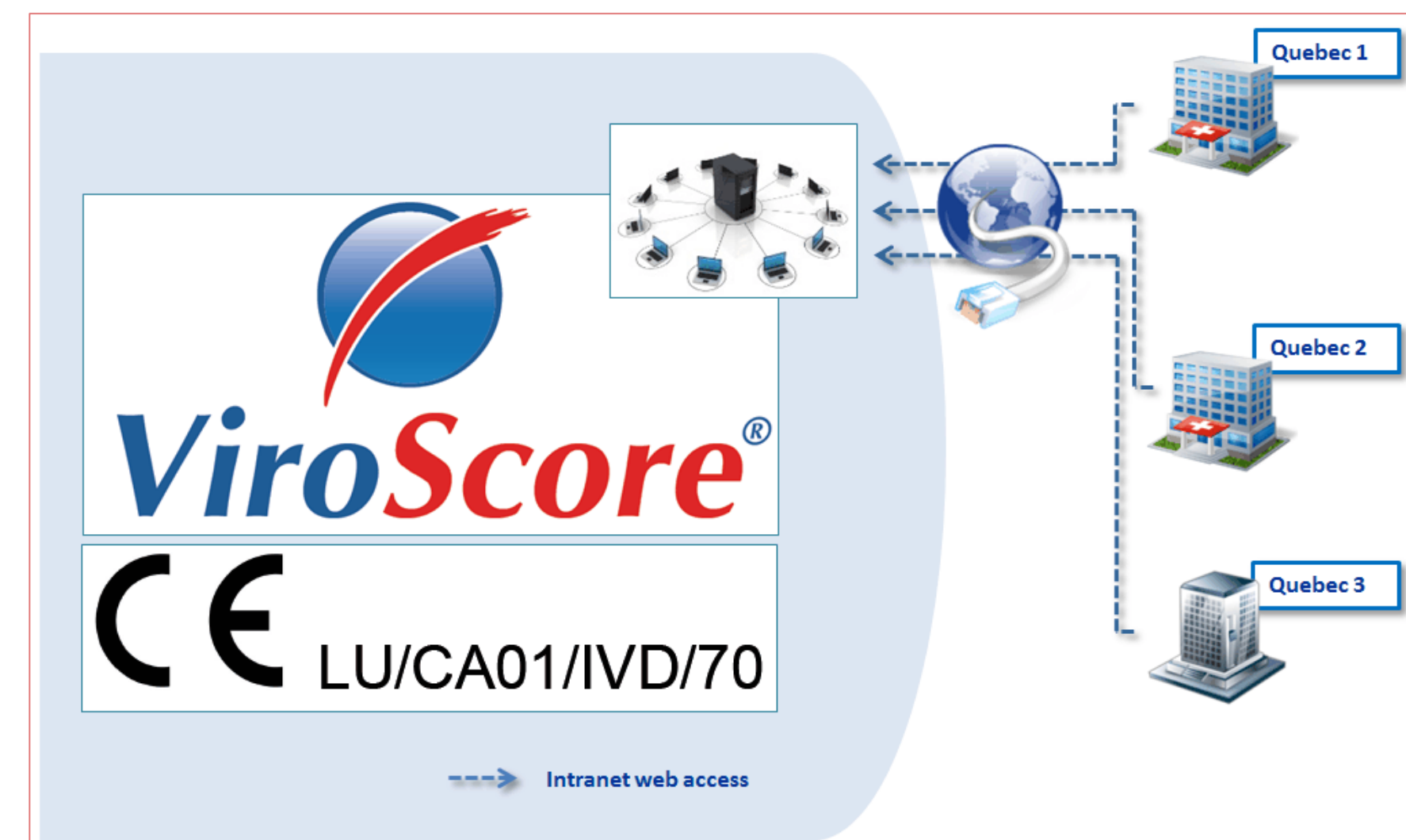
Fig. 2: Overview of the ViroScore installation and IT infrastructure.

Results

- ViroScore-HIV was installed on a central server and configured according to the needs of each site to optimize data workflows and improve timing constraints.

- During November 2013, 50 samples coming from our reference laboratories were first analyzed.

- In most cases, Virtual-phenotyping interpretations from the latest version of the geno2pheno algorithm recently integrated in ViroScore gave results comparable to the VircoType interpretations.

- The provincial ViroScore-HIV genotyping reports provides a virtual-phenotyping algorithm (geno2pheno[resistance] v3.3) with mutational interpretations from the Stanford HIVdb v6.3.1 algorithm.

- The ViroScore-HIV subtyping tool has been updated to include a recently developed High Performance Subtyping tool.

- As the intent is to use ViroScore-HIV for daily diagnostic use, reports (*Fig. 3*) were exchanged with clinicians who confirmed their usefulness.

- Since January 2014, ViroScore-HIV has been used in routine by our laboratories to generate 115 reports.
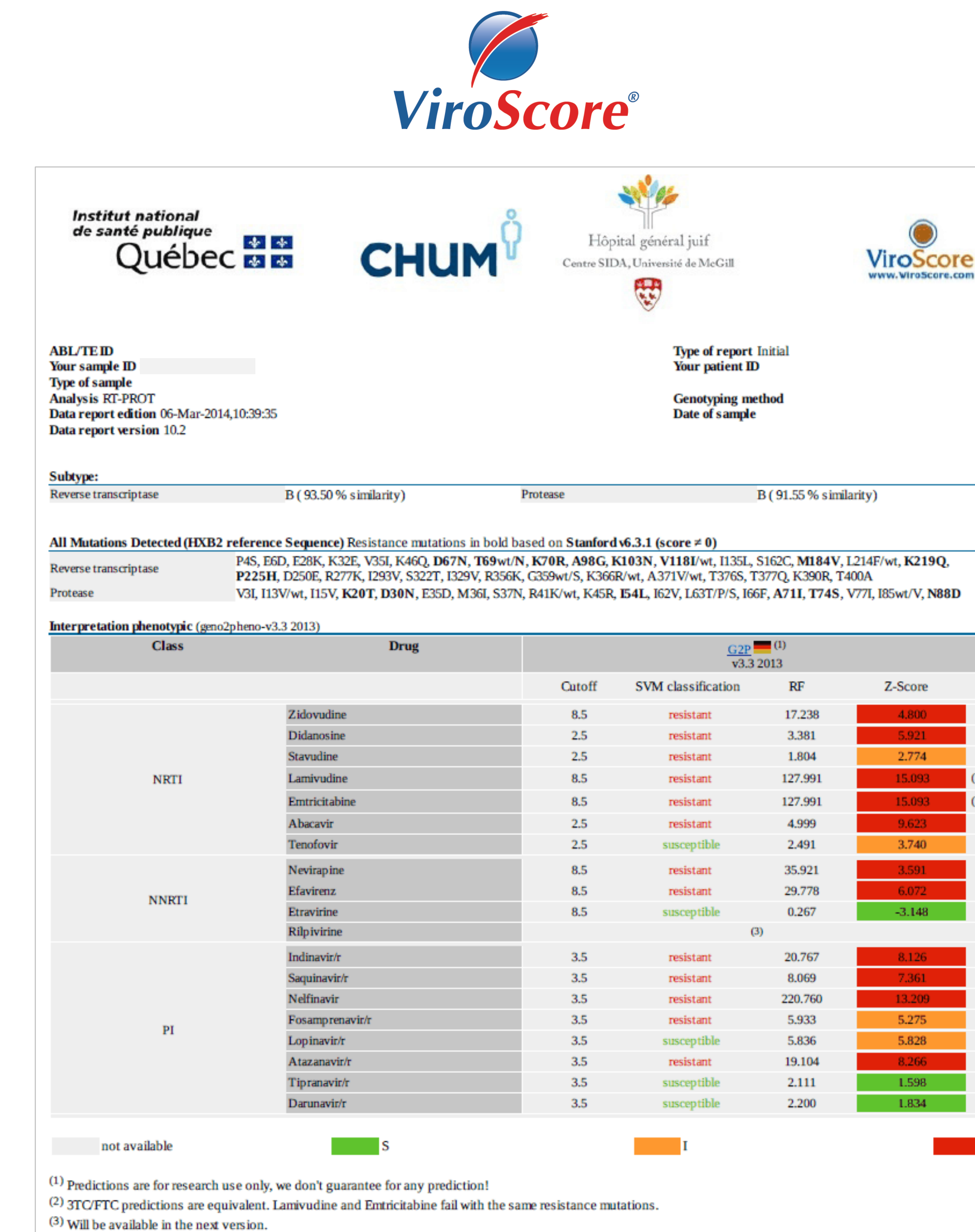
Fig. 3: Diagnostic use configuration of the ViroScore-HIV report.

Fig. 4: Data mining through VisibleChek for research and clinical studies applications.

Conclusions

- Using the advanced ViroScore-HIV information systems, combining genotypic and phenotypic algorithms for drug resistance determinations helped in routine diagnostics and facilitated the daily management of HIV infection.

- In addition, analysis of the results within VisibleChek, may assist in defining emergent resistance patterns for newer second and third generation antiretroviral drugs.

- Furthermore, the technology also enables research activities via the use of easy-to-use interfaces and data workflows tailored to the specificity of a network of hospitals.