DeepChek®–HIV

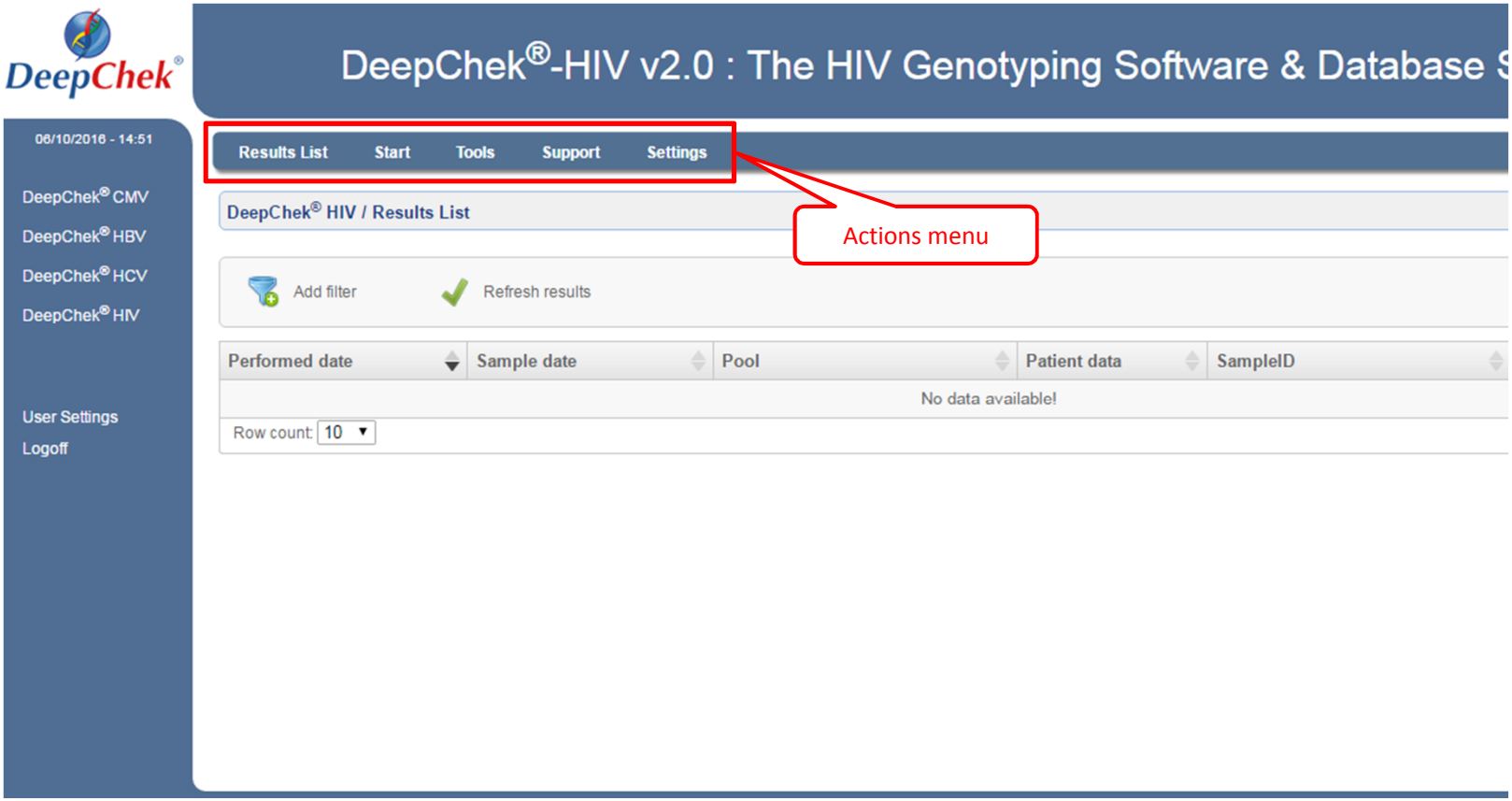
Quick Start Guide

October 2016

DeepChek HIV - Log in screen

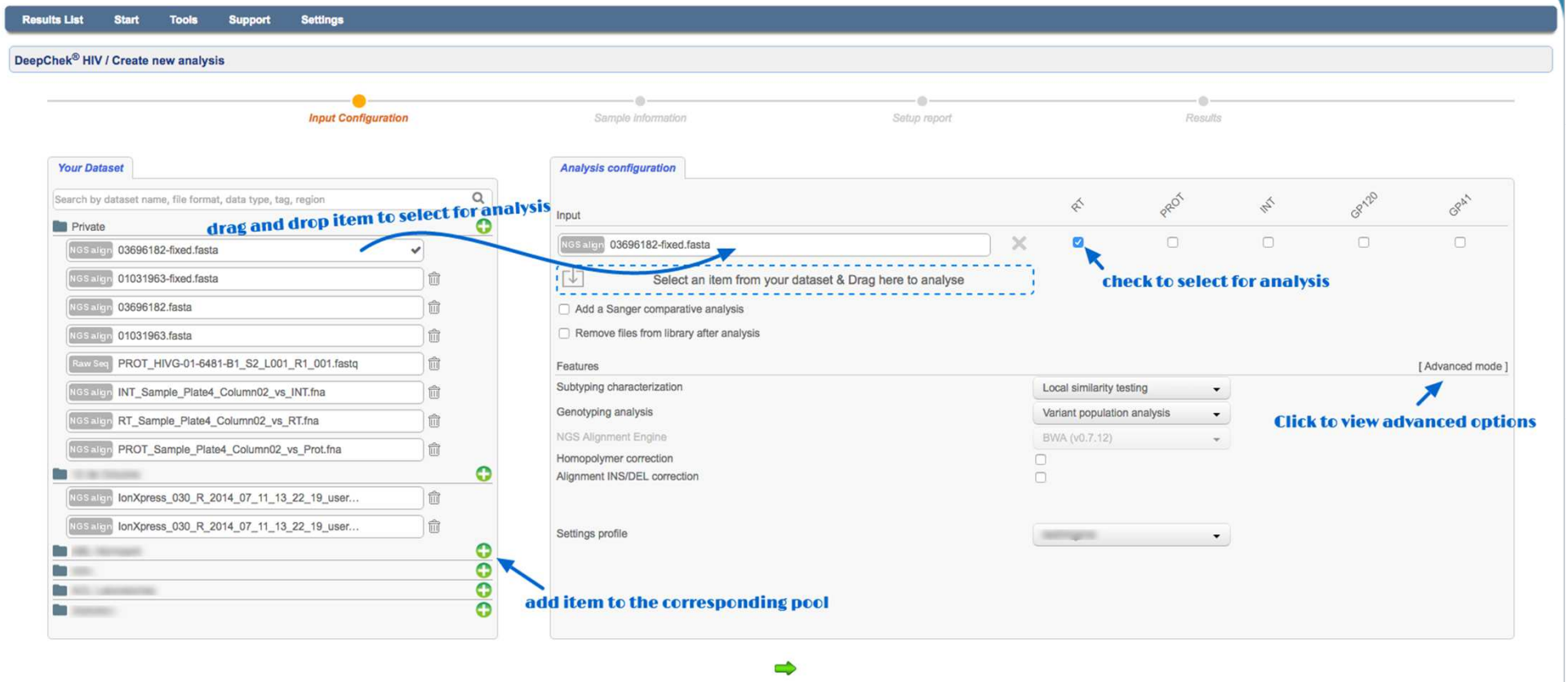
- After typing the URL in the address bar, the system will display the login screen.
- Type your username and password, select “User login” and click on “Sign-in”.
- The system will redirect you to the main DC screen.

DeepChek HIV – Main screen



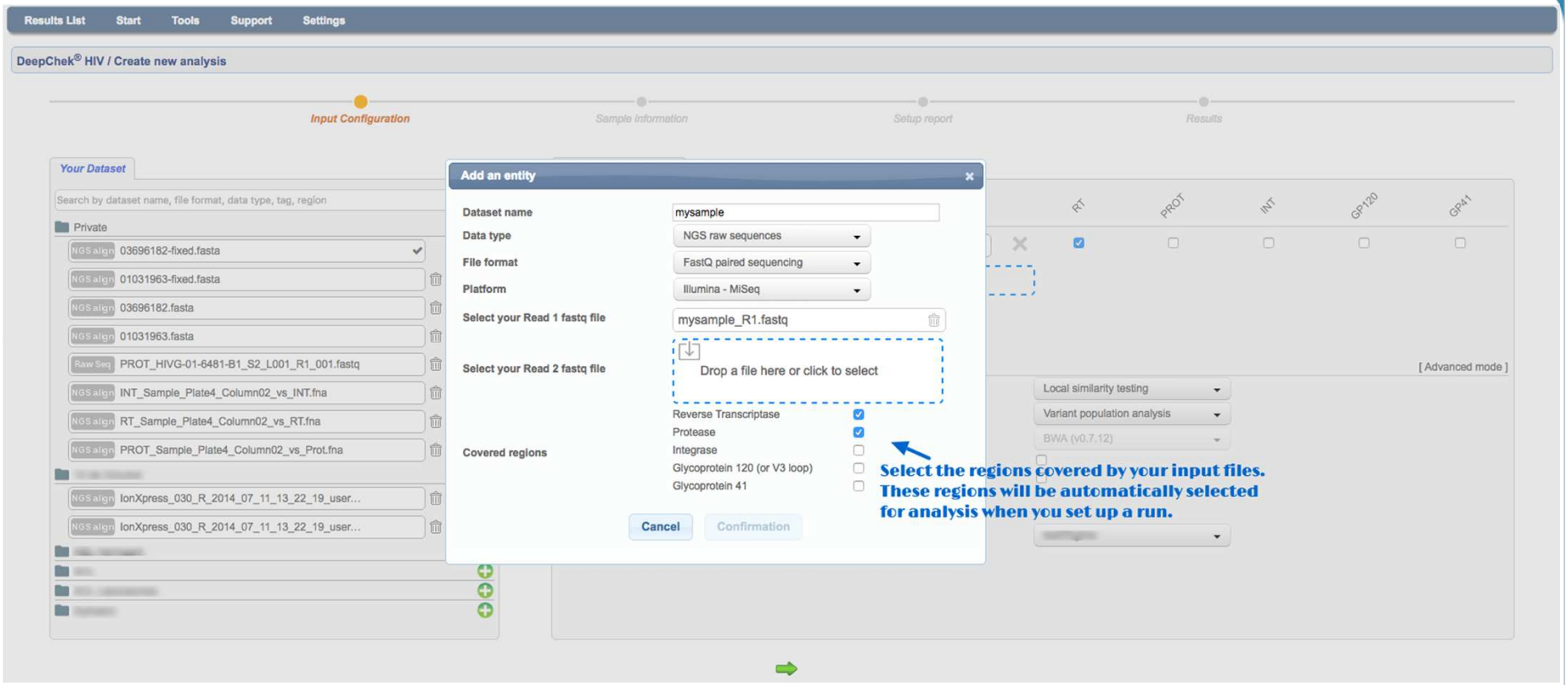
- Once you are logged in to the software, you will see the DeepChek (DC) HIV main screen.
- On the top blue bar, you will find all the actions you can perform with DC HIV.
- By clicking on “Start” > “Start new analysis”, you will be able to start the process of generating a new report.

DeepChek HIV – New analysis (1)



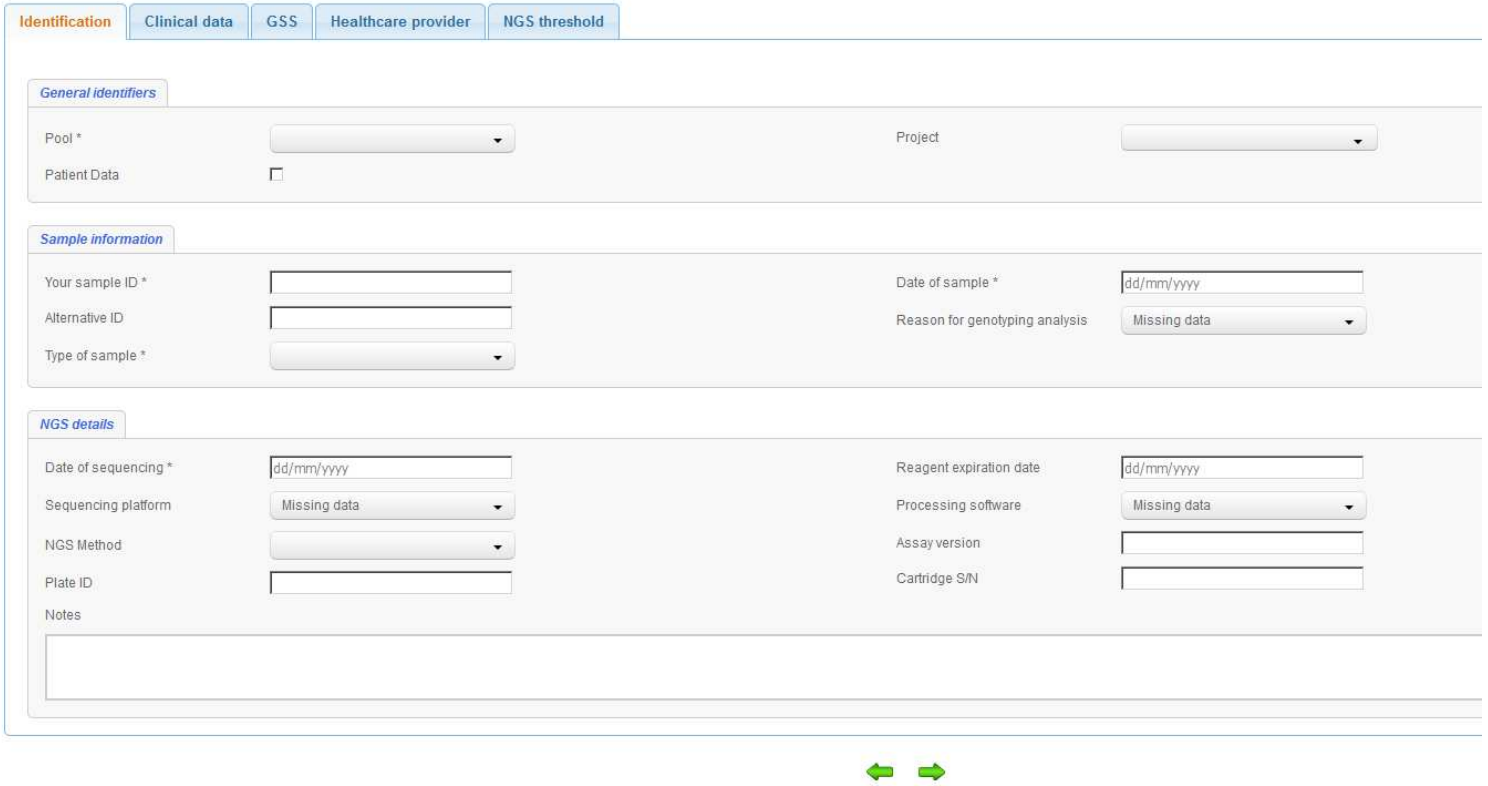
- On this first page you select the dataset on which you want to do the analysis.
- You can also add a new dataset to an existing pool by clicking on the corresponding green button with the white plus sign (detailed in the next page).
- You will go to the second page by clicking on the green arrow pointing to the right.

DeepChek HIV – New analysis (1.1)



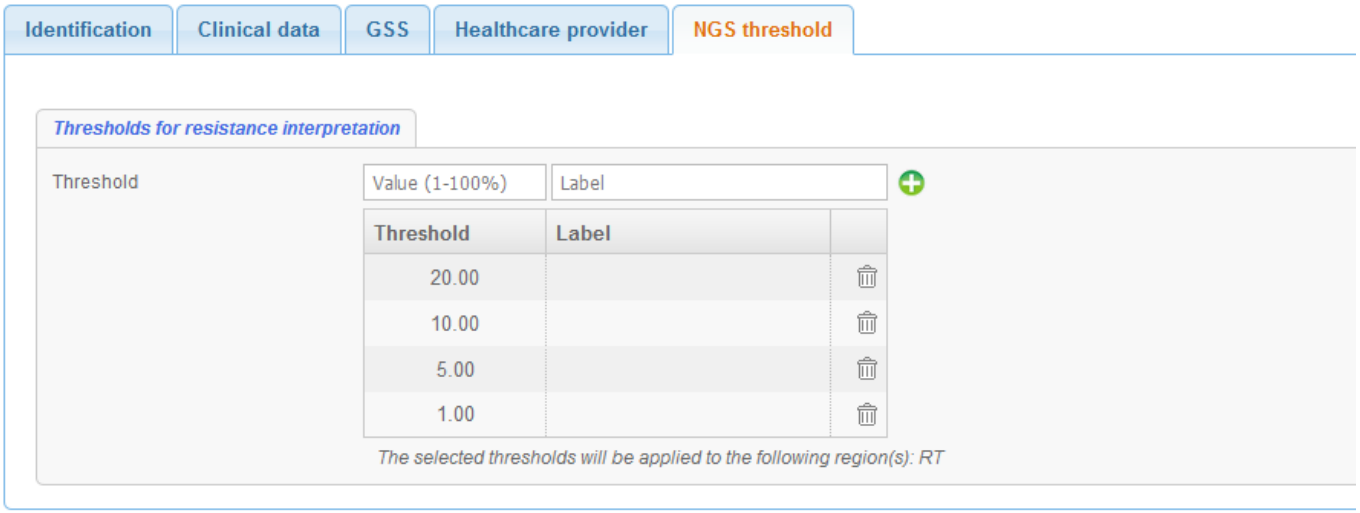
- On the popup window to add a new dataset you will need to:
  - ✓ *Choose the appropriate options from the dropdown menus.*
  - ✓ *Upload the input file by clicking inside the blue dashed rectangle to select the file or directly dragging the file from your local folder and dropping it inside the rectangle.*
  - ✓ *Select the regions covered by the reads in your input file.*

DeepChek HIV – New analysis (2)



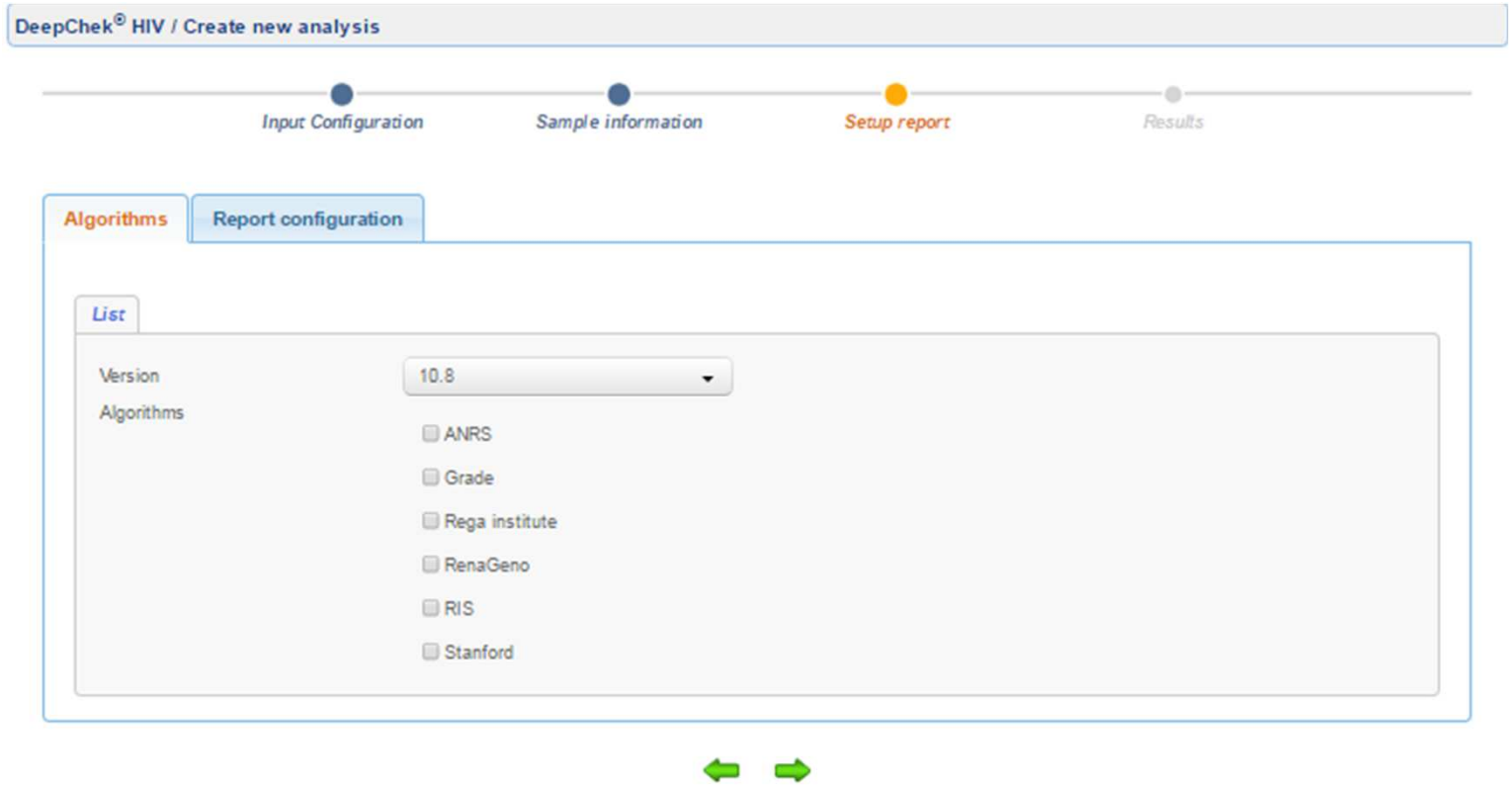
- On this second page you will have to type all the information regarding the files you have just introduced in the previous page.
- Please note that mandatory fields are marked with an asterisk.
- All the information you type here will appear in the generated report.
- Navigate through the tabs at the top to add as much information you want/have.

DeepChek HIV – New analysis (3)



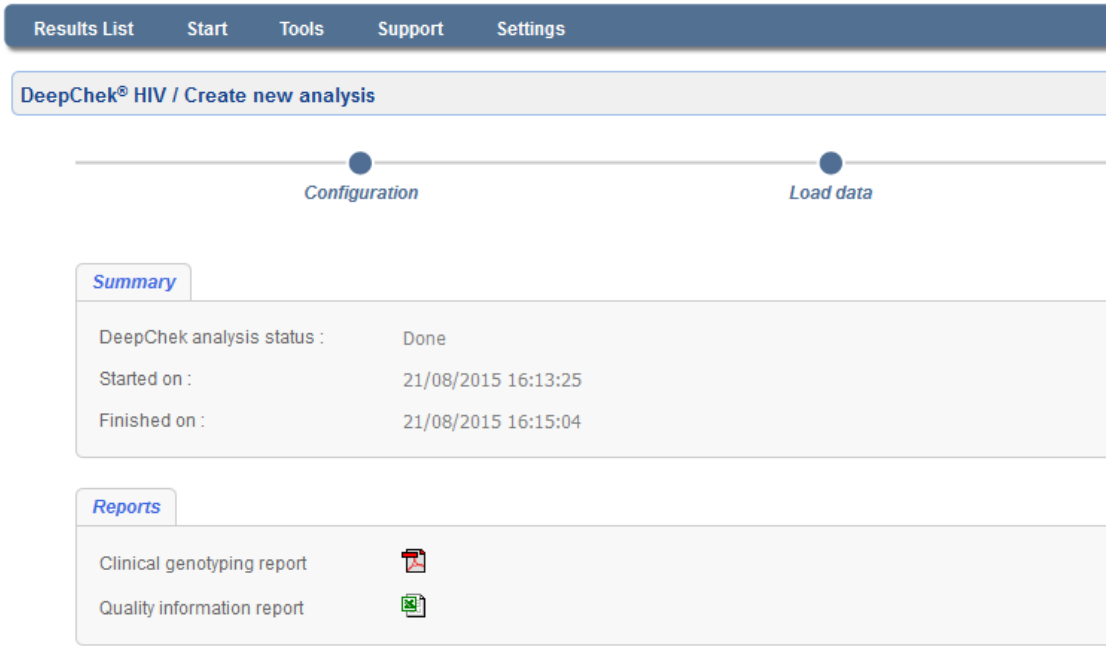
- Under the fifth tab, you will find the "NGS thresholds" you should add in order for the system to analyse your input files. The cut-offs will be used to group the mutations and provide the corresponding drug resistance interpretations.
  For example, if you select two thresholds 1% and 20%, the systems will build a first list containing all the mutations with a frequency superior to 1% and another for the ones superior to 20%. Based on those 2 lists, it will determine 2 different sets of interpretations.
  - ✓ *Note that the 20% is more or less equivalent to the Sanger method.*
- When you have finished adding all the information on the five tabs, just click on the green arrow pointing to the right and the system will proceed to the next page.

DeepChek HIV – New analysis (4)



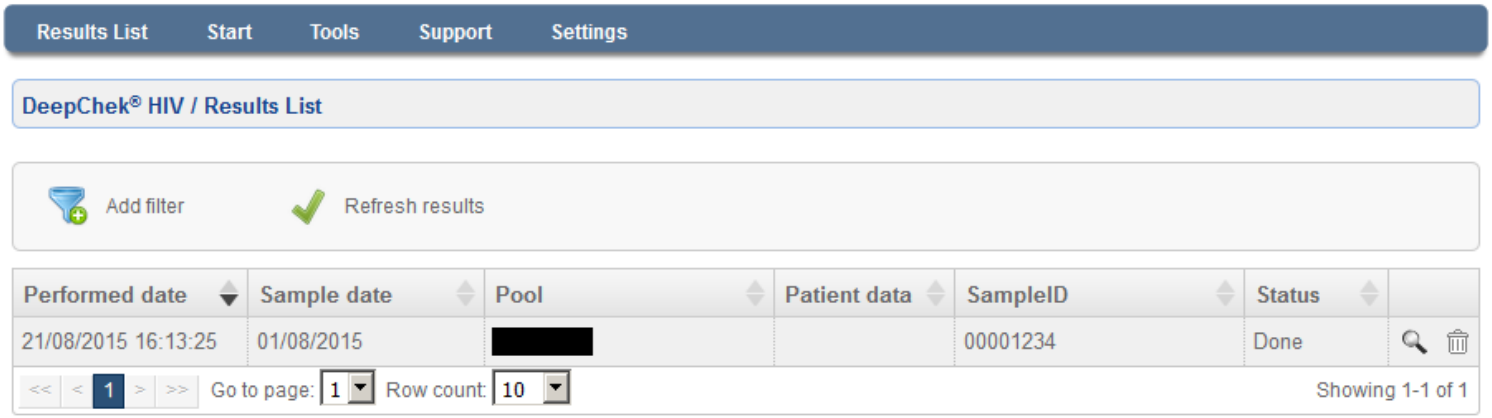
- On the third page you will be able to add as many algorithms as you want into the report. The version of the algorithms corresponds to a global version given by ABL, incremented each time ABL updates one of the algorithms. The version used will be indicated on the first page of the report.
- Click on the “Report configuration” tab for other settings for the final report.
- Finally, click on the green arrow to launch the analysis.

DeepChek HIV – Report done



- You can either wait for the system to finish processing the report or you can go to the DC HIV main page to start another analysis. If you wait, you should soon get the reports as shown in this screenshot.
- If you prefer to go to the DC HIV's main page, just click on "Results List" from the action menu blue bar (see next page).

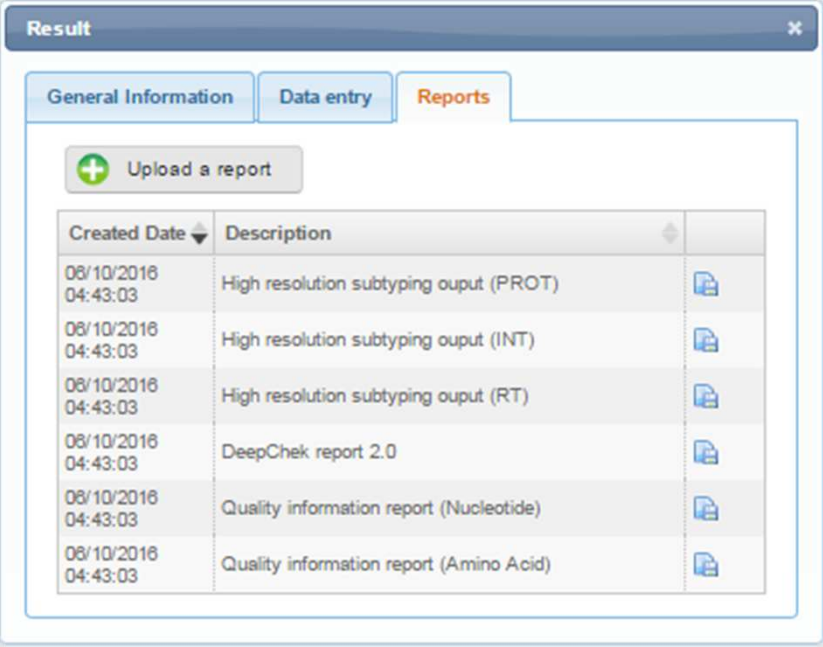
DeepChek HIV – Report done



- On the “Results List” page you can retrieve the reports of finished runs by clicking on the magnifier on the last column of the table (see next page).
- You can also delete an analysis by clicking on the bin icon.

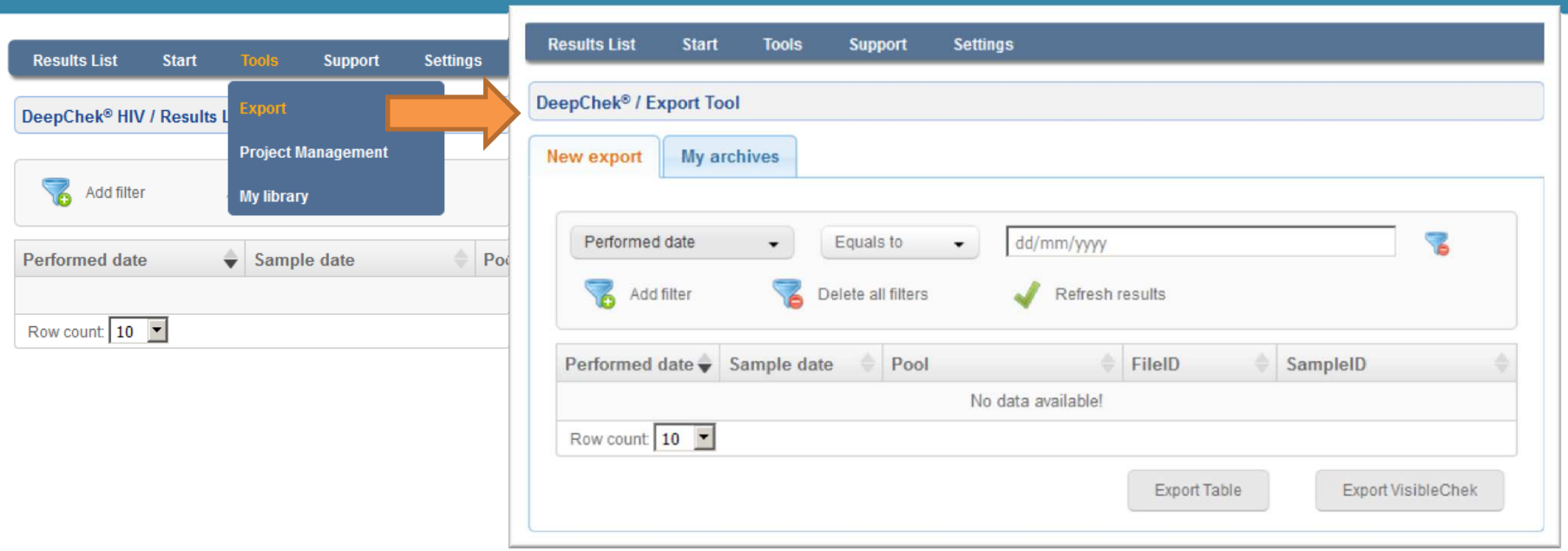
DeepChek HIV – Report done

- Clicking on the magnifier icon will launch the pop-up screen you see below, which contains three new tabs:
  - "General Information" will display basic information on your analysis.
  - "Data entry" will allow you to download the input files the system processed to generate the report
  - "Reports" will allow you to download the reports the system built for your analysis:



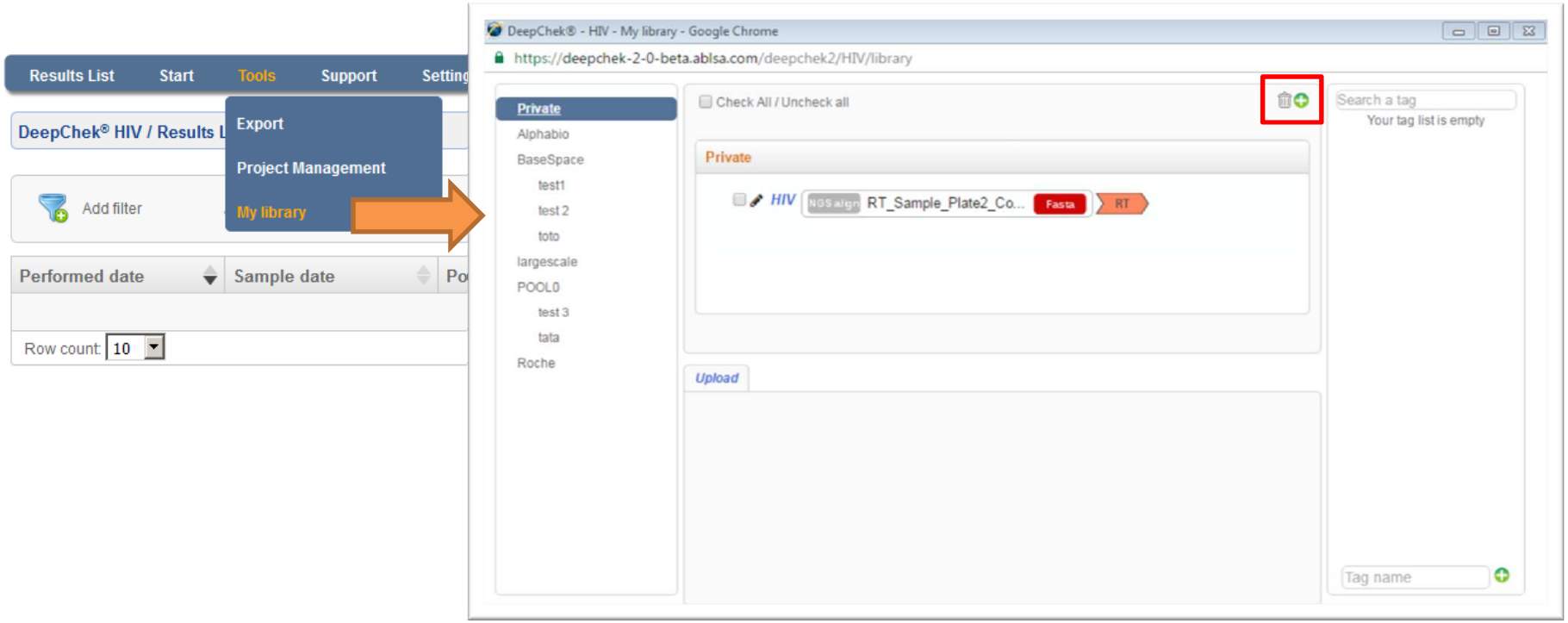
- "DeepChek report" is a PDF file where you will find color-coded visual information, well validated mutations (only the variant that passed our expert system), subtyping results, drug resistance determination and other information you have asked for in the report configuration steps.
- The "Quality information" reports are CSV tabulated files where you can find all the mutations (even the ones that didn't pass our expert system) found in your data along with more detailed information bout each mutation.
- "High resolution subtyping output" are CSV tabulated files with the detailed high resolution subtyping results per region.

DeepChek HIV – Export



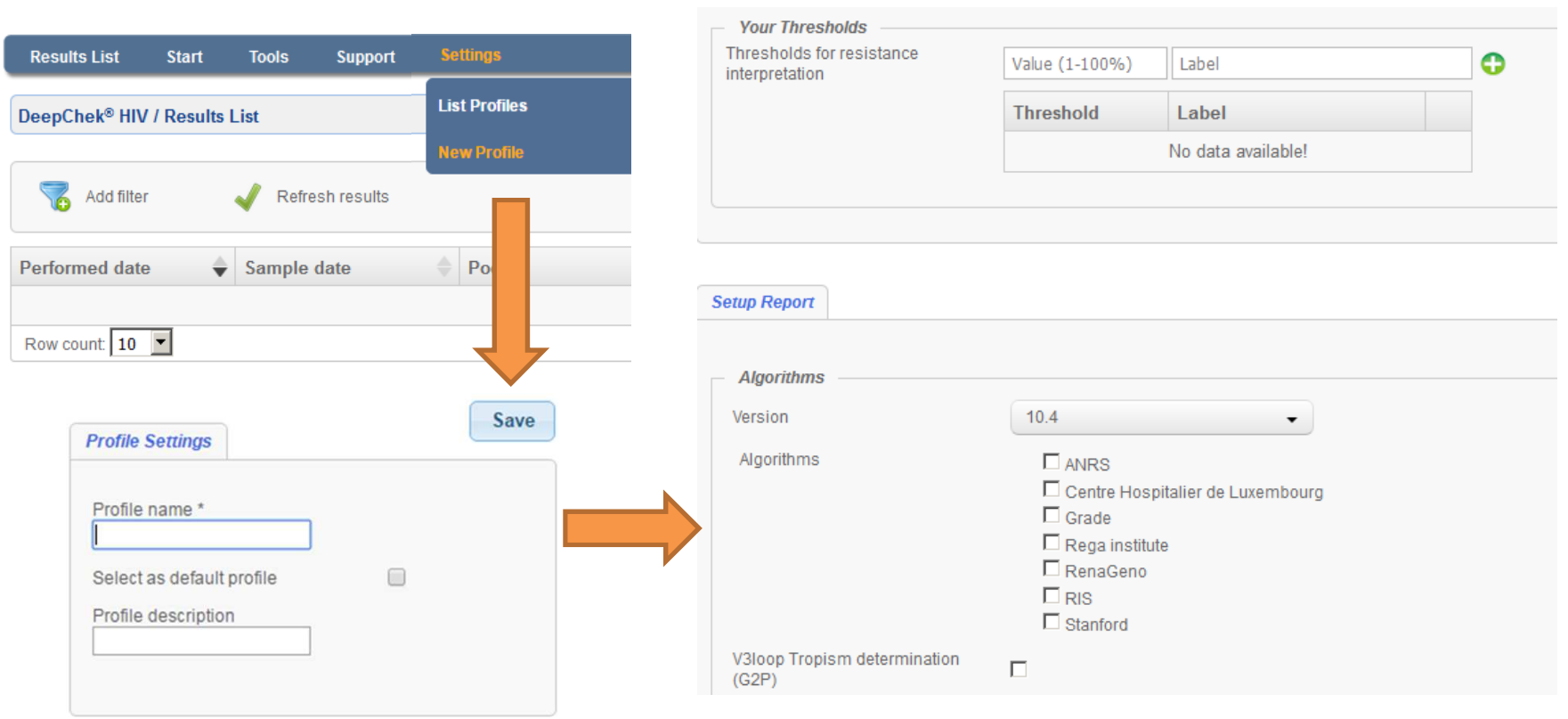
- Data can easily be exported by clicking on the “Tools” > ”Export” link placed on the blue bar action menu.
- If you want to export a specific set of data in order to be analysed by a third-party statistical software, just click on the “Export Table” button after configuring the filters your want. If you want all data to be exported, do not configure any filter.
- Each time you set a new filter, you should click on “Refresh results”.
- All the exports generated by the “Export Table” button will be in the standard CSV format.

DeepChek HIV – Library



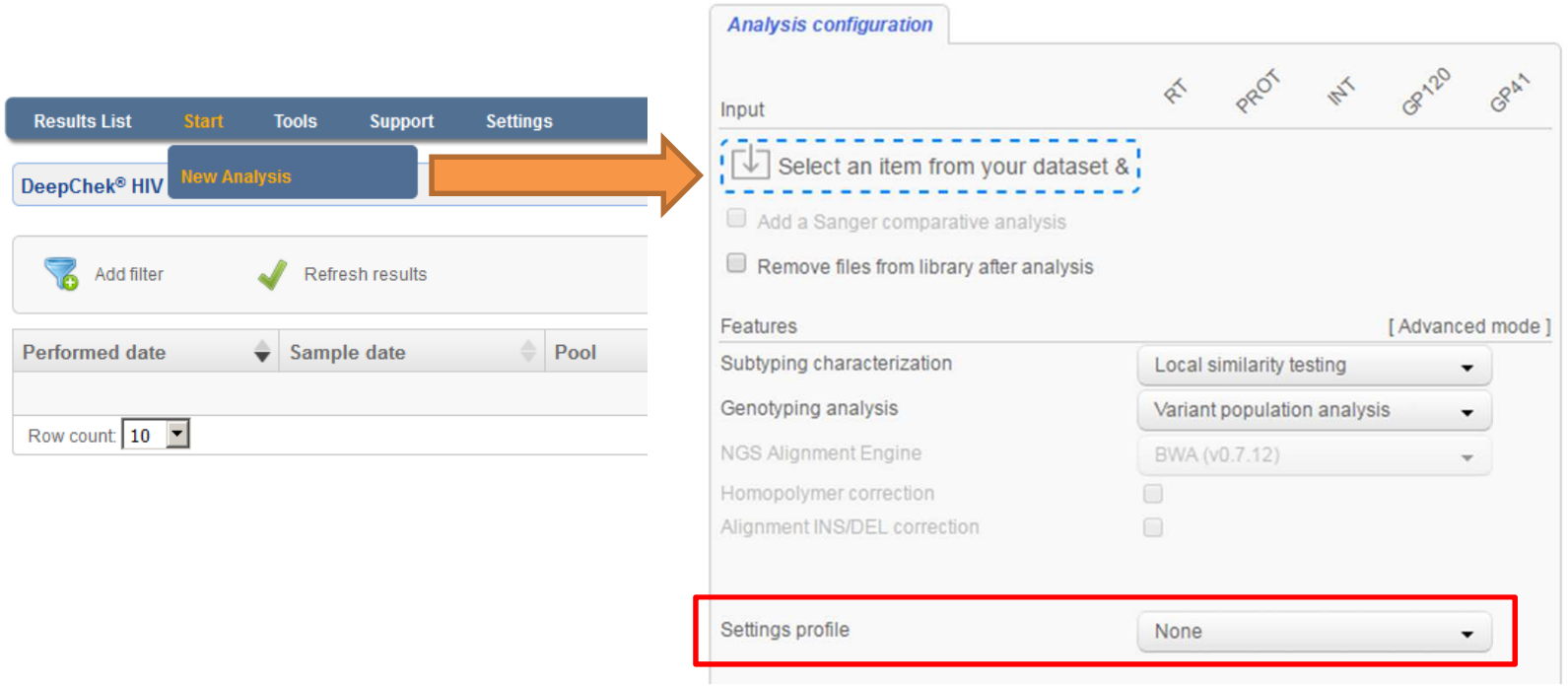
- Easily access the library by clicking on the “Tools” > ”My Library” link placed on the blue bar action menu.
- A new window appears and you can use the buttons at the top of the window (highlighted in the above screenshot) to add (button with the white cross) or delete (bin icon) datasets. When you click on the button to add a new dataset the popup window described on page 5 will be displayed.
- When you are done uploading or deleting datasets, close the window and click on the “Leave” button in the confirmation dialog that will popup next.

DeepChek HIV – Settings (1)



- To add a new Settings Profile, click on the "Settings" > "New Profile" link placed on the blue bar action menu.
- You will be asked for the new Settings Profile name and after you click on the "Save" button you will see a large set of options you can use to configure future analysis/reports. Don't forget to click on the "Save" button once you're done.
  - ✓ *Setting up a profile with your preferred choices will save you time when launching a new analysis.*

DeepChek HIV – Settings (2)



- After setting up all the options and saving this profile, you can select this settings profile in the first step when starting a new analysis.
- Just click on “Start” > “New analysis” and select the profile you saved with the desired options from the “Settings profile” drop list.
- Even if you select a profile, the system will allow you to check or uncheck the different options automatically set by the profile.

SUPPORT: https://org.ablsa.com/

You can submit your questions to our support team and developers using the above webpage or by sending an email to support@ablsa.com.