



DeepChek[®]–HIV

Quick Start Guide



October 2016

Confidential & Proprietary, ABL SA

DeepChek HIV - Log in screen

DeepChek[®] 2.0

The NGS Genotyping Software & Database Solution

DEEPCHEK 2.0 BETA SERVER

If you have lost your password or username please click [here](#).
If you need assistance logging in, please [email customer support](#) or call our support line at (352)26389676

Login:

Password:

☒ User login
☐ Administrator login

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- 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

DeepChek®-HIV v2.0 : The HIV Genotyping Software & Database S

Results List Start Tools Support Settings

DeepChek® HIV / Results List

Add filter Refresh results

Performed date Sample date Pool Patient data SampleID

No data available!

Row count: 10

- 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)

Results List Start Tools Support Settings

DeepChek® HIV / Create new analysis

Input Configuration Sample information Setup report Results

Your Dataset

Search by dataset name, file format, data type, tag, region

Private

- NGS align 03696182-fixed.fasta ✓
- NGS align 01031963-fixed.fasta
- NGS align 03696182.fasta
- NGS align 01031963.fasta
- Raw Seq PROT_HIVG-01-6481-B1_S2_L001_R1_001.fastq
- NGS align INT_Sample_Plate4_Column02_vs_INT.fna
- NGS align RT_Sample_Plate4_Column02_vs_RT.fna
- NGS align PROT_Sample_Plate4_Column02_vs_Prot.fna

Public

- NGS align IonXpress_030_R_2014_07_11_13_22_19_user...
- NGS align IonXpress_030_R_2014_07_11_13_22_19_user...

Analysis configuration

Input

NGS align 03696182-fixed.fasta

Select an item from your dataset & Drag here to analyse

☐ Add a Sanger comparative analysis

☐ Remove files from library after analysis

Features

Subtyping characterization

Genotyping analysis

NGS Alignment Engine

Homopolymer correction

Alignment INS/DEL correction

Settings profile

RT ☒ PROT ☐ INT ☐ GP120 ☐ GP41 ☐

check to select for analysis

Local similarity testing

Variant population analysis

BWA (v0.7.12)

[Advanced mode]

Click to view advanced options

drag and drop item to select for analysis

add item to the corresponding pool

➡

- 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)

Results List Start Tools Support Settings

DeepChek® HIV / Create new analysis

Input Configuration Sample Information Setup report Results

Your Dataset

Search by dataset name, file format, data type, tag, region

Private

- NGS align 03696182-fixed.fasta
- NGS align 01031963-fixed.fasta
- NGS align 03696182.fasta
- NGS align 01031963.fasta
- Raw Seq PROT_HIVG-01-6481-B1_S2_L001_R1_001.fastq
- NGS align INT_Sample_Plate4_Column02_vs_INT.fna
- NGS align RT_Sample_Plate4_Column02_vs_RT.fna
- NGS align PROT_Sample_Plate4_Column02_vs_Prot.fna
- NGS align IonXpress_030_R_2014_07_11_13_22_19_user...
- NGS align IonXpress_030_R_2014_07_11_13_22_19_user...

Add an entity

Dataset name: mysample

Data type: NGS raw sequences

File format: FastQ paired sequencing

Platform: Illumina - MiSeq

Select your Read 1 fastq file: mysample_R1.fastq

Select your Read 2 fastq file: Drop a file here or click to select

Covered regions:

- Reverse Transcriptase ☒
- Protease ☒
- Integrase ☐
- Glycoprotein 120 (or V3 loop) ☐
- Glycoprotein 41 ☐

Cancel Confirmation

RT PROT INT GP120 GP41

Local similarity testing

Variant population analysis

BWA (v0.7.12)

[Advanced mode]

Select the regions covered by your input files. These regions will be automatically selected for analysis when you set up a run.

- 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)

Identification Clinical data GSS Healthcare provider NGS threshold

General identifiers

Pool * Project

Patient Data ☐

Sample information

Your sample ID * Date of sample *

Alternative ID Reason for genotyping analysis

Type of sample *

NGS details

Date of sequencing * Reagent expiration date

Sequencing platform Processing software

NGS Method

Assay version

Plate ID Cartridge S/N

Notes



- 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)

Identification Clinical data GSS Healthcare provider **NGS threshold**

Thresholds for resistance interpretation

Threshold	Value (1-100%)	Label

The selected thresholds will be applied to the following region(s): RT



- 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)

DeepChek® HIV / Create new analysis

Input Configuration Sample information **Setup report** Results

Algorithms Report configuration

List

Version: 10.8

Algorithms:

- ☐ ANRS
- ☐ Grade
- ☐ Rega institute
- ☐ RenaGeno
- ☐ RIS
- ☐ Stanford



← →

- 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

The screenshot displays the DeepChek HIV web interface. At the top is a navigation bar with links: Results List, Start, Tools, Support, and Settings. Below this is a header for 'DeepChek® HIV / Create new analysis'. A progress bar shows two steps: 'Configuration' (completed) and 'Load data' (in progress). The main content area has two tabs: 'Summary' and 'Reports'. The 'Summary' tab shows the analysis status as 'Done', with start and finish times from 21/08/2015. The 'Reports' tab lists two reports: 'Clinical genotyping report' (with a PDF icon) and 'Quality information report' (with an Excel icon).

Summary	
DeepChek analysis status :	Done
Started on :	21/08/2015 16:13:25
Finished on :	21/08/2015 16:15:04



Reports	
Clinical genotyping report	
Quality information report	



- 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

Results List	Start	Tools	Support	Settings
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DeepChek® HIV / Results List

 Add filter  Refresh results

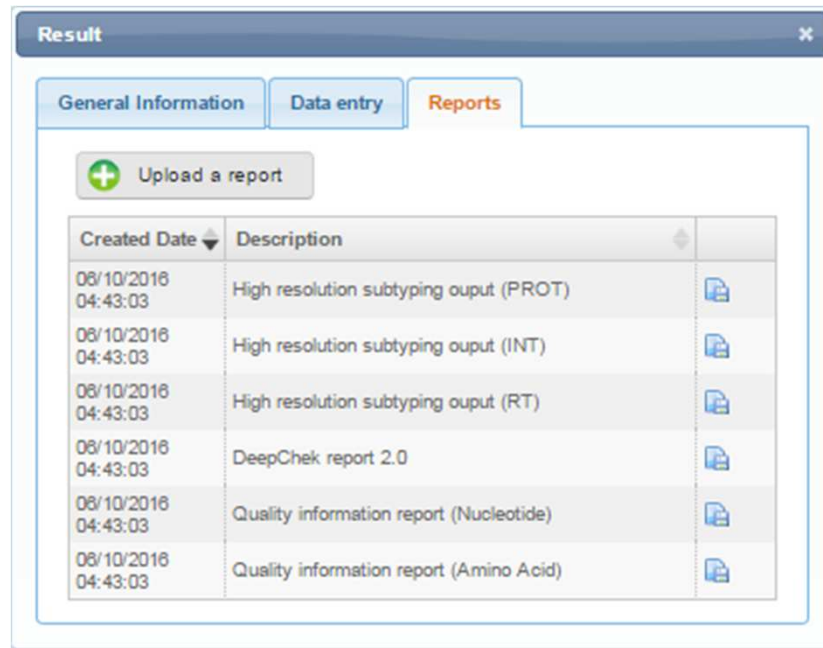
Performed date ▾	Sample date ▾	Pool ▾	Patient data ▾	SampleID ▾	Status ▾	
21/08/2015 16:13:25	01/08/2015	██████		00001234	Done	 

<< < 1 > >> Go to page: 1 ▾ Row count: 10 ▾ Showing 1-1 of 1

- 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.

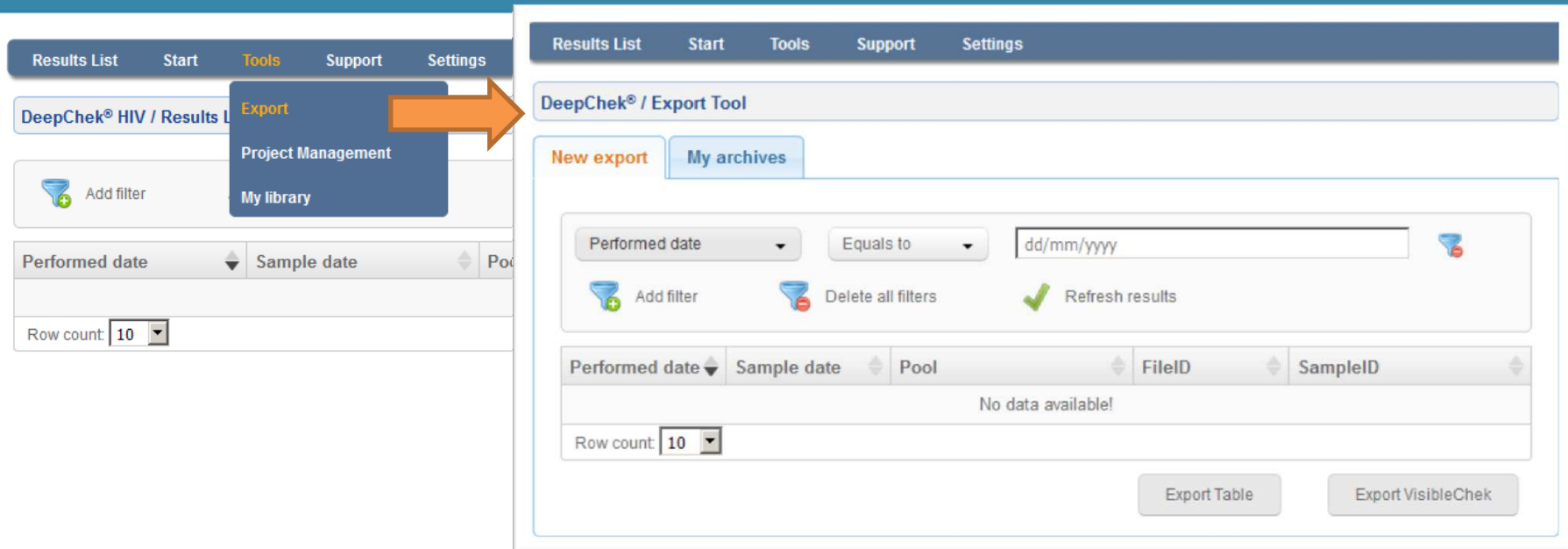
DeepChek HIV – Report done

- 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:



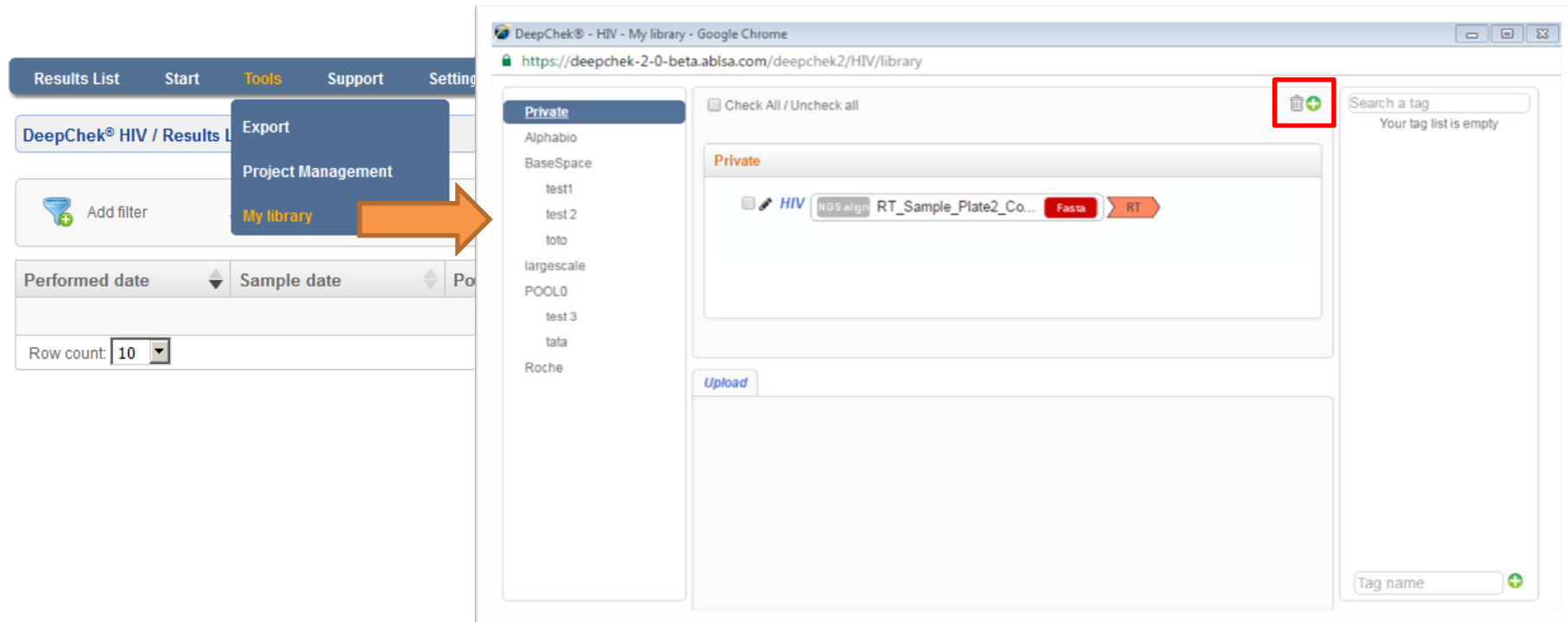
- “DeepChek report” is a PDF file where you will find color-coded visual information, well validated mutations (only the variant that passed our expert system), subtyping results, drug resistance determination and other information you have asked for in the report configuration steps.
- The “Quality 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 about 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)

The screenshot illustrates the process of creating a new settings profile in the DeepChek HIV application. It is divided into three main sections:

- Top Navigation:** A blue bar contains links for 'Results List', 'Start', 'Tools', 'Support', and 'Settings'. The 'Settings' link is highlighted. Below it, a dropdown menu shows 'List Profiles' and 'New Profile' (highlighted in orange).
- Left Panel:** Contains filters like 'Add filter' and 'Refresh results', and a 'Row count' dropdown set to '10'. An orange arrow points from the 'New Profile' link to the 'Save' button in the 'Profile Settings' modal.
- Profile Settings Modal:** A form with fields for 'Profile name *', 'Select as default profile' (checkbox), and 'Profile description'. An orange arrow points from this modal to the 'Algorithms' section.
- Algorithms Section:** Displays a 'Version' dropdown (set to 10.4) and a list of algorithms with checkboxes: ANRS, Centre Hospitalier de Luxembourg, Grade, Rega institute, RenaGeno, RIS, and Stanford. At the bottom, there is a checkbox for 'V3loop Tropism determination (G2P)'.
- Right Panel:** Shows 'Your Thresholds' for resistance interpretation with a table for 'Value (1-100%)' and 'Label', and a 'Setup Report' tab.

- 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)

Results List **Start** Tools Support Settings

DeepChek® HIV **New Analysis**

Add filter Refresh results

Performed date Sample date Pool

Row count: 10

Analysis configuration

Input RT PROT INT GP120 GP41

Select an item from your dataset &

☐ Add a Sanger comparative analysis

☐ Remove files from library after analysis

Features [Advanced mode]

Subtyping characterization Local similarity testing

Genotyping analysis Variant population analysis

NGS Alignment Engine BWA (v0.7.12)

Homopolymer correction ☐

Alignment INS/DEL correction ☐

Settings profile None

- 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.



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