Targets

Hands-on-training

info@genexplain.com

Part 1: Upstream analysis workflow in geneXplain platform

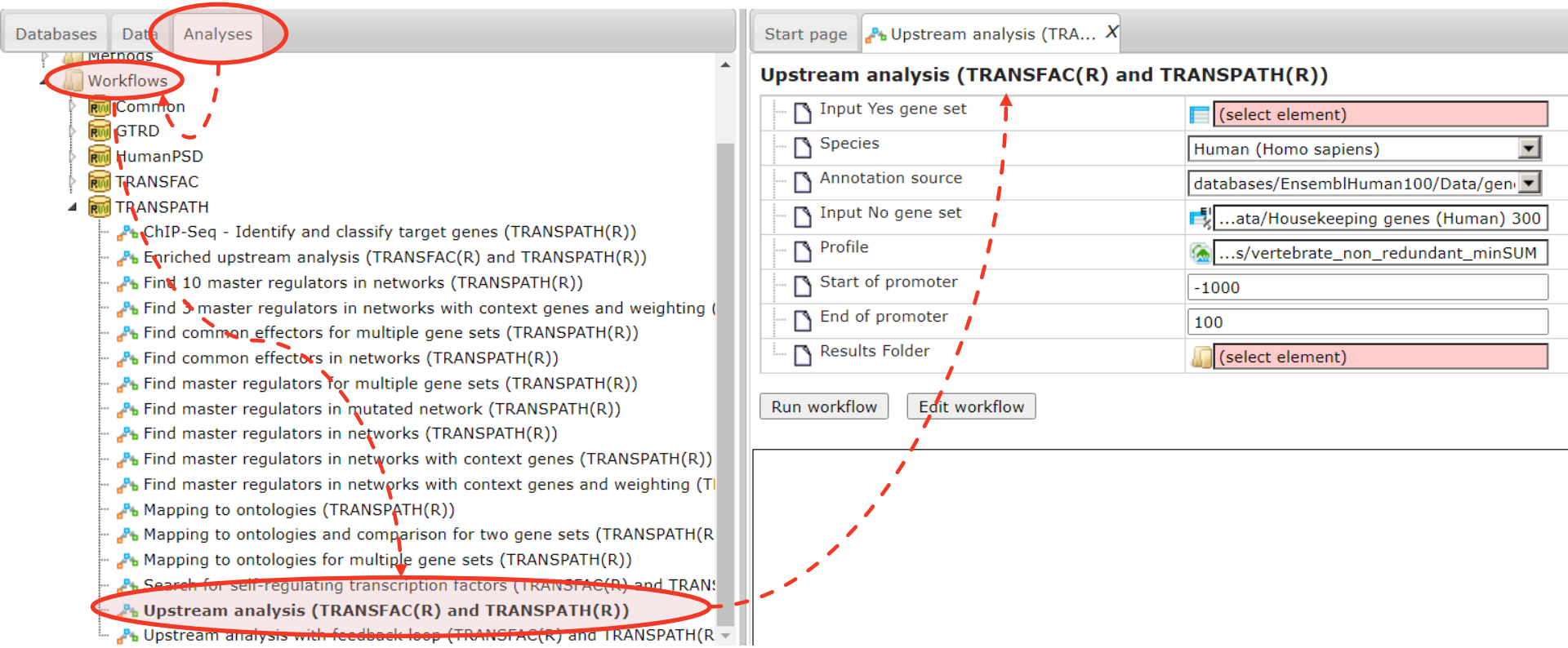
Part 2: Look and feel of Genome Enhancer software

Part 1

Run a complete upstream analysis with the geneXplain platform.

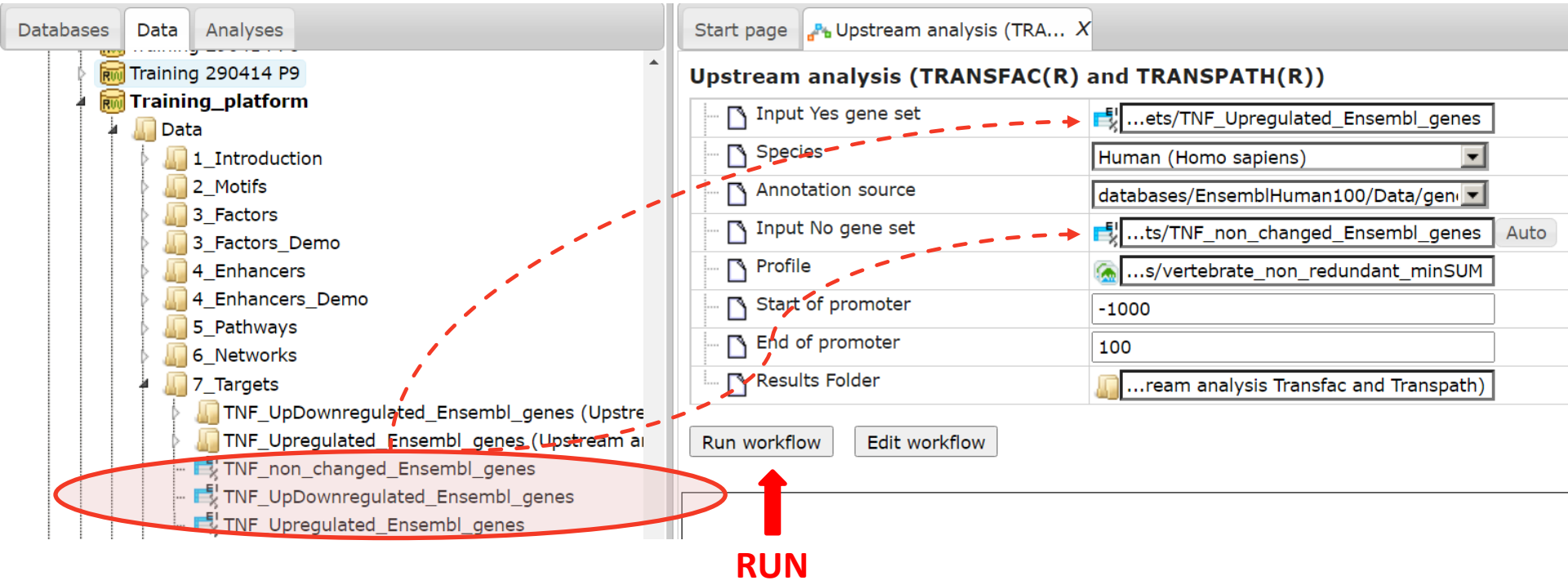
Part 1 – Run a complete upstream analysis with the geneXplain platform.

Open the **Upstream analysis (TRANSFAC(R)) and TRANSPATH®** workflow as shown below.



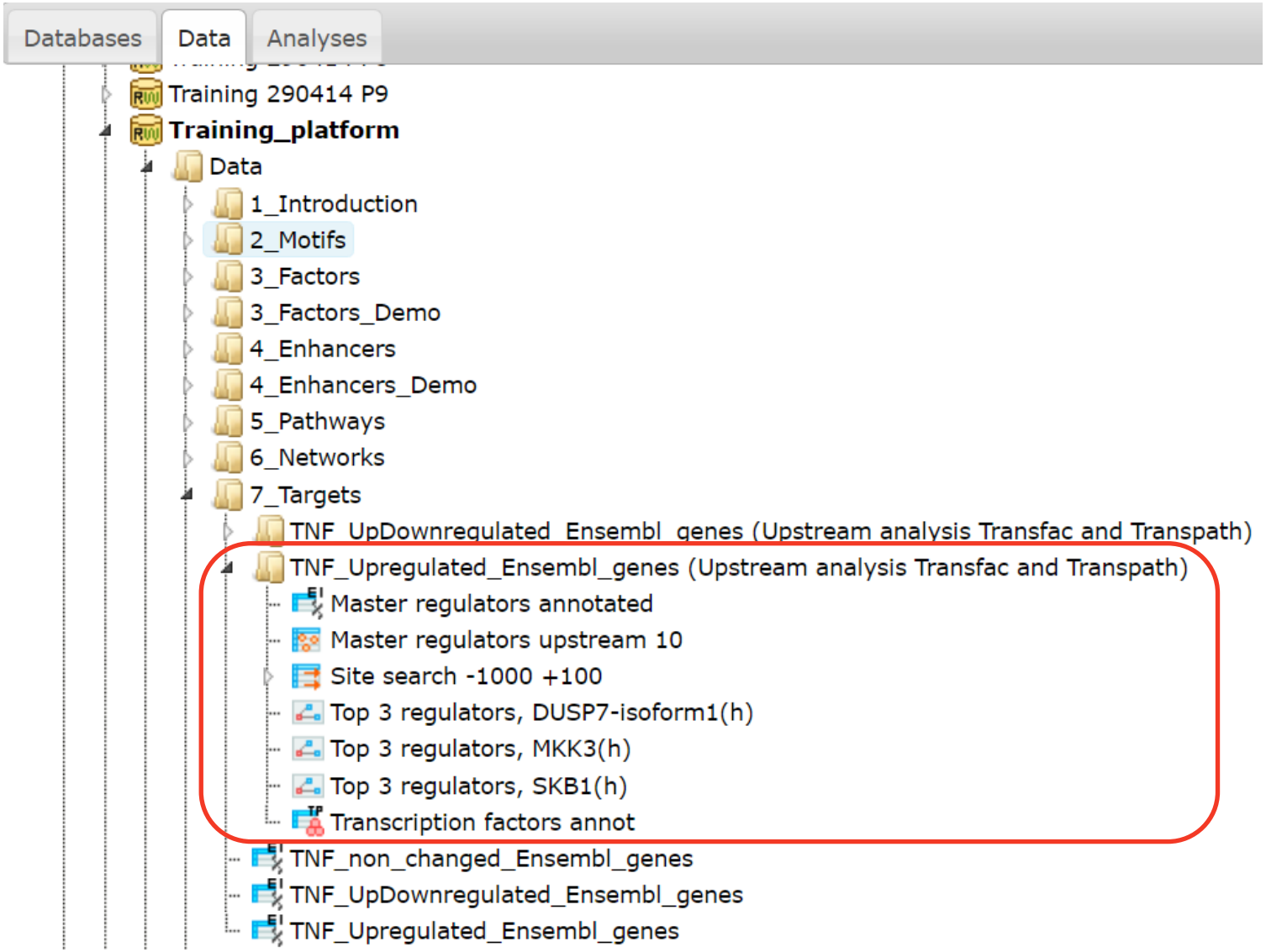
Part 1 – Run a complete upstream analysis with the geneXplain platform.

Navigate to the *GSM558469_E2F1_hg19 filtered exp1000 dist1000 L<600* track and drag-and-drop it to the **Input Yes track** field of the workflow input mask. Navigate to the *Housekeeping genes (Human) track -100000 to -98000 filtered chr 1* track and drag-and-drop it to the **Input No track** field of the workflow input mask. The field **Sequence source** should be set to Ensembl Human 75 genome build. Click **Run workflow** when parameters are set as shown below.



Part 1 – Run a complete upstream analysis with the geneXplain platform.

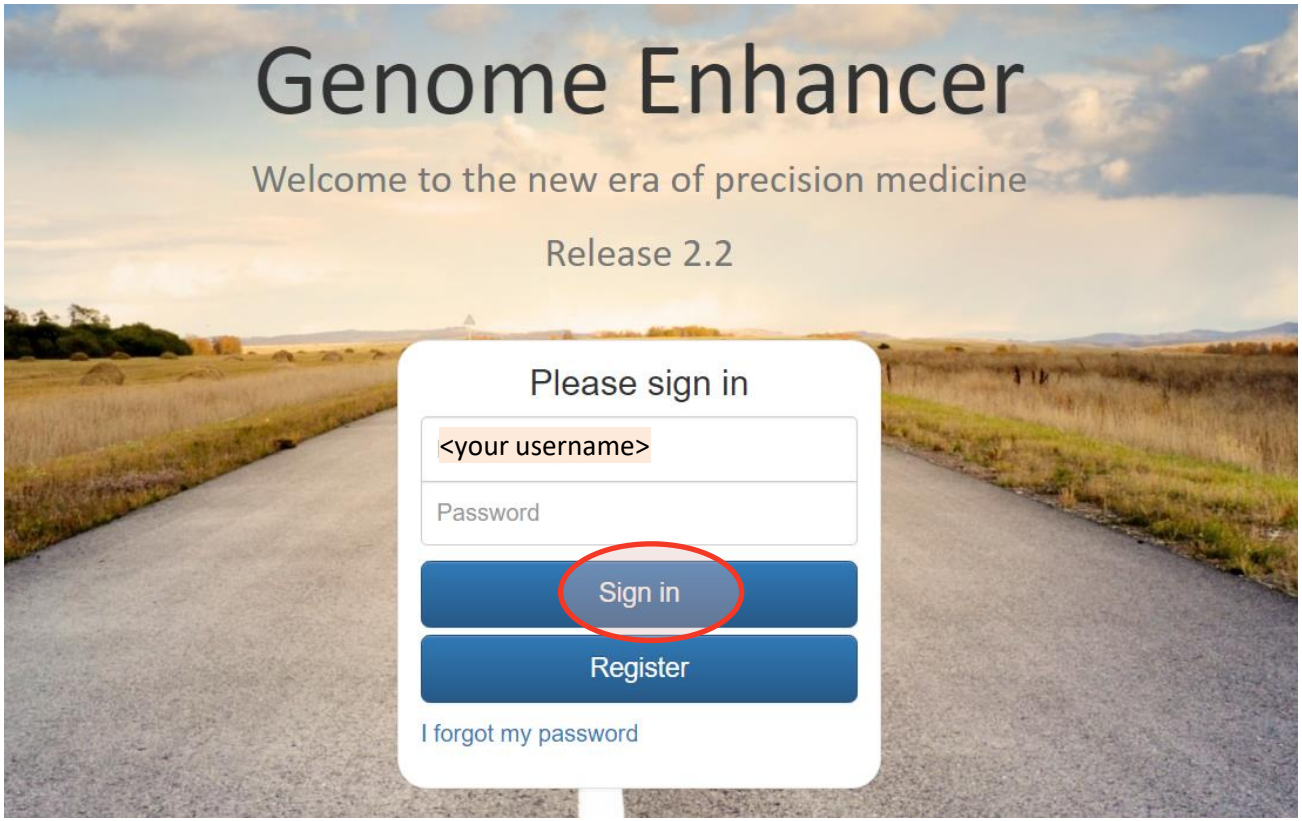
Have a look to the results folder and corresponding files.

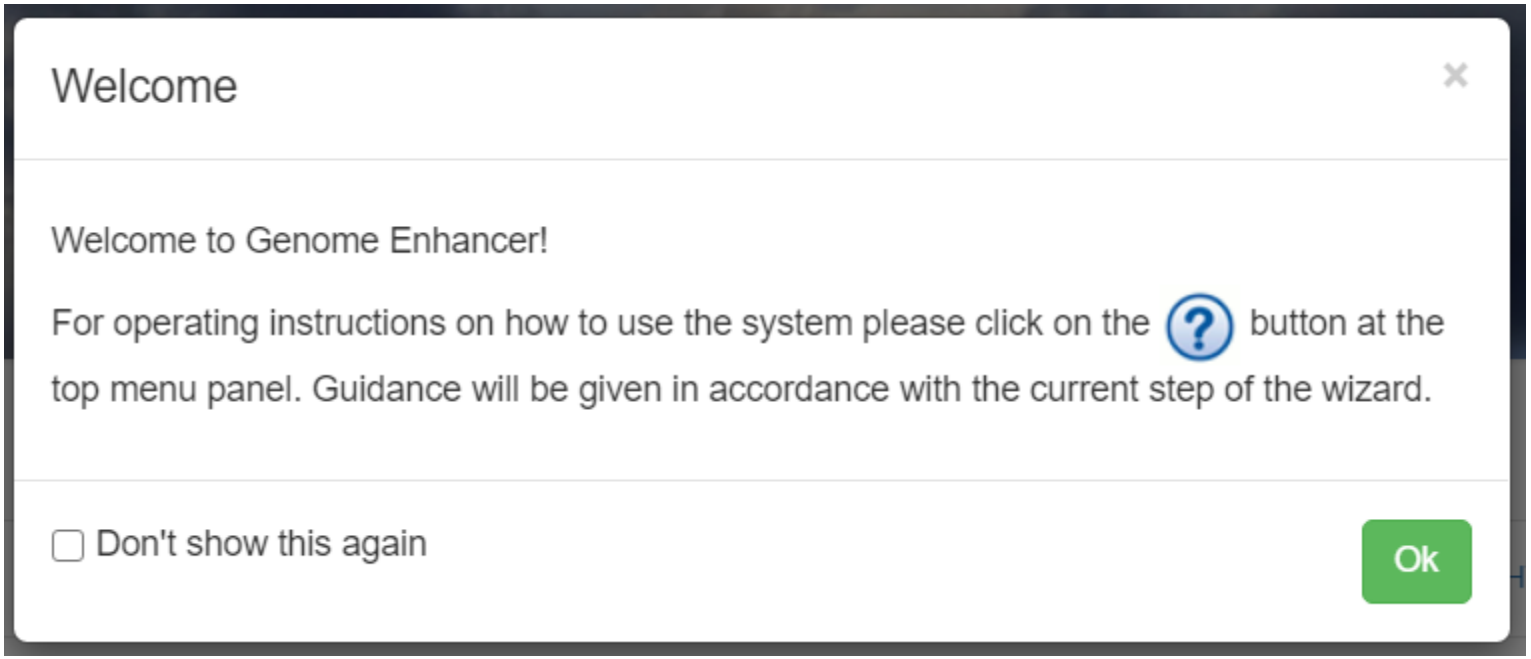


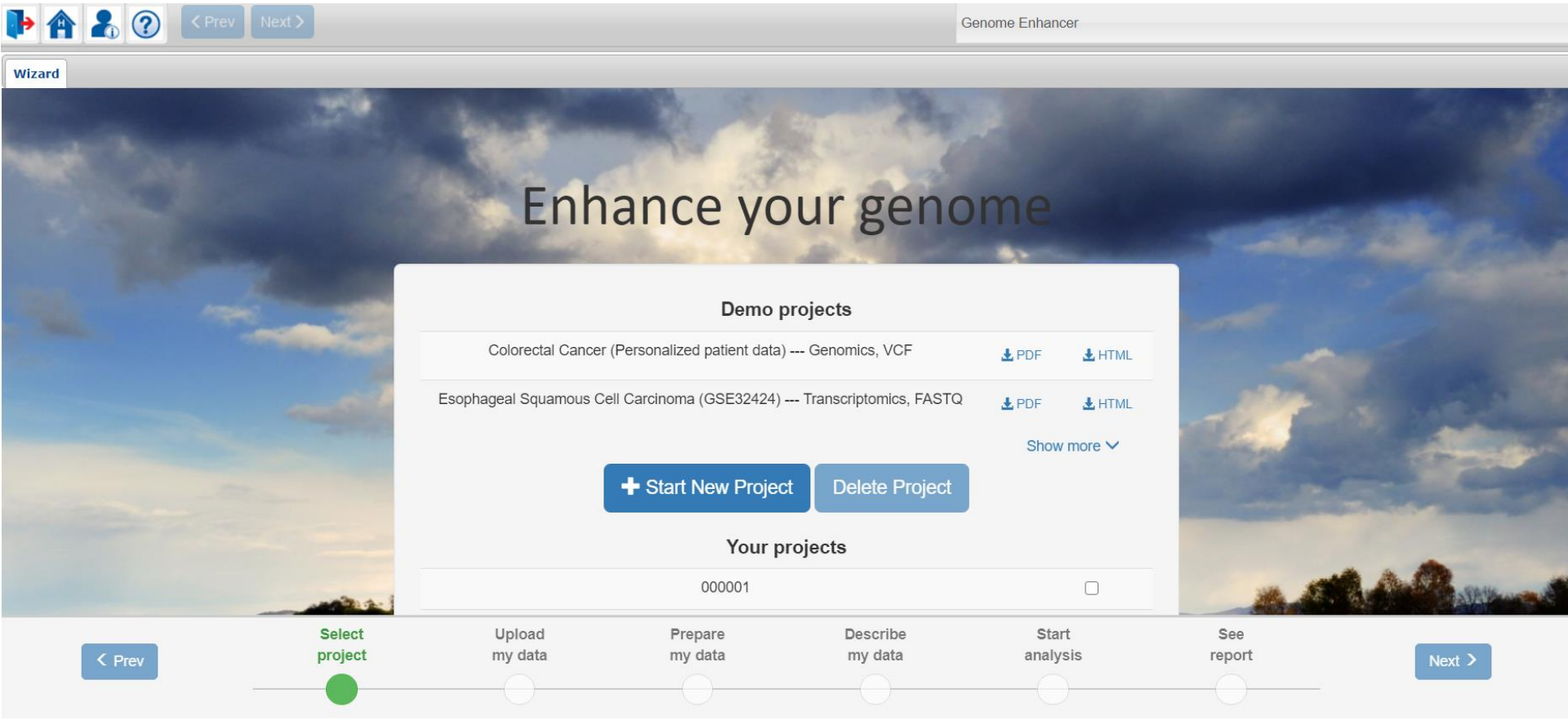
Part 2 – Genome Enhancer tour

Genome Enhancer page in your browser: *https://genexplain-platform.com/bioumlweb/*

Specify your credentials and click **Login**.




Welcome
Welcome to Genome Enhancer!
For operating instructions on how to use the system please click on the button at the top menu panel. Guidance will be given in accordance with the current step of the wizard.
Don't show this again
Ok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Describe my data
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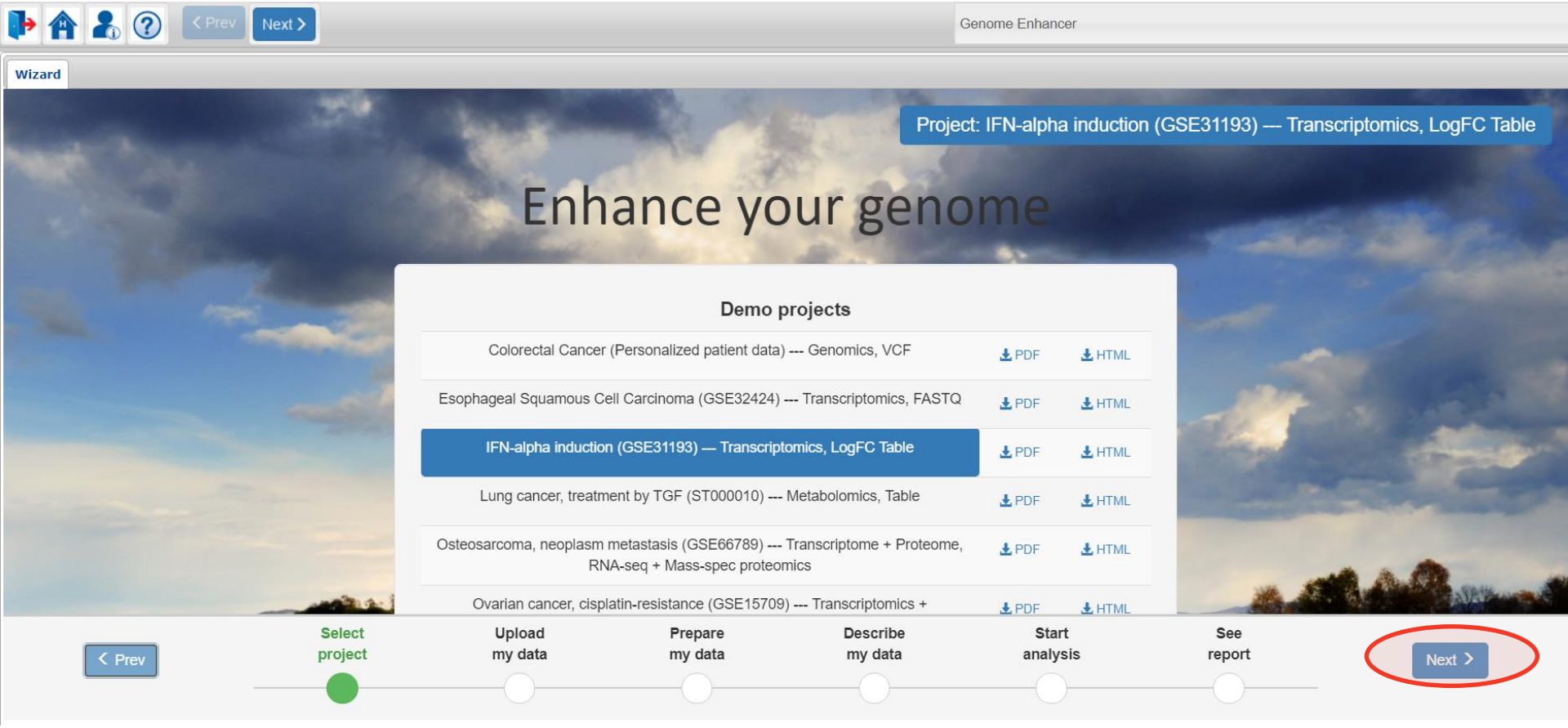
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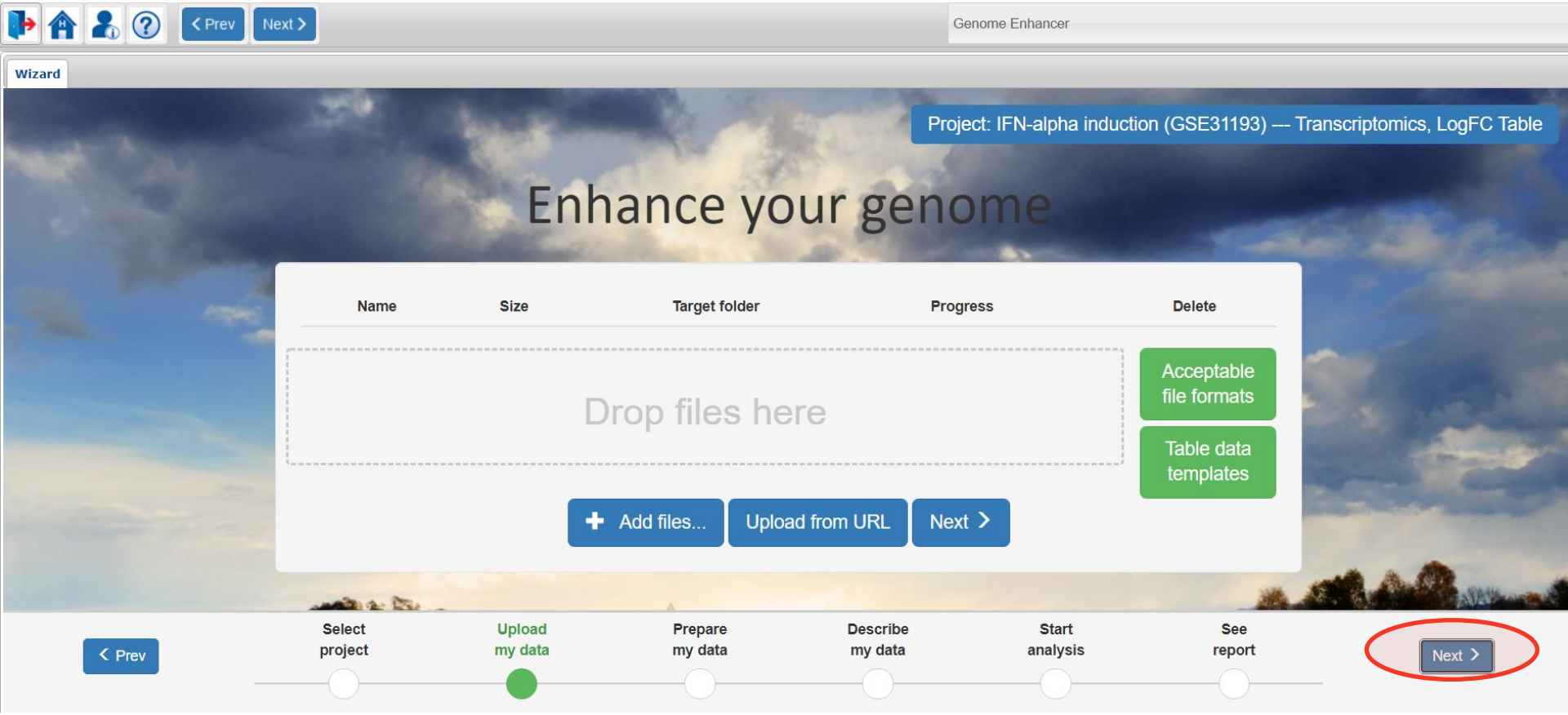
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Table data templates
Add files...
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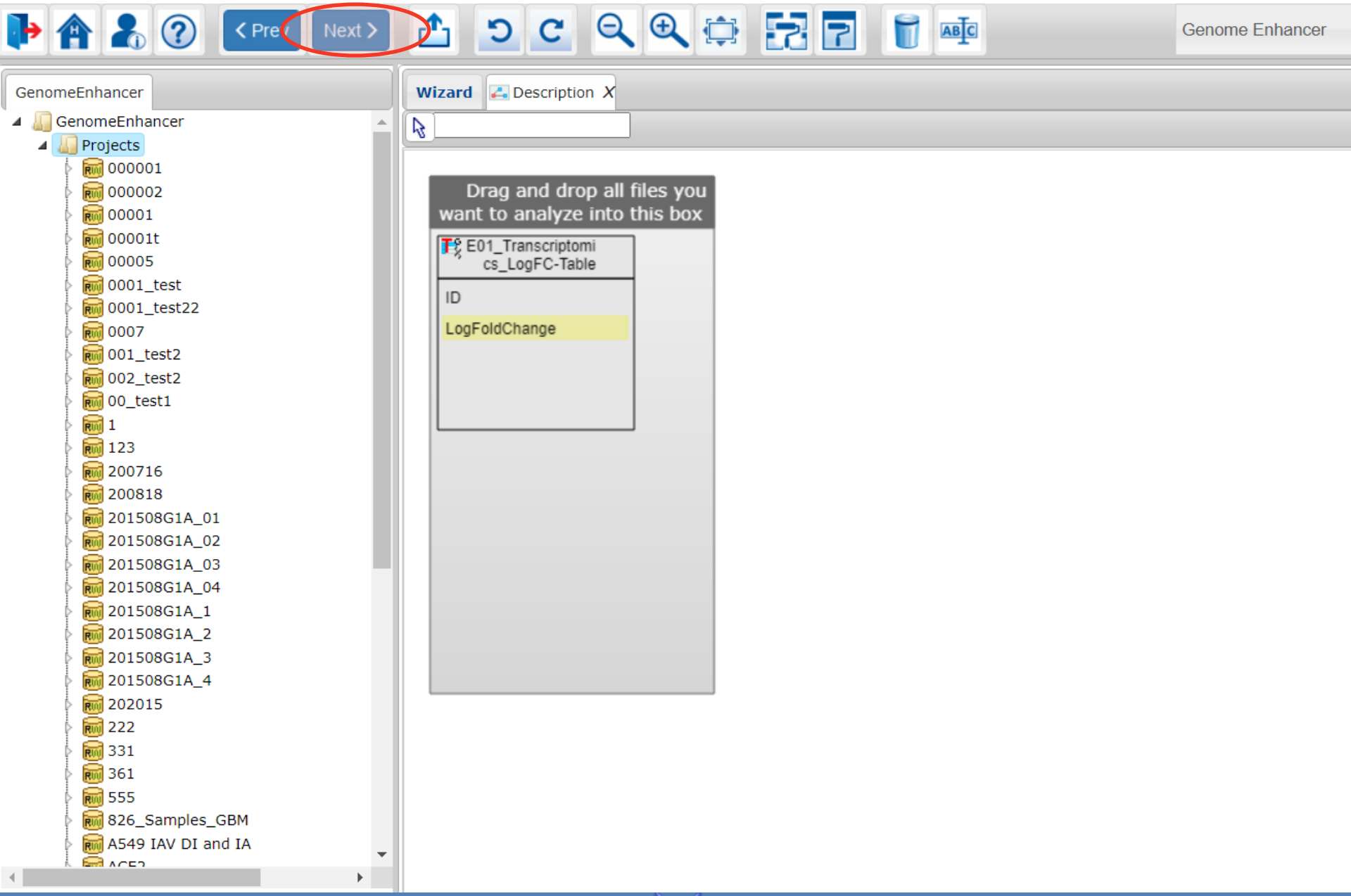
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201508G1A_02
201508G1A_03
201508G1A_04
201508G1A_1
201508G1A_2
201508G1A_3
201508G1A_4
202015
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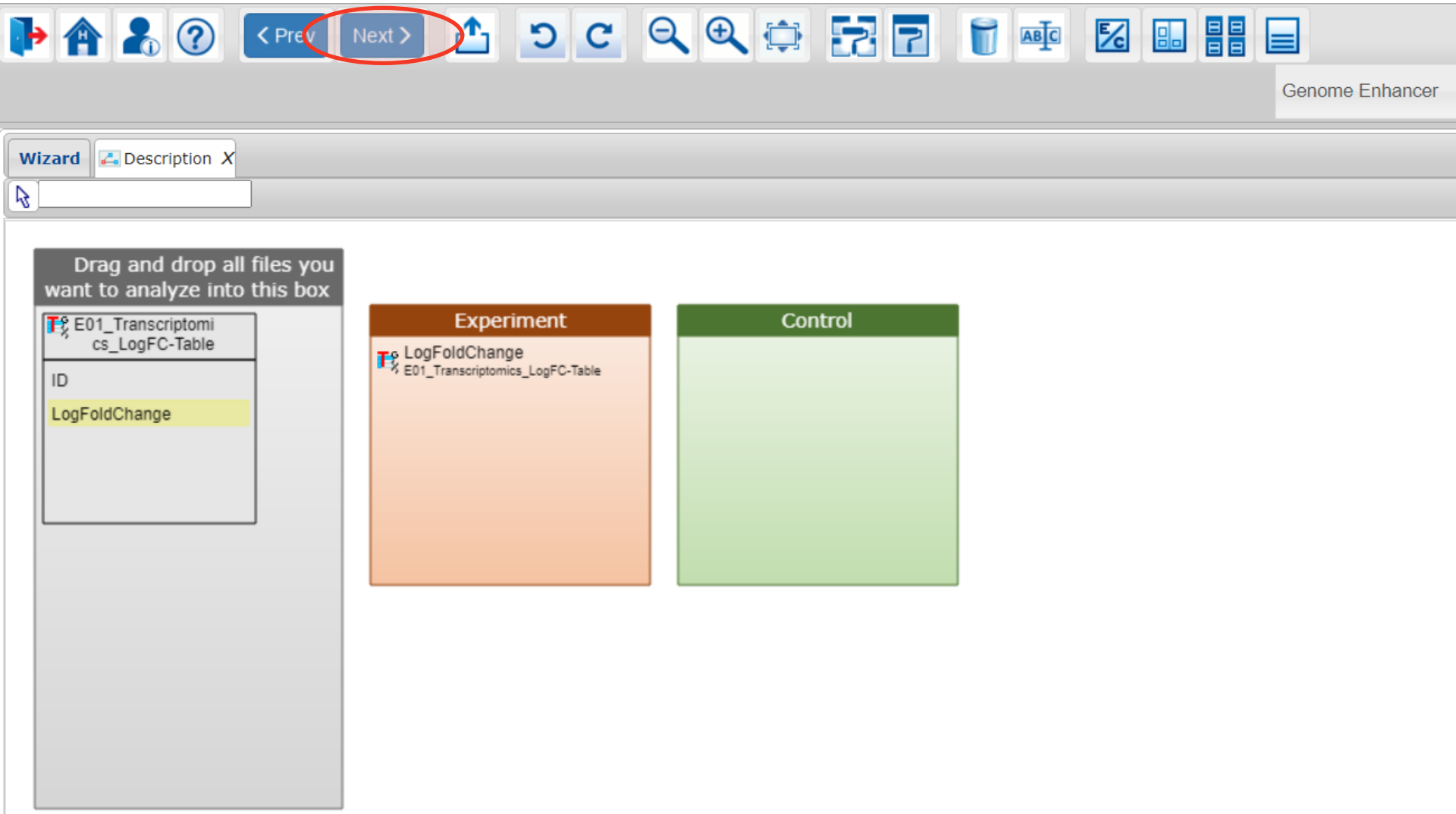
361
555
826_Samples_GBM
A549 IAV DI and IA
Wizard
Description
Drag and drop all files you want to analyze into this box
E01_Transcriptomics_LogFC-Table
ID
LogFoldChange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Genome Enhancer
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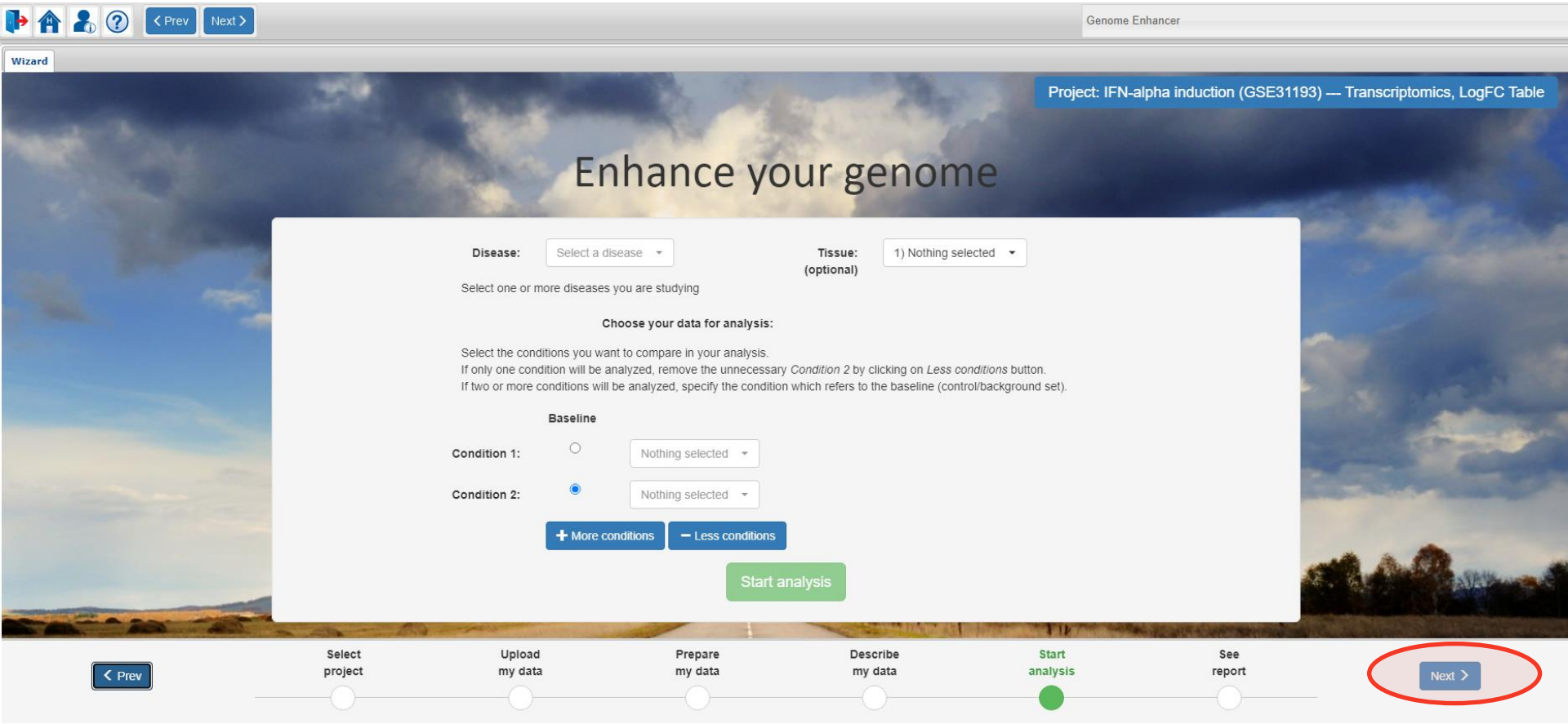
Description
Drag and drop all files you want to analyze into this box
E01_Transcriptomics_LogFC-Table
ID
LogFoldChange
Experiment
LogFoldChange
E01_Transcriptomics_LogFC-Table
Control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Project: IFN-alpha induction (GSE31193) — Transcriptomics, LogFC Table
Enhance your genome
Disease:
Select a disease
Tissue: (optional)
1) Nothing selected
Select one or more diseases you are studying
Choose your data for analysis:
Select the conditions you want to compare in your analysis.
If only one condition will be analyzed, remove the unnecessary Condition 2 by clicking on Less conditions button.
If two or more conditions will be analyzed, specify the condition which refers to the baseline (control/background set).
Baseline
Condition 1:
Nothing selected
Condition 2:
Nothing selected
+ More conditions
− Less conditions
Start analysis
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Select project
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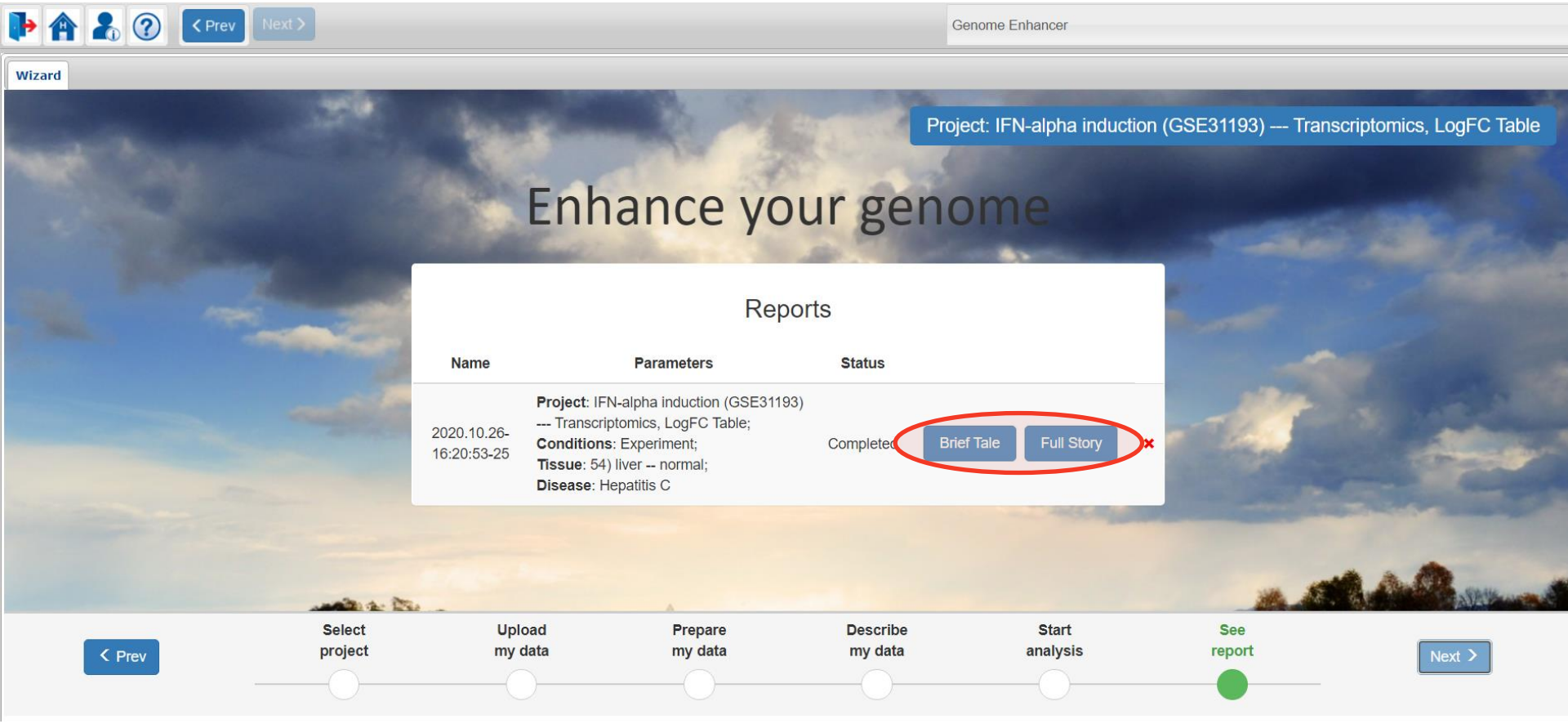
Part 1 – Genome Enhancer tour

Have a look to the results with clicking **Brief Tale** and **Full Story**.



Report on promising druggable targets and drugs for treating Hepatitis C that are identified on the basis of analysis of differentially expressed genes in liver tissue

Demo User
geneXplain GmbH
info@genexplain.com

Project IFN-alpha induction (GSE31193) --- Transcriptomics, LogFC Table
Data received on 13/08/2019; Run on 26/10/2020; Report generated on 26/10/2020

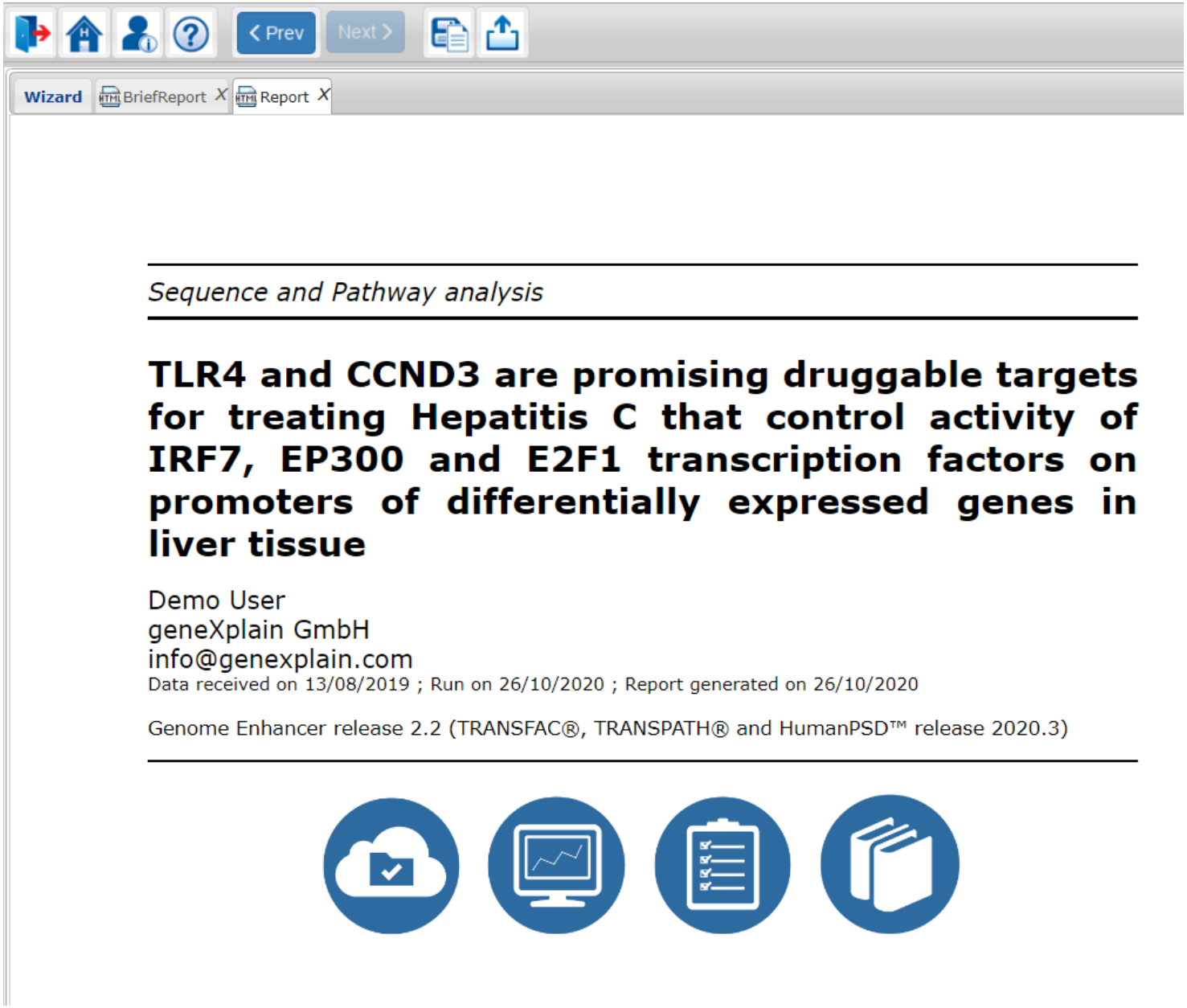
Based on the performed analysis, the following drugs were proposed as most promising candidates for treating the pathology under study: **Naloxone, Tofacitinib and Perindopril**.

These drugs were selected for acting on the following targets: TLR4, JAK2 and ITGA2B. The targets were identified by analysis of molecular mechanism of the pathology under study.

Proposed drugs are top ranked drug candidates, that were found to be active on the identified targets and were selected from 4 categories:

1. FDA approved drugs or used in clinical trials drugs for the studied pathology;
2. Repurposing drugs used in clinical trials for other pathologies;
3. Drugs, predicted by PASS to be active against identified drug targets and against the studied pathology;
4. Drugs, predicted by PASS to be active against identified drug targets but for other pathologies.

Proposed drugs were selected on the basis of Drug rank which was computed from two scores: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Report
Sequence and Pathway analysis
TLR4 and CCND3 are promising druggable targets for treating Hepatitis C that control activity of IRF7, EP300 and E2F1 transcription factors on promoters of differentially expressed genes in liver tissue
Demo User
geneXplain GmbH
info@genexplain.com
Data received on 13/08/2019 ; Run on 26/10/2020 ; Report generated on 26/10/2020
Genome Enhancer release 2.2 (TRANSFAC®, TRANSPATH® and HumanPSD™ release 2020.3)

Part 1 – Genome Enhancer Help page

Click the link below and read through the description of the Genome Enhancer Software.

https://ge.genexplain.com/bioumlweb/ge/help/step-project.shtml

Practical session completed

info@genexplain.com