**User Manual of ImmunoCompare**

**February 10, 2022**

ImmunoCompare is an omics-based target validation tool, which can query candidate targets and biological conditions (e.g. diseases, organisms, treatments, tissues or cell types) together to reveal whether candidates are differentially expressed under conditions (e.g. whether a gene has significantly higher expression in non-responders than responders in most of IBD transcriptomic datasets). ImmunoCompare can also query candidate targets from AbbVie internal target lists and from multiple public databases (e.g. DrugBank, PharmGKB, and GWAS Catalog). Currently, ImmunoCompare contains 13 microarray datasets, 25 bulk RNASeq datasets, 24 proteomics datasets, 16 single-cell RNASeq datasets, and 3 AbbVie target lists spanning 12 diseases and can query 9 external databases.

1. Input query genes

Clicking the “GENES” menu, a user can input the interesting genes. Multiple genes should be separated by comma.

Graphical user interface, diagram

Description automatically generated

Figure 1. Interesting gene input

2. Select disease of interest

Clicking on the “DISEASE” menu, a user can select one or multiple diseases of interest from the dropdown menu.

Graphical user interface

Description automatically generated

Figure 2. Selection of interesting diseases

3. Select technology of interest

Clicking “TECHNOLOGY” menu and then clicking “Experiment Type” menu, the user can select one or multiple experiment types (e.g. Microarray and RNASeq) from the dropdown menu.

Graphical user interface, diagram

Description automatically generated with medium confidence

Figure 3. Selection of interesting experiment types

**The user can set other interesting parameters (e.g. organism or treatment) based on the same method.**

4. Comparison Summary

After setting the parameters, the user can click “Run ImmunoCompare” button to get the query results, which may take 20-30 seconds.

“Comparison Summary” tab shows the summary of query results based on datasets and comparisons in each disease. For example, “TNF – found in 6 datasets (44 comparisons)” means TNF is included in 6 datasets that contain totally 44 comparisons. “Summary Metrics” shows the number of datasets and comparisons that the TNF is significant based on the significant threshold (default is p<0.05 & logFC>0.5).

Graphical user interface, text, application

Description automatically generated

Figure 4. Summary of Comparisons

5. Comparison Tables and Expression Visuals

Clicking the “Comparison Tables” tab, the user can get all detailed information about “Summary Metrics” in the “Comparison Summary” tab. The table includes the description of each dataset and comparison and whether the interesting genes are significant in the comparison. “NS” means interesting gene is not significant in the comparison while red and blue “info” button represent the interesting gene is significantly up- or down-regulated in the comparison. Hanging over the “info” button can get the detailed statistic result. The directionality of the comparison can be found in the “comparison” column. For example, “NonInvolvedArea vs InflammedArea” means up-regulated gene has higher expression in NonInvolvedArea compared with InflammedArea.

Graphical user interface, text, application

Description automatically generated

Figure 5. Comparison table

Selecting the one or multiple comparisons from one or multiple datasets using “Row/Plot Selection” checkboxes and clicking “Generate Visuals” button, the user can plot the boxplots related to the selected comparisons.

Graphical user interface

Description automatically generated

Figure 6. Expression Visuals

5. Geneset View and Database View

Under the “Geneset View”, the user can check whether the interesting genes are included in the genesets related to query parameters (e.g. disease).

“Database View” tab provides the links of interesting genes in the public databases.

Graphical user interface

Description automatically generated

Figure 7 Geneset View

Graphical user interface, application

Description automatically generated

Figure 8. Database View