User Manual of IBDCompare
October 2, 2023

IBDCompare is a data comparison and visualization tool based on interesting genes/pathways. Users began IBDCompare by selecting "GENE" or "PATHWAY" options (red box in Figure 1). If selecting "GENE" option, users need to input the query genes in the blue box (genes must be separated by commas). If selecting "PATHWAY" option, users need to select a pathway database from KEGG and Reactome and then select interesting pathways from a drop-down list that include 311 KEGG pathways or 1414 Reactome pathways. Then, after selecting the diseases (CD or UC) and other optional attributes (e.g. tissues or treatments) in green box, the related datasets will be shown in the table. Users can click the "select all" button (grey box) to select all datasets or manually refine the datasets. Clicking the "Compare Datasets" button (yellow box), IBDCompare will compare the comparisons from all selected datasets for the query genes or pathways.

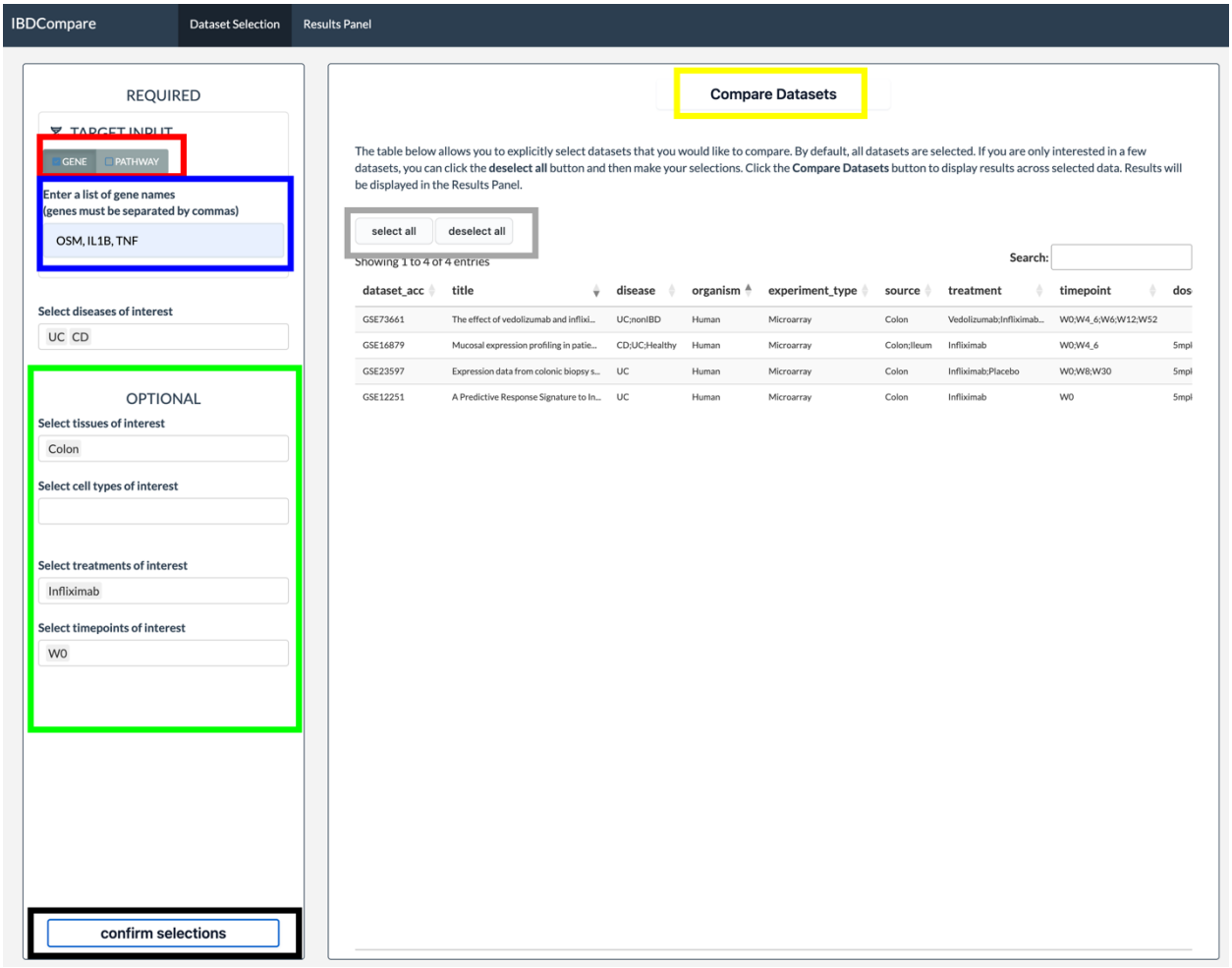

Figure 1. Data selection in IBDCompare.

The comparison results are shown in the “Results Panel” tab. This tab includes four sub-tabs: Summary, Comparison Tables (Results), Expression Visuals, Database View. Summary tab show the query parameters and number of datasets and comparisons that include the query genes/pathways for each disease.

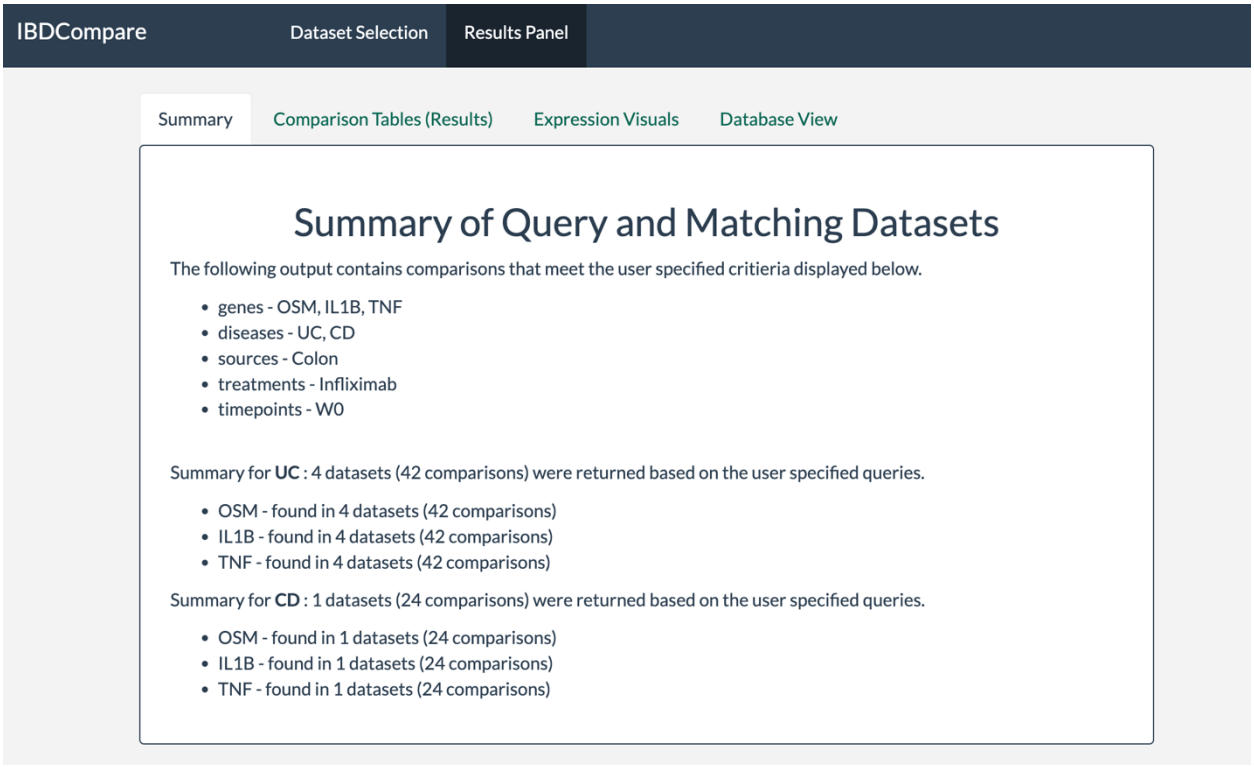

Figure 2. Summary tab in the Results Panel

In the “Comparison Tables (Results)” tab, “Summary of Results” panel includes the number of datasets and comparisons related to each query gene/pathway based on each disease and each platform (red box in Figure 3). “Results” panel includes the comparison results. The tables are first separated by disease and then by dataset. The top panel of each dataset table includes the details of the dataset and bottom panel is the significant status of each gene/pathway in each comparison. “up”, “down” and “NS” mean gene/pathway is up-regulated, down-regulated or not significant in the comparison, respectively. For example, IL1B is up-regulated in the comparison “CD responder at W0 vs Healthy”. Hovering the mouse over each cell can get detailed statistic values. Users can modify the threshold to change the status of each gene/pathway in each comparison by clicking the “Table Options” button (orange box).
After selecting one or multiple comparisons, users can click the “Filter Comparisons” button (blue box) to only remove all unselected comparisons or check “Include similar comparisons” in the pop-up dialog to only keep the comparisons with the same name with the selected comparisons. For the gene-level query, users can also click “Visualize Comparisons” to plot the boxplots for each gene in each comparison in the “Expression Visuals” panel.

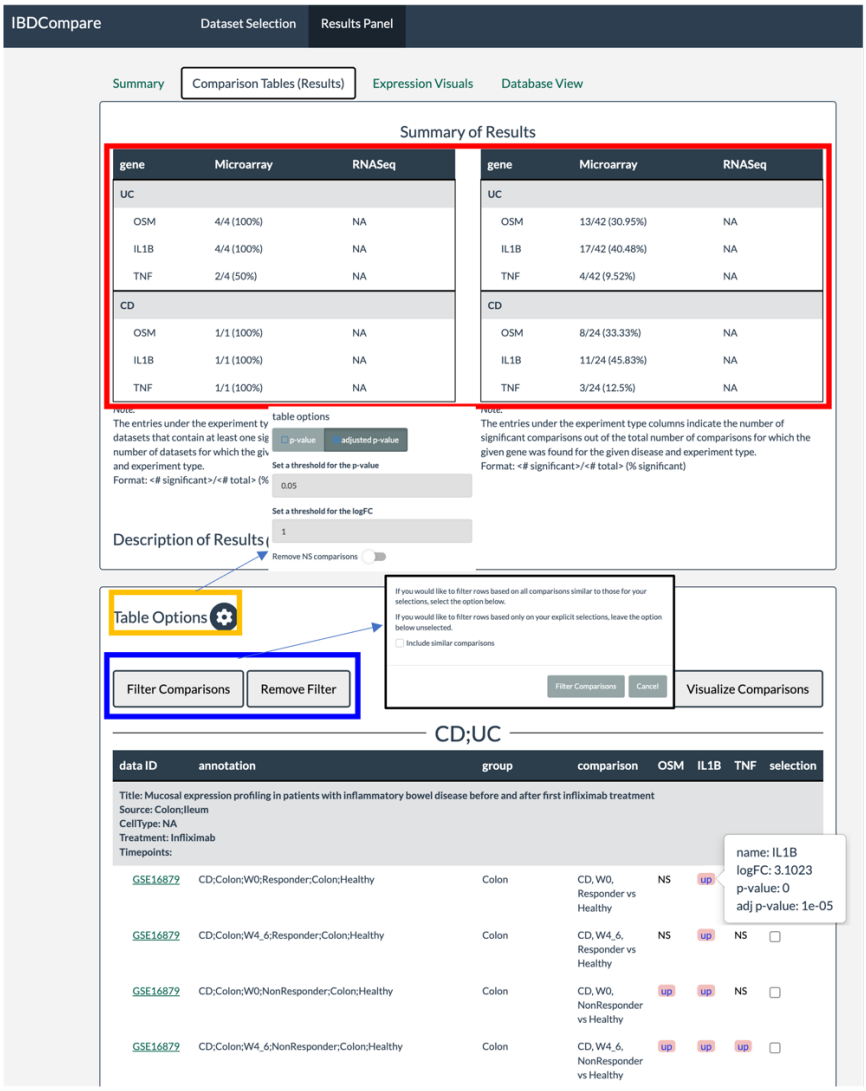

Figure 3. Comparison Tables tab in the Results Panel

In the “Expression Visuals” tab, each row represents a query gene and each column represents a comparison. Users can change the layout by clicking the top-left button (red box in Figure 4). Users can also perform meta analysis by clicking the “Run Meta Analysis” button (blue box). The meta result table will be shown under the boxplots. The table includes gene name, meta p value, meta adjusted p value and directionality. Clicking the triangle button can show the details of each gene in all selected comparisons.

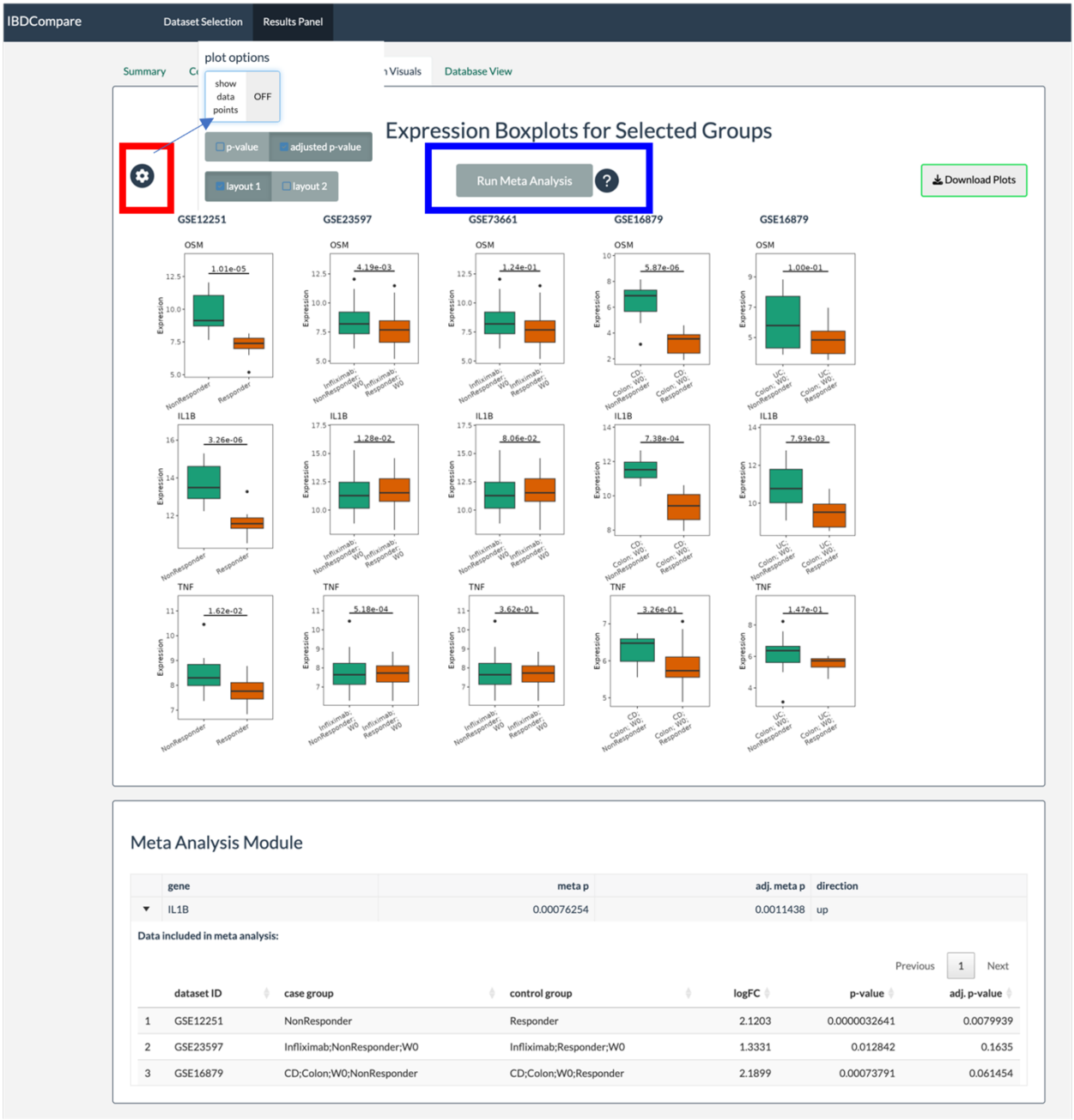

Figure 4. Expression Visuals tab in the Results Panel

“Database View” tab provides the information of the query genes in nine public databases. Clicking the “link” can check the gene information in each database.

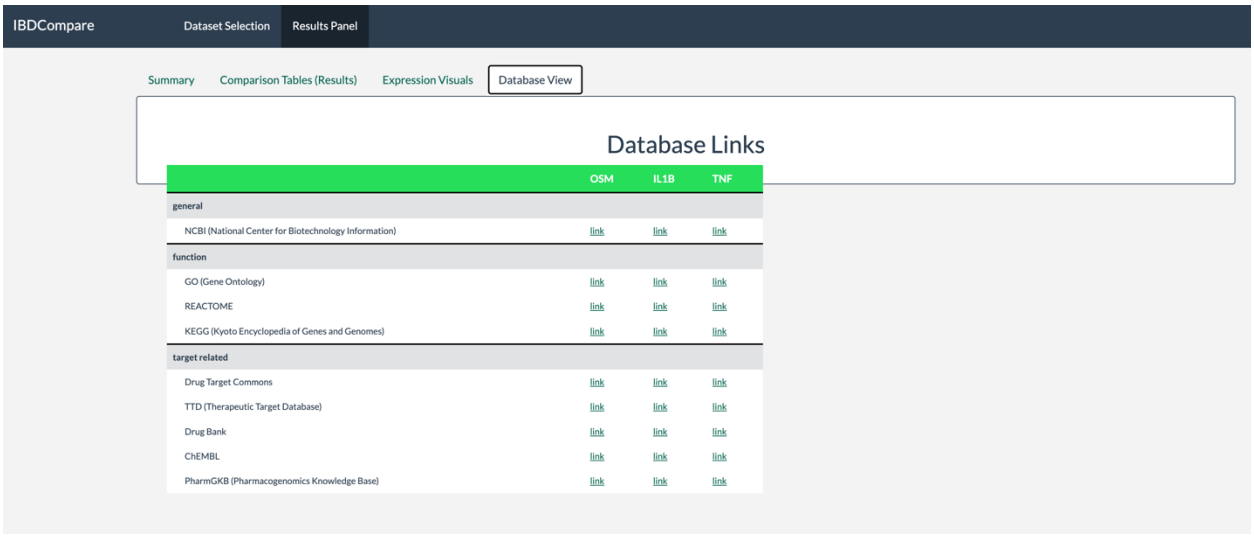

Figure 5. Database View tab in the Results Panel