

Understand the biology behind your QluCore Omics Explorer data

MetaCore

Introduction

This is a guide for biologists who are using QluCore Omics Explorer (QOE) visualization and statistical analysis tools and who want to gain additional insight into the underlying biology that drives your omics. The combination of QluCore Omics Explorer with Clarivate's MetaCore™ allows you to analyze huge amounts of complex omics data and rationalize the biological processes behind that data in one easy workflow.

QluCore Omics Explorer allows you to quickly explore, analyze and visualize large complex datasets to find discriminating variables (genes, proteins, metabolites etc) and to identify potentially new, interesting groups in the datasets. The built-in analytics allow you to quickly perform statistical tests such as t-test, ANOVA and regression analyses and identify discriminating variables. The results are visualized in plots that are updated in real time. QOE supports many different types of data. For gene expression analysis, data is typically loaded as RNA-seq BAM-files, pre-normalized txt or csv files. It is also possible to download and analyze public datasets from, for example, GEO and TCGA.

MetaCore is a molecular interactions database that allows you to upload gene lists from QOE and understand the biological pathways and processes that are driving your disease or treatment-response of interest. Various analysis workflows will guide you through mapping your data to manually curated interactions, signalling pathways, process networks and other ontologies to identify disrupted biological process in your studies. In addition, search across the wealth of information in MetaCore for relationships between genes, diseases, pathways, and other biological topics to understand disease mechanisms and identify potential targets and biomarkers for further investigation.

Use Case: Acute Lymphoblastic Leukemia

As an example of how QOE and MetaCore can be combined, we will analyze a gene expression dataset from pediatric acute lymphoblastic leukemia (ALL) patients, described by Ross et al., "Classification of pediatric acute lymphoblastic leukemia by gene expression profiling". *Blood* (2003), 102: 2951-9

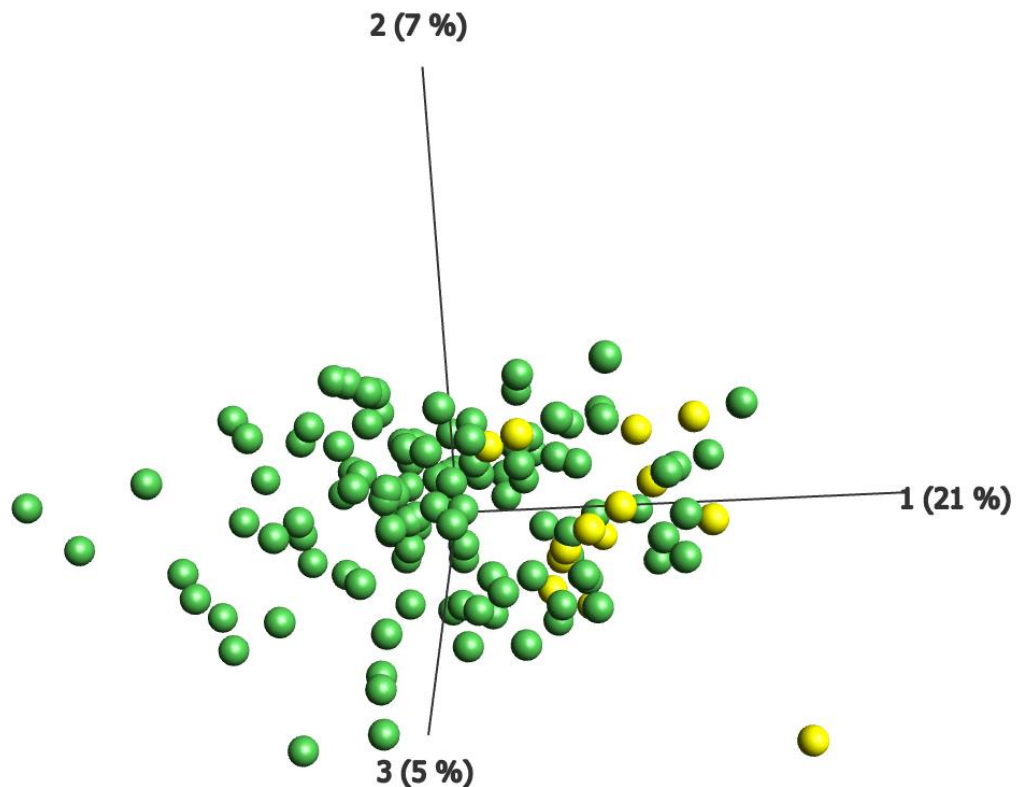
(<https://www.stjuderesearch.org/site/data/ALL3/>).

1. Using QOE to refine the data to a set of genes most likely to be driving the disease.
2. Exporting the gene list and expression fold-change so it can be imported into MetaCore.
3. Using MetaCore enrichment analysis to identify the disrupted pathways and biological processes in the pediatric ALL patients in this experiment.

Basic Statistical analysis in QluCore Omics Explorer

See the **Additional Support** section below for how to upload different types of data into QOE.

Once the data set is loaded, it is instantly visualized in a sample principal component analysis (PCA) plot:



132 samples from patients with Acute Lymphoblastic Leukemia (ALL) belonging to two subgroups – T-ALL (yellow) and B-ALL (green) visualized in a sample PCA plot. No filtering is done – the plot is based on all 22282 gene probes. The sample coloring was based on the annotations from the data set.

To separate the groups, a t-test (Two-group comparison) is applied, and the filters are set to a false discovery rate (FDR q-value) cutoff of 0.0019 and a Fold-change cutoff of 2,75.

Statistics

Variance

Statistics

Extended

Input: Variables after variance filter 22282/22282 v.

Filter by

Two Group Comparison

Leukemia Type

≠

T-ALL

B-ALL

Restriction

+

Eliminated factors

+

p =

3.9e-4

q =

0.0019516

|t₁₃₀| ≥ 3.6416

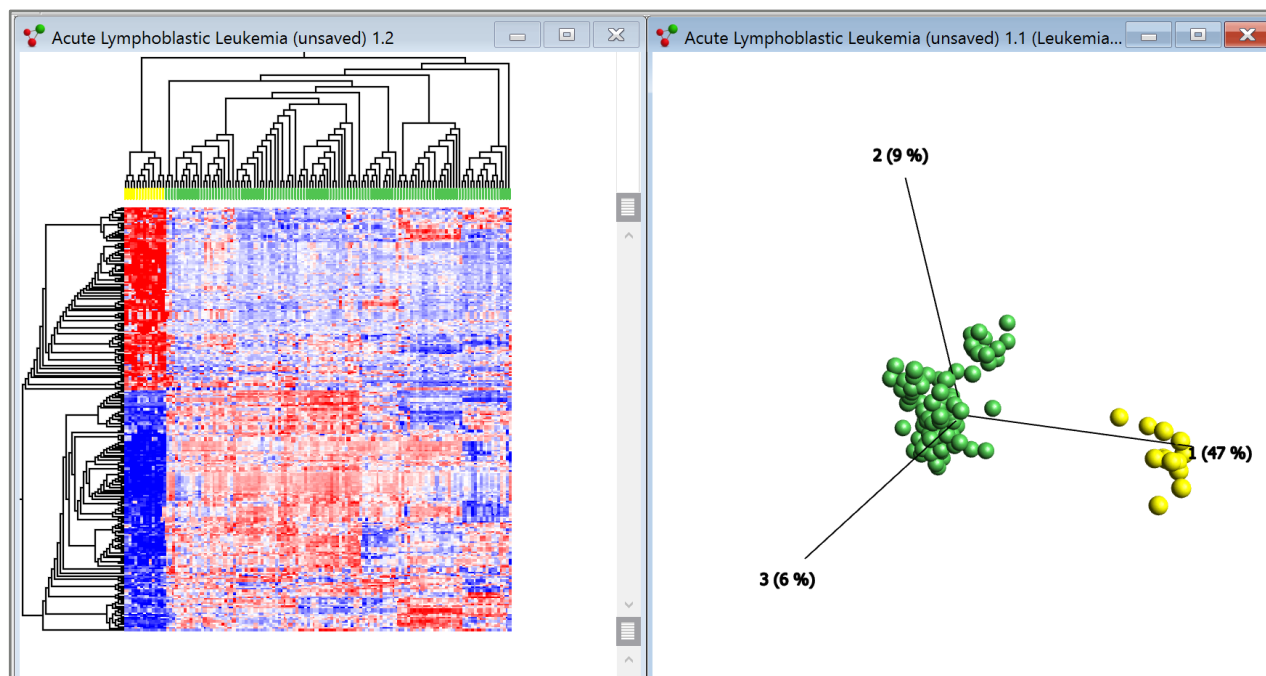
|R| ≥ 0.30425

Filter by

Fold Change

2.75

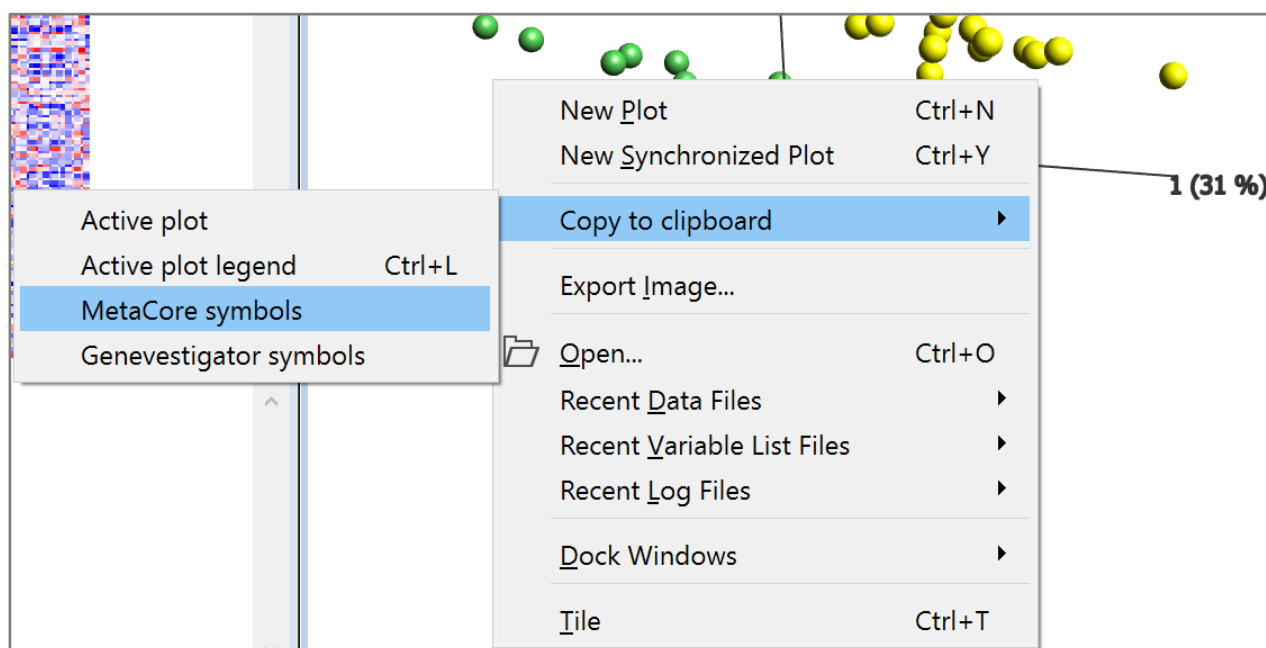
This results in 250 highly discriminating genes, as shown in the plots below.



The PCA plot and heatmap show a clear discrimination between genes that are over/under expressed in B-ALL versus T-ALL.

Exporting omics data for analysis in MetaCore

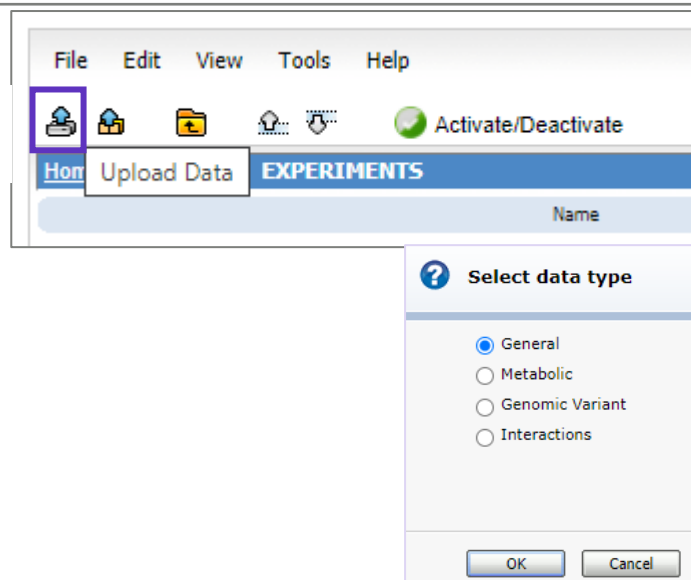
Having refined the data to a list of 250 highly discriminating genes, they can now be easily exported to MetaCore by right clicking in one of the plots, selecting Copy to clipboard > MetaCore symbols. The probe IDs and log expression fold-change is exported. This information should then be pasted into Excel and saved as a tab delimited text file.



Uploading omics data to MetaCore

Below is a quick reference guide to uploading the data:

1. Click "Upload Data" in the top left of your screen.



2. Select data type, General, to upload gene or proteins.
3. Select your file to upload in step 1 of the Data Analysis Wizard, then click "Next".
4. In Step 2, check the details are correct and select the column headers, then click "Next"
5. Choose the species in Step 3 > Next

Data Analysis Wizard (General parser)

Step 1

Click "browse" to select file(s) to upload:

[Choose File](#) Gene list 25...and B-all.txt

Background processing status

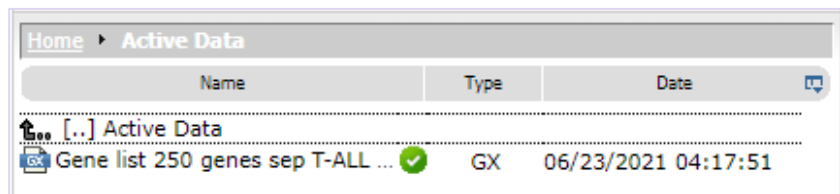
#	Start time	End time	Type	Experiment name	File location	Network objects	Status	Auto refresh
1	07/02/2021 13:41:54	13:41:58	General	250 genes sep T-all and B-all with log fold change	Show location	view	<div><div></div></div> Done	<input checked="" type="checkbox"/>

6. A status bar will let you know when your data is ready to analyze
7. Click the Experiment Name to activate your dataset in the Data Manager window

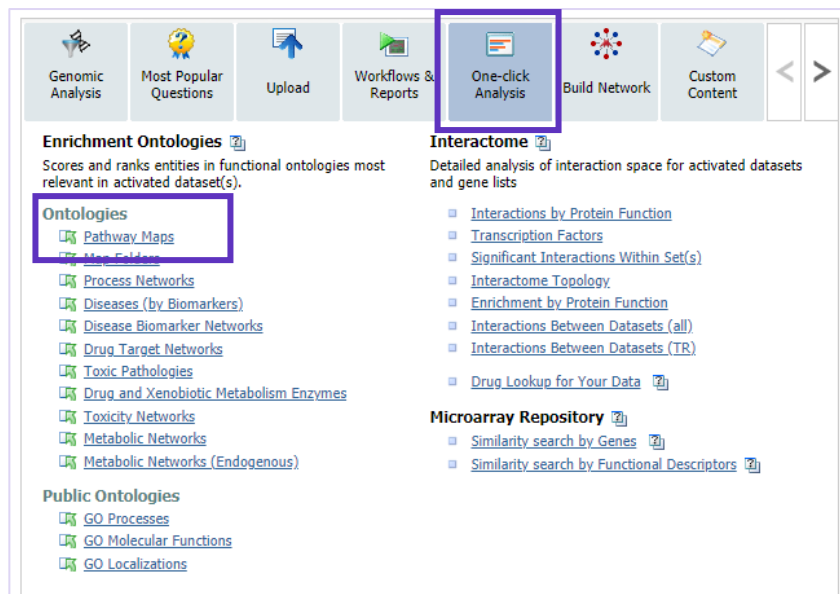
Metacore pathway enrichment

So far, we have refined the data using QOE and uploaded it to MetaCore for analysis. In this example, we'll use enrichment analysis to explore the most relevant pathways, processes, targets, biomarkers, and molecular functions in the dataset. The following steps will guide you through pathway map enrichment.

1. Make sure your dataset is in the "Active Data" window in the lower left panel of your screen



2. From the control panel on the upper right, select > One-Click Analysis, then > Pathway Maps



Interpreting the pathway map enrichment results

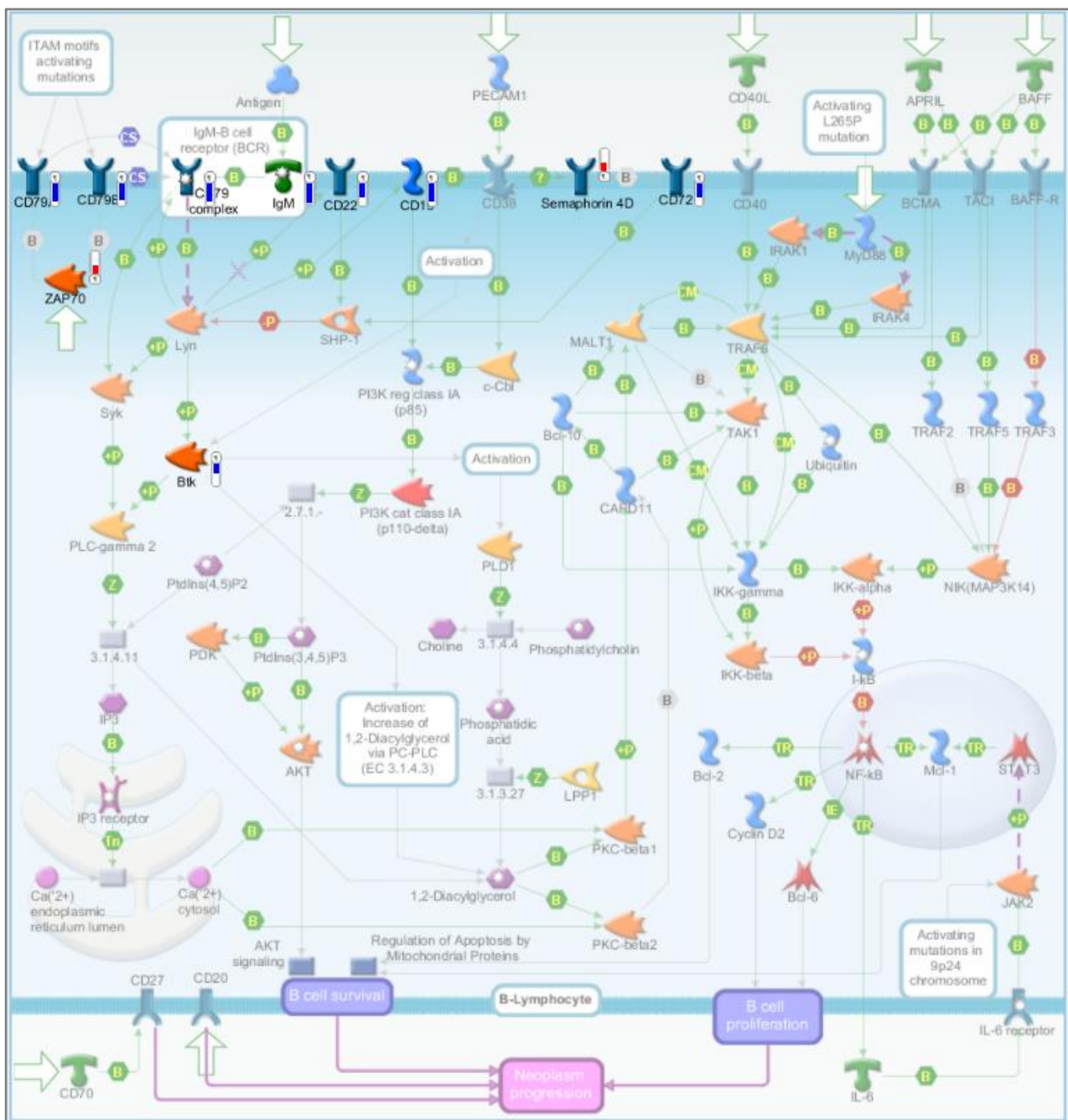
The pediatric ALL data has been mapped onto MetaCore's high quality, manually curated pathway maps.

Pathway Maps		Network Objects									
		Filter by Map Categories									
		0	2	4	6	8	10	-log(pvalue)	pValue	FDR	Ratio
<input type="checkbox"/>	1							3.040e-14	2.696e-11		13/51
<input type="checkbox"/>	2							1.443e-12	6.399e-10		12/53
<input type="checkbox"/>	3							3.408e-10	9.348e-8		10/49
<input type="checkbox"/>	4							4.216e-10	9.348e-8		10/50
<input type="checkbox"/>	5							1.343e-9	2.383e-7		9/41
<input type="checkbox"/>	6							2.181e-9	3.225e-7		13/118
<input type="checkbox"/>	7							3.450e-9	4.295e-7		12/100
<input type="checkbox"/>	8							3.874e-9	4.295e-7		12/101
<input type="checkbox"/>	9							8.114e-9	7.997e-7		8/35
<input type="checkbox"/>	10							3.384e-8	3.001e-6		10/77
<input type="checkbox"/>	11							1.573e-7	1.269e-5		7/34
<input type="checkbox"/>	12							2.060e-7	1.523e-5		6/22

The overlap between the dataset and pathway maps is calculated using a hypergeometric mean, and the P value of the mean overlap is used to sort the maps with the most significant overlap at the top of the list.

A quick scan of the map names shows highly enriched maps related to T- and B-Cell immune responses, which makes sense given the dataset came from ALL patients, and the disruptions occurring in their lymphocytes.

Click on the map name to see the map itself. For this example, the “B-cell signalling in hematologic malignancies” map was selected to demonstrate the visualization of the experimental pediatric ALL data in the context of this disease map:



This map shows a series of B-cell surface receptors have been under or over-expressed in the experimental dataset, displayed as thermometers where the amount of blue/red indicates the level of under/over-expression, activating a signal cascade that results in B-cell survival and progression of the neoplasm.

In Summary

The initial analysis with Qlucore Omics Explorer was able to differentiate B-Cell and T-Cell lymphomas in the dataset. From the differences in expression between the B-cell and T-cell lymphomas, we can hypothesize that the cell surface receptors shown above are driving the B-cell lymphoma in this subset of patients.

What next?

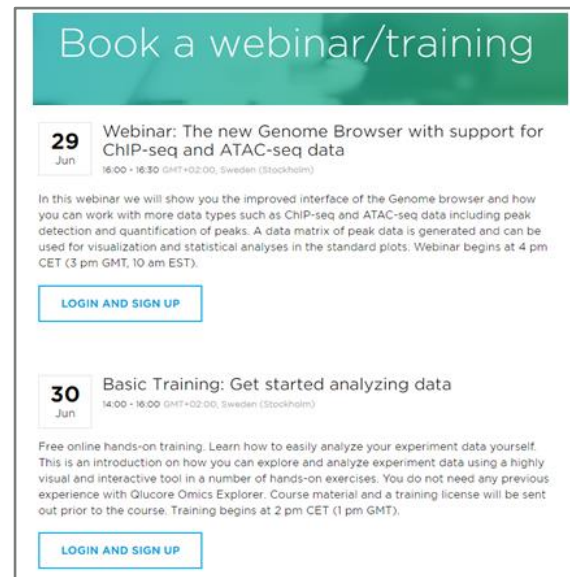
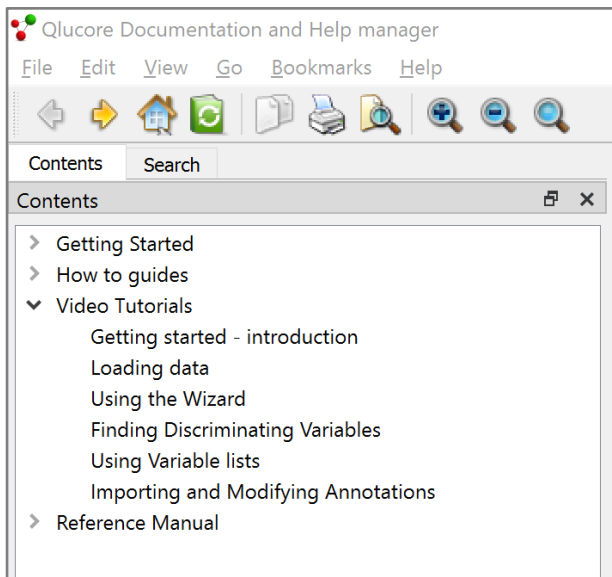
Having used QOE with MetaCore to rationalize the mechanistic drivers behind the ALL in these pediatric patients, you could go on to use MetaCore to explore possible biomarkers to differentiate the B- and T-Cell subtypes using the biomarker enrichment ontologies; or hypothesize druggable targets using the target enrichment.

The example above is for analysis of differential gene expression data from microarrays. The following datatypes can also be exported from QOE for analysis in MetaCore; and note that data from multiple different experiments on the same population can be combined in MetaCore with the Compare Experiments workflow.

- Gene expression (RNA-Seq and Array)
- Single-cell RNA-Seq
- Proteomics
- Metabolomics
- miRNA data
- qPCR data
- NGS module: RNA-Seq, DNA-Seq, ChIP-Seq and ATAC-Seq data (in QOE export to .txt file for analysis in MetaCore)

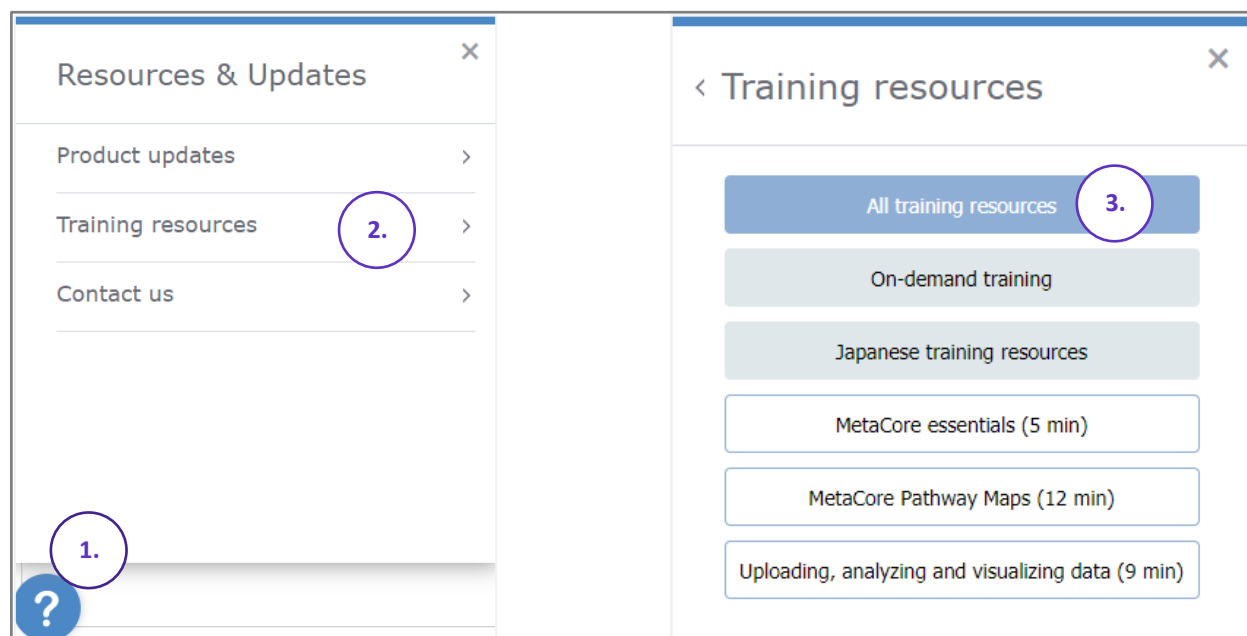
Additional Support

Learn more about how to explore, analyze and visualize your data with Qlucore Omics Explorer from the Video tutorials in the Help menu or join a webinar or hands-on training from [here](#)



Or contact Qlucore directly from [here](#)

Explore MetaCore's library of training resources to understand enrichment, interactome and network analysis:



Or use the “Contact us” link shown above to contact Clarivate Support.

For more information contact Customer Service at **LS Product Support**