Advanced IPA Training Based on a Long COVID Multi-Omics Study

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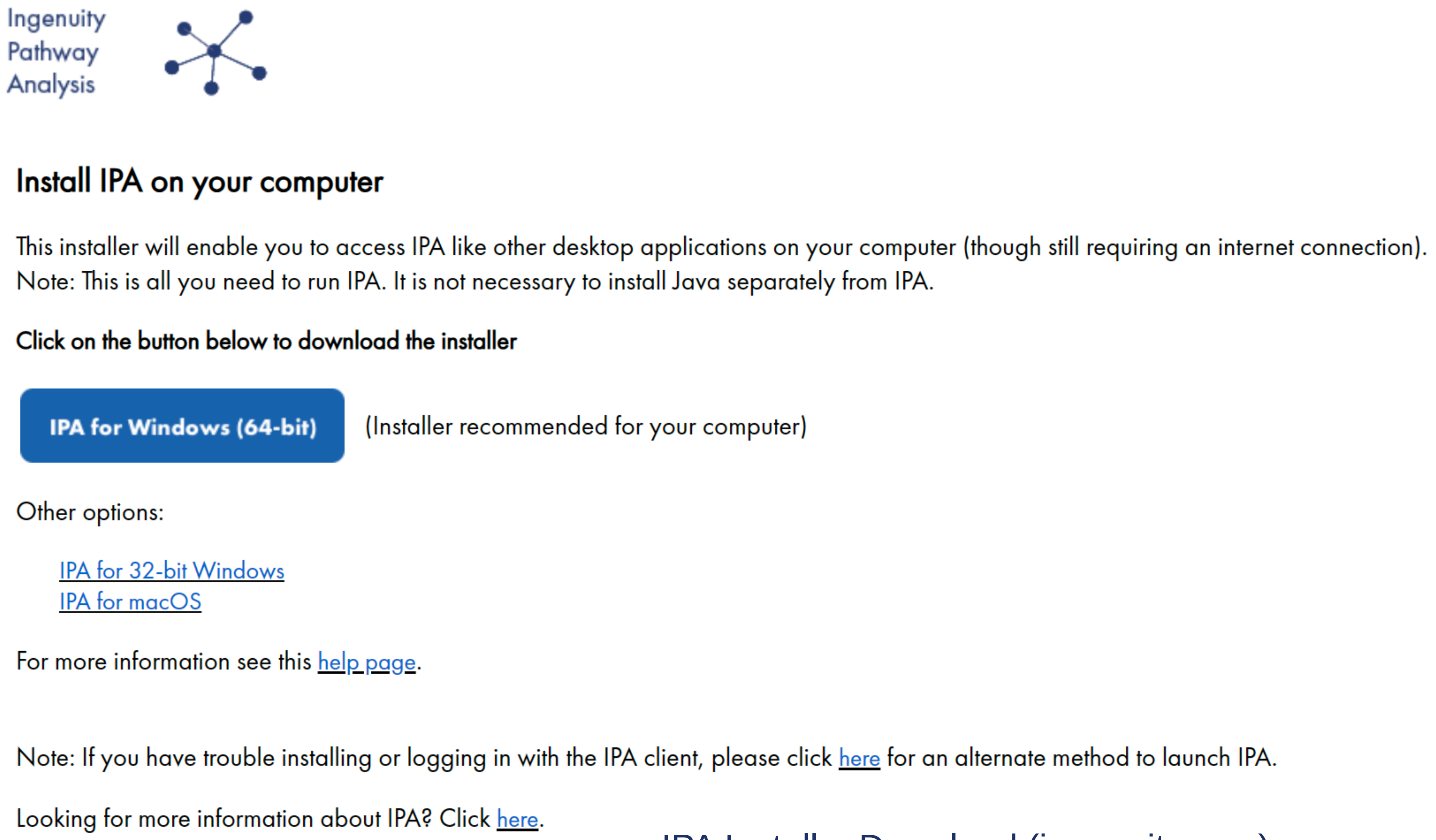
Choose your IPA installer



Install IPA on your computer

This installer will enable you to access IPA like other desktop applications on your computer (though still requiring an internet connection).
Note: This is all you need to run IPA. It is not necessary to install Java separately from IPA.

Click on the button below to download the installer

(Installer recommended for your computer)

Other options:

- IPA for 32-bit Windows
- IPA for macOS

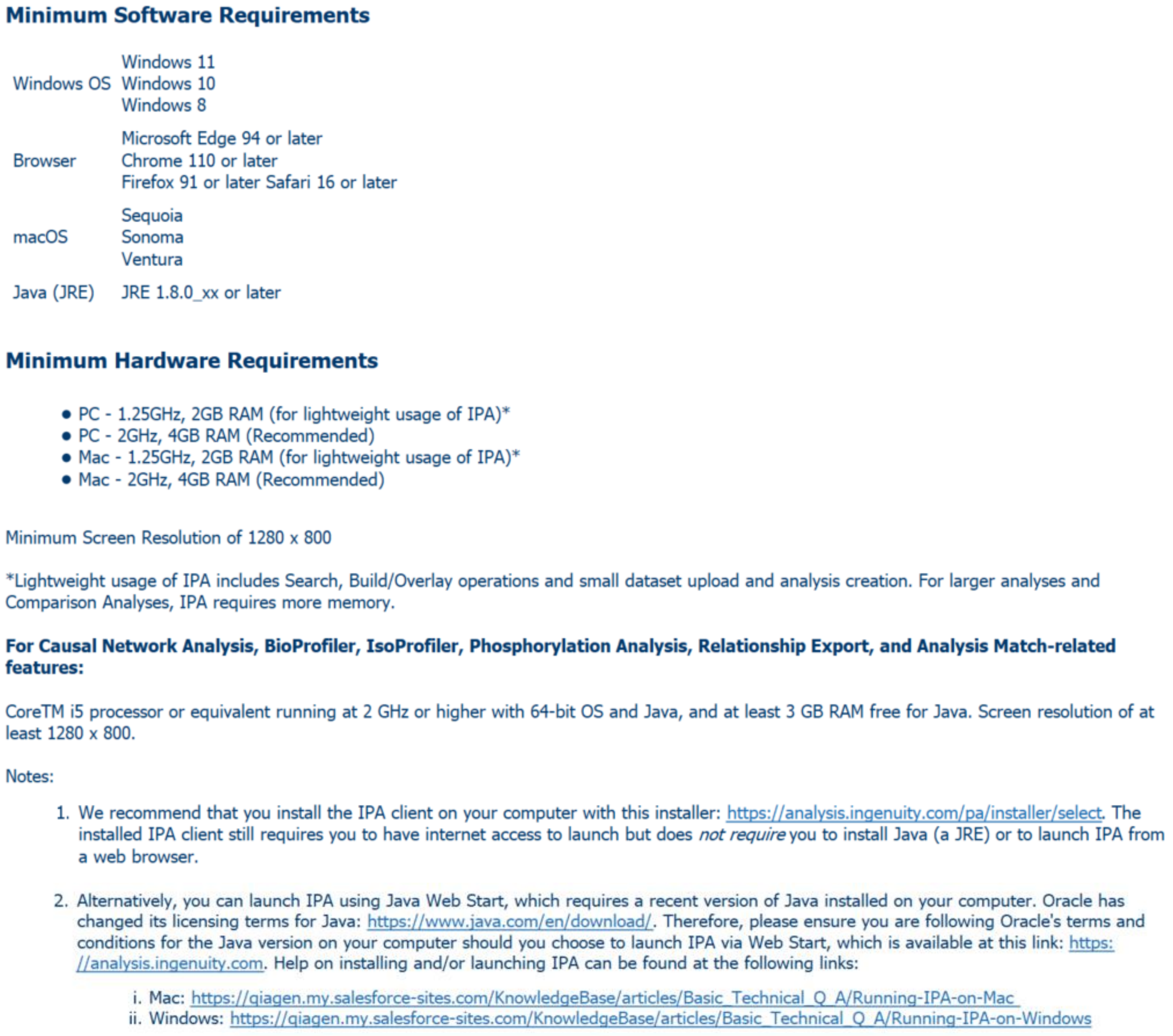
For more information see this help page.

Note: If you have trouble installing or logging in with the IPA client, please click here for an alternate method to launch IPA.

Looking for more information about IPA? Click here.

IPA Installer Download (ingenuity.com)

System Requirements



Minimum Software Requirements

Windows OS	Windows 11 Windows 10 Windows 8
Browser	Microsoft Edge 94 or later Chrome 110 or later Firefox 91 or later Safari 16 or later
macOS	Sequoia Sonoma Ventura
Java (JRE)	JRE 1.8.0_xx or later

Minimum Hardware Requirements

- PC - 1.25GHz, 2GB RAM (for lightweight usage of IPA)*
- PC - 2GHz, 4GB RAM (Recommended)
- Mac - 1.25GHz, 2GB RAM (for lightweight usage of IPA)*
- Mac - 2GHz, 4GB RAM (Recommended)

Minimum Screen Resolution of 1280 x 800

*Lightweight usage of IPA includes Search, Build/Overlay operations and small dataset upload and analysis creation. For larger analyses and Comparison Analyses, IPA requires more memory.

For Causal Network Analysis, BioProfiler, IsoProfiler, Phosphorylation Analysis, Relationship Export, and Analysis Match-related features:

CoreTM i5 processor or equivalent running at 2 GHz or higher with 64-bit OS and Java, and at least 3 GB RAM free for Java. Screen resolution of at least 1280 x 800.

Notes:

1. We recommend that you install the IPA client on your computer with this installer: https://analysis.ingenuity.com/pa/installer/select. The installed IPA client still requires you to have internet access to launch but does *not require* you to install Java (a JRE) or to launch IPA from a web browser.

2. Alternatively, you can launch IPA using Java Web Start, which requires a recent version of Java installed on your computer. Oracle has changed its licensing terms for Java: https://www.java.com/en/download/. Therefore, please ensure you are following Oracle's terms and conditions for the Java version on your computer should you choose to launch IPA via Web Start, which is available at this link: https://analysis.ingenuity.com. Help on installing and/or launching IPA can be found at the following links:
   i. Mac: https://qiagen.my.salesforce-sites.com/KnowledgeBase/articles/Basic_Technical_Q_A/Running-IPA-on-Mac
   ii. Windows: https://qiagen.my.salesforce-sites.com/KnowledgeBase/articles/Basic_Technical_Q_A/Running-IPA-on-Windows

IPA Installer Download (ingenuity.com)

Agenda

Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

- Introduction of Ingenuity Pathway Analysis
- What's new in Ingenuity Pathway Analysis

Create networks from scratch

Interpreting your ′omics data using IPA

- Data upload and analysis setup
- Canonical pathways and upstream regulators
- Comparison analysis
- Diseases and functions/Tox analysis

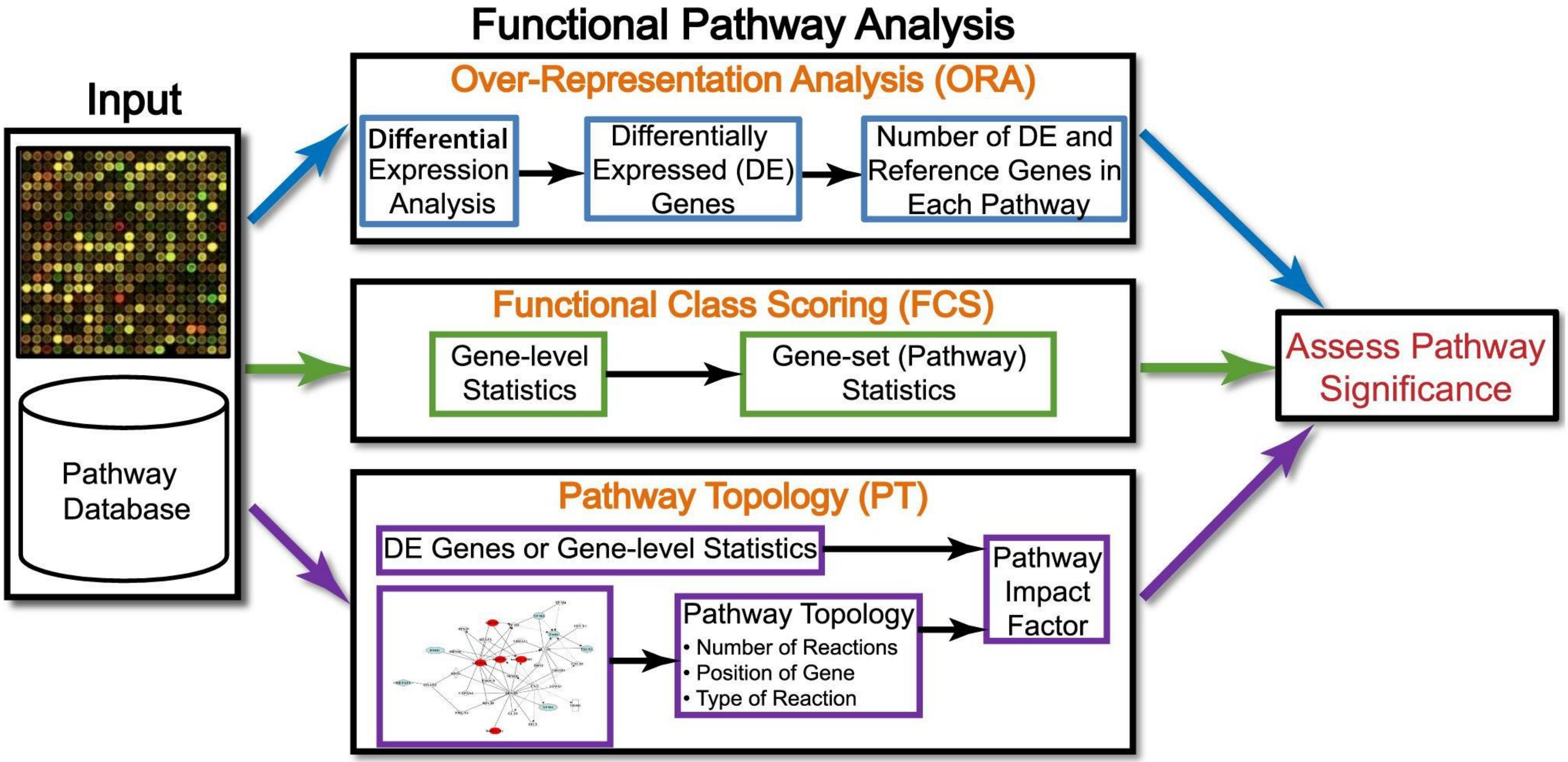
Creating networks from gene list

Bioprofiler

Comparison analysis

Summary

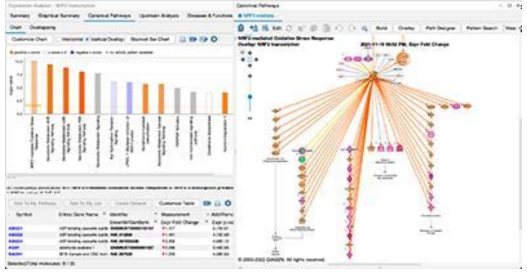
Introduction of pathway analysis



Khatri, Sirota, and Butte. *PLoS Comp Bio*. 2012.

QIAGEN – from Sample to Insight

An example: Analyzing variant data from Sample to Insight



Sample to data

NGS library prep
Sequencing

- Platform- and assay-agnostic
- Whole genome, whole exome, custom panels

Data to information

Normalization and quality control

Read mapping

Variant calling

- **QIAGEN CLC Genomics Workbench, Server and Cloud Computation**

BaseSpace ad Amazon Web Service integration

Information to knowledge

Data integration

Metadata exploration

Differential expression

- **QIAGEN OmicSoft Suite, Lands, and APIs**

Curated experiments

- **QIAGEN OmicSoft Lands: OncoLand, DiseaseLand, Single Cell Land**

Knowledge to insight

Interpretation

Pathway analysis

- **QIAGEN IPA**

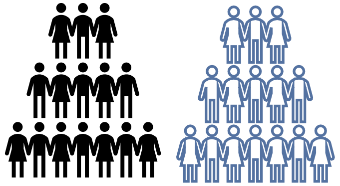
Variant interpretation

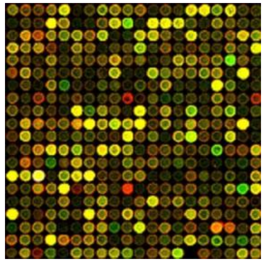
- **QCI Translational, HSMD, HGMD and COSMIC**

Portfolio designed to transition complex ′omics data into high-value actionable insights without the need for deep expertise

Why are we using Qiagen Ingenuity Pathway analysis?

Your dataset





PDE6A
SLC6A14
LPCAT1
C2
CFB
REG4
CD55
TIMP1
DPP10
PDIA4
PRKG2
NAT8B
SHISA5
LCN2
CDH3
ACAT1
NAALADL1
APOBEC3B
NMT2
KYNU
TMEM63C
S100A11
PI3
CDC25B
CNNM2
CHRNA1
LRRN2
RMDN2
CNTFR
CDC14A
C7orf31
BACE2
CXCL1
SLC36A1
WDR78
PKM

→

Public /commercial database

Drugs and chemicals

Pathway

Disease

Function

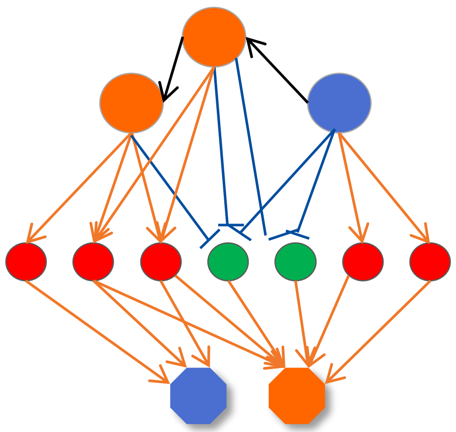
Network

ORA/FCS/Topology Pathway Analysis

Machine learning

→

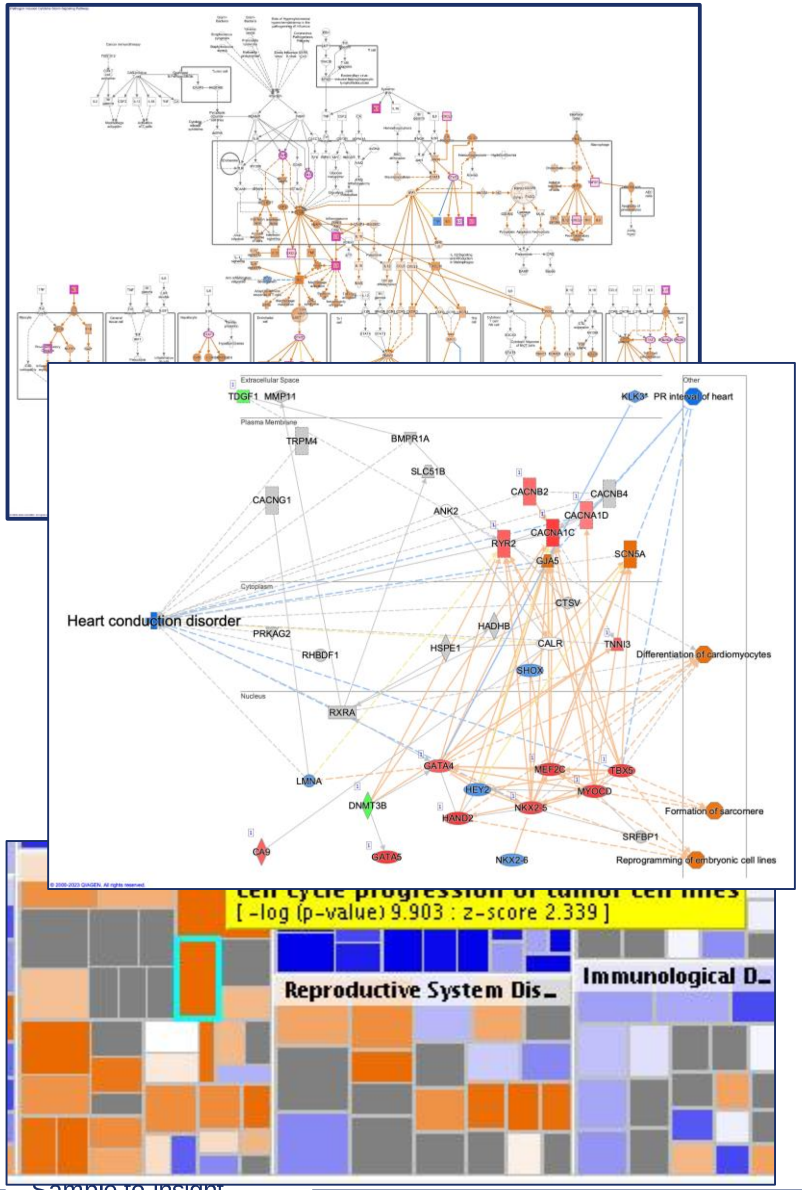
What do they relate to each other?

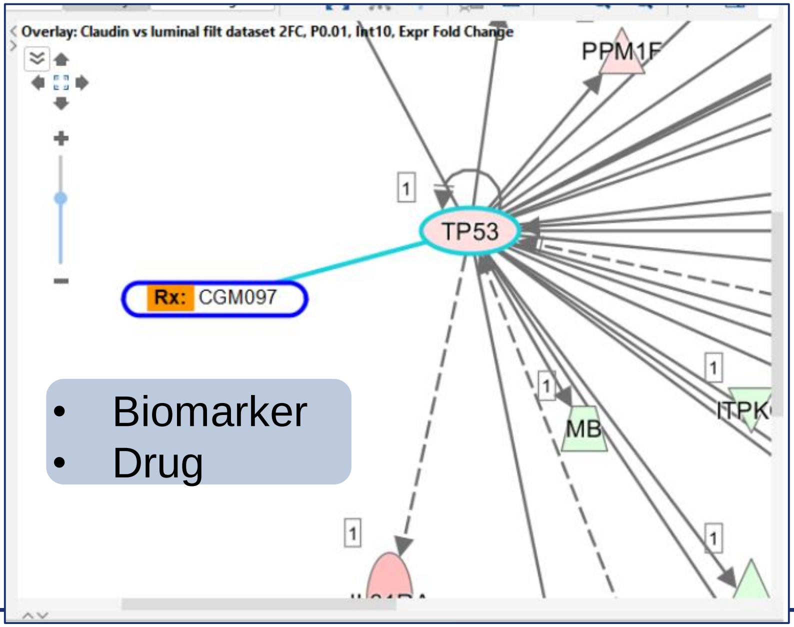


What are the relationship between each molecules?

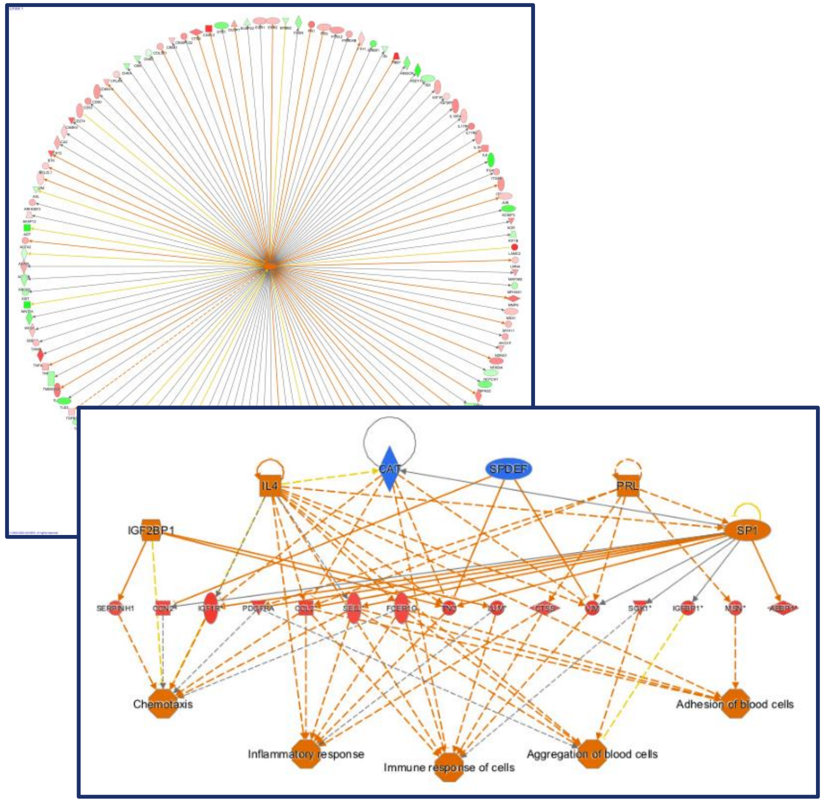
What Can We Achieve with IPA?

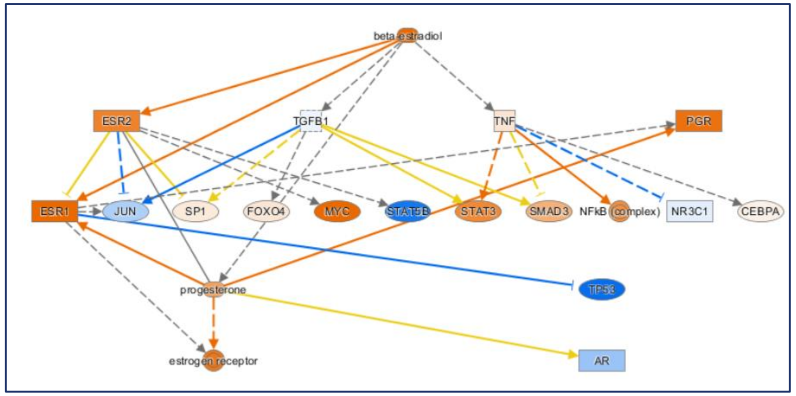
1. Canonical pathway
2. Machine Learning disease pathway
3. Disease and function
4. Upstream regulator
5. Regulate effect
6. Network





- Biomarker
- Drug





Publication using Qiagen Ingenuity Pathway Analysis

訊聯基因數位

> Hepatol Commun. 2020 Mar 15;4(5):724-738. doi: 10.1002/hep4.1497. eCollection 2020 May.

Integrated GWAS and mRNA Microarray Analysis Identified IFNG and CD40L as the Central Upstream Regulators in Primary Biliary Cholangitis

GWAS

1,738 results

☐ 1 **Ingenuity pathway analysis** of alpha-synuclein predicts potential signaling pathways, network molecules, biological functions, and its role in neurological diseases.
Suthar SK, Lee SY.
Front Mol Neurosci. 2022 Nov 29;15:1029682. doi: 10.3389/fnmol.2022.1029682. eCollection 2022.
PMID: 36523604 Free PMC article.
We have taken the advantage of such a Bioinformatics tool, **ingenuity pathway analysis** (IPA) to decipher the signaling pathways, interactome, biological functions, and role of alpha-synuclein. ...

☐ 2 Gene set enrichment analysis and **ingenuity pathway analysis** to verify the impact of Wnt signaling in psoriasis treated with Taodan granules.
Chen Y, Zhang Z, Zhang Y, Jiang J, Luo Y, Fei X, Ru Y, Li B, Zhang H, Liu T, Yang Y, Kuai L, Song J, Luo Y.
Am J Transl Res. 2023 Jan 15;15(1):422-434. eCollection 2023.
PMID: 36777818 Free PMC article.
MATERIALS AND METHODS: Primarily, transcriptional profiling was applied to identi expressed genes (DEGs), proceeding with Gene ontology (GO) and Kyoto Encyclope Genomes (KEGG) analysis. Gene Set Enrichment Analysis (GSEA) and **Ingenuity P** ...

☐ 3 Gene set enrichment analysis and **ingenuity pathway analysis** t biomarkers in Sheng-ji Hua-yu formula treated diabetic ulcers.
Ru Y, Zhang Y, Xiang YW, Luo Y, Luo Y, Jiang JS, Song JK, Fei XY, Yang D, Zhang Z, Zh SY, Li B, Kuai L.
J Ethnopharmacol. 2022 Mar 1;285:114845. doi: 10.1016/j.jep.2021.114845. Epub 20
PMID: 34800645
GO and KEGG enrichment analysis were used to identify the mechanisms underlying effect of SJHY formula, and then gene set enrichment analysis and **ingenuity pathway analysis** were conducted for functional analysis. ...

From 2019-2025
2,127literatures

> J Neuroinflammation. 2024 Mar 20;21(1):69. doi: 10.1186/s12974-024-03065-z.

Deletion of Slc9a1 in $Cx3cr1^+$ cells stimulated microglial subcluster CREB1 signaling and microglia-oligodendrocyte crosstalk

transcriptomic

> Stem Cells Transl Med. 2024 Mar 15;13(3):293-308. doi: 10.1093/stcltm/szad090.

Histone Trimethylations and HDAC5 Regulate Spheroid Subpopulation and Differentiation Signaling of Human Adipose-Derived Stem Cells

Single-cell RNA-seq

> J Allergy Clin Immunol. 2024 May;153(5):1268-1281. doi: 10.1016/j.jaci.2023.12.030. Epub 2024 Mar 29.

Galectin-10 in serum extracellular vesicles reflects asthma pathophysiology

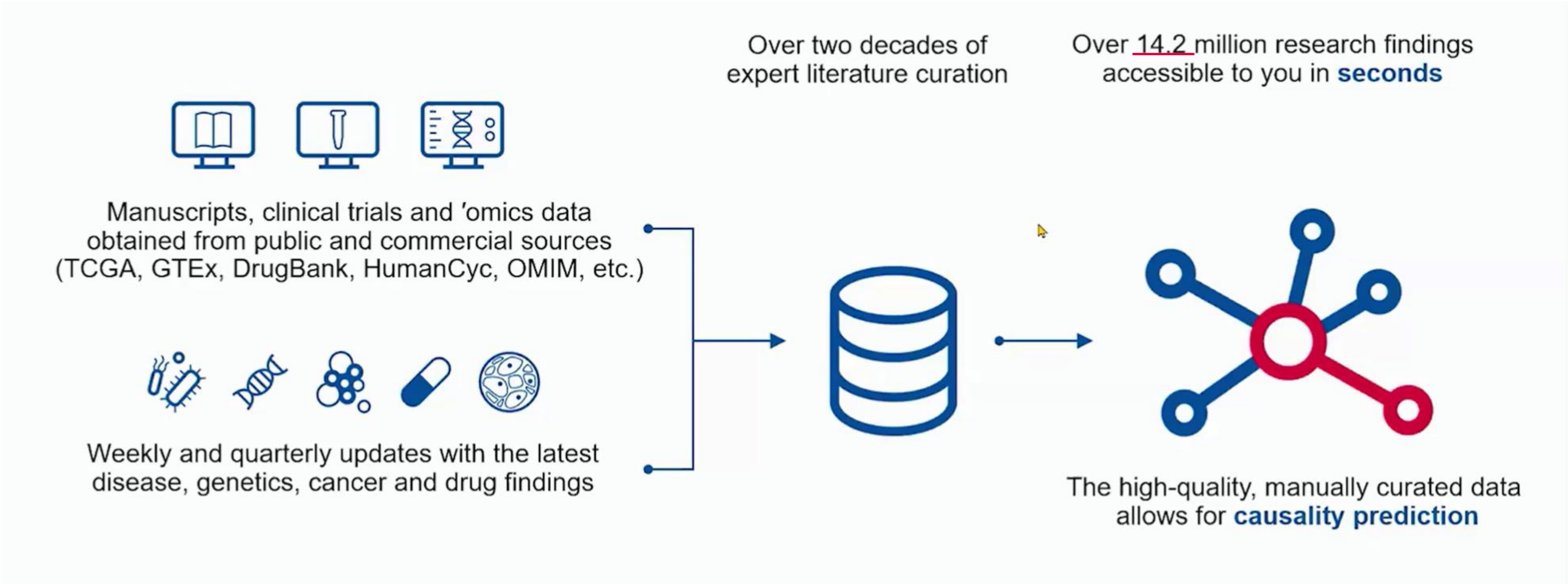
proteinomics

> Chin Med. 2022 Jun 15;17(1):71. doi: 10.1186/s13020-022-00632-5.

Serum metabolomics analysis of deficiency pattern and excess pattern in patients with rheumatoid arthritis

metabolomics

Ingenuity Pathway Analysis is powered by QIAGEN knowledge base



Over two decades of expert literature curation

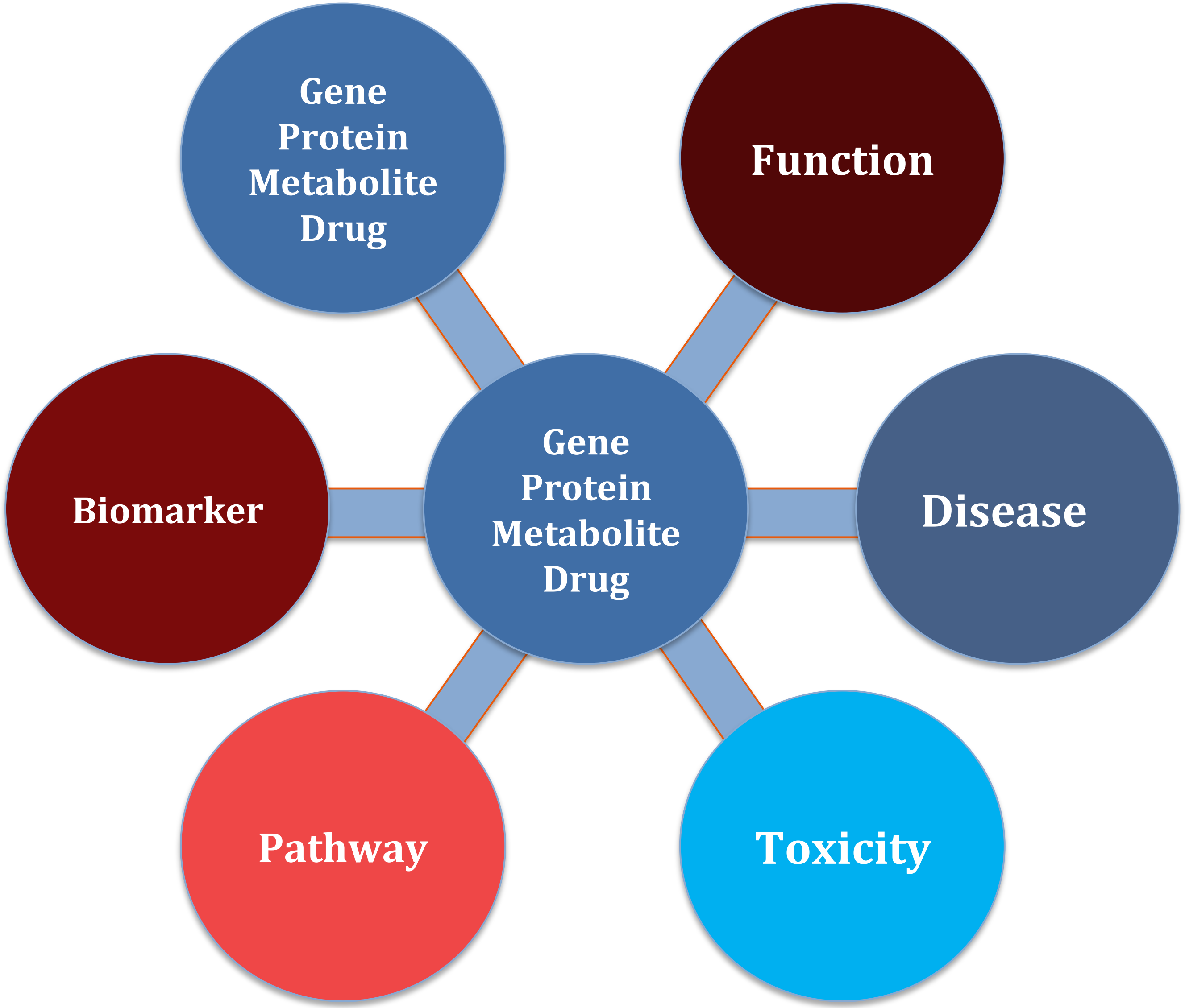
Over 14.2 million research findings accessible to you in **seconds**

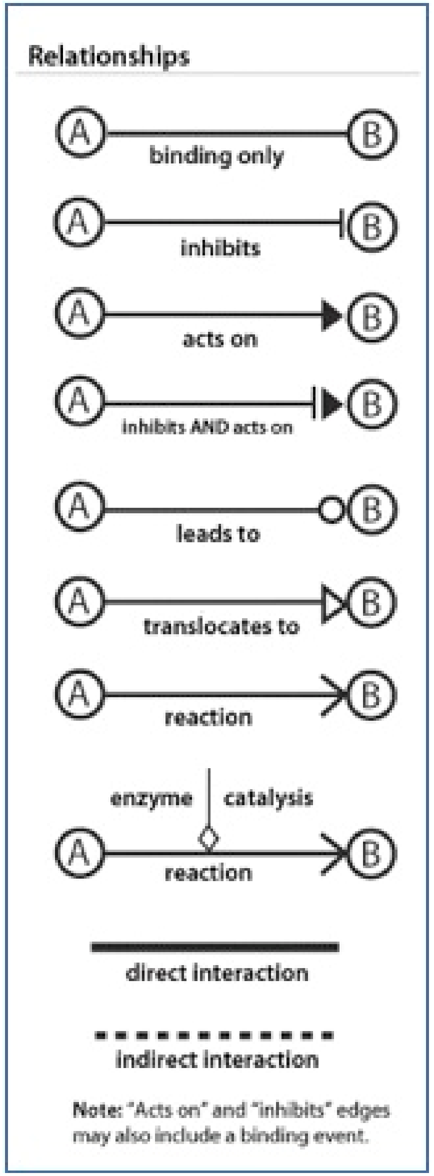
Manuscripts, clinical trials and 'omics data obtained from public and commercial sources (TCGA, GTEx, DrugBank, HumanCyc, OMIM, etc.)

Weekly and quarterly updates with the latest disease, genetics, cancer and drug findings

The high-quality, manually curated data allows for **causality prediction**

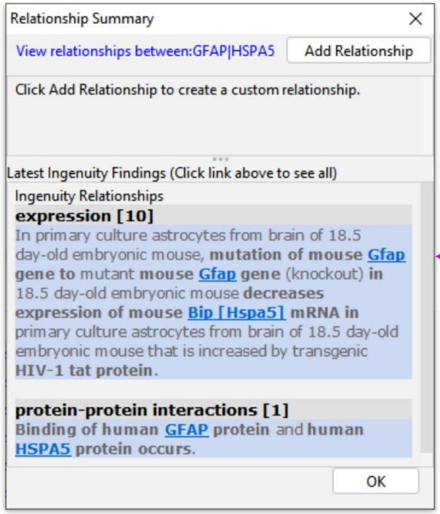
Using IPA to Discover Relationships in Experimental Data





Note: "Acts on" and "inhibits" edges may also include a binding event.

Every connection in IPA is backed by literature findings



View relationships between:GFAP|HSPA5

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

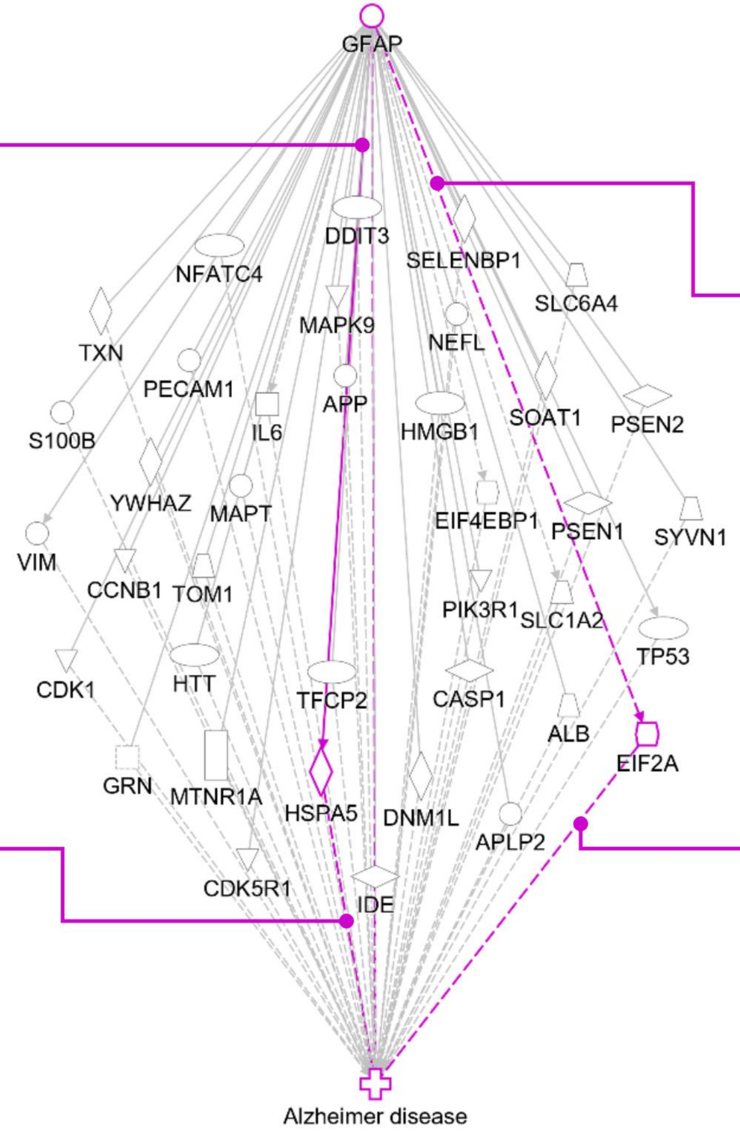
Ingenuity Relationships

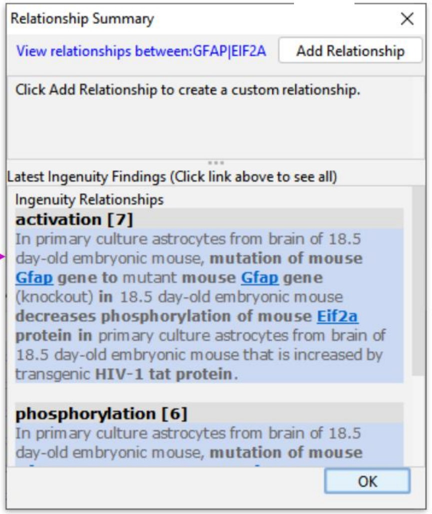
expression [10]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse Gfap gene to mutant mouse Gfap gene** (knockout) **in** 18.5 day-old embryonic mouse **decreases expression of mouse Bip [Hspa5] mRNA in** primary culture astrocytes from brain of 18.5 day-old embryonic mouse that is increased by transgenic **HIV-1 tat protein**.

protein-protein interactions [1]

Binding of human GFAP protein and **human HSPA5 protein occurs.**





View relationships between:GFAP|EIF2A

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

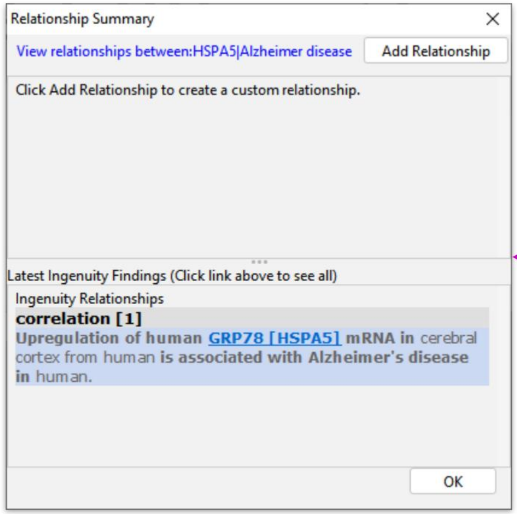
Ingenuity Relationships

activation [7]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse Gfap gene to mutant mouse Gfap gene** (knockout) **in** 18.5 day-old embryonic mouse **decreases phosphorylation of mouse Eif2a protein in** primary culture astrocytes from brain of 18.5 day-old embryonic mouse that is increased by transgenic **HIV-1 tat protein**.

phosphorylation [6]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse**



View relationships between:HSPA5|Alzheimer disease

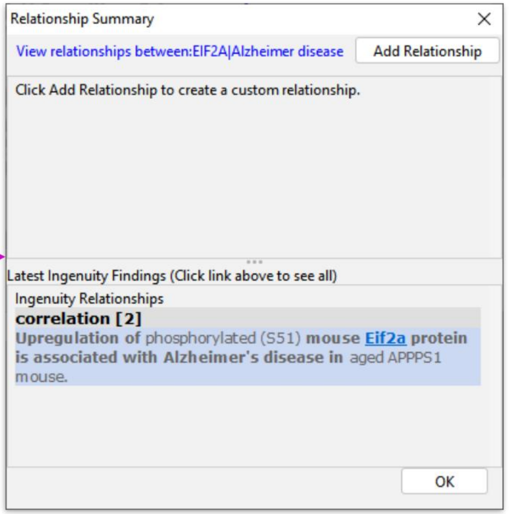
Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [1]

Upregulation of human GRP78 [HSPA5] mRNA in cerebral cortex from human **is associated with Alzheimer's disease in** human.



View relationships between:EIF2A|Alzheimer disease

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [2]

Upregulation of phosphorylated (S51) **mouse Eif2a protein is associated with Alzheimer's disease in** aged APPPS1 mouse.

Species Support within IPA

Fully supported:

Human

Mouse

Rat

What species identifiers are accepted for analysis by IPA?

- ✓ Atlantic Salmon (*Salmo salar*)
- ✓ Thale cress (*Arabidopsis thaliana)*
- ✓ Bat (Greater horseshoe bat, *Rhinolophus ferrumequinum*)
- ✓ Brewer's yeast (*Saccharomyces cerevisiae)*
- ✓ Cat (domestic, *Felis catus*)
- ✓ Chicken (*Gallus gallus*)
- ✓ Chimpanzee (*Pan troglodytes*)
- ✓ Chinese hamster (*Cricetulus griseus*)
- ✓ Cow (*Bos taurus*)
- ✓ Crab-eating macaque (*Macaca fascicularis*)
- ✓ Dog (*Canis lupus familiaris*)
- ✓ Fission yeast (*Schizosaccharomyces pombe)*
- ✓ Fruit fly (*Drosophila melanogaster*)
- ✓ Golden hamster (*Mesocricetus auratus*)
- ✓ Guinea pig, domestic (*Cavia porcellus*)
- ✓ Horse (*Equus caballus*)
- ✓ Human (*Homo sapiens*)
- ✓ Mouse (*Mus musculus*)
- ✓ Pig (*Sus scrofa*)
- ✓ Rabbit (*Oryctolagus cuniculus*)
- ✓ Rainbow trout (*Oncorhynchus mykiss*)
- ✓ Rat (*Rattus norvegicus*)
- ✓ Rhesus Monkey (*Macaca mulatta*)
- ✓ Roundworm (*Caenorhabditis elegans)*
- ✓ Sheep (*Ovis aries*)
- ✓ Western clawed frog (*Xenopus tropicalis*)
- ✓ Zebrafish (*Danio rerio*)

Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

Supported Identifiers for Data Upload

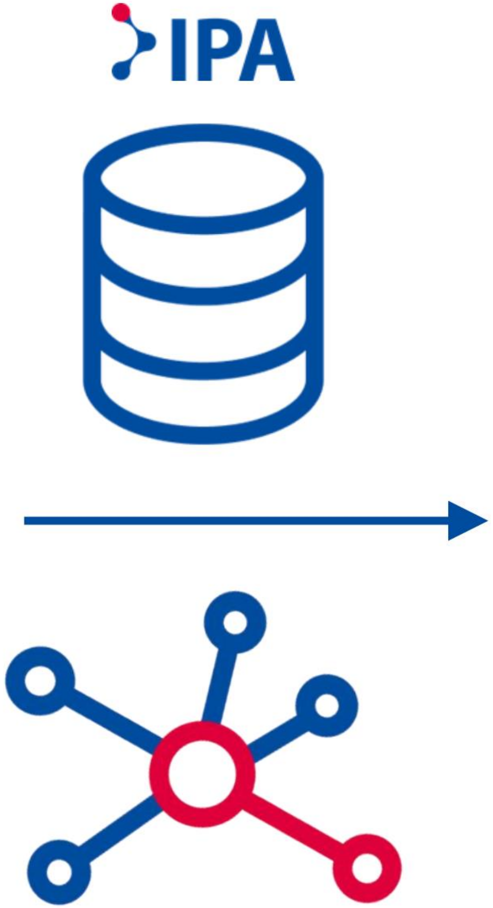
Get more complete mapping during dataset upload!

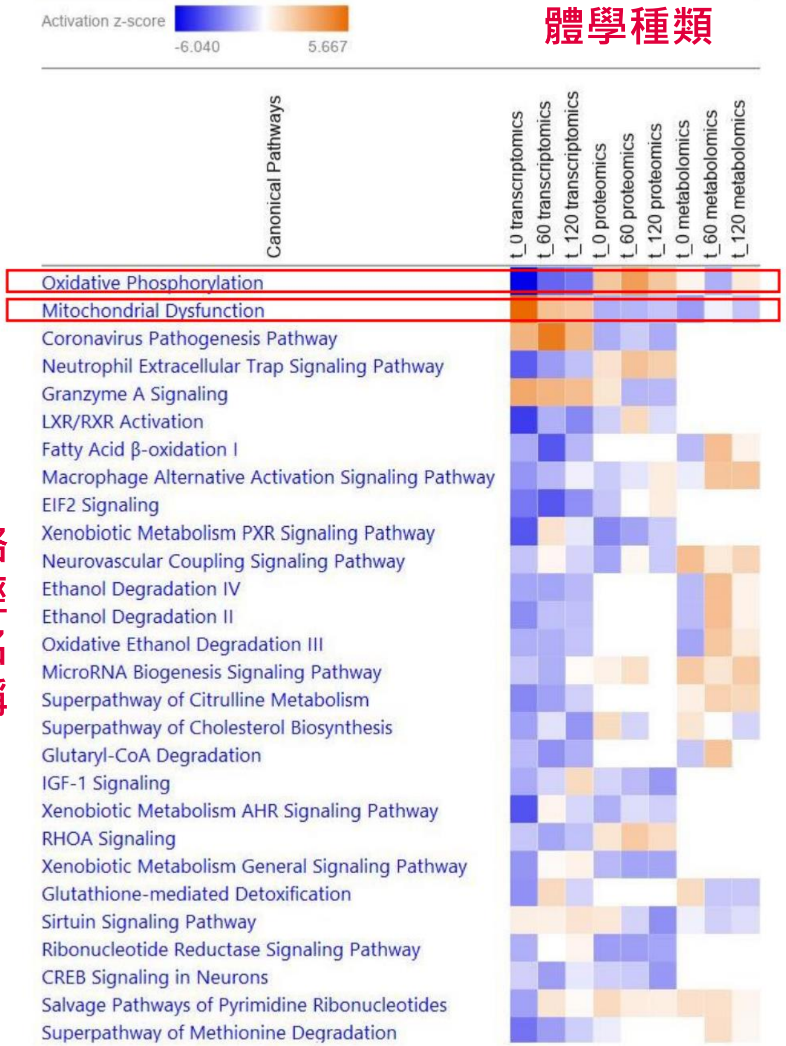
Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2023/8)	GenPept	Ensembl (110)	miRbase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (257)	International Protein Index (IPI)	RefSeq (human、mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human (HUGO/ HGNC, EG)	UniProt/ Swiss-Prot Accession (2022_02)	UCSC (hg18)			KEGG
Codelink	Symbol- mouse (EG)		UCSC (hg19)			PubChem CID
Illumina	Symbol- rat (EG)		UCSC (hg38)			
Ingenuity	GI Number					
	UniGene					

Multi-omics data analysis using QIAGEN IPA

Omics data type

- RNA-seq
- scRNA-seq
- Microarray
- Nanostring
- qPCR
- ChIP-seq
- Proteomics
- Metabolomics
- RNAi
- CRISPR
- WGS/WES etc.





體學種類

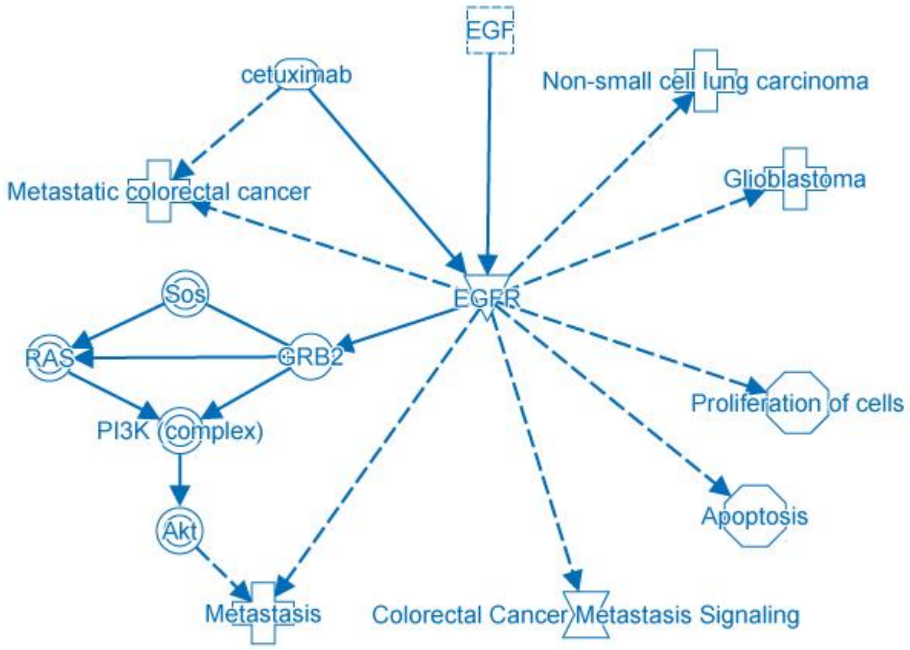
路徑名稱

QIAGEN IPA – a dual approach to data analysis

With dataset	Without dataset
• Find connections in your data	• Search and explore the QIAGEN Knowledge Base
• Identify novel biomarkers	• Test hypothesis in silico
• Uncover key targets and regulators	• Identify degree of novelty in a hypothesis
• Discover novel disease mechanisms	
• Compare across experiments	

Example of Biomedical Knowledge Base findings

Selected biomedical relationships between different types of Attributes for selected biomedical relationships entities



Cetuximab is a metastatic colorectal cancer drug. EGFR is a target of cetuximab. Molecular interactions enable you to reconstruct a pathway between EFG, EGFR and the pathological process metastasis. EGFR is a known member of the canonical pathway Colorectal Cancer Metastasis Signaling. In addition to metastatic colorectal cancer, EGFR is involved in other diseases, for example non-small cell lung carcinoma and glioblastoma. Activation of cell proliferation and inhibition of apoptosis by EGFR are known oncology mechanisms.

EGF – EGFR

[one of many]

Type: activation
Direction: directional
Effect: increases
Directness: direct
Tissue or primary cell: epithelial cells
Subcellular location: plasma membrane
Source: PubMed PMID: 17909010

cetuximab – EGFR

[one of many]

Type: phosphorylation
Direction: directional
Effect: decreases
Cell line: CaR1 cells
Organism: human
Experiment: anti-phosphoresidue immunoblot
Source: PubMed PMID: 23213241

EGFR – Proliferation of cells

[one of many]

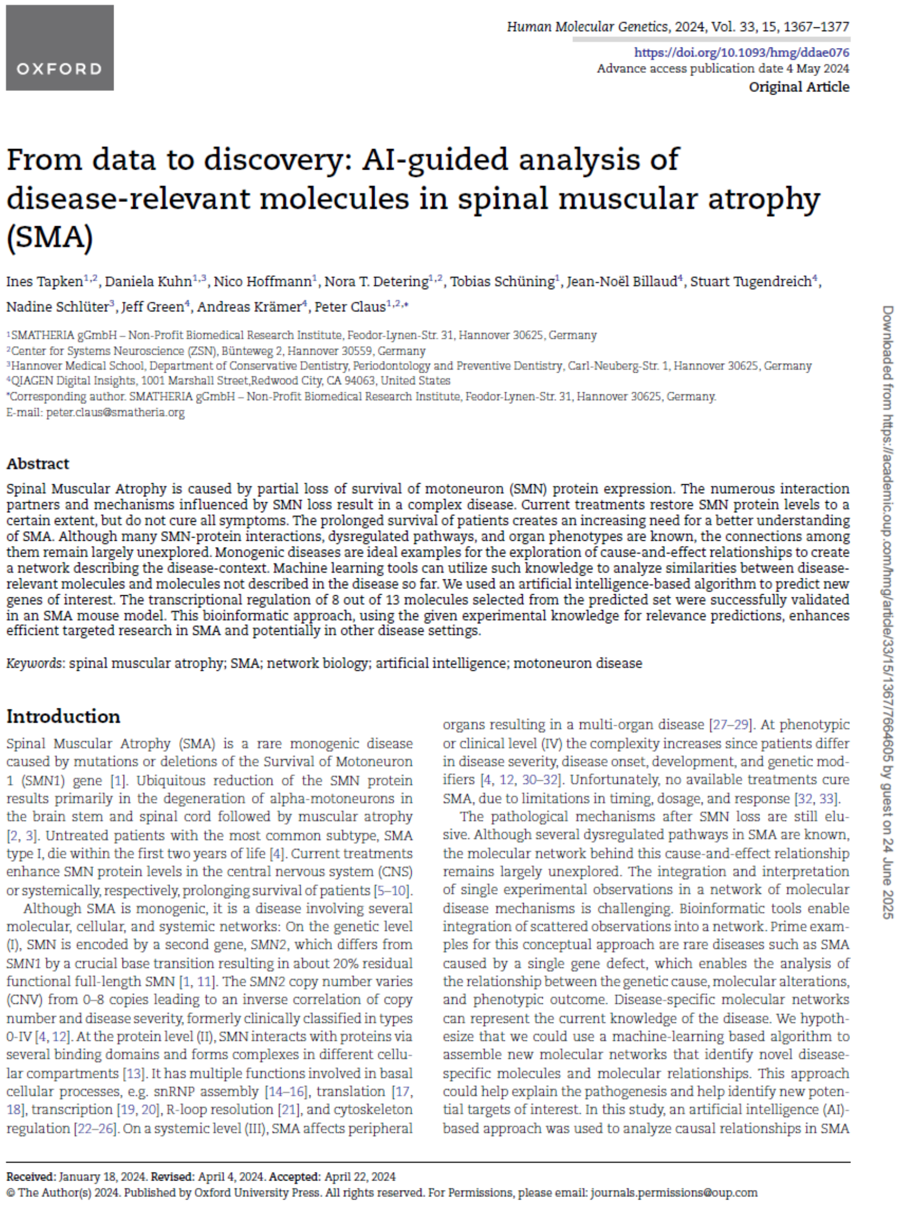
Type: causation
Direction: directional
Effect: increases
Tissue or primary cell: epithelial cells
Subcellular location: plasma membrane
Source: PubMed PMID: 22674072

EGFR – Glioblastoma

[one of many]

Type: causation
Direction: directional
Effect: increases
Organism: human
Source: PubMed PMID: 24782454

Dig into biology and test hypotheses in silico



OXFORD

Human Molecular Genetics, 2024, Vol. 33, 15, 1367–1377
https://doi.org/10.1093/hmg/ddae076
Advance access publication date 4 May 2024
Original Article

From data to discovery: AI-guided analysis of disease-relevant molecules in spinal muscular atrophy (SMA)

Ines Tapken[1,2], Daniela Kuhn[1,3], Nico Hoffmann[1], Nora T. Detering[1,2], Tobias Schüning[1], Jean-Noël Billaud[4], Stuart Tugendreich[4], Nadine Schlüter[3], Jeff Green[4], Andreas Krämer[4], Peter Claus[1,2,*]

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E-mail: peter.claus@smatheria.org

Abstract

Spinal Muscular Atrophy is caused by partial loss of survival of motoneuron (SMN) protein expression. The numerous interaction partners and mechanisms influenced by SMN loss result in a complex disease. Current treatments restore SMN protein levels to a certain extent, but do not cure all symptoms. The prolonged survival of patients creates an increasing need for a better understanding of SMA. Although many SMN-protein interactions, dysregulated pathways, and organ phenotypes are known, the connections among them remain largely unexplored. Monogenic diseases are ideal examples for the exploration of cause-and-effect relationships to create a network describing the disease-context. Machine learning tools can utilize such knowledge to analyze similarities between disease-relevant molecules and molecules not described in the disease so far. We used an artificial intelligence-based algorithm to predict new genes of interest. The transcriptional regulation of 8 out of 13 molecules selected from the predicted set were successfully validated in an SMA mouse model. This bioinformatic approach, using the given experimental knowledge for relevance predictions, enhances efficient targeted research in SMA and potentially in other disease settings.

Keywords: spinal muscular atrophy; SMA; network biology; artificial intelligence; motoneuron disease

Introduction

Spinal Muscular Atrophy (SMA) is a rare monogenic disease caused by mutations or deletions of the Survival of Motoneuron 1 (SMN1) gene [1]. Ubiquitous reduction of the SMN protein results primarily in the degeneration of alpha-motoneurons in the brain stem and spinal cord followed by muscular atrophy [2, 3]. Untreated patients with the most common subtype, SMA type I, die within the first two years of life [4]. Current treatments enhance SMN protein levels in the central nervous system (CNS) or systemically, respectively, prolonging survival of patients [5–10].

Although SMA is monogenic, it is a disease involving several molecular, cellular, and systemic networks: On the genetic level (I), SMN is encoded by a second gene, SMN2, which differs from SMN1 by a crucial base transition resulting in about 20% residual functional full-length SMN [1, 11]. The *SMN2* copy number varies (CNV) from 0–8 copies leading to an inverse correlation of copy number and disease severity, formerly clinically classified in types 0-IV [4, 12]. At the protein level (II), SMN interacts with proteins via several binding domains and forms complexes in different cellular compartments [13]. It has multiple functions involved in basal cellular processes, e.g. snRNP assembly [14–16], translation [17, 18], transcription [19, 20], R-loop resolution [21], and cytoskeleton regulation [22–26]. On a systemic level (III), SMA affects peripheral organs resulting in a multi-organ disease [27–29]. At phenotypic or clinical level (IV) the complexity increases since patients differ in disease severity, disease onset, development, and genetic modifiers [4, 12, 30–32]. Unfortunately, no available treatments cure SMA, due to limitations in timing, dosage, and response [32, 33].

The pathological mechanisms after SMN loss are still elusive. Although several dysregulated pathways in SMA are known, the molecular network behind this cause-and-effect relationship remains largely unexplored. The integration and interpretation of single experimental observations in a network of molecular disease mechanisms is challenging. Bioinformatic tools enable integration of scattered observations into a network. Prime examples for this conceptual approach are rare diseases such as SMA caused by a single gene defect, which enables the analysis of the relationship between the genetic cause, molecular alterations, and phenotypic outcome. Disease-specific molecular networks can represent the current knowledge of the disease. We hypothesize that we could use a machine-learning based algorithm to assemble new molecular networks that identify novel disease-specific molecules and molecular relationships. This approach could help explain the pathogenesis and help identify new potential targets of interest. In this study, an artificial intelligence (AI)-based approach was used to analyze causal relationships in SMA

Received: January 18, 2024. **Revised**: April 4, 2024. **Accepted**: April 22, 2024

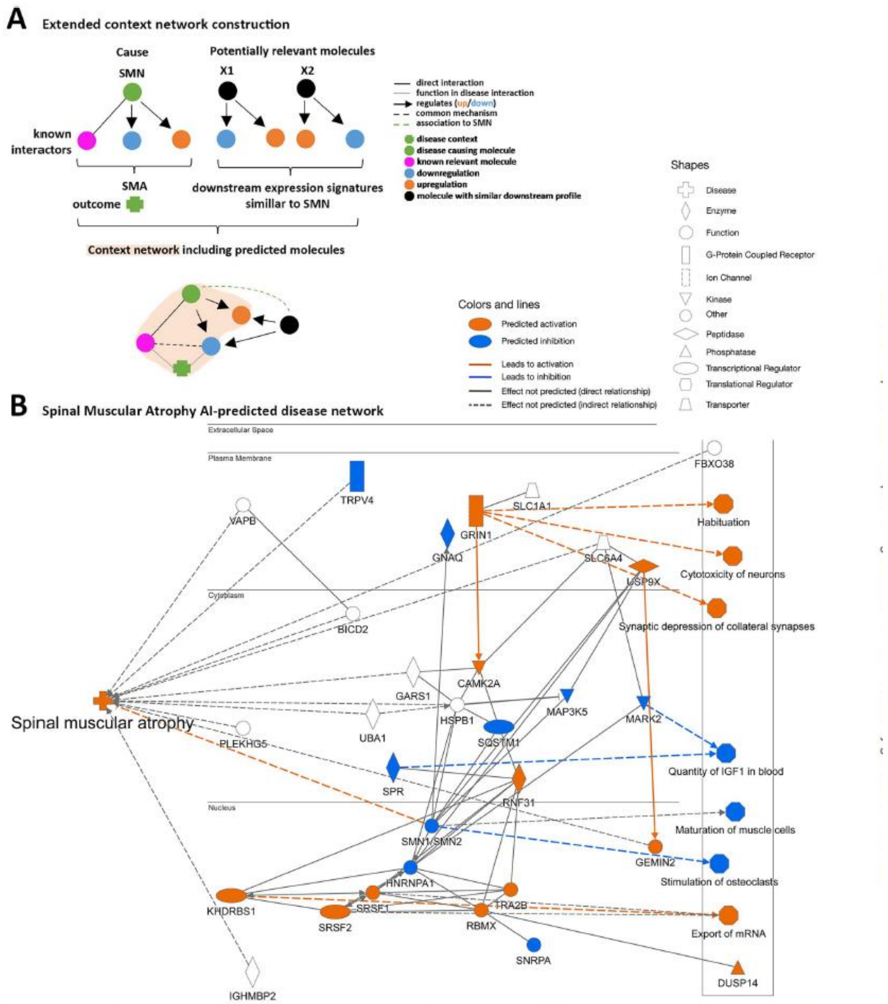
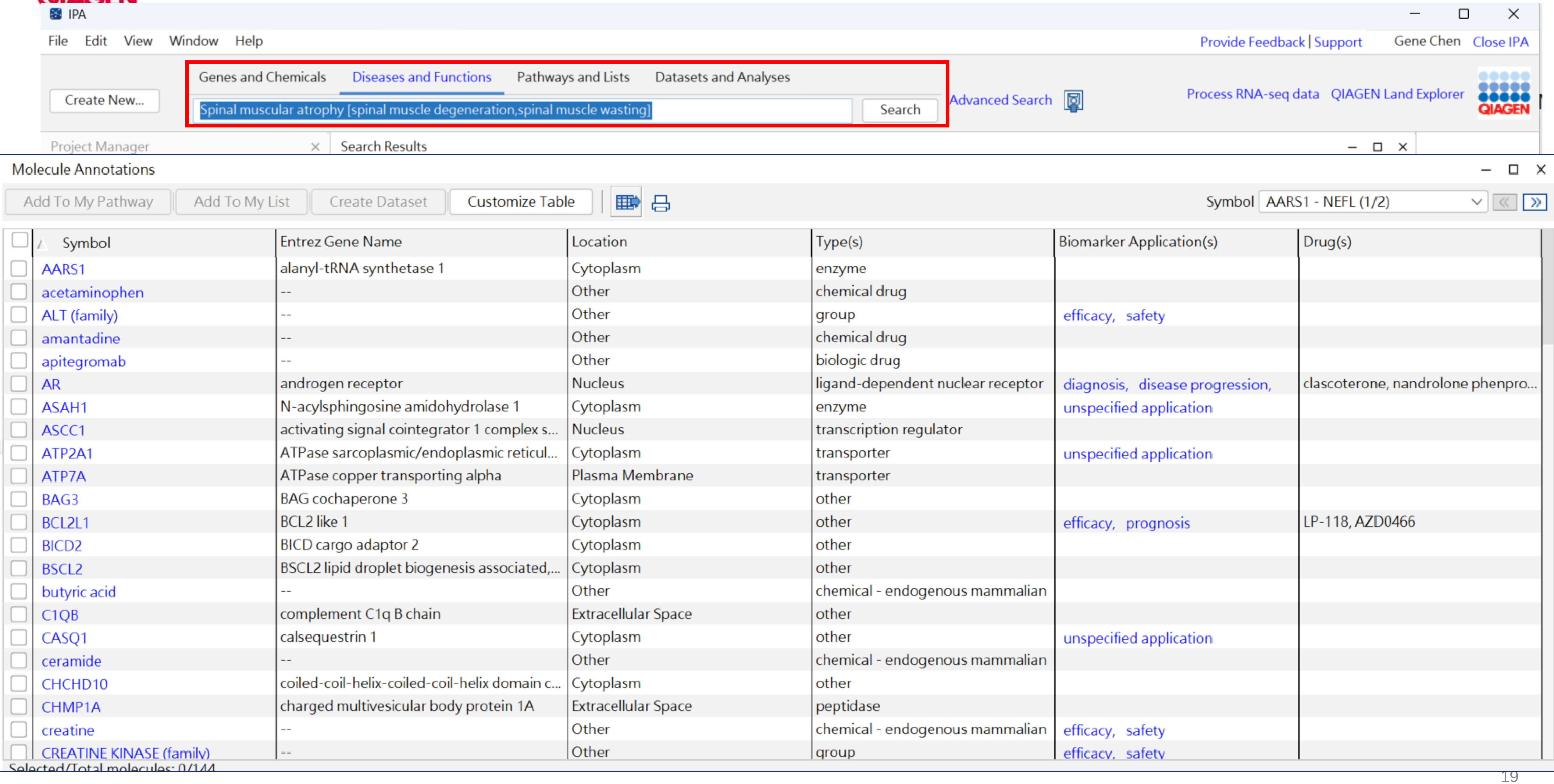


Figure 1. Artificial intelligence-predicted context network for spinal muscular atrophy. (A) Schematic representation of the AI-prediction algorithm and network construction. SMN (green circle) is the genetic cause and SMA (green cross) the disease outcome. In the QIAGEN Knowledge Base (QKB), interactors (pink circle) and causal relationships (black line: protein-protein interaction (PPI); grey line: Function), and dependency keywords (arrow: Direction; orange circle: Increases; blue circle: Decreases) are curated. The downstream profile of the disease-causing molecule is compared to other molecules (X) and similarities are ranked for potential relevance in the disease context. A context network is displayed including known and predicted disease-relevant molecules. Those were selected based on their connectivity to present a network to a size that could be reasonably interpreted. (B) IPA context network for SMA. The network includes known disease relevant molecules (connected to SMA) and predicted potentially relevant molecules with their direction of regulation (orange, blue). Functional outcomes are displayed on the right. Prediction activation (orange)/inhibition (blue): Regulation is predicted from interacting molecule measurements. Color codes for lines are based on the same concept. Molecule shapes represent their type.

Diseases and Function



Spinal muscular atrophy [spinal muscle degeneration,spinal muscle wasting]

Symbol: AARS1 - NEFL (1/2)

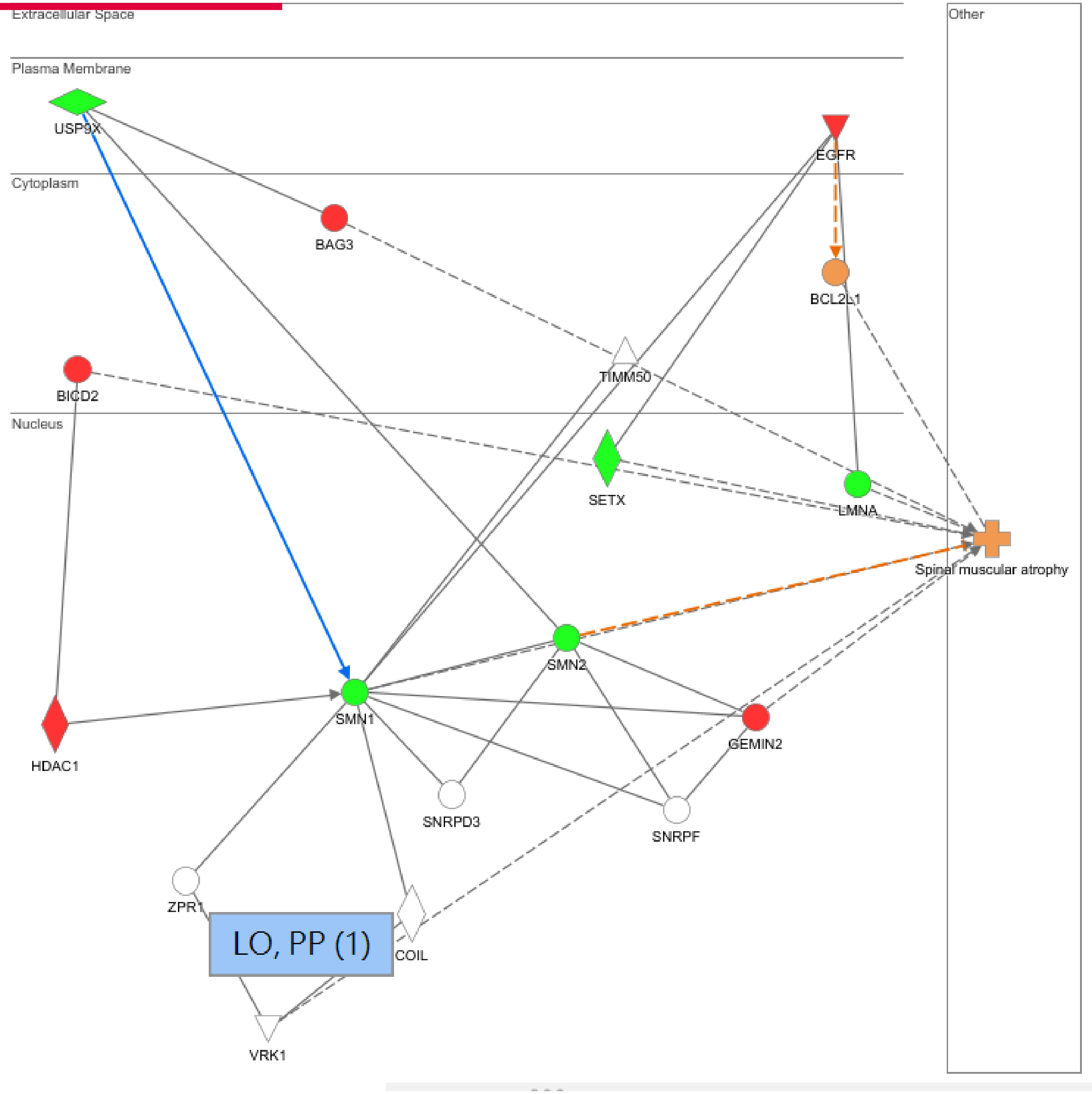
	Symbol	Entrez Gene Name	Location	Type(s)	Biomarker Application(s)	Drug(s)
☐	AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme		
☐	acetaminophen	--	Other	chemical drug		
☐	ALT (family)	--	Other	group	efficacy, safety	
☐	amantadine	--	Other	chemical drug		
☐	apitegromab	--	Other	biologic drug		
☐	AR	androgen receptor	Nucleus	ligand-dependent nuclear receptor	diagnosis, disease progression,	clascoterone, nandrolone phenpro...
☐	ASAH1	N-acylsphingosine amidohydrolase 1	Cytoplasm	enzyme	unspecified application	
☐	ASCC1	activating signal cointegrator 1 complex s...	Nucleus	transcription regulator		
☐	ATP2A1	ATPase sarcoplasmic/endoplasmic reticul...	Cytoplasm	transporter	unspecified application	
☐	ATP7A	ATPase copper transporting alpha	Plasma Membrane	transporter		
☐	BAG3	BAG cochaperone 3	Cytoplasm	other		
☐	BCL2L1	BCL2 like 1	Cytoplasm	other	efficacy, prognosis	LP-118, AZD0466
☐	BICD2	BICD cargo adaptor 2	Cytoplasm	other		
☐	BSCL2	BSCL2 lipid droplet biogenesis associated,...	Cytoplasm	other		
☐	butyric acid	--	Other	chemical - endogenous mammalian		
☐	C1QB	complement C1q B chain	Extracellular Space	other		
☐	CASQ1	calsequestrin 1	Cytoplasm	other	unspecified application	
☐	ceramide	--	Other	chemical - endogenous mammalian		
☐	CHCHD10	coiled-coil-helix-coiled-coil-helix domain c...	Cytoplasm	other		
☐	CHMP1A	charged multivesicular body protein 1A	Extracellular Space	peptidase		
☐	creatine	--	Other	chemical - endogenous mammalian	efficacy, safety	
☐	CREATINE KINASE (family)	--	Other	group	efficacy, safety	

Selected/Total molecules: 0/144

Create networks from scratch and test activity in silico

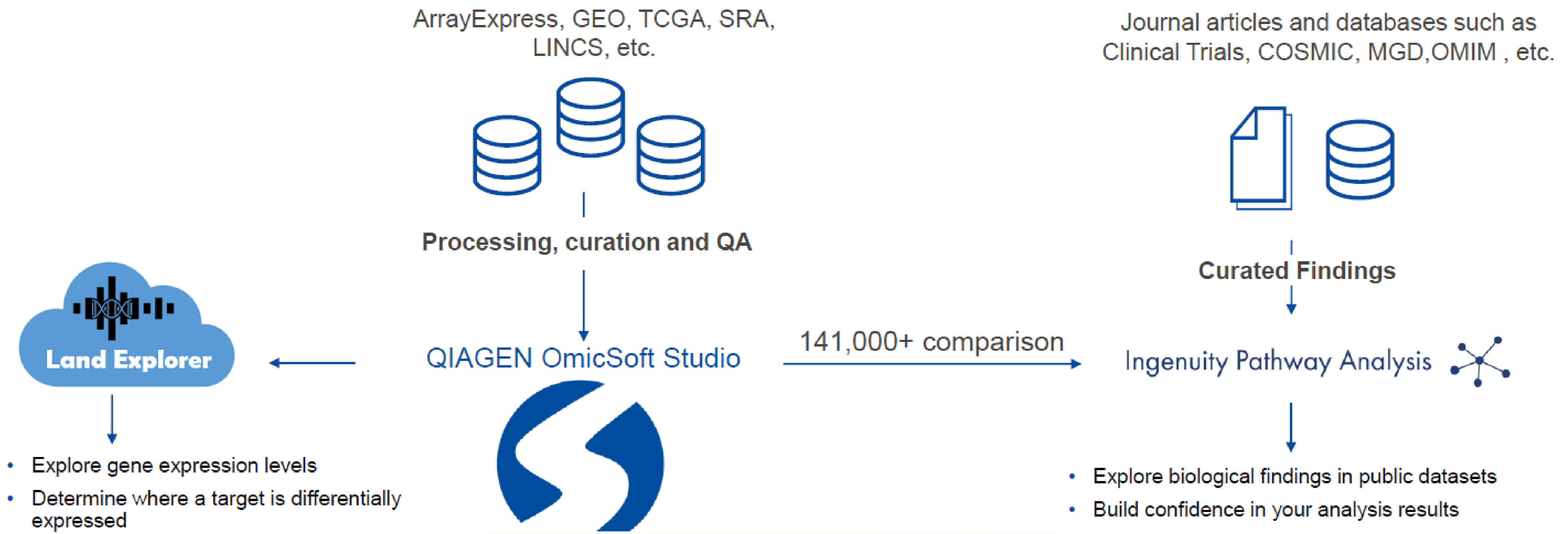
New feature:
Cells and Tissues overlay

Predict cell types associated with the genes on your network or pathway using data from The Human Protein Atlas



- Search for genes
- Build: grow (molecular or disease a function)
- Overlay: Molecule activity predictor, Drug, Cells & Tissues
- Drug: IPA Chem View

QIAGEN IPA Analysis Match and Land Explorer



ArrayExpress, GEO, TCGA, SRA, LINCS, etc.

Processing, curation and QA

QIAGEN OmicSoft Studio

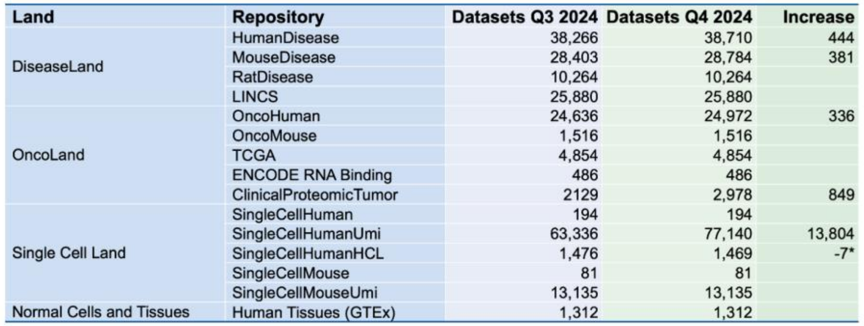
141,000+ comparison

Journal articles and databases such as Clinical Trials, COSMIC, MGD,OMIM , etc.

Curated Findings

Ingenuity Pathway Analysis

- Explore gene expression levels
- Determine where a target is differentially expressed
- Understand how ‘omics data influences survival
- Identify mutation status of a target



Land	Repository	Datasets Q3 2024	Datasets Q4 2024	Increase
DiseaseLand	HumanDisease	38,266	38,710	444
	MouseDisease	28,403	28,784	381
	RatDisease	10,264	10,264	
	LINCS	25,880	25,880	
OncoLand	OncoHuman	24,636	24,972	336
	OncoMouse	1,516	1,516	
	TCGA	4,854	4,854	
	ENCODE RNA Binding	486	486	
	ClinicalProteomicTumor	2129	2,978	849
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	63,336	77,140	13,804
	SingleCellHumanHCL	1,476	1,469	-7*
	SingleCellMouse	81	81	
	SingleCellMouseUmi	13,135	13,135	
Normal Cells and Tissues	Human Tissues (GTEx)	1,312	1,312	

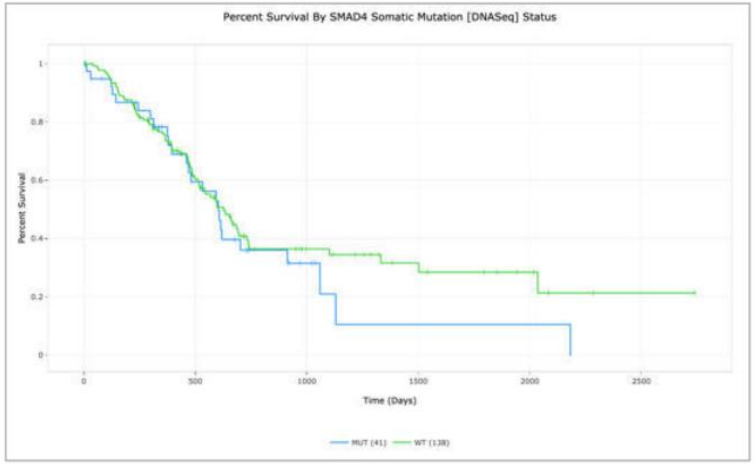
- Explore biological findings in public datasets
- Build confidence in your analysis results
- Make unexpected insights into shared mechanisms between studies
- “Anti-matches” may provide insights

IPA with OmicSoft Land Explorer

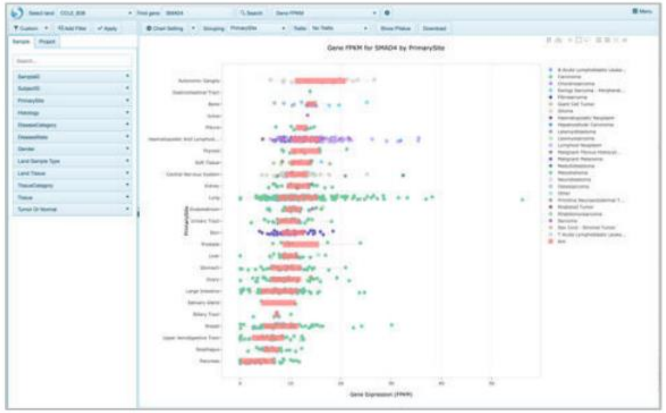
Expression in Rat, Mouse, and Human Disease


Select land TCGA_B38
Find gene SMAD4
Somatic Mutation Distribution
Grouping Tumor Type
Trellis No Trellis

Mutation frequency

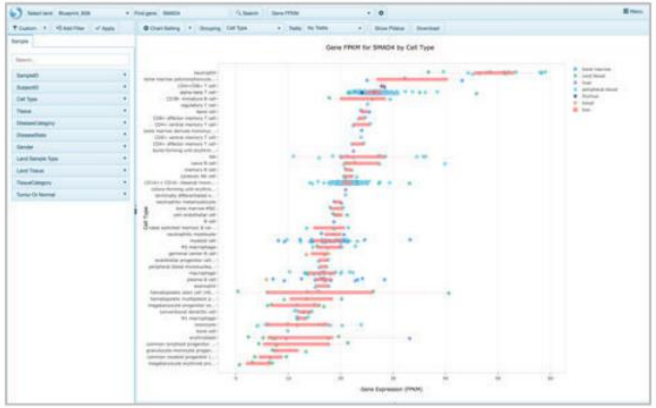


Survival plots



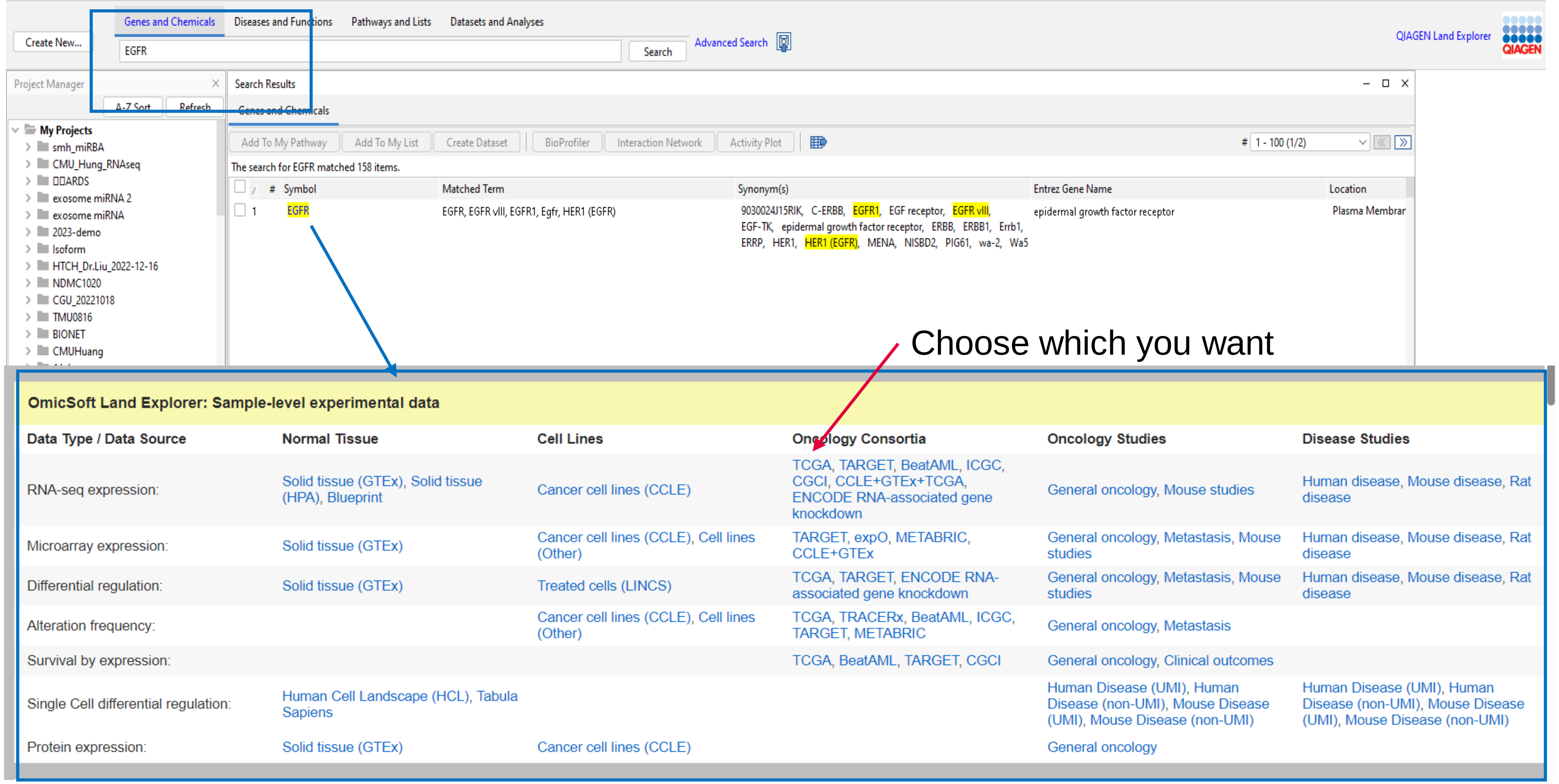
Cell line expression

Tumor expression



Hematopoietic expression (BluePrint)

IPA with OmicSoft Land Explorer



The search for EGFR matched 158 items.

☐	#	Symbol	Matched Term	Synonym(s)	Entrez Gene Name	Location
☐	1	EGFR	EGFR, EGFR vIII, EGFR1, Egfr, HER1 (EGFR)	9030024J15RIK, C-ERBB, EGFR1, EGF receptor, EGFR vIII, EGF-TK, epidermal growth factor receptor, ERBB, ERBB1, Errb1, ERRP, HER1, HER1 (EGFR), MENA, NISBD2, PIG61, wa-2, Wa5	epidermal growth factor receptor	Plasma Membrar

Choose which you want

OmicSoft Land Explorer: Sample-level experimental data

Data Type / Data Source	Normal Tissue	Cell Lines	Oncology Consortia	Oncology Studies	Disease Studies
RNA-seq expression:	Solid tissue (GTEx), Solid tissue (HPA), Blueprint	Cancer cell lines (CCLE)	TCGA, TARGET, BeatAML, ICGC, CGCI, CCLE+GTEx+TCGA, ENCODE RNA-associated gene knockdown	General oncology, Mouse studies	Human disease, Mouse disease, Rat disease
Microarray expression:	Solid tissue (GTEx)	Cancer cell lines (CCLE), Cell lines (Other)	TARGET, expO, METABRIC, CCLE+GTEx	General oncology, Metastasis, Mouse studies	Human disease, Mouse disease, Rat disease
Differential regulation:	Solid tissue (GTEx)	Treated cells (LINCS)	TCGA, TARGET, ENCODE RNA-associated gene knockdown	General oncology, Metastasis, Mouse studies	Human disease, Mouse disease, Rat disease
Alteration frequency:		Cancer cell lines (CCLE), Cell lines (Other)	TCGA, TRACERx, BeatAML, ICGC, TARGET, METABRIC	General oncology, Metastasis	
Survival by expression:			TCGA, BeatAML, TARGET, CGCI	General oncology, Clinical outcomes	
Single Cell differential regulation:	Human Cell Landscape (HCL), Tabula Sapiens			Human Disease (UMI), Human Disease (non-UMI), Mouse Disease (UMI), Mouse Disease (non-UMI)	Human Disease (UMI), Human Disease (non-UMI), Mouse Disease (UMI), Mouse Disease (non-UMI)
Protein expression:	Solid tissue (GTEx)	Cancer cell lines (CCLE)		General oncology	

IPA Gene View :OmicSoft Land Explorer

IPA with OmicSoft Land Explorer

- **TCGA-B38-G33**

Land selection

Search bar

View selection

View controller

Download data for current view

Metadata filtering

Select land: TCGA_B38_GC33

Find gene: egfr

Gene FPKM

Grouping: Tumor Type

Trellis: No Trellis

Sample

- ☑ ovarian serous cystadenocarcinoma (OV)
- ☑ pancreas adenocarcinoma (PAAD)
- ☑ papillary renal cell carcinoma (KIRP)
- ☑ pheochromocytoma and paraganglioma (PCPG)
- ☑ prostate adenocarcinoma (PRAD)
- ☑ rectum adenocarcinoma (READ)
- ☑ renal clear cell carcinoma (KIRC)
- ☑ sarcoma (SARC)
- ☑ skin melanoma (SKCM)
- ☑ testicular germ cell tumor (TGCT)
- ☑ thymoma (THYM)
- ☑ thyroid carcinoma (THCA)
- ☑ uterine carcinosarcoma (UCS)
- ☑ uveal melanoma (UVM)
- ☑ -missing-

Gender

Check All Check None Invert

- ☑ female
- ☑ male
- ☐ NA
- ☐ -missing-

Race

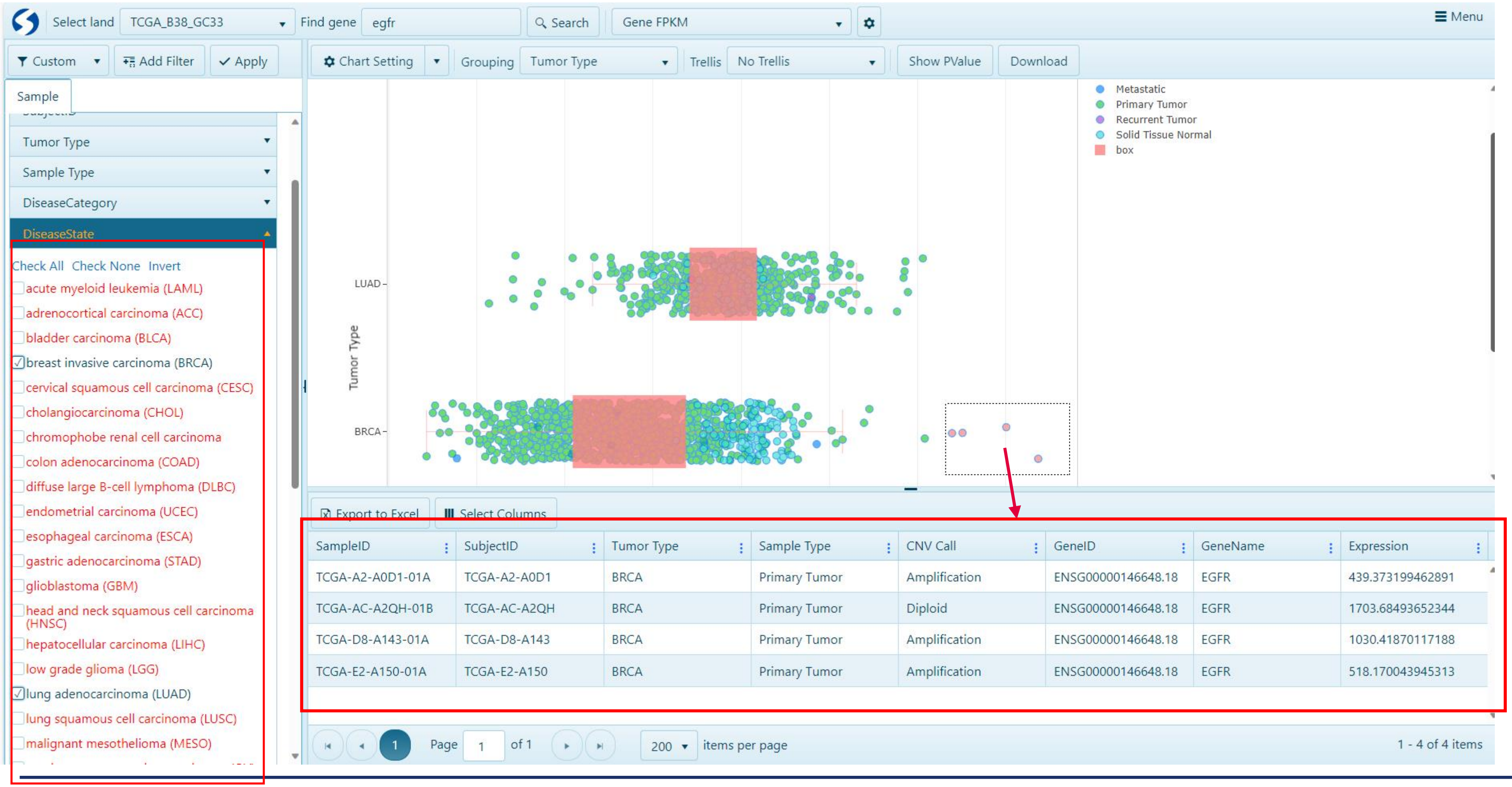
Tissue Category

Tissue

https://explorer.omicland.com/IPA/Home/MainPage?landName=TCGA_B38_GC33&geneID=EGFR&viewID=RnaSeq_Transcript.GeneVariable&grouping=Tumor Type&trellis=No Trellis

IPA with OmicSoft Land Explorer

- Through DiseaseState filter, to observe the expression difference of EGFR gene in cancer type in TCGA
- Select a specific experimental group to view more detailed information.



Select land TCGA_B38_GC33

Find gene egfr

Gene FPKM

Grouping Tumor Type

Trellis No Trellis

DiseaseState

Check All Check None Invert

☐ acute myeloid leukemia (LAML)
☐ adrenocortical carcinoma (ACC)
☐ bladder carcinoma (BLCA)
☑ breast invasive carcinoma (BRCA)
☐ cervical squamous cell carcinoma (CESC)
☐ cholangiocarcinoma (CHOL)
☐ chromophobe renal cell carcinoma
☐ colon adenocarcinoma (COAD)
☐ diffuse large B-cell lymphoma (DLBC)
☐ endometrial carcinoma (UCEC)
☐ esophageal carcinoma (ESCA)
☐ gastric adenocarcinoma (STAD)
☐ glioblastoma (GBM)
☐ head and neck squamous cell carcinoma (HNSC)
☐ hepatocellular carcinoma (LIHC)
☐ low grade glioma (LGG)
☑ lung adenocarcinoma (LUAD)
☐ lung squamous cell carcinoma (LUSC)
☐ malignant mesothelioma (MESO)

SampleID	SubjectID	Tumor Type	Sample Type	CNV Call	GeneID	GeneName	Expression
TCGA-A2-A0D1-01A	TCGA-A2-A0D1	BRCA	Primary Tumor	Amplification	ENSG00000146648.18	EGFR	439.373199462891
TCGA-AC-A2QH-01B	TCGA-AC-A2QH	BRCA	Primary Tumor	Diploid	ENSG00000146648.18	EGFR	1703.68493652344
TCGA-D8-A143-01A	TCGA-D8-A143	BRCA	Primary Tumor	Amplification	ENSG00000146648.18	EGFR	1030.41870117188
TCGA-E2-A150-01A	TCGA-E2-A150	BRCA	Primary Tumor	Amplification	ENSG00000146648.18	EGFR	518.170043945313

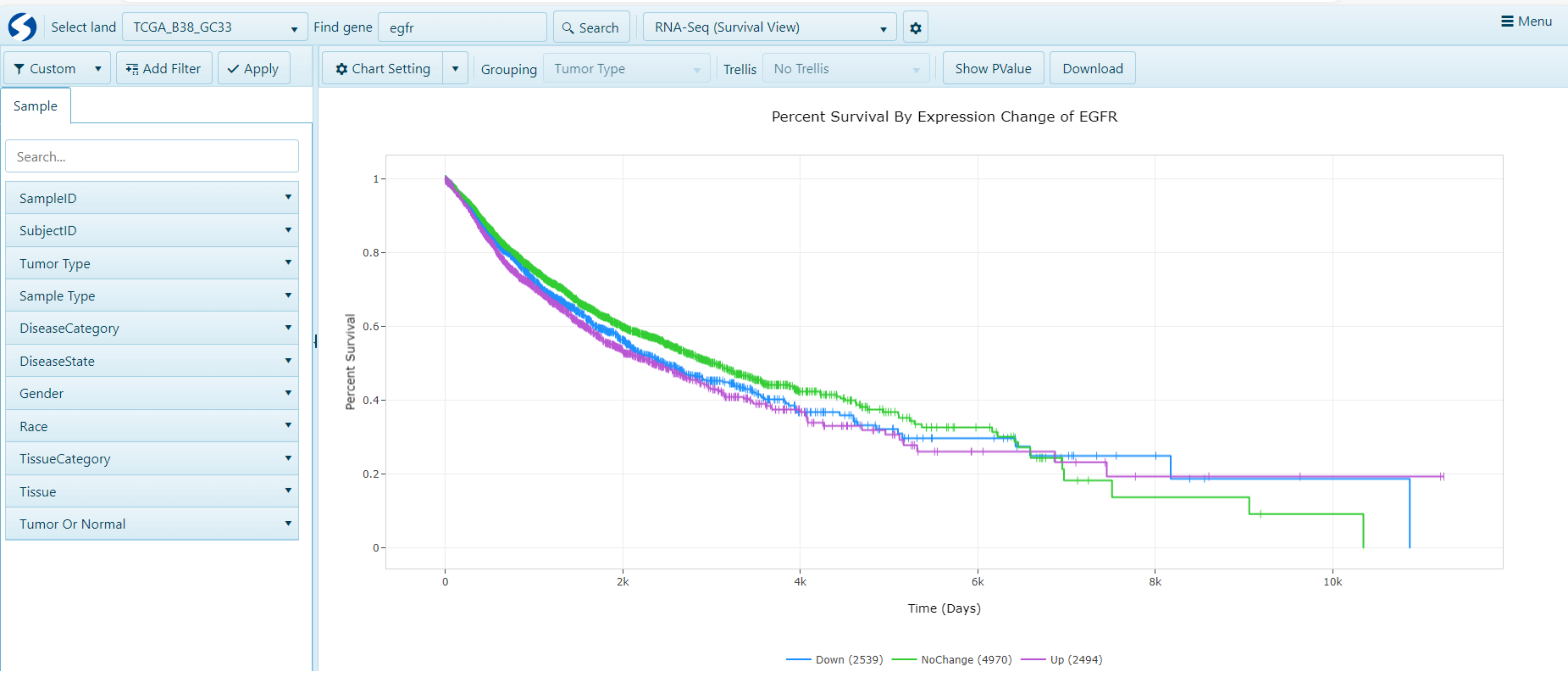
1 Page 1 of 1

200 items per page

1 - 4 of 4 items

SURVIVAL ANALYSIS RESULT IN TCGA DATASET

TCGA_B38_GC33



Select land: TCGA_B38_GC33

Find gene: egfr

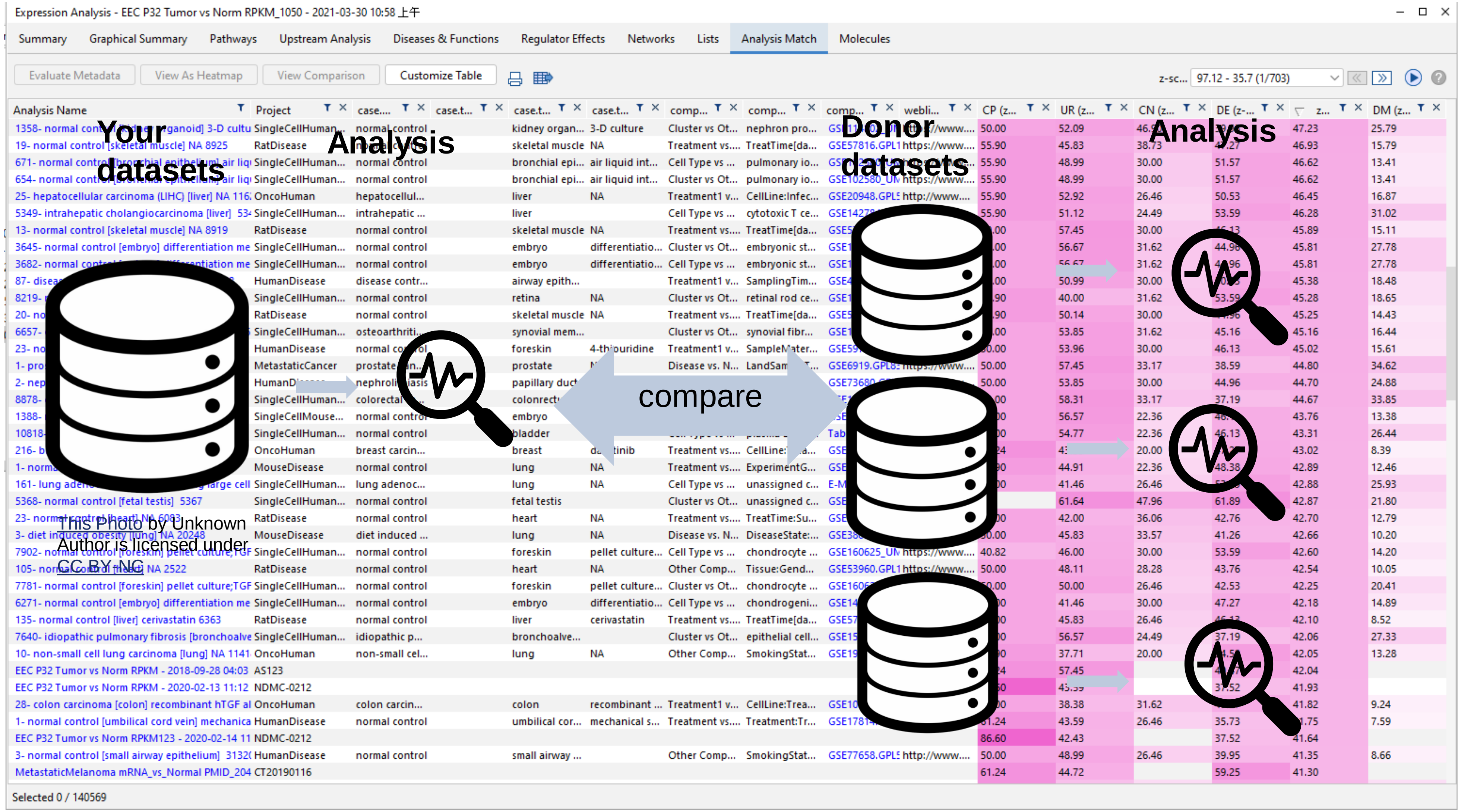
RNA-Seq (Survival View)

Grouping: Tumor Type

Trellis: No Trellis

Analysis matching

Automatically discover other IPA Core Analyses with similar (or opposite) biological results as compared to yours, to help confirm your interpretation of the results or to provide unexpected insights into underlying shared biological mechanisms



Expression Analysis - EEC P32 Tumor vs Norm RPKM_1050 - 2021-03-30 10:58 上午

z-sc... 97.12 - 35.7 (1/703)

Analysis Name	Project	case....	case.t...	case.t...	case.t...	comp...	comp...	comp...	webli...	CP (z...	UR (z...	CN (z...	DE (z-...	z...	DM (z...
1358- normal con[illegible]rganoid] 3-D cultu	SingleCellHuman...	normal control		kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GS[illegible]	[illegible]//www....	50.00	52.09	46.9[illegible]	[illegible]	47.23	25.79
19- normal control [skeletal muscle] NA 8925	RatDisease	[illegible]		skeletal muscle	NA	Treatment vs....	TreatTime[da...	GSE57816.GPL1	https://www....	55.90	45.83	38.73	[illegible]	46.93	15.79
671- normal contr[illegible]air liqu	SingleCellHuman...	normal control		bronchial epi...	air liquid int...	Cell Type vs ...	pulmonary io...	GS[illegible]	[illegible]	55.90	48.99	30.00	51.57	46.62	13.41
654- normal cont[illegible]air liqu	SingleCellHuman...	normal control		bronchial epi...	air liquid int...	Cluster vs Ot...	pulmonary io...	GSE102580_UN	https://www....	55.90	48.99	30.00	51.57	46.62	13.41
25- hepatocellular carcinoma (LIHC) [liver] NA 116:	OncoHuman	hepatocellul...		liver	NA	Treatment1 v...	CellLine:Infec...	GSE20948.GPL5	http://www....	55.90	52.92	26.46	50.53	46.45	16.87
5349- intrahepatic cholangiocarcinoma [liver] 534	SingleCellHuman...	intrahepatic ...		liver		Cell Type vs ...	cytotoxic T ce...	GSE1427[illegible]	[illegible]	55.90	51.12	24.49	53.59	46.28	31.02
13- normal control [skeletal muscle] NA 8919	RatDisease	normal control		skeletal muscle	NA	Treatment vs....	TreatTime[da...	GSE5[illegible]	[illegible]	[illegible].00	57.45	30.00	[illegible]	45.89	15.11
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control		embryo	differentiatio...	Cluster vs Ot...	embryonic st...	GSE1[illegible]	[illegible]	[illegible].00	56.67	31.62	44.9[illegible]	45.81	27.78
3682- normal cont[illegible]ifferentiation me	SingleCellHuman...	normal control		embryo	differentiatio...	Cell Type vs ...	embryonic st...	GSE1[illegible]	[illegible]	[illegible].00	[illegible]	31.62	[illegible]96	45.81	27.78
87- disea[illegible]	HumanDisease	disease contr...		airway epith...		Treatment1 v...	SamplingTim...	GSE4[illegible]	[illegible]	[illegible].00	50.99	30.00	[illegible]	45.38	18.48
8219- [illegible]	SingleCellHuman...	normal control		retina	NA	Cluster vs Ot...	retinal rod ce...	GSE1[illegible]	[illegible]	[illegible].90	40.00	31.62	53.59	45.28	18.65
20- no[illegible]	RatDisease	normal control		skeletal muscle	NA	Treatment vs....	TreatTime[da...	GSE5[illegible]	[illegible]	[illegible].90	50.14	30.00	[illegible]	45.25	14.43
6657- [illegible]	SingleCellHuman...	osteoarthriti...		synovial mem...		Cluster vs Ot...	synovial fibr...	GSE1[illegible]	[illegible]	[illegible].00	53.85	31.62	45.16	45.16	16.44
23- no[illegible]	HumanDisease	normal co[illegible]ol		foreskin	4-thiouridine	Treatment1 v...	SampleMater...	GSE59[illegible]	[illegible]	[illegible]0.00	53.96	30.00	46.13	45.02	15.61
1- pro[illegible]	MetastaticCancer	prostate [illegible]an...		prostate	N[illegible]	Disease vs. N...	LandSam[illegible]T...	GSE6919.GPL8:	[illegible]	50.00	57.45	33.17	38.59	44.80	34.62
2- nep[illegible]	HumanD[illegible]	nephroli[illegible]iasis		papillary duct	[illegible]	[illegible]	[illegible]	GSE73680[illegible]	[illegible]	50.00	53.85	30.00	44.96	44.70	24.88
8878- [illegible]	SingleCellHuman...	colorectal [illegible]		colonrect[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible].00	58.31	33.17	37.19	44.67	33.85
1388- [illegible]	SingleCellMouse...	normal contro[illegible]		embryo	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]00	56.57	22.36	46.[illegible]	43.76	13.38
10818-[illegible]	SingleCellHuman...	normal control		bladder	[illegible]	[illegible]	[illegible]	Tab[illegible]	[illegible]	[illegible]00	54.77	22.36	46.13	43.31	26.44
216- b[illegible]	OncoHuman	breast carcin...		breast	da[illegible]tinib	Treatment vs....	CellLine:[illegible]a...	GSE[illegible]	[illegible]	[illegible]24	43[illegible]	20.00	[illegible]	43.02	8.39
1- norma[illegible]	MouseDisease	normal control		lung	NA	Treatment vs....	ExperimentG...	GSE[illegible]	[illegible]	[illegible]90	44.91	22.36	48.38	42.89	12.46
161- lung ade[illegible]large cell	SingleCellHuman...	lung adenoc...		lung	NA	Cell Type vs ...	unassigned c...	E-M[illegible]	[illegible]	[illegible]00	41.46	26.46	[illegible]	42.88	25.93
5368- normal control [fetal testis] 5367	SingleCellHuman...	normal control		fetal testis		Cluster vs Ot...	unassigned c...	GSE[illegible]	[illegible]		61.64	47.96	61.89	42.87	21.80
23- normal control [heart] NA 6083	RatDisease	normal control		heart	NA	Treatment vs....	TreatTime:Su...	GSE[illegible]	[illegible]	[illegible]00	42.00	36.06	42.76	42.70	12.79
3- diet induced obesity [lung] NA 20248	MouseDisease	diet induced ...		lung	NA	Disease vs. N...	DiseaseState:...	GSE38[illegible]	[illegible]	[illegible]0.00	45.83	33.57	41.26	42.66	10.20
7902- normal control [foreskin] pellet culture;TGF	SingleCellHuman...	normal control		foreskin	pellet culture...	Cell Type vs ...	chondrocyte ...	GSE160625_UN	https://www....	40.82	46.00	30.00	53.59	42.60	14.20
105- normal control [heart] NA 2522	RatDisease	normal control		heart	NA	Other Comp...	Tissue:Gend...	GSE53960.GPL1	https://www....	50.00	48.11	28.28	43.76	42.54	10.05
7781- normal control [foreskin] pellet culture;TGF	SingleCellHuman...	normal control		foreskin	pellet culture...	Cluster vs Ot...	chondrocyte ...	GSE1606[illegible]	[illegible]	[illegible]0.00	50.00	26.46	42.53	42.25	20.41
6271- normal control [embryo] differentiation me	SingleCellHuman...	normal control		embryo	differentiatio...	Cell Type vs ...	chondrogeni...	GSE14[illegible]	[illegible]	[illegible]00	41.46	30.00	47.27	42.18	14.89
135- normal control [liver] cerivastatin 6363	RatDisease	normal control		liver	cerivastatin	Treatment vs....	TreatTime[da...	GSE57[illegible]	[illegible]	[illegible]00	45.83	26.46	[illegible]	42.10	8.52
7640- idiopathic pulmonary fibrosis [bronchoalve	SingleCellHuman...	idiopathic p...		bronchoalve...		Cluster vs Ot...	epithelial cell...	GSE15[illegible]	[illegible]	[illegible]00	56.57	24.49	37.19	42.06	27.33
10- non-small cell lung carcinoma [lung] NA 1141	OncoHuman	non-small cel...		lung	NA	Other Comp...	SmokingStat...	GSE19[illegible]	[illegible]	[illegible]90	37.71	20.00	[illegible]	42.05	13.28
EEC P32 Tumor vs Norm RPKM - 2018-09-28 04:03	AS123									[illegible]24	57.45		[illegible]	42.04	
EEC P32 Tumor vs Norm RPKM - 2020-02-13 11:12	NDMC-0212									[illegible]50	43.[illegible]		37.52	41.93	
28- colon carcinoma [colon] recombinant hTGF al	OncoHuman	colon carcin...		colon	recombinant ...	Treatment1 v...	CellLine:Trea...	GSE10[illegible]	[illegible]	[illegible]00	38.38	31.62	[illegible]	41.82	9.24
1- normal control [umbilical cord vein] mechanica	HumanDisease	normal control		umbilical cor...	mechanical s...	Treatment vs....	Treatment:Tr...	GSE1781[illegible]	[illegible]	[illegible]1.24	43.59	26.46	35.73	[illegible]1.75	7.59
EEC P32 Tumor vs Norm RPKM123 - 2020-02-14 11	NDMC-0212									86.60	42.43		37.52	41.64	
3- normal control [small airway epithelium] 3132(	HumanDisease	normal control		small airway ...		Other Comp...	SmokingStat...	GSE77658.GPL5	http://www....	50.00	48.99	26.46	39.95	41.35	8.66
MetastaticMelanoma mRNA_vs_Normal PMID_204	CT20190116									61.24	44.72		59.25	41.30	

Selected 0 / 140569

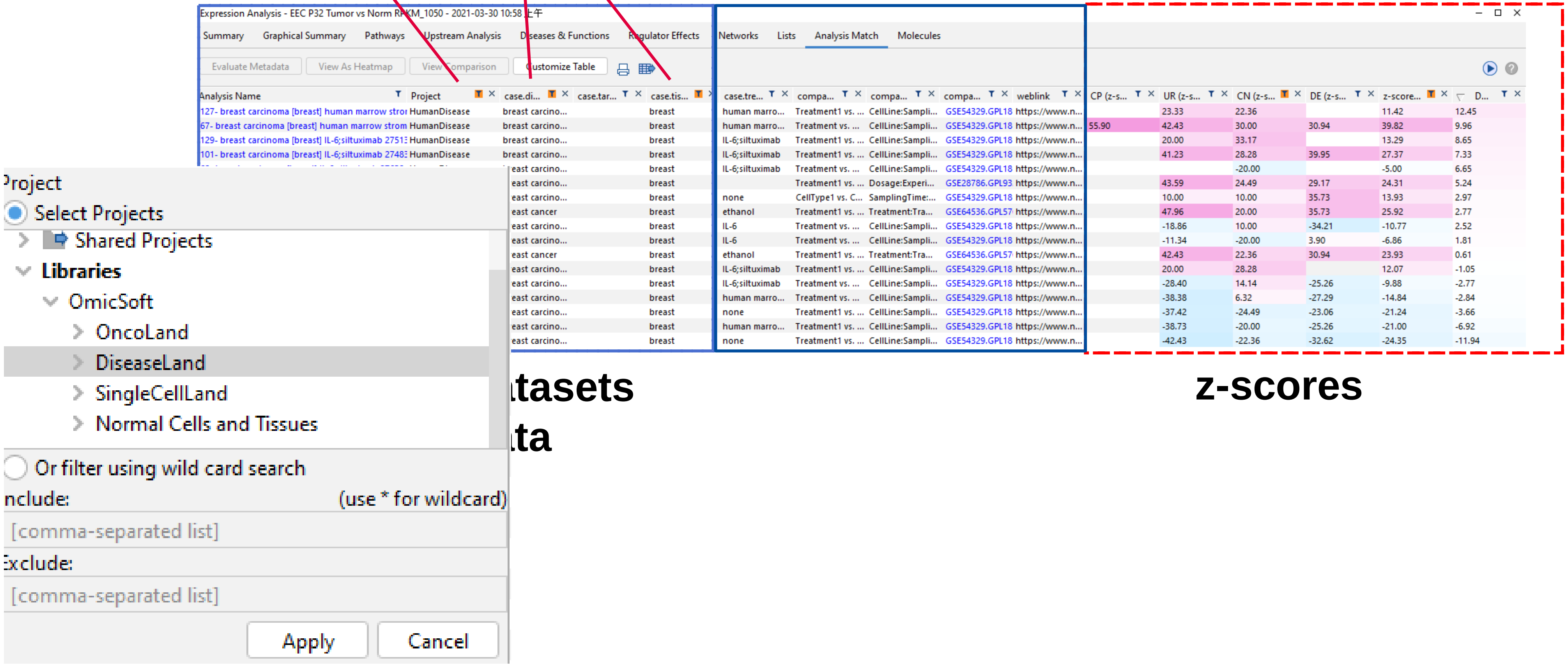
Analysis matching

Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project **Cell & Tissue**

Datasets information

similar **opposite**



Expression Analysis - EEC P32 Tumor vs Norm RPKM_1050 - 2021-03-30 10:58 上午

Analysis Name	Project	case.di...	case.tar...	case.tis...	case.tre...	compa...	compa...	compa...	weblink	CP (z-s...	UR (z-s...	CN (z-s...	DE (z-s...	z-score...	D...
127- breast carcinoma [breast] human marrow stroı	HumanDisease	breast carcino...		breast	human marro...	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		23.33	22.36		11.42	12.45
67- breast carcinoma [breast] human marrow strom	HumanDisease	breast carcino...		breast	human marro...	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...	55.90	42.43	30.00	30.94	39.82	9.96
129- breast carcinoma [breast] IL-6;siltuximab 2751	HumanDisease	breast carcino...		breast	IL-6;siltuximab	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		20.00	33.17		13.29	8.65
101- breast carcinoma [breast] IL-6;siltuximab 2748	HumanDisease	breast carcino...		breast	IL-6;siltuximab	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		41.23	28.28	39.95	27.37	7.33
		east carcino...		breast	IL-6;siltuximab	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...			-20.00		-5.00	6.65
		east carcino...		breast		Treatment1 vs. ...	Dosage:Experi...	GSE28786.GPL93	https://www.n...		43.59	24.49	29.17	24.31	5.24
		east carcino...		breast	none	CellType1 vs. C...	SamplingTime:...	GSE54329.GPL18	https://www.n...		10.00	10.00	35.73	13.93	2.97
		east cancer		breast	ethanol	Treatment1 vs. ...	Treatment:Tra...	GSE64536.GPL57	https://www.n...		47.96	20.00	35.73	25.92	2.77
		east carcino...		breast	IL-6	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-18.86	10.00	-34.21	-10.77	2.52
		east carcino...		breast	IL-6	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-11.34	-20.00	3.90	-6.86	1.81
		east cancer		breast	ethanol	Treatment1 vs. ...	Treatment:Tra...	GSE64536.GPL57	https://www.n...		42.43	22.36	30.94	23.93	0.61
		east carcino...		breast	IL-6;siltuximab	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		20.00	28.28		12.07	-1.05
		east carcino...		breast	IL-6;siltuximab	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-28.40	14.14	-25.26	-9.88	-2.77
		east carcino...		breast	human marro...	Treatment vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-38.38	6.32	-27.29	-14.84	-2.84
		east carcino...		breast	none	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-37.42	-24.49	-23.06	-21.24	-3.66
		east carcino...		breast	human marro...	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-38.73	-20.00	-25.26	-21.00	-6.92
		east carcino...		breast	none	Treatment1 vs. ...	CellLine:Sampli...	GSE54329.GPL18	https://www.n...		-42.43	-22.36	-32.62	-24.35	-11.94

roject

● Select Projects

○ Or filter using wild card search

nclude: (use * for wildcard)

[comma-separated list]

xclude:

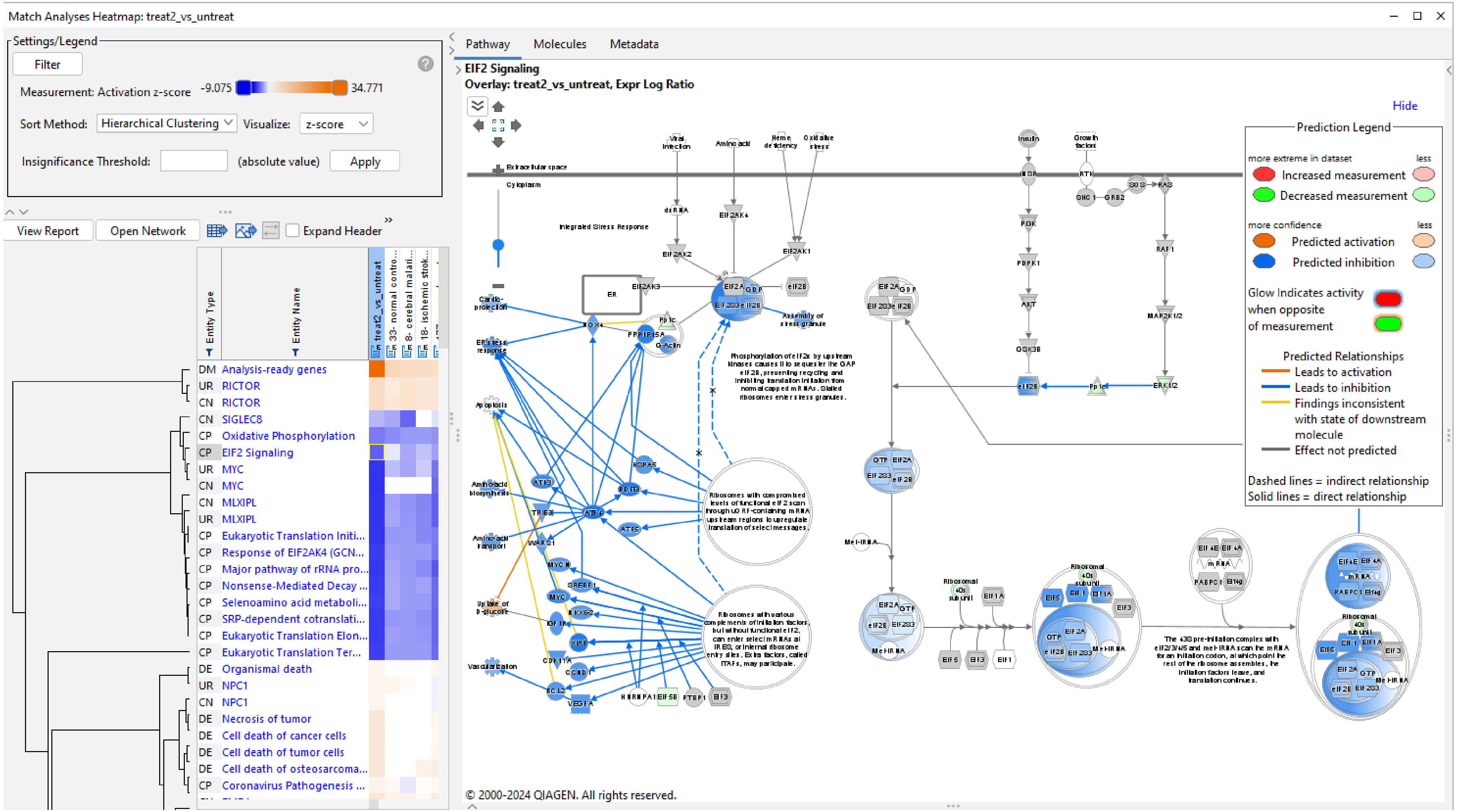
[comma-separated list]

tasets

ta

z-scores

Analysis Match



Match Analyses Heatmap: treat2_vs_untreat

Settings/Legend

Measurement: Activation z-score -9.075 34.771

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value)

Entity Type	Entity Name
DM	Analysis-ready genes
UR	RICTOR
CN	RICTOR
CN	SIGLEC8
CP	Oxidative Phosphorylation
CP	EIF2 Signaling
UR	MYC
CN	MYC
CN	MLXIPL
UR	MLXIPL
CP	Eukaryotic Translation Initi...
CP	Response of EIF2AK4 (GCN...
CP	Major pathway of rRNA pro...
CP	Nonsense-Mediated Decay ...
CP	Selenoamino acid metaboli...
CP	SRP-dependent cotranslati...
CP	Eukaryotic Translation Elon...
CP	Eukaryotic Translation Ter...
DE	Organismal death
UR	NPC1
CN	NPC1
DE	Necrosis of tumor
DE	Cell death of cancer cells
DE	Cell death of tumor cells
DE	Cell death of osteosarcoma...
CP	Coronavirus Pathogenesis ...

EIF2 Signaling

Overlay: treat2_vs_untreat, Expr Log Ratio

Prediction Legend

more extreme in dataset		less
🟥	Increased measurement	🟥
🟩	Decreased measurement	🟩

more confidence		less
●	Predicted activation	●
●	Predicted inhibition	●

Glow Indicates activity when opposite of measurement

Predicted Relationships
- Leads to activation
- Leads to inhibition
- Findings inconsistent with state of downstream molecule
- Effect not predicted

Dashed lines = indirect relationship
Solid lines = direct relationship

Phosphorylation of eIF2α by upstream kinases causes it to sequester the GAP eIF2B, preventing recycling and inhibiting translation initiation from normal capped mRNAs. Stalled ribosomes enter stress granules.

Ribosomes with compromised levels of functional eIF2 scan through uORF-containing mRNA upstream regions to upregulate translation of select messages.

Ribosomes with various complements of initiation factors, but without functional eIF2, can enter select mRNAs at IRES, or internal ribosome entry sites. Extra factors, called ITAFs, may participate.

The 43S pre-initiation complex with eIF2/3/4/5 and met-tRNA scans the mRNA for an initiation codon, at which point the rest of the ribosome assembles, the initiation factors leave, and translation continues.

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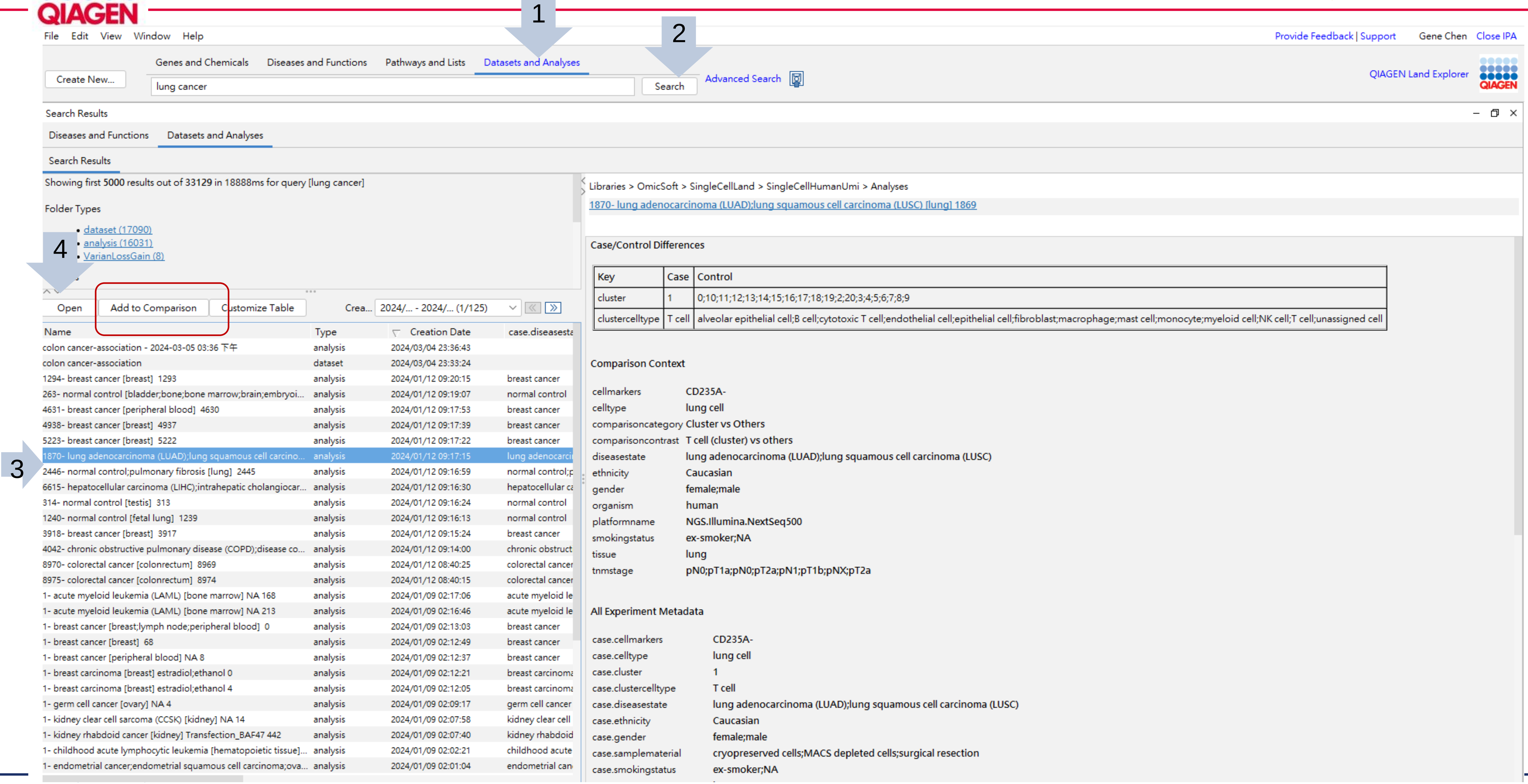
Dataset and analysis search



Showing first 5000 results out of 33129 in 18888ms for query [lung cancer]

Folder Types

- dataset (17090)
- analysis (16031)
- VarianLossGain (8)

Name	Type	Creation Date	case.diseasesta
colon cancer-association - 2024-03-05 03:36 下午	analysis	2024/03/04 23:36:43	
colon cancer-association	dataset	2024/03/04 23:33:24	
1294- breast cancer [breast] 1293	analysis	2024/01/12 09:20:15	breast cancer
263- normal control [bladder;bone;bone marrow;brain;embryoi...	analysis	2024/01/12 09:19:07	normal control
4631- breast cancer [peripheral blood] 4630	analysis	2024/01/12 09:17:53	breast cancer
4938- breast cancer [breast] 4937	analysis	2024/01/12 09:17:39	breast cancer
5223- breast cancer [breast] 5222	analysis	2024/01/12 09:17:22	breast cancer
1870- lung adenocarcinoma (LUAD);lung squamous cell carcino...	analysis	2024/01/12 09:17:15	lung adenocarci
2446- normal control;pulmonary fibrosis [lung] 2445	analysis	2024/01/12 09:16:59	normal control;p
6615- hepatocellular carcinoma (LIHC);intrahepatic cholangiocar...	analysis	2024/01/12 09:16:30	hepatocellular ca
314- normal control [testis] 313	analysis	2024/01/12 09:16:24	normal control
1240- normal control [fetal lung] 1239	analysis	2024/01/12 09:16:13	normal control
3918- breast cancer [breast] 3917	analysis	2024/01/12 09:15:24	breast cancer
4042- chronic obstructive pulmonary disease (COPD);disease co...	analysis	2024/01/12 09:14:00	chronic obstruct
8970- colorectal cancer [colonrectum] 8969	analysis	2024/01/12 08:40:25	colorectal cancer
8975- colorectal cancer [colonrectum] 8974	analysis	2024/01/12 08:40:15	colorectal cancer
1- acute myeloid leukemia (LAML) [bone marrow] NA 168	analysis	2024/01/09 02:17:06	acute myeloid le
1- acute myeloid leukemia (LAML) [bone marrow] NA 213	analysis	2024/01/09 02:16:46	acute myeloid le
1- breast cancer [breast;lymph node;peripheral blood] 0	analysis	2024/01/09 02:13:03	breast cancer
1- breast cancer [breast] 68	analysis	2024/01/09 02:12:49	breast cancer
1- breast cancer [peripheral blood] NA 8	analysis	2024/01/09 02:12:37	breast cancer
1- breast carcinoma [breast] estradiol;ethanol 0	analysis	2024/01/09 02:12:21	breast carcinoma
1- breast carcinoma [breast] estradiol;ethanol 4	analysis	2024/01/09 02:12:05	breast carcinoma
1- germ cell cancer [ovary] NA 4	analysis	2024/01/09 02:09:17	germ cell cancer
1- kidney clear cell sarcoma (CCSK) [kidney] NA 14	analysis	2024/01/09 02:07:58	kidney clear cell
1- kidney rhabdoid cancer [kidney] Transfection_BAF47 442	analysis	2024/01/09 02:07:40	kidney rhabdoid
1- childhood acute lymphocytic leukemia [hematopoietic tissue]...	analysis	2024/01/09 02:02:21	childhood acute
1- endometrial cancer;endometrial squamous cell carcinoma;ova...	analysis	2024/01/09 02:01:04	endometrial can

Libraries > OmicSoft > SingleCellLand > SingleCellHumanUmi > Analyses

1870- lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC) [lung] 1869

Case/Control Differences

Key	Case	Control
cluster	1	0;10;11;12;13;14;15;16;17;18;19;2;20;3;4;5;6;7;8;9
clustercelltype	T cell	alveolar epithelial cell;B cell;cytotoxic T cell;endothelial cell;epithelial cell;fibroblast;macrophage;mast cell;monocyte;myeloid cell;NK cell;T cell;unassigned cell

Comparison Context

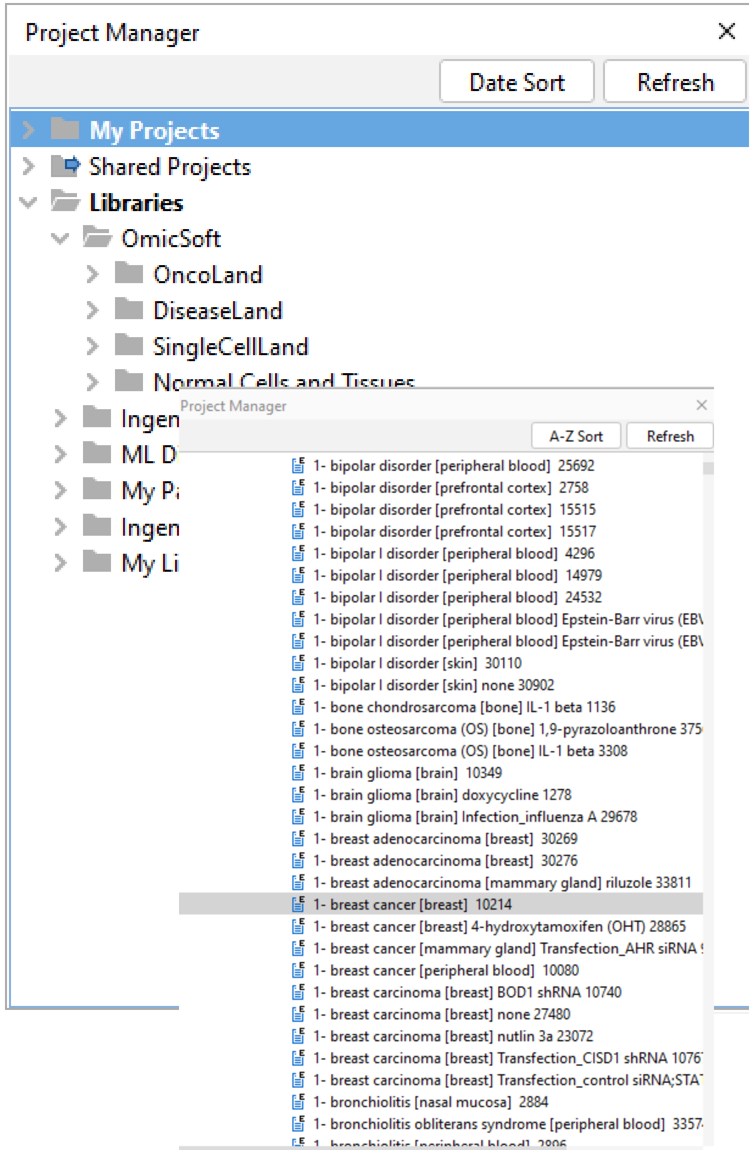
cellmarkers	CD235A-
celltype	lung cell
comparisoncategory	Cluster vs Others
comparisoncontrast	T cell (cluster) vs others
diseasestate	lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)
ethnicity	Caucasian
gender	female;male
organism	human
platformname	NGS.Illumina.NextSeq500
smokingstatus	ex-smoker;NA
tissue	lung
tnmstage	pN0;pT1a;pN0;pT2a;pN1;pT1b;pNX;pT2a

All Experiment Metadata

case.cellmarkers	CD235A-
case.celltype	lung cell
case.cluster	1
case.clustercelltype	T cell
case.diseasestate	lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)
case.ethnicity	Caucasian
case.gender	female;male
case.samplematerial	cryopreserved cells;MACS depleted cells;surgical resection
case.smokingstatus	ex-smoker;NA

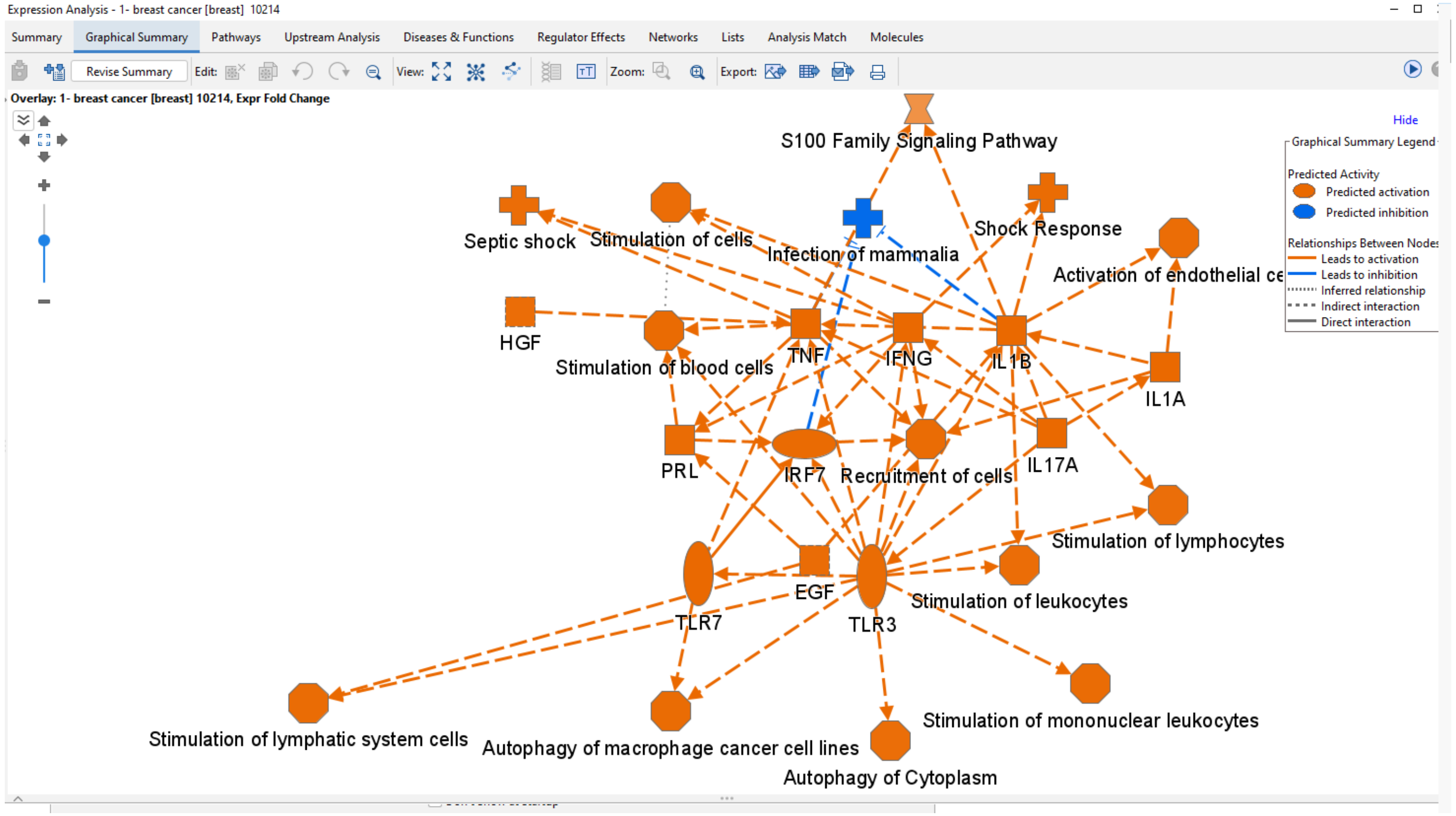
OmicSoft data storage and analysis in IPA

You can also use the repository without your own analysis, just by searching for available analyses of interest.



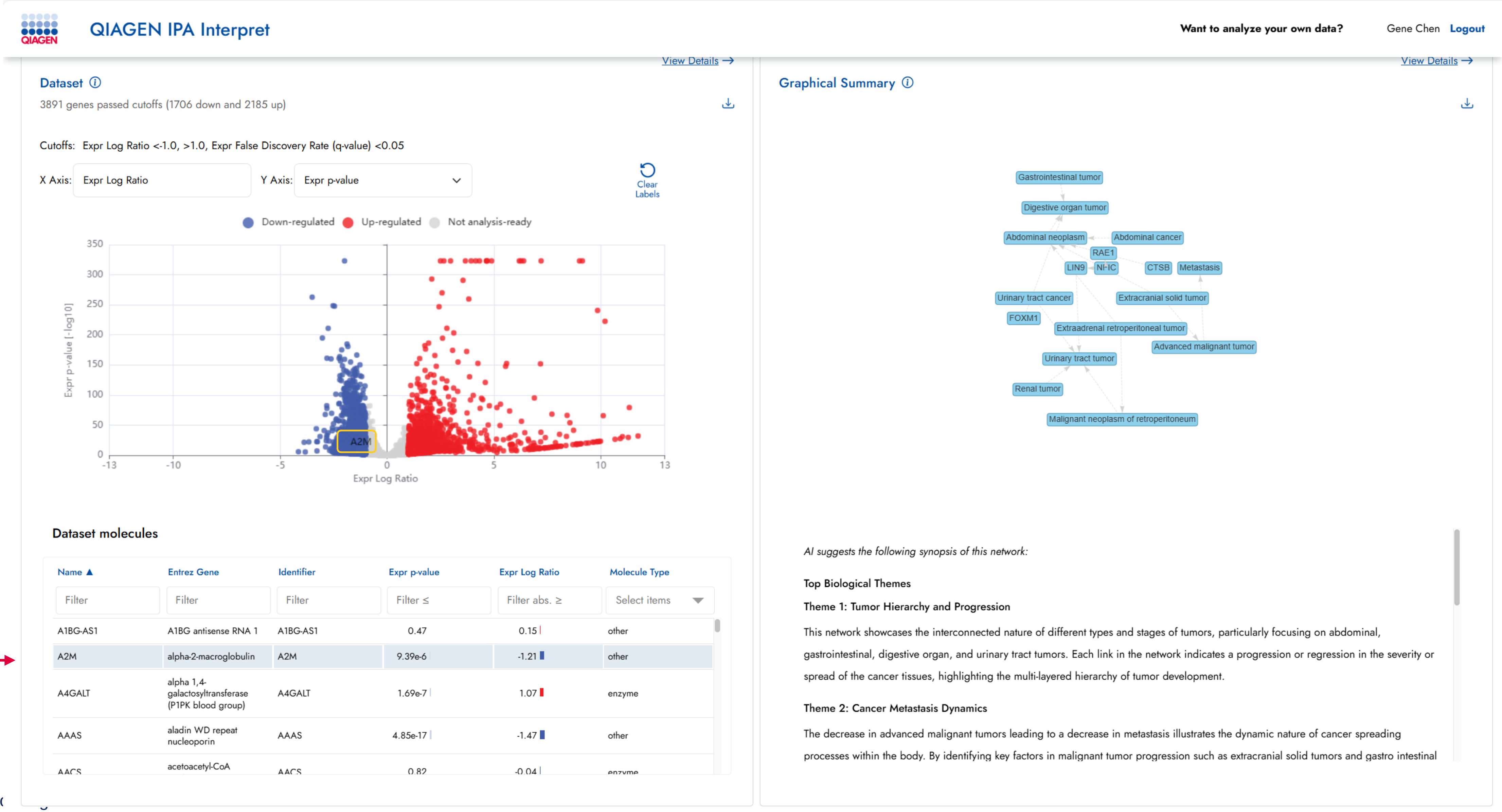
1- bipolar disorder [peripheral blood] 25692
1- bipolar disorder [prefrontal cortex] 2758
1- bipolar disorder [prefrontal cortex] 15515
1- bipolar disorder [prefrontal cortex] 15517
1- bipolar I disorder [peripheral blood] 4296
1- bipolar I disorder [peripheral blood] 14979
1- bipolar I disorder [peripheral blood] 24532
1- bipolar I disorder [peripheral blood] Epstein-Barr virus (EB
1- bipolar I disorder [peripheral blood] Epstein-Barr virus (EB
1- bipolar I disorder [skin] 30110
1- bipolar I disorder [skin] none 30902
1- bone chondrosarcoma [bone] IL-1 beta 1136
1- bone osteosarcoma (OS) [bone] 1,9-pyrazoloanthrone 375
1- bone osteosarcoma (OS) [bone] IL-1 beta 3308
1- brain glioma [brain] 10349
1- brain glioma [brain] doxycycline 1278
1- brain glioma [brain] Infection_influenza A 29678
1- breast adenocarcinoma [breast] 30269
1- breast adenocarcinoma [breast] 30276
1- breast adenocarcinoma [mammary gland] riluzole 33811
1- breast cancer [breast] 10214
1- breast cancer [breast] 4-hydroxytamoxifen (OHT) 28865
1- breast cancer [mammary gland] Transfection_AHR siRNA
1- breast cancer [peripheral blood] 10080
1- breast carcinoma [breast] BOD1 shRNA 10740
1- breast carcinoma [breast] none 27480
1- breast carcinoma [breast] nutlin 3a 23072
1- breast carcinoma [breast] Transfection_CISD1 shRNA 1076
1- breast carcinoma [breast] Transfection_control siRNA;STA
1- bronchiolitis [nasal mucosa] 2884
1- bronchiolitis obliterans syndrome [peripheral blood] 3357

Graphical summary



What’s new in the QIAGEN® Ingenuity Pathway Analysis Fall Release (2024)

IPA interpret



QIAGEN IPA Interpret

Want to analyze your own data? Gene Chen **Logout**

View Details →

Dataset ⓘ

3891 genes passed cutoffs (1706 down and 2185 up)

Cutoffs: Expr Log Ratio <-1.0, >1.0, Expr False Discovery Rate (q-value) <0.05

X Axis: Expr Log Ratio

Y Axis: Expr p-value

Dataset molecules

Name ▲	Entrez Gene	Identifier	Expr p-value	Expr Log Ratio	Molecule Type
Filter	Filter	Filter	Filter ≤	Filter abs. ≥	Select items
A1BG-AS1	A1BG antisense RNA 1	A1BG-AS1	0.47	0.15	other
A2M	alpha-2-macroglobulin	A2M	9.39e-6	-1.21	other
A4GALT	alpha 1,4-galactosyltransferase (P1PK blood group)	A4GALT	1.69e-7	1.07	enzyme
AAAS	aladin WD repeat nucleoporin	AAAS	4.85e-17	-1.47	other
AACS	acetoacetyl-CoA	AACS	0.82	-0.04	enzyme

View Details →

Graphical Summary ⓘ

AI suggests the following synopsis of this network:

Top Biological Themes

Theme 1: Tumor Hierarchy and Progression

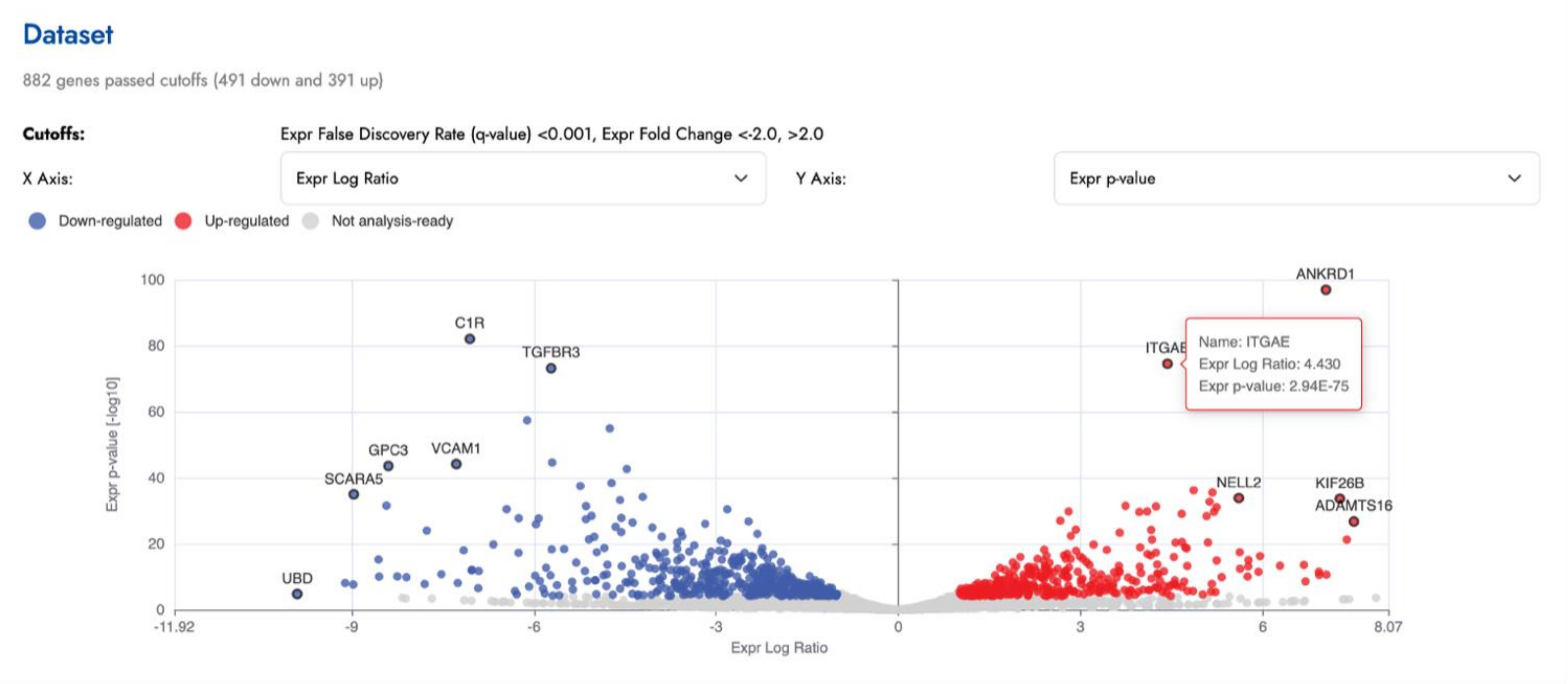
This network showcases the interconnected nature of different types and stages of tumors, particularly focusing on abdominal, gastrointestinal, digestive organ, and urinary tract tumors. Each link in the network indicates a progression or regression in the severity or spread of the cancer tissues, highlighting the multi-layered hierarchy of tumor development.

Theme 2: Cancer Metastasis Dynamics

The decrease in advanced malignant tumors leading to a decrease in metastasis illustrates the dynamic nature of cancer spreading processes within the body. By identifying key factors in malignant tumor progression such as extracranial solid tumors and gastro intestinal

Sample t

Label gene names of interest in the volcano plot



Dataset

882 genes passed cutoffs (491 down and 391 up)

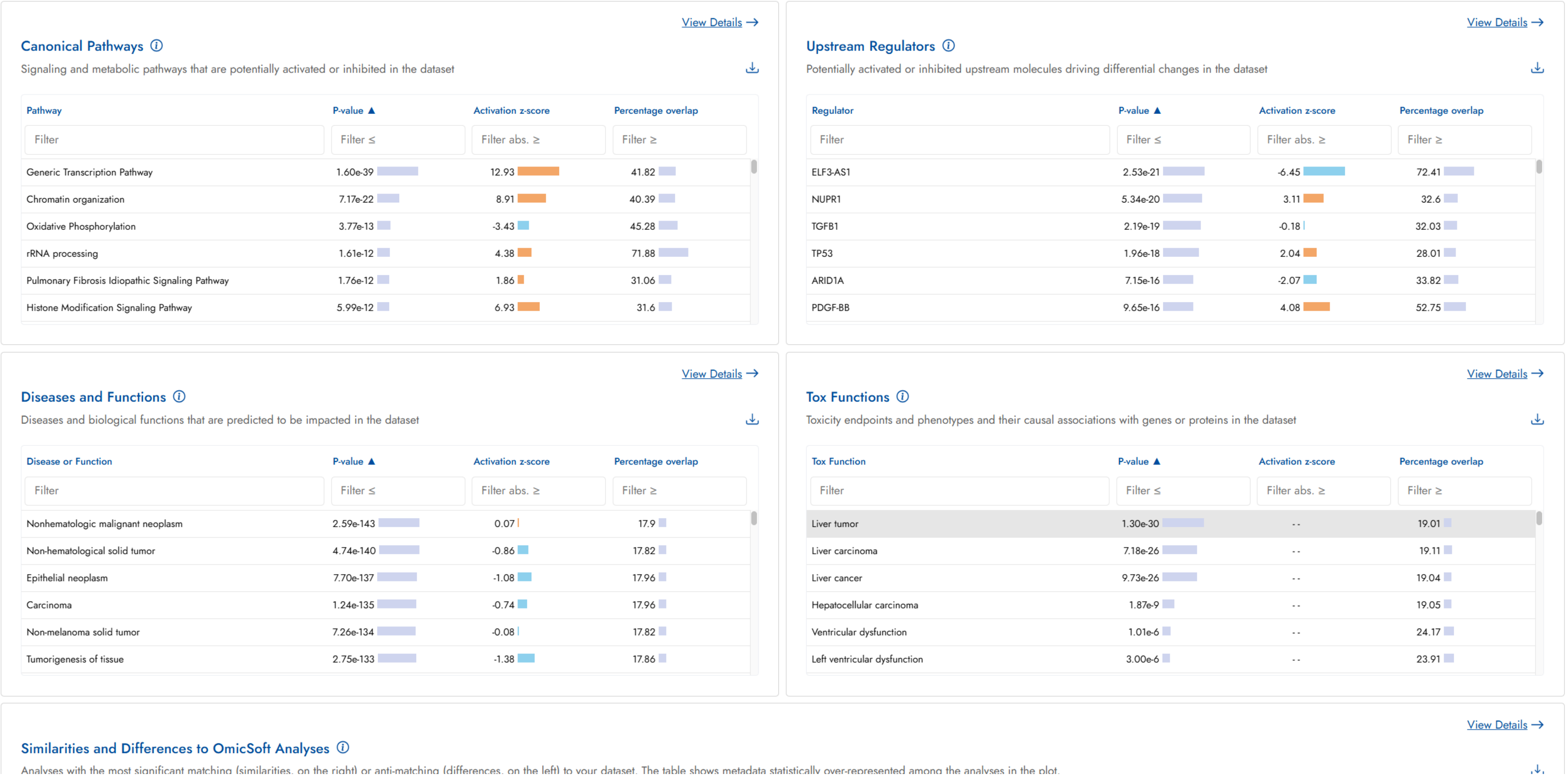
Cutoffs: Expr False Discovery Rate (q-value) <0.001, Expr Fold Change <-2.0, >2.0

X Axis: Expr Log Ratio

Y Axis: Expr p-value

Name: ITGAE
Expr Log Ratio: 4.430
Expr p-value: 2.94E-75

IPA interpret (2024 fall release)



View Details →

Canonical Pathways ⓘ

Signaling and metabolic pathways that are potentially activated or inhibited in the dataset

Pathway	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Generic Transcription Pathway	1.60e-39	12.93	41.82
Chromatin organization	7.17e-22	8.91	40.39
Oxidative Phosphorylation	3.77e-13	-3.43	45.28
rRNA processing	1.61e-12	4.38	71.88
Pulmonary Fibrosis Idiopathic Signaling Pathway	1.76e-12	1.86	31.06
Histone Modification Signaling Pathway	5.99e-12	6.93	31.6

View Details →

Upstream Regulators ⓘ

Potentially activated or inhibited upstream molecules driving differential changes in the dataset

Regulator	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter ≤	Filter abs. ≥	Filter ≥
ELF3-AS1	2.53e-21	-6.45	72.41
NUPR1	5.34e-20	3.11	32.6
TGFB1	2.19e-19	-0.18	32.03
TP53	1.96e-18	2.04	28.01
ARID1A	7.15e-16	-2.07	33.82
PDGF-BB	9.65e-16	4.08	52.75

View Details →

Diseases and Functions ⓘ

Diseases and biological functions that are predicted to be impacted in the dataset

Disease or Function	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Nonhematologic malignant neoplasm	2.59e-143	0.07	17.9
Non-hematological solid tumor	4.74e-140	-0.86	17.82
Epithelial neoplasm	7.70e-137	-1.08	17.96
Carcinoma	1.24e-135	-0.74	17.96
Non-melanoma solid tumor	7.26e-134	-0.08	17.82
Tumorigenesis of tissue	2.75e-133	-1.38	17.86

View Details →

Tox Functions ⓘ

Toxicity endpoints and phenotypes and their causal associations with genes or proteins in the dataset

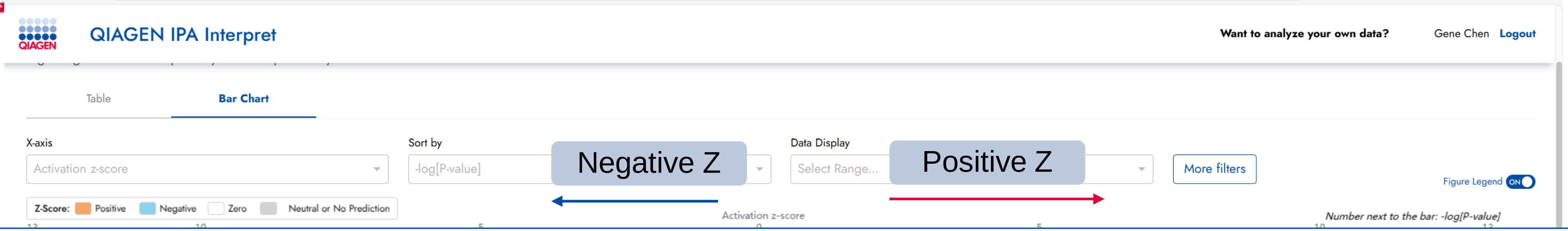
Tox Function	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Liver tumor	1.30e-30	--	19.01
Liver carcinoma	7.18e-26	--	19.11
Liver cancer	9.73e-26	--	19.04
Hepatocellular carcinoma	1.87e-9	--	19.05
Ventricular dysfunction	1.01e-6	--	24.17
Left ventricular dysfunction	3.00e-6	--	23.91

View Details →

Similarities and Differences to OmicSoft Analyses ⓘ

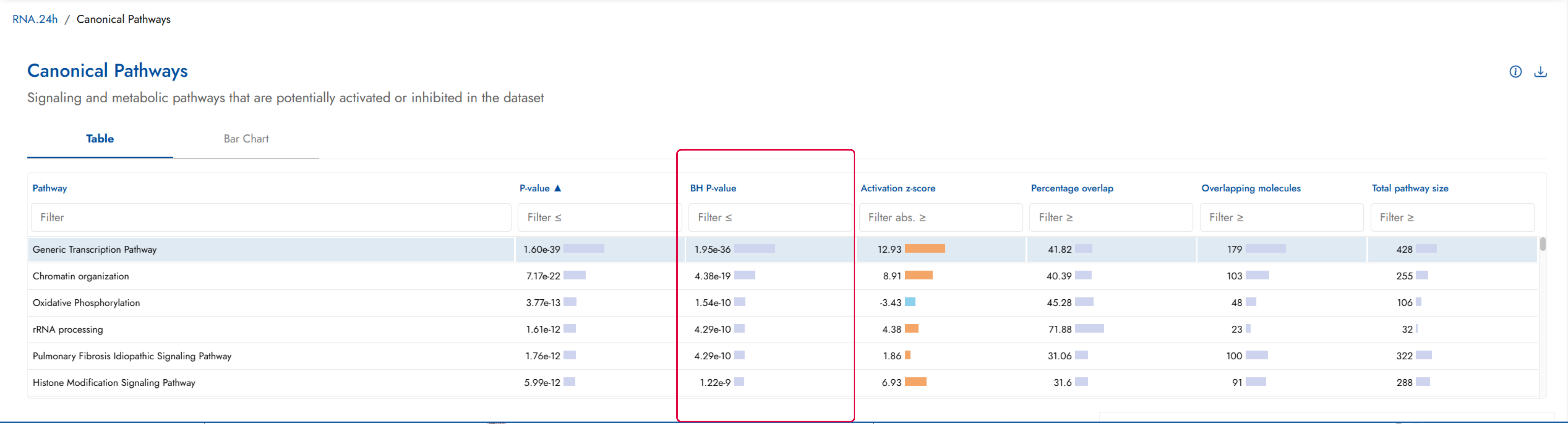
Analyses with the most significant matching (similarities, on the right) or anti-matching (differences, on the left) to your dataset. The table shows metadata statistically over-represented among the analyses in the plot.

IPA interpret canonical pathway bar chart (2025 spring release)



Negative Z

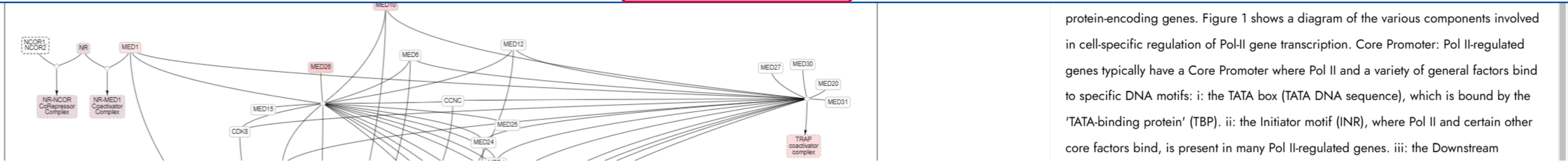
Positive Z



Canonical Pathways

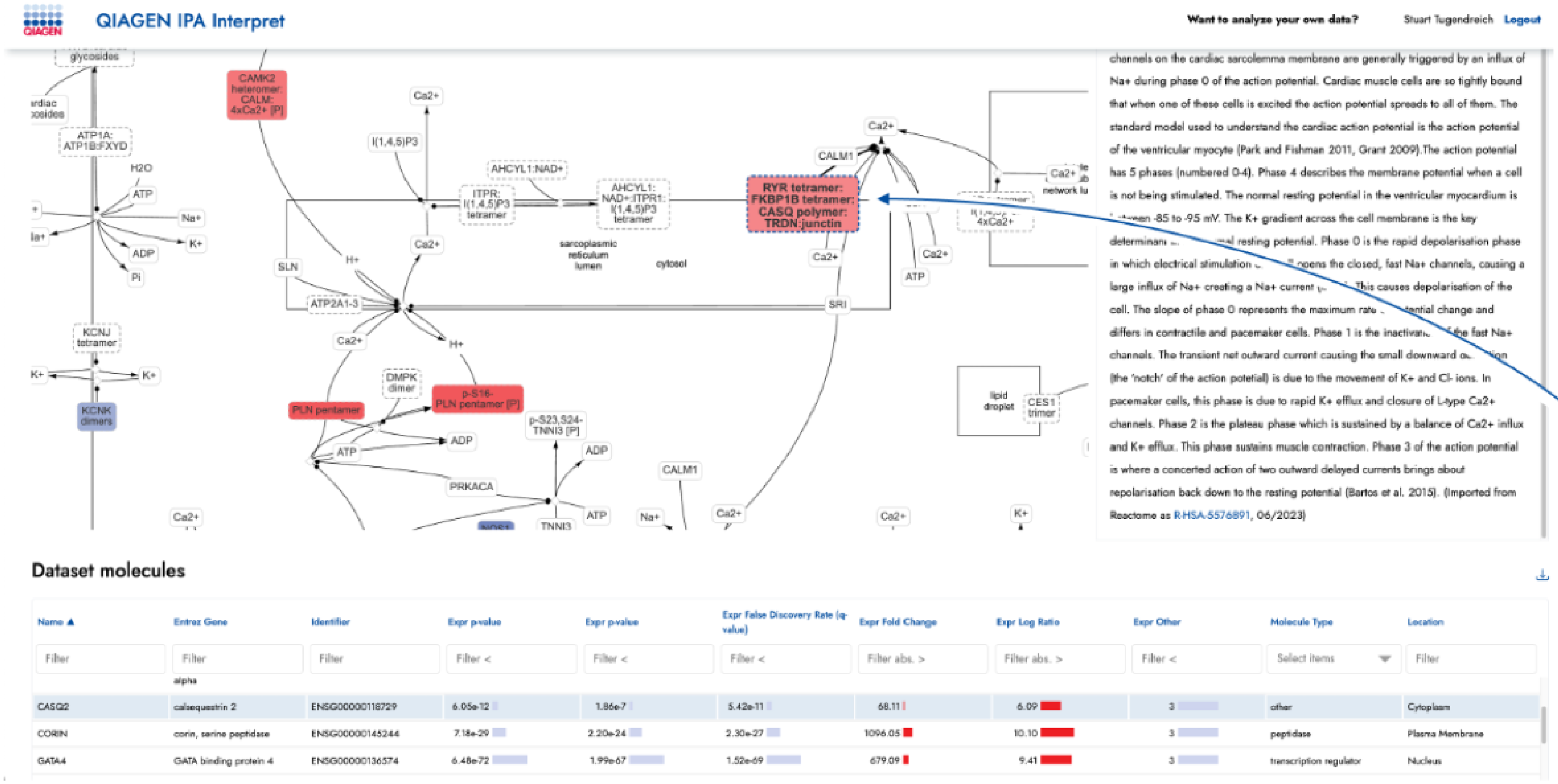
Signaling and metabolic pathways that are potentially activated or inhibited in the dataset

Pathway	P-value ▲	BH P-value	Activation z-score	Percentage overlap	Overlapping molecules	Total pathway size
Filter	Filter ≤	Filter ≤	Filter abs. ≥	Filter ≥	Filter ≥	Filter ≥
Generic Transcription Pathway	1.60e-39	1.95e-36	12.93	41.82	179	428
Chromatin organization	7.17e-22	4.38e-19	8.91	40.39	103	255
Oxidative Phosphorylation	3.77e-13	1.54e-10	-3.43	45.28	48	106
rRNA processing	1.61e-12	4.29e-10	4.38	71.88	23	32
Pulmonary Fibrosis Idiopathic Signaling Pathway	1.76e-12	4.29e-10	1.86	31.06	100	322
Histone Modification Signaling Pathway	5.99e-12	1.22e-9	6.93	31.6	91	288



protein-encoding genes. Figure 1 shows a diagram of the various components involved in cell-specific regulation of Pol-II gene transcription. Core Promoter: Pol II-regulated genes typically have a Core Promoter where Pol II and a variety of general factors bind to specific DNA motifs: i: the TATA box (TATA DNA sequence), which is bound by the 'TATA-binding protein' (TBP). ii: the Initiator motif (INR), where Pol II and certain other core factors bind, is present in many Pol II-regulated genes. iii: the Downstream

Highlight nodes of interest in a canonical pathway or network



channels on the cardiac sarcolemma membrane are generally triggered by an influx of Na+ during phase 0 of the action potential. Cardiac muscle cells are so tightly bound that when one of these cells is excited the action potential spreads to all of them. The standard model used to understand the cardiac action potential is the action potential of the ventricular myocyte (Park and Fishman 2011, Grant 2009).The action potential has 5 phases (numbered 0-4). Phase 4 describes the membrane potential when a cell is not being stimulated. The normal resting potential in the ventricular myocardium is [illegible]tween -85 to -95 mV. The K+ gradient across the cell membrane is the key determinan[illegible] [illegible]al resting potential. Phase 0 is the rapid depolarisation phase in which electrical stimulation [illegible] opens the closed, fast Na+ channels, causing a large influx of Na+ creating a Na+ current [illegible]. This causes depolarisation of the cell. The slope of phase 0 represents the maximum rat[illegible] [illegible]tential change and differs in contractile and pacemaker cells. Phase 1 is the inactiva[illegible] [illegible] the fast Na+ channels. The transient net outward current causing the small downward [illegible]tion (the 'notch' of the action potetial) is due to the movement of K+ and Cl- ions. In pacemaker cells, this phase is due to rapid K+ efflux and closure of L-type Ca2+ channels. Phase 2 is the plateau phase which is sustained by a balance of Ca2+ influx and K+ efflux. This phase sustains muscle contraction. Phase 3 of the action potential is where a concerted action of two outward delayed currents brings about repolarisation back down to the resting potential (Bartos et al. 2015). (Imported from Reactome as R-HSA-5576891, 06/2023)

Dataset molecules

Name ▲	Entrez Gene	Identifier	Expr p-value	Expr p-value	Expr False Discovery Rate (q-value)	Expr Fold Change	Expr Log Ratio	Expr Other	Molecule Type	Location
Filter	Filter	Filter	Filter <	Filter <	Filter <	Filter abs. >	Filter abs. >	Filter <	Select items	Filter
	alpha									
CASQ2	calsequestrin 2	ENSG00000118729	6.05e-12	1.86e-7	5.42e-11	68.11	6.09	3	other	Cytoplasm
CORIN	corin, serine peptidase	ENSG00000145244	7.18e-29	2.20e-24	2.30e-27	1096.05	10.10	3	peptidase	Plasma Membrane
GATA4	GATA binding protein 4	ENSG00000136574	6.48e-72	1.99e-67	1.52e-69	679.09	9.41	3	transcription regulator	Nucleus

2) Highlights the corresponding node(s) even if inside a group or complex

1) Clicking row(s) here

IPA interpret Canonical Pathway Bubble Plot (2025 summer release)

IPA interpret

In canonical pathway, could show volcano bubble plot

1. Z-score
2. P-value
3. Overlay molecules
4. Percentage overlap
5. Pathway type
6. Total pathway size

protein.24 / Canonical Pathways

Canonical Pathways

Signaling and metabolic pathways that are potentially activated or inhibited in the dataset

Chart Type: Bubble chart

X-axis: Activation z-score

Y-axis: Pathway name

Sort by: -log[P-value]

Bubble size: Overlapping molecules

Bubble color: Pathway type

Data display: Select Range...

Cerebral Malformation Signaling Pathway

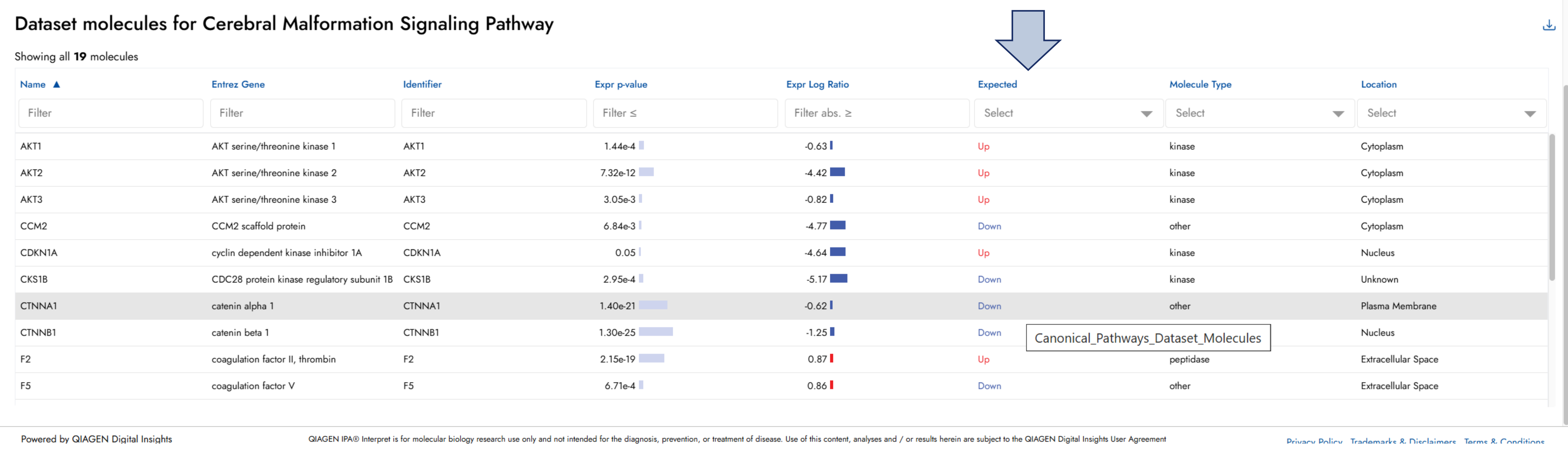
-log(p-value)	7.154
p-value	7.02e-8
Activation z-score	0.471
Percentage overlap	16.52 % (19/115)
Overlapping Molecules	19
Total Pathway Size	115

IPA interpret Canonical Pathway Bubble Plot (2025 summer release)

訊聯基因數位

IPA interpret

In canonical pathway, could show each molecules overlap in this pathway



Dataset molecules for Cerebral Malformation Signaling Pathway

Showing all **19** molecules

Name ▲	Entrez Gene	Identifier	Expr p-value	Expr Log Ratio	Expected	Molecule Type	Location
Filter	Filter	Filter	Filter ≤	Filter abs. ≥	Select	Select	Select
AKT1	AKT serine/threonine kinase 1	AKT1	1.44e-4	-0.63	Up	kinase	Cytoplasm
AKT2	AKT serine/threonine kinase 2	AKT2	7.32e-12	-4.42	Up	kinase	Cytoplasm
AKT3	AKT serine/threonine kinase 3	AKT3	3.05e-3	-0.82	Up	kinase	Cytoplasm
CCM2	CCM2 scaffold protein	CCM2	6.84e-3	-4.77	Down	other	Cytoplasm
CDKN1A	cyclin dependent kinase inhibitor 1A	CDKN1A	0.05	-4.64	Up	kinase	Nucleus
CKS1B	CDC28 protein kinase regulatory subunit 1B	CKS1B	2.95e-4	-5.17	Down	kinase	Unknown
CTNNA1	catenin alpha 1	CTNNA1	1.40e-21	-0.62	Down	other	Plasma Membrane
CTNNB1	catenin beta 1	CTNNB1	1.30e-25	-1.25	Down		Nucleus
F2	coagulation factor II, thrombin	F2	2.15e-19	0.87	Up	peptidase	Extracellular Space
F5	coagulation factor V	F5	6.71e-4	0.86	Down	other	Extracellular Space

Canonical_Pathways_Dataset_Molecules

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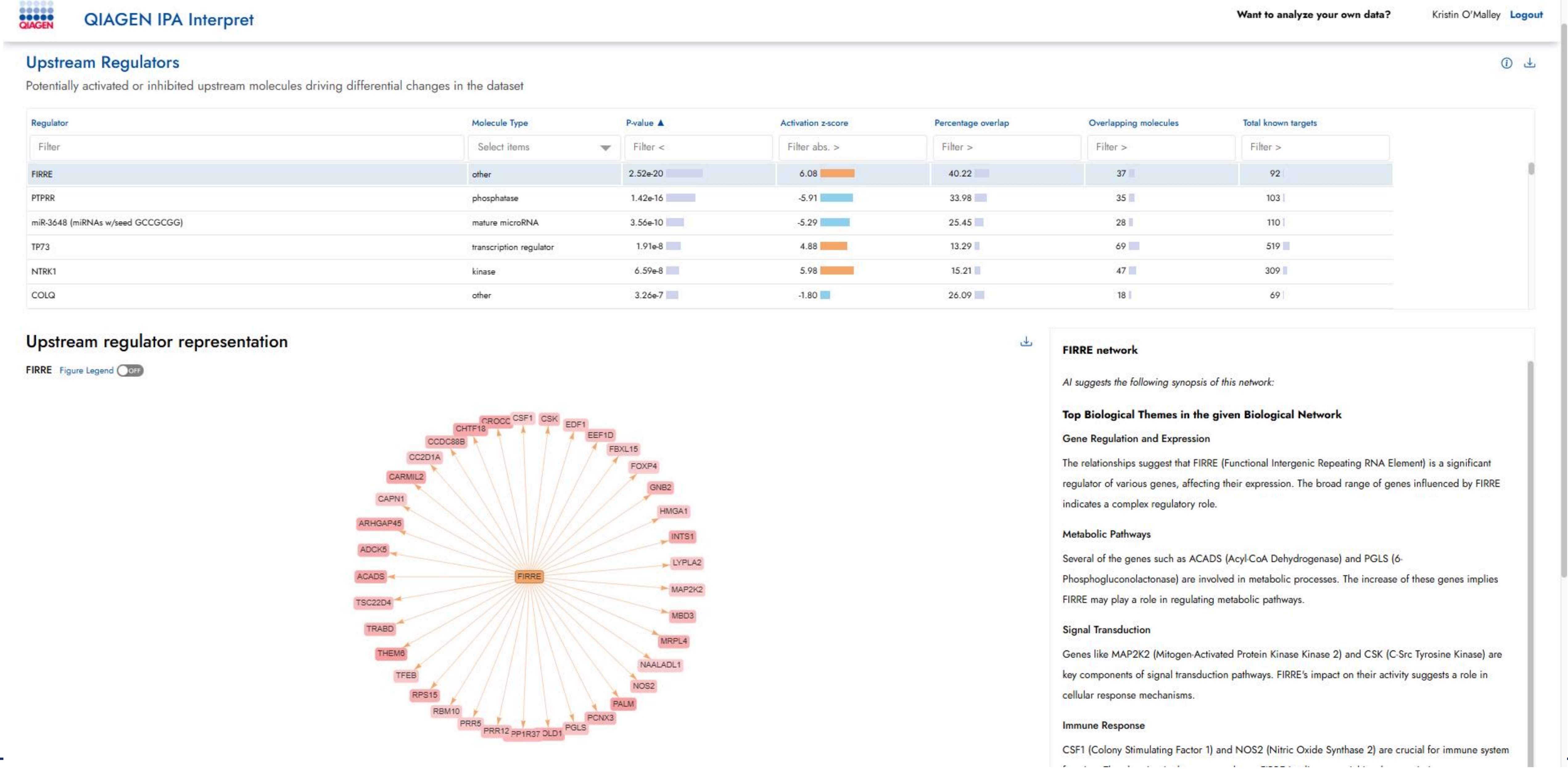
IPA interpret in upstream regulator



Upstream Regulators

Potentially activated or inhibited upstream molecules driving differential changes in the dataset

Regulator	Molecule Type	P-value ▲	Activation z-score	Percentage overlap	Overlapping molecules	Total known targets
Filter	Select items	Filter <	Filter abs. >	Filter >	Filter >	Filter >
FIRRE	other	2.52e-20	6.08	40.22	37	92
PTPRR	phosphatase	1.42e-16	-5.91	33.98	35	103
miR-3648 (miRNAs w/seed GCCGCGG)	mature microRNA	3.56e-10	-5.29	25.45	28	110
TP73	transcription regulator	1.91e-8	4.88	13.29	69	519
NTRK1	kinase	6.59e-8	5.98	15.21	47	309
COLQ	other	3.26e-7	-1.80	26.09	18	69

Upstream regulator representation

FIRRE Figure Legend OFF

FIRRE network

AI suggests the following synopsis of this network:

Top Biological Themes in the given Biological Network

Gene Regulation and Expression

The relationships suggest that FIRRE (Functional Intergenic Repeating RNA Element) is a significant regulator of various genes, affecting their expression. The broad range of genes influenced by FIRRE indicates a complex regulatory role.

Metabolic Pathways

Several of the genes such as ACADS (Acyl-CoA Dehydrogenase) and PGLS (6-Phosphogluconolactonase) are involved in metabolic processes. The increase of these genes implies FIRRE may play a role in regulating metabolic pathways.

Signal Transduction

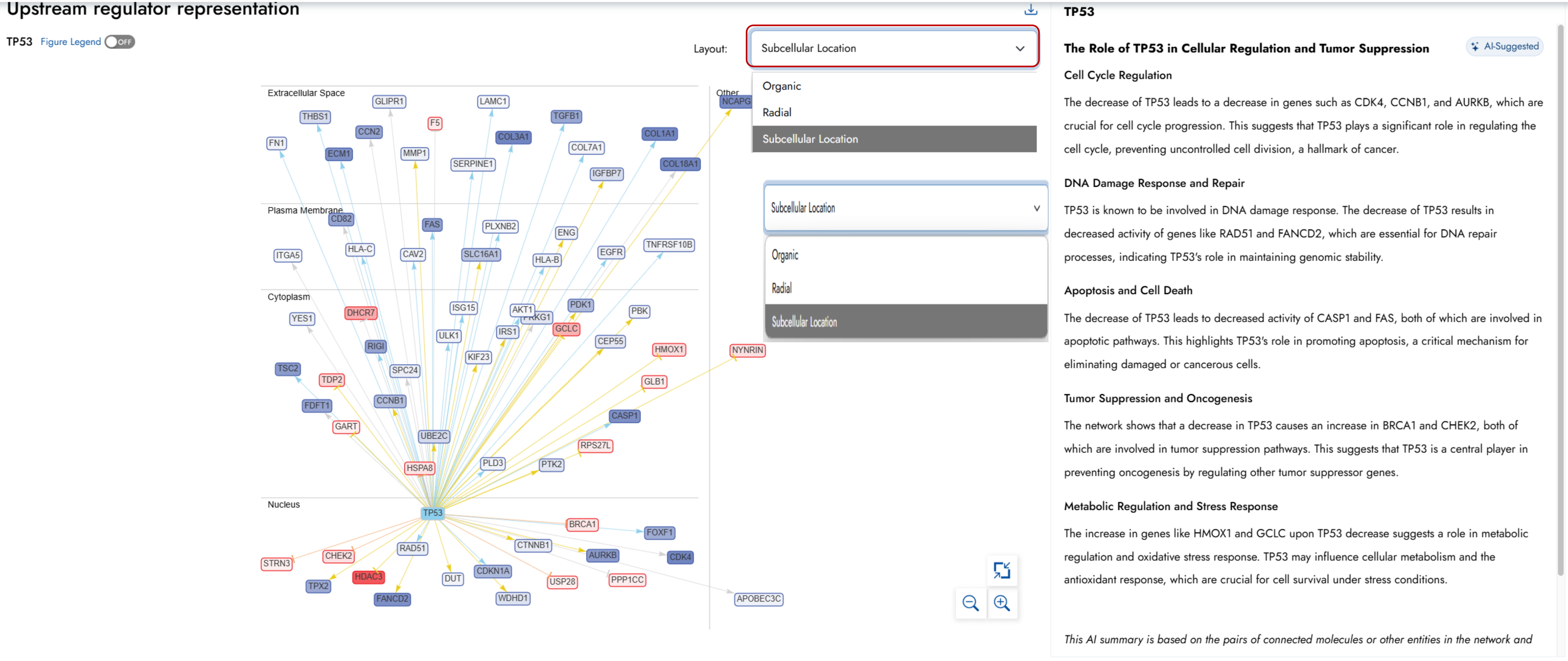
Genes like MAP2K2 (Mitogen-Activated Protein Kinase Kinase 2) and CSK (C-Src Tyrosine Kinase) are key components of signal transduction pathways. FIRRE's impact on their activity suggests a role in cellular response mechanisms.

Immune Response

CSF1 (Colony Stimulating Factor 1) and NOS2 (Nitric Oxide Synthase 2) are crucial for immune system

What's new in the QIAGEN® Ingenuity Pathway Analysis Spring Release (2025)

IPA interpret



The Role of TP53 in Cellular Regulation and Tumor Suppression

Cell Cycle Regulation

The decrease of TP53 leads to a decrease in genes such as CDK4, CCNB1, and AURKB, which are crucial for cell cycle progression. This suggests that TP53 plays a significant role in regulating the cell cycle, preventing uncontrolled cell division, a hallmark of cancer.

DNA Damage Response and Repair

TP53 is known to be involved in DNA damage response. The decrease of TP53 results in decreased activity of genes like RAD51 and FANCD2, which are essential for DNA repair processes, indicating TP53's role in maintaining genomic stability.

Apoptosis and Cell Death

The decrease of TP53 leads to decreased activity of CASP1 and FAS, both of which are involved in apoptotic pathways. This highlights TP53's role in promoting apoptosis, a critical mechanism for eliminating damaged or cancerous cells.

Tumor Suppression and Oncogenesis

The network shows that a decrease in TP53 causes an increase in BRCA1 and CHEK2, both of which are involved in tumor suppression pathways. This suggests that TP53 is a central player in preventing oncogenesis by regulating other tumor suppressor genes.

Metabolic Regulation and Stress Response

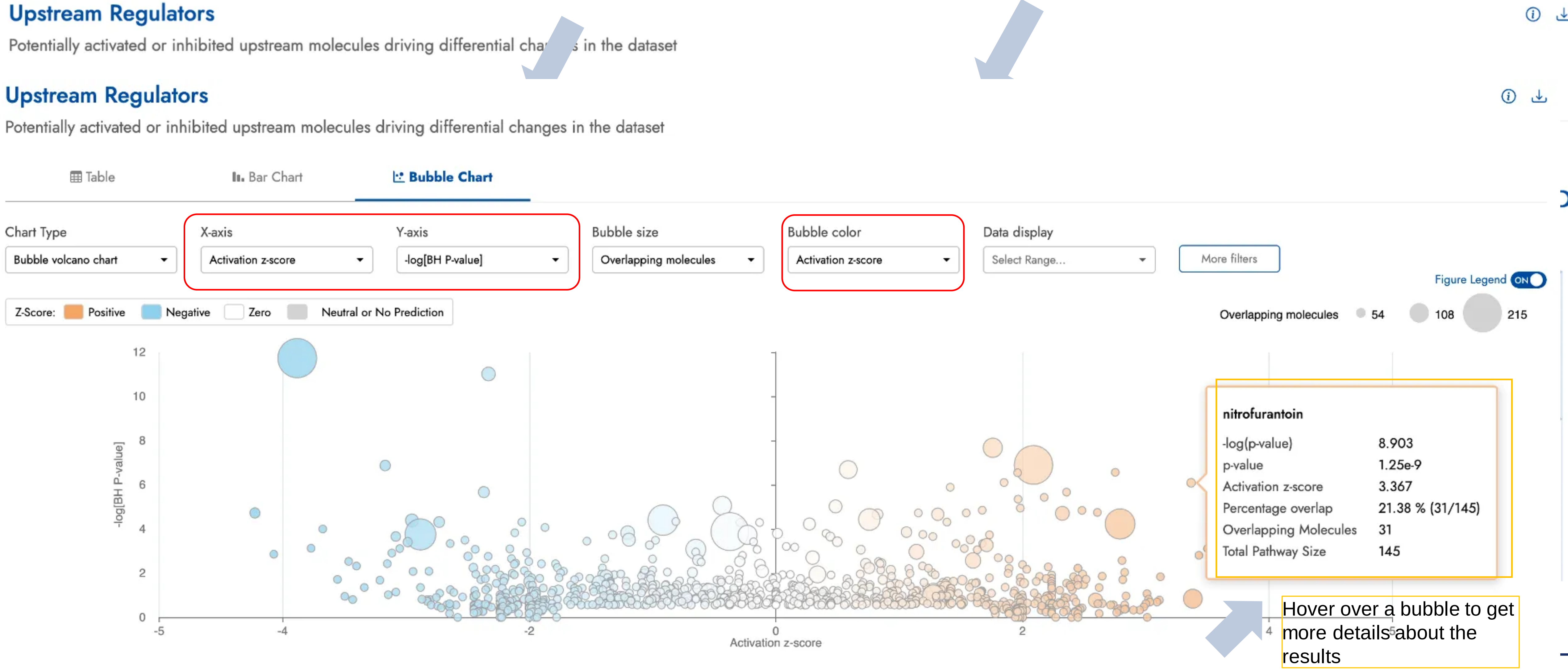
The increase in genes like HMOX1 and GCLC upon TP53 decrease suggests a role in metabolic regulation and oxidative stress response. TP53 may influence cellular metabolism and the antioxidant response, which are crucial for cell survival under stress conditions.

This AI summary is based on the pairs of connected molecules or other entities in the network and

IPA interpret in Upstream Regulator

We can change the X-axis Y-axis

Color showed the Z-score



Upstream Regulators

Potentially activated or inhibited upstream molecules driving differential cha s in the dataset

Upstream Regulators

Potentially activated or inhibited upstream molecules driving differential changes in the dataset

Chart Type: Bubble volcano chart

X-axis: Activation z-score

Y-axis: -log[BH P-value]

Bubble size: Overlapping molecules

Bubble color: Activation z-score

Data display: Select Range...

Z-Score: 🟧 Positive 🟦 Negative ☐ Zero ⬜ Neutral or No Prediction

Overlapping molecules ● 54 ● 108 ● 215

nitrofurantoin

-log(p-value)	8.903
p-value	1.25e-9
Activation z-score	3.367
Percentage overlap	21.38 % (31/145)
Overlapping Molecules	31
Total Pathway Size	145

Hover over a bubble to get more details about the results

IPA interpret Canonical Pathway Bubble Plot (2025 summer release)

IPA interpret in Upstream Regulator

If we selected a upstream regulator, there was show molecules which affected by FGF7

Dataset molecules for TP53

Showing all **72** molecules

Name ▲	Entrez Gene	Identifier	Expr p-value	Expr Log Ratio	Expected	Molecule Type	Location
Filter	Filter	Filter	Filter ≤	Filter abs. ≥	Select ▾	Select ▾	Select ▾
AKT1	AKT serine/threonine kinase 1	AKT1	1.44e-4	-0.63	Up	kinase	Cytoplasm
APOBEC3C	apolipoprotein B mRNA editing enzyme catalytic subunit 3C	APOBEC3C	7.69e-20	-0.90	- -	enzyme	Unknown
AURKB	aurora kinase B	AURKB	1.62e-22	-6.69	Down	kinase	Nucleus
BRCA1	BRCA1 DNA repair associated	BRCA1	0.04	0.97	Down	transcription regulator	Nucleus
CASP1	caspase 1	CASP1	2.00e-30	-7.39	Up	peptidase	Cytoplasm
CAV2	caveolin 2	CAV2	4.84e-3	-0.83	Up	other	Plasma Membrane
CCN2	cellular communication network factor 2	CCN2	1.41e-11	-6.04	- -	growth factor	Extracellular Space
CCNB1	cyclin B1	CCNB1	0.04	-4.32	Down	enzyme	Cytoplasm
CD82	CD82 molecule	CD82	1.13e-4	-6.00	- -	other	Plasma Membrane
CDK4	cyclin dependent kinase 4	CDK4	2.00e-30	-9.17	- -	kinase	Nucleus

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What’s new in the QIAGEN® Ingenuity Pathway Analysis Summer Release (2025)

IPA interpret in Disease and Function

In disease and functional, It also could show Bubble Chart

For Disease and Function
We could use more filter to select our interested disease and function

Diseases and Functions

Diseases and biological processes predicted to be impacted in the dataset

Chart Type: Bubble volcano chart

X-axis: Activation z-score

Y-axis: -log[BH P-value]

Bubble size: Percentage overlap

Bubble color: Activation z-score

Data display: Active Filters: Z-Score, P-Value

More Data Filters

Filter by Gene(s)

Include (e.g. BRCA1, TP5:

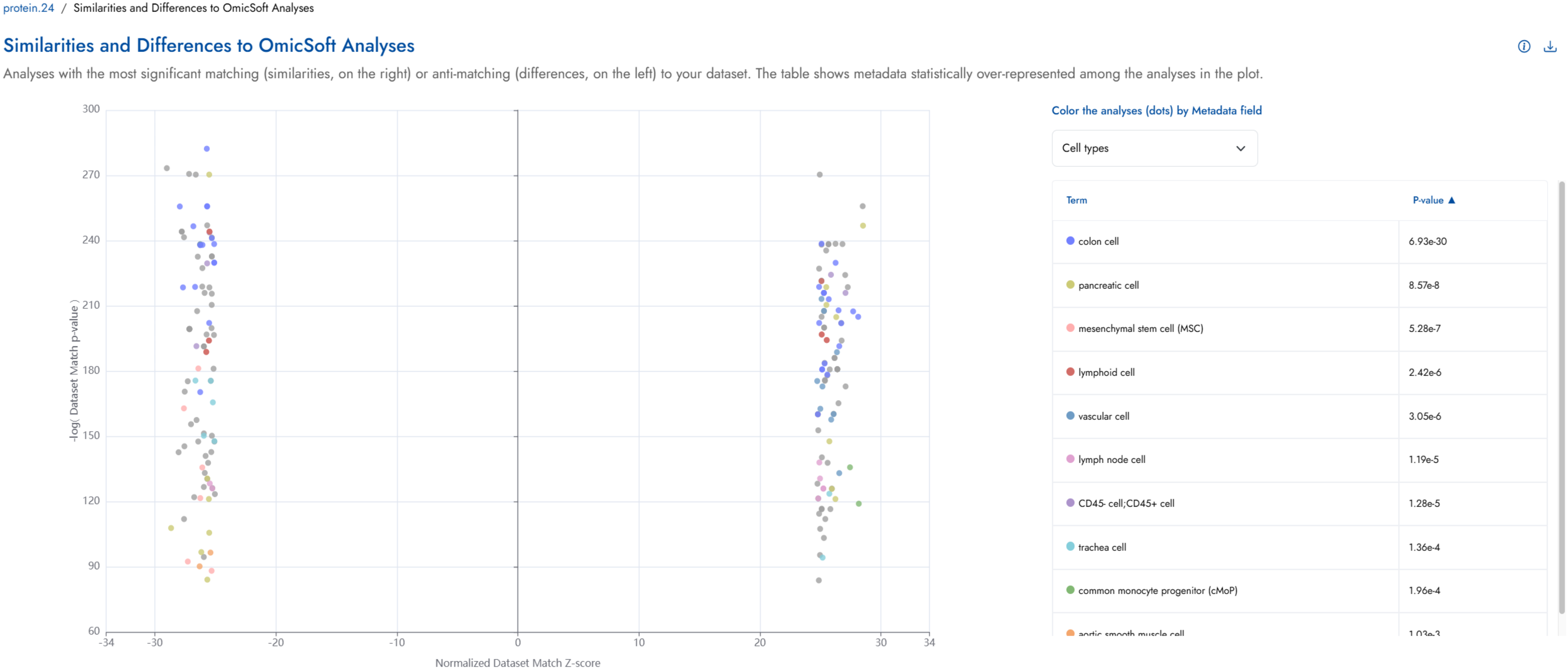
Exclude (e.g. ALAS2, IRF:

Diseases and Functions Display

Search list (Unselect all, then search to filter results)

- ☐ All Diseases and Functions (2761)
  - ☑ Embryonic Development (111)
  - ☐ Organismal Development (138)
  - ☐ Organismal Injury and Abnormalities (670)
  - ☐ Cardiovascular Disease (172)
  - ☐ Tissue Development (123)

Analysis match of Omicsoft analysis



protein.24 / Similarities and Differences to OmicSoft Analyses

Similarities and Differences to OmicSoft Analyses

Analyses with the most significant matching (similarities, on the right) or anti-matching (differences, on the left) to your dataset. The table shows metadata statistically over-represented among the analyses in the plot.

Color the analyses (dots) by Metadata field

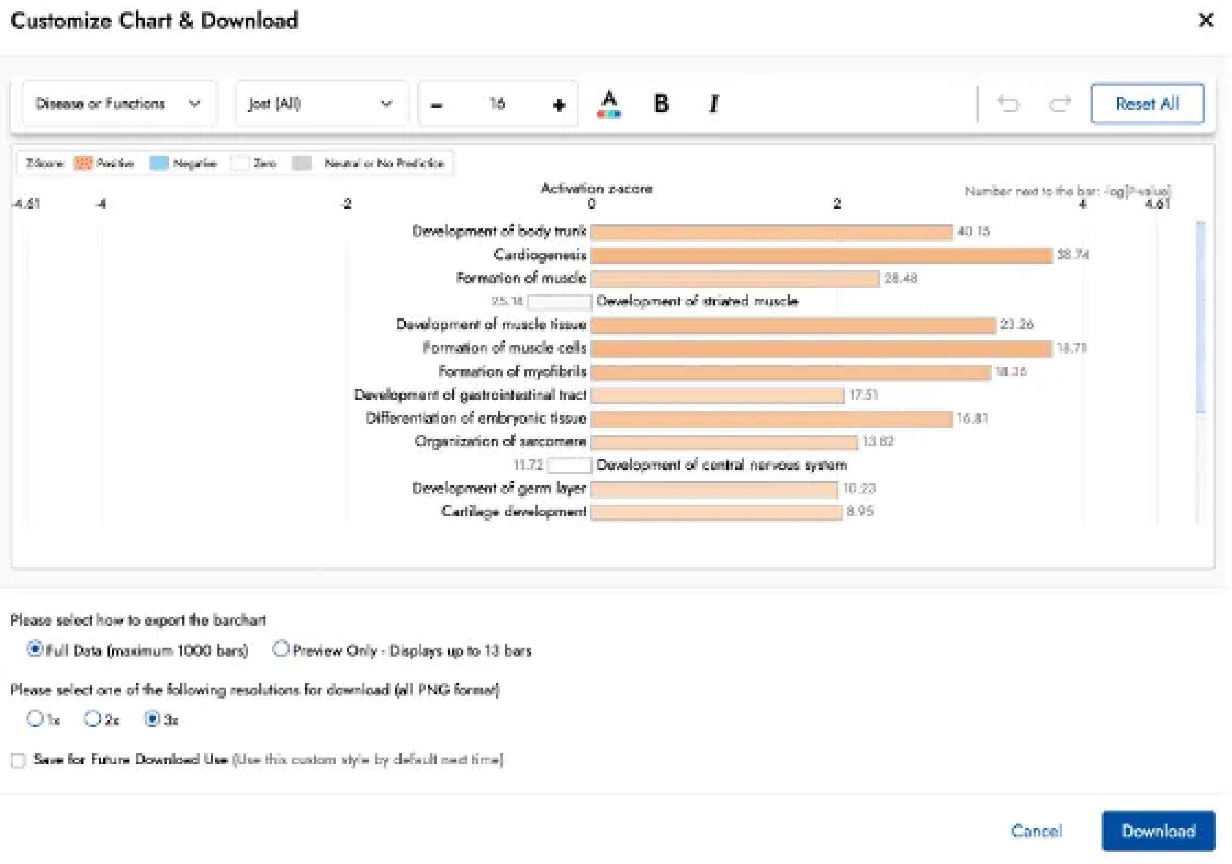
Cell types

Term	P-value ▲
● colon cell	6.93e-30
● pancreatic cell	8.57e-8
● mesenchymal stem cell (MSC)	5.28e-7
● lymphoid cell	2.42e-6
● vascular cell	3.05e-6
● lymph node cell	1.19e-5
● CD45- cell;CD45+ cell	1.28e-5
● trachea cell	1.36e-4
● common monocyte progenitor (cMoP)	1.96e-4
● aortic smooth muscle cell	1.03e-3

Customize bar charts for image export

Canonical Pathways

Signaling and metabolic pathways that are potentially activated or inhibited in the dataset



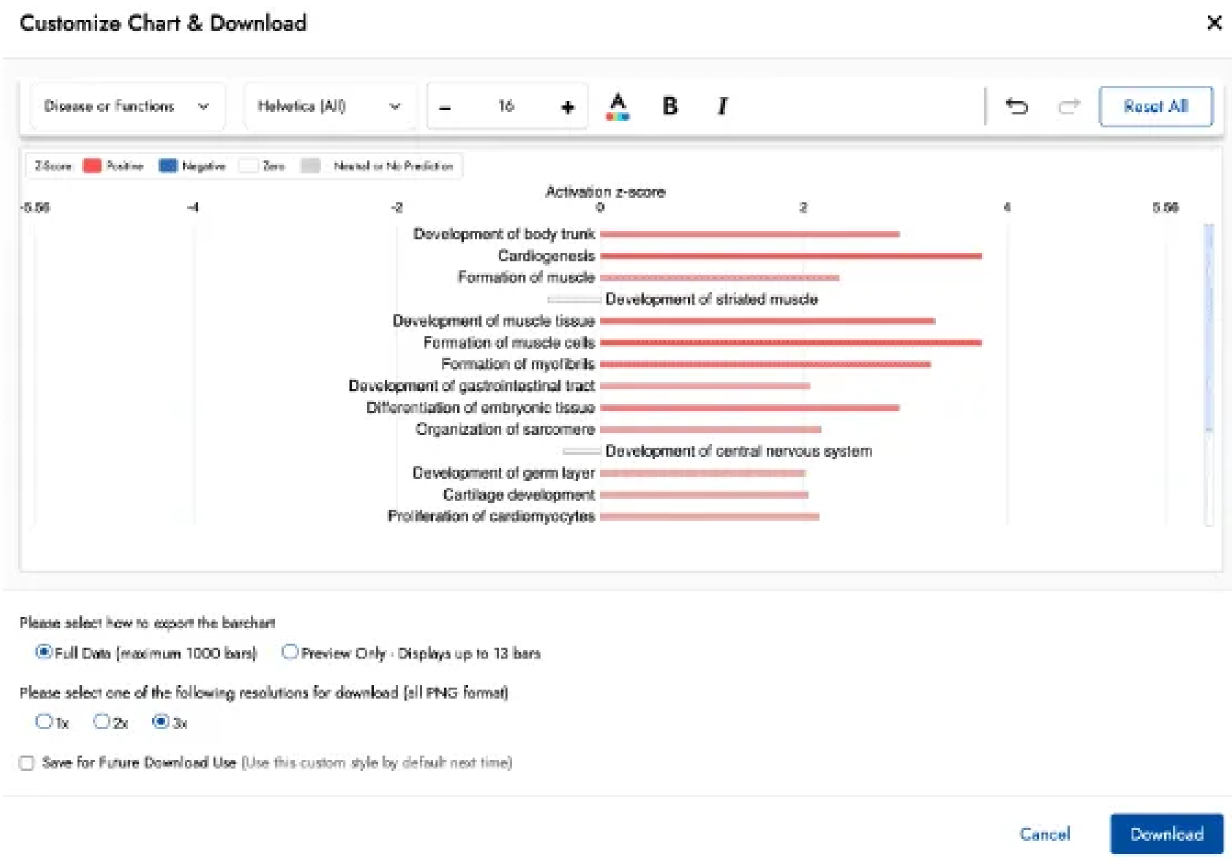
Please select how to export the barchart

● Full Data (maximum 1000 bars) ○ Preview Only - Displays up to 13 bars

Please select one of the following resolutions for download (all PNG format)

○ 1x ○ 2x ● 3x

☐ Save for Future Download Use (Use this custom style by default next time)



Please select how to export the barchart

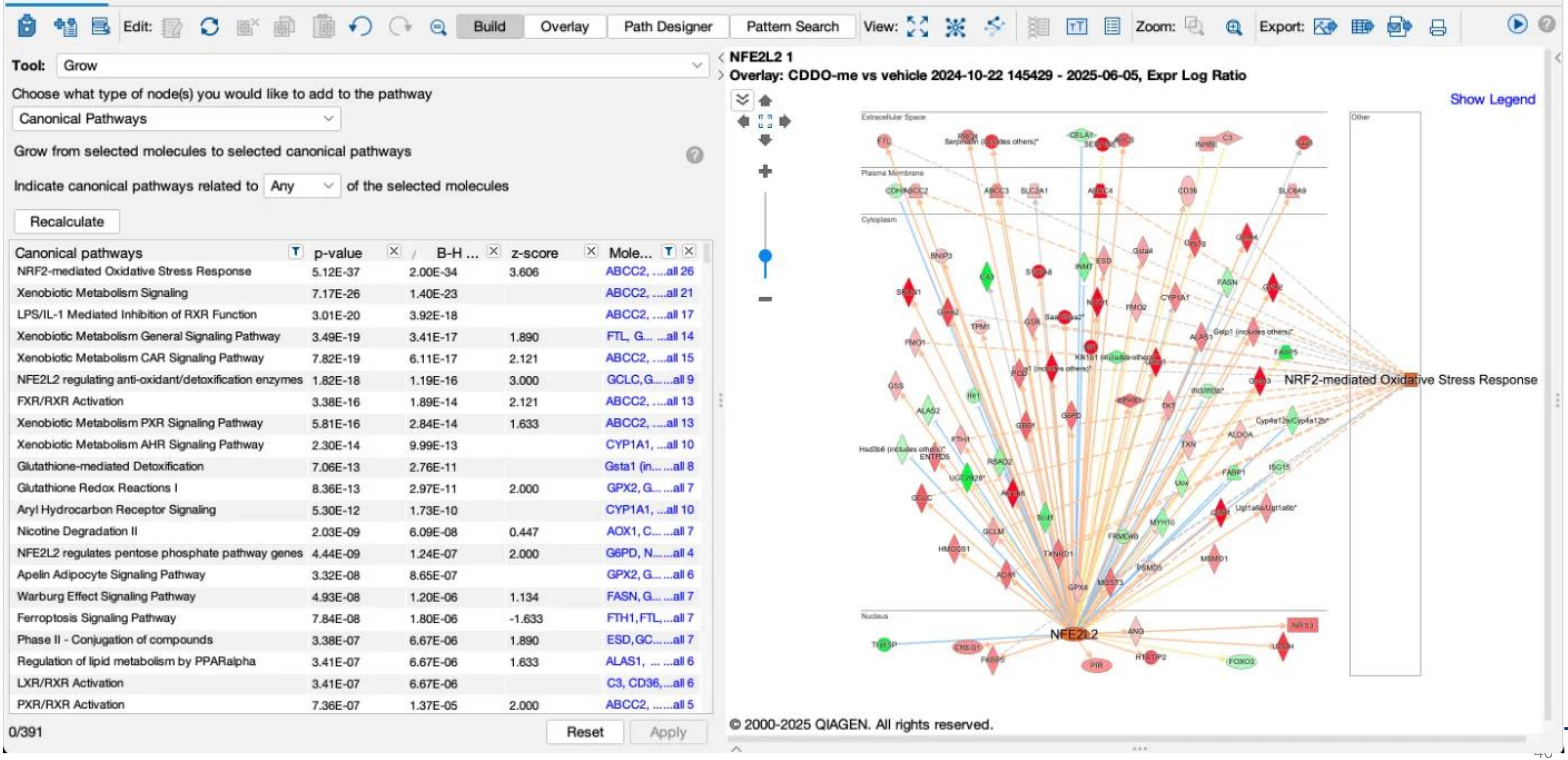
● Full Data (maximum 1000 bars) ○ Preview Only - Displays up to 13 bars

Please select one of the following resolutions for download (all PNG format)

○ 1x ○ 2x ● 3x

☐ Save for Future Download Use (Use this custom style by default next time)

Grow function



Tool: Grow

Choose what type of node(s) you would like to add to the pathway: Canonical Pathways

Grow from selected molecules to selected canonical pathways

Indicate canonical pathways related to Any of the selected molecules

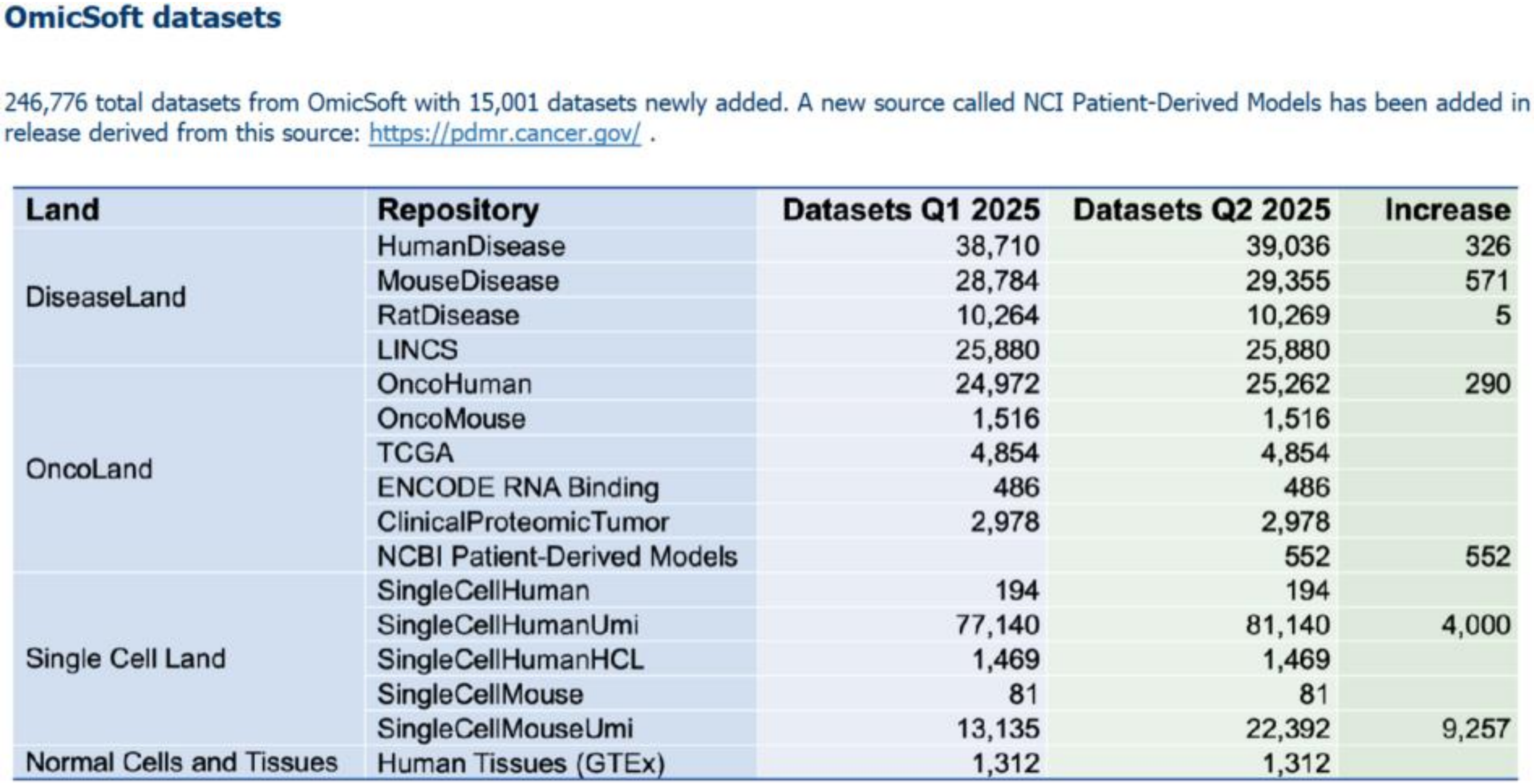
Canonical pathways	p-value	B-H ...	z-score	Mole...
NRF2-mediated Oxidative Stress Response	5.12E-37	2.00E-34	3.606	ABCC2, ...all 26
Xenobiotic Metabolism Signaling	7.17E-26	1.40E-23		ABCC2, ...all 21
LPS/IL-1 Mediated Inhibition of RXR Function	3.01E-20	3.92E-18		ABCC2, ...all 17
Xenobiotic Metabolism General Signaling Pathway	3.49E-19	3.41E-17	1.890	FTL, G... ...all 14
Xenobiotic Metabolism CAR Signaling Pathway	7.82E-19	6.11E-17	2.121	ABCC2, ...all 15
NFE2L2 regulating anti-oxidant/detoxification enzymes	1.82E-18	1.19E-16	3.000	GCLC,G.....all 9
FXR/RXR Activation	3.38E-16	1.89E-14	2.121	ABCC2, ...all 13
Xenobiotic Metabolism PXR Signaling Pathway	5.81E-16	2.84E-14	1.633	ABCC2, ...all 13
Xenobiotic Metabolism AHR Signaling Pathway	2.30E-14	9.99E-13		CYP1A1, ...all 10
Glutathione-mediated Detoxification	7.06E-13	2.76E-11		Gsta1 (in... ...all 8
Glutathione Redox Reactions I	8.36E-13	2.97E-11	2.000	GPX2, G... ...all 7
Aryl Hydrocarbon Receptor Signaling	5.30E-12	1.73E-10		CYP1A1, ...all 10
Nicotine Degradation II	2.03E-09	6.09E-08	0.447	AOX1, C... ...all 7
NFE2L2 regulates pentose phosphate pathway genes	4.44E-09	1.24E-07	2.000	G6PD, N.....all 4
Apelin Adipocyte Signaling Pathway	3.32E-08	8.65E-07		GPX2, G... ...all 6
Warburg Effect Signaling Pathway	4.93E-08	1.20E-06	1.134	FASN, G... ...all 7
Ferroptosis Signaling Pathway	7.84E-08	1.80E-06	-1.633	FTH1,FTL,...all 7
Phase II - Conjugation of compounds	3.38E-07	6.67E-06	1.890	ESD,GC.....all 7
Regulation of lipid metabolism by PPARalpha	3.41E-07	6.67E-06	1.633	ALAS1, ...all 6
LXR/RXR Activation	3.41E-07	6.67E-06		C3, CD36,...all 6
PXR/RXR Activation	7.36E-07	1.37E-05	2.000	ABCC2, ...all 5

0/391

NFE2L2 1

Overlay: CDDO-me vs vehicle 2024-10-22 145429 - 2025-06-05, Expr Log Ratio

Omicsoft datasets update



OmicSoft datasets

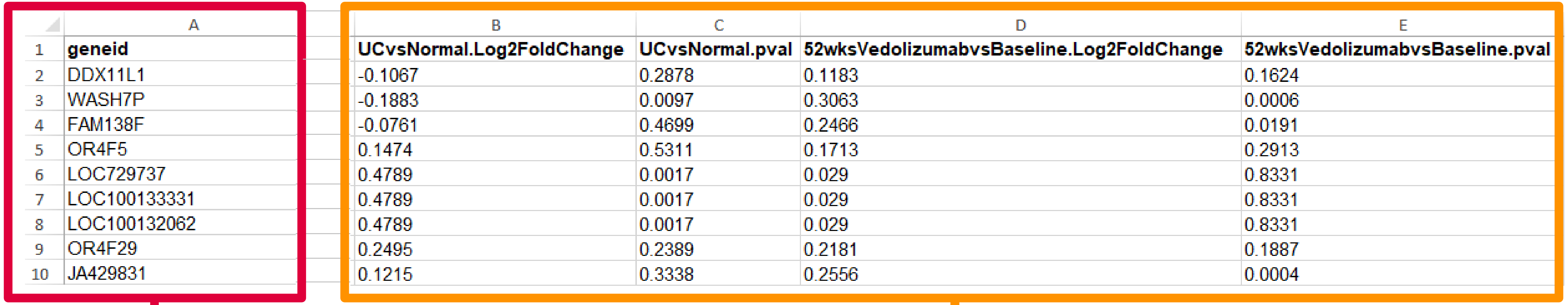
246,776 total datasets from OmicSoft with 15,001 datasets newly added. A new source called NCI Patient-Derived Models has been added in this release derived from this source: https://pdmr.cancer.gov/ .

Land	Repository	Datasets Q1 2025	Datasets Q2 2025	Increase
DiseaseLand	HumanDisease	38,710	39,036	326
	MouseDisease	28,784	29,355	571
	RatDisease	10,264	10,269	5
	LINCS	25,880	25,880	
OncoLand	OncoHuman	24,972	25,262	290
	OncoMouse	1,516	1,516	
	TCGA	4,854	4,854	
	ENCODE RNA Binding	486	486	
	ClinicalProteomicTumor	2,978	2,978	
	NCBI Patient-Derived Models		552	552
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	77,140	81,140	4,000
	SingleCellHumanHCL	1,469	1,469	
	SingleCellMouse	81	81	
	SingleCellMouseUmi	13,135	22,392	9,257
Normal Cells and Tissues	Human Tissues (GTEx)	1,312	1,312	

Formatting ‘omics data before uploading to IPA

Observation 1

Observation 2



	A	B	C	D	E
1	**geneid**	**UCvsNormal.Log2FoldChange**	**UCvsNormal.pval**	**52wksVedolizumabvsBaseline.Log2FoldChange**	**52wksVedolizumabvsBaseline.pval**
2	DDX11L1	-0.1067	0.2878	0.1183	0.1624
3	WASH7P	-0.1883	0.0097	0.3063	0.0006
4	FAM138F	-0.0761	0.4699	0.2466	0.0191
5	OR4F5	0.1474	0.5311	0.1713	0.2913
6	LOC729737	0.4789	0.0017	0.029	0.8331
7	LOC100133331	0.4789	0.0017	0.029	0.8331
8	LOC100132062	0.4789	0.0017	0.029	0.8331
9	OR4F29	0.2495	0.2389	0.2181	0.1887
10	JA429831	0.1215	0.3338	0.2556	0.0004

Analyte identifier REQUIRED to explore enrichment

RNA examples: Gene symbols, array identifiers from Affymetrix, Ensembl, etc.

Protein examples: UniProt, GenPept, Gene symbols, Ensembl. etc.

Metabolite examples: KEGG, CAS registry number, etc. **add multiple columns of ids to ensure best mapping*

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

Significance values: P-values **optional but recommended to enable filtering for significance*

Accepted file formats:

- ✓ .txt (tab-delimited text files)
- ✓ .xls, .xlsx, .csv (Excel tables
- ✓ .diff (Cuffdiff output

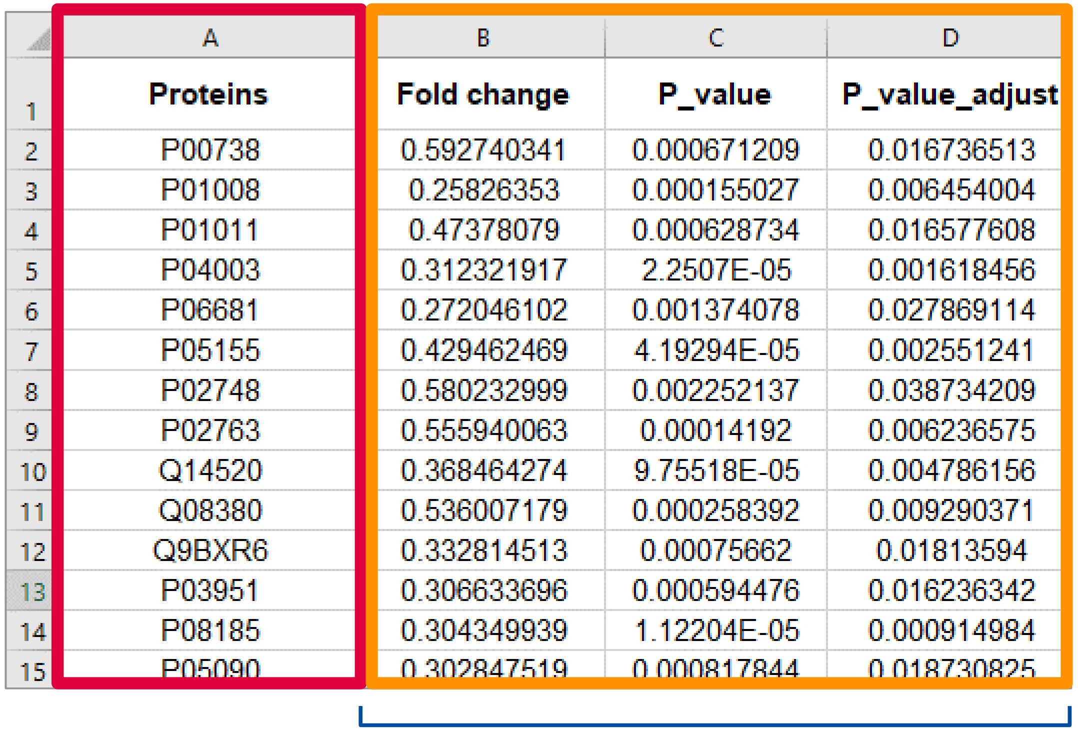
Multiple comparisons or observations may be uploaded in one file

Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)



	A	B	C	D
1	**Proteins**	**Fold change**	**P_value**	**P_value_adjust**
2	P00738	0.592740341	0.000671209	0.016736513
3	P01008	0.25826353	0.000155027	0.006454004
4	P01011	0.47378079	0.000628734	0.016577608
5	P04003	0.312321917	2.2507E-05	0.001618456
6	P06681	0.272046102	0.001374078	0.027869114
7	P05155	0.429462469	4.19294E-05	0.002551241
8	P02748	0.580232999	0.002252137	0.038734209
9	P02763	0.555940063	0.00014192	0.006236575
10	Q14520	0.368464274	9.75518E-05	0.004786156
11	Q08380	0.536007179	0.000258392	0.009290371
12	Q9BXR6	0.332814513	0.00075662	0.01813594
13	P03951	0.306633696	0.000594476	0.016236342
14	P08185	0.304349939	1.12204E-05	0.000914984
15	P05090	0.302847519	0.000817844	0.018730825

Common protein IDs

- Ensembl
- Gene symbols (Entrez or HUGO)
- GenPept and GenBank
- International Protein Index
- UniProt and SwissProt

UniProt ID conversion tool:

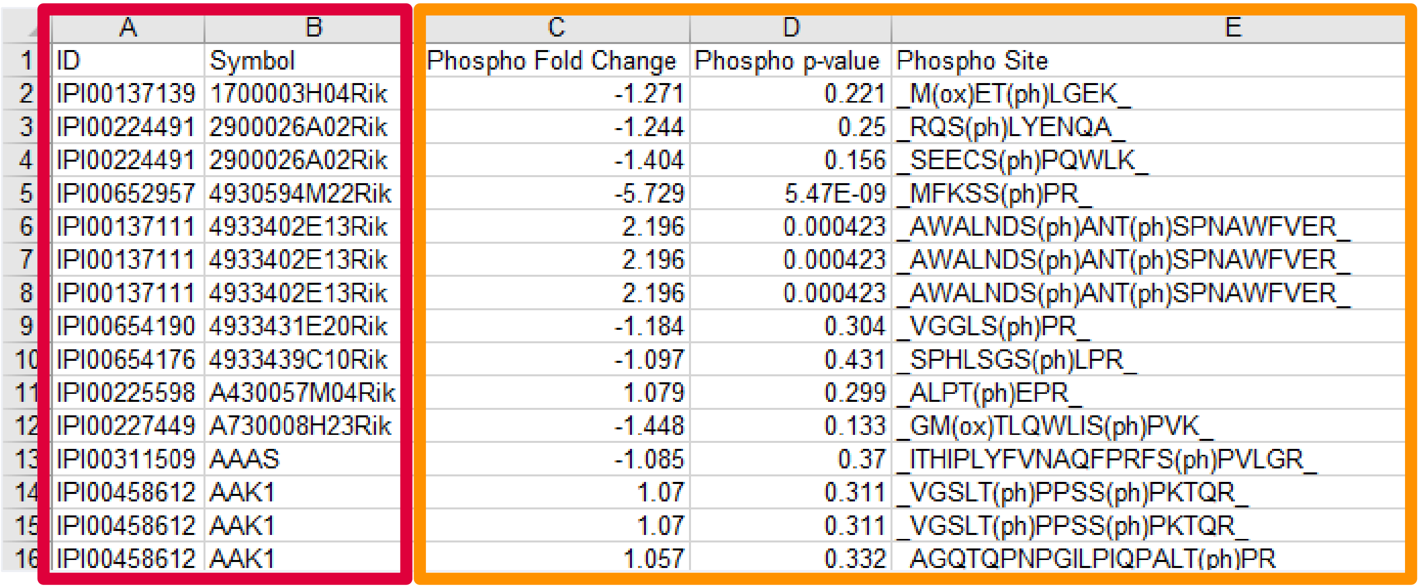
- https://www.uniprot.org/mapping/

Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)



	A	B	C	D	E
1	ID	Symbol	Phospho Fold Change	Phospho p-value	Phospho Site
2	IPI00137139	1700003H04Rik	-1.271	0.221	_M(ox)ET(ph)LGEK_
3	IPI00224491	2900026A02Rik	-1.244	0.25	_RQS(ph)LYENQA_
4	IPI00224491	2900026A02Rik	-1.404	0.156	_SEECS(ph)PQWLK_
5	IPI00652957	4930594M22Rik	-5.729	5.47E-09	_MFKSS(ph)PR_
6	IPI00137111	4933402E13Rik	2.196	0.000423	_AWALNDS(ph)ANT(ph)SPNAWFVER_
7	IPI00137111	4933402E13Rik	2.196	0.000423	_AWALNDS(ph)ANT(ph)SPNAWFVER_
8	IPI00137111	4933402E13Rik	2.196	0.000423	_AWALNDS(ph)ANT(ph)SPNAWFVER_
9	IPI00654190	4933431E20Rik	-1.184	0.304	_VGGLS(ph)PR_
10	IPI00654176	4933439C10Rik	-1.097	0.431	_SPHLSGS(ph)LPR_
11	IPI00225598	A430057M04Rik	1.079	0.299	_ALPT(ph)EPR_
12	IPI00227449	A730008H23Rik	-1.448	0.133	_GM(ox)TLQWLIS(ph)PVK_
13	IPI00311509	AAAS	-1.085	0.37	_ITHIPLYFVNAQFPRFS(ph)PVLGR_
14	IPI00458612	AAK1	1.07	0.311	_VGSLT(ph)PPSS(ph)PKTQR_
15	IPI00458612	AAK1	1.07	0.311	_VGSLT(ph)PPSS(ph)PKTQR_
16	IPI00458612	AAK1	1.057	0.332	_AGQTQPNPGILPIQPALT(ph)PR_

Observation 1

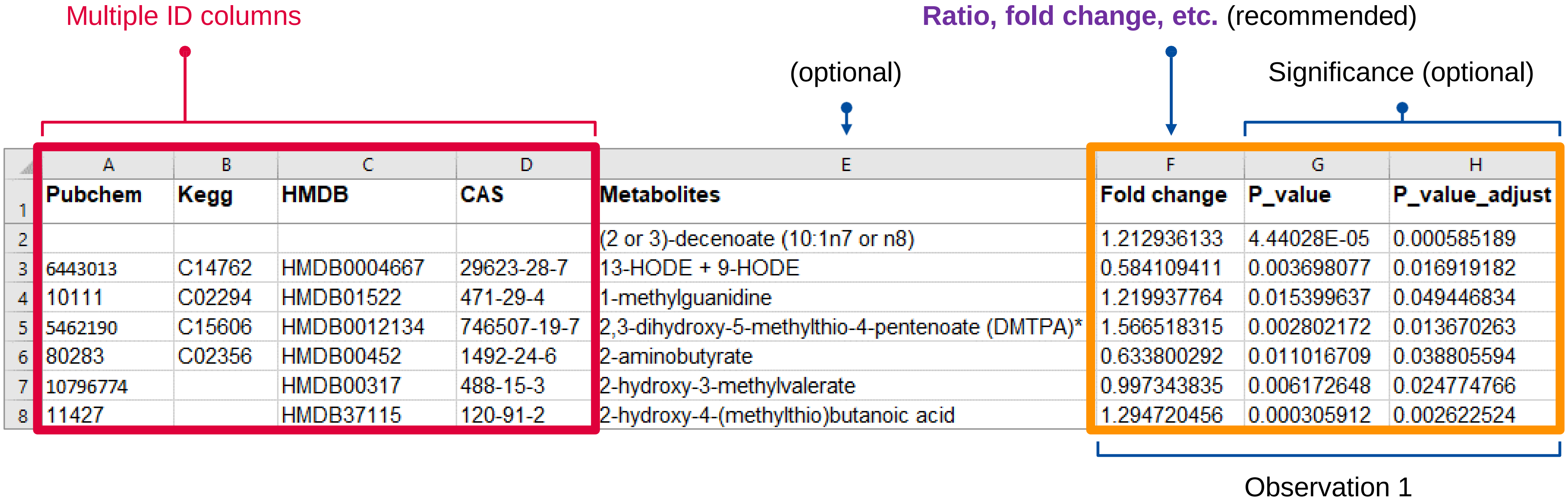
Common protein IDs

- Ensembl
- Gene symbols (Entrez or HUGO)
- GenPept and GenBank
- International Protein Index
- UniProt and SwissProt

UniProt ID conversion tool:

- https://www.uniprot.org/mapping/

Formatting metabolomics data before uploading to IPA



Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

	A	B	C	D	E	F	G	H
1	**Pubchem**	**Kegg**	**HMDB**	**CAS**	**Metabolites**	**Fold change**	**P_value**	**P_value_adjust**
2					(2 or 3)-decenoate (10:1n7 or n8)	1.212936133	4.44028E-05	0.000585189
3	6443013	C14762	HMDB0004667	29623-28-7	13-HODE + 9-HODE	0.584109411	0.003698077	0.016919182
4	10111	C02294	HMDB01522	471-29-4	1-methylguanidine	1.219937764	0.015399637	0.049446834
5	5462190	C15606	HMDB0012134	746507-19-7	2,3-dihydroxy-5-methylthio-4-pentenoate (DMTPA)*	1.566518315	0.002802172	0.013670263
6	80283	C02356	HMDB00452	1492-24-6	2-aminobutyrate	0.633800292	0.011016709	0.038805594
7	10796774		HMDB00317	488-15-3	2-hydroxy-3-methylvalerate	0.997343835	0.006172648	0.024774766
8	11427		HMDB37115	120-91-2	2-hydroxy-4-(methylthio)butanoic acid	1.294720456	0.000305912	0.002622524

Observation 1

Common metabolite IDs

- CAS registry number
- Human Metabolome Database
- KEGG
- PubChem CID

Metabolite ID conversion tools:

- https://biodbnet-abcc.ncifcrf.gov/db/db2db.php
- https://cts.fiehnlab.ucdavis.edu/batch
- http://csbg.cnb.csic.es/mbrole2/conversion.php

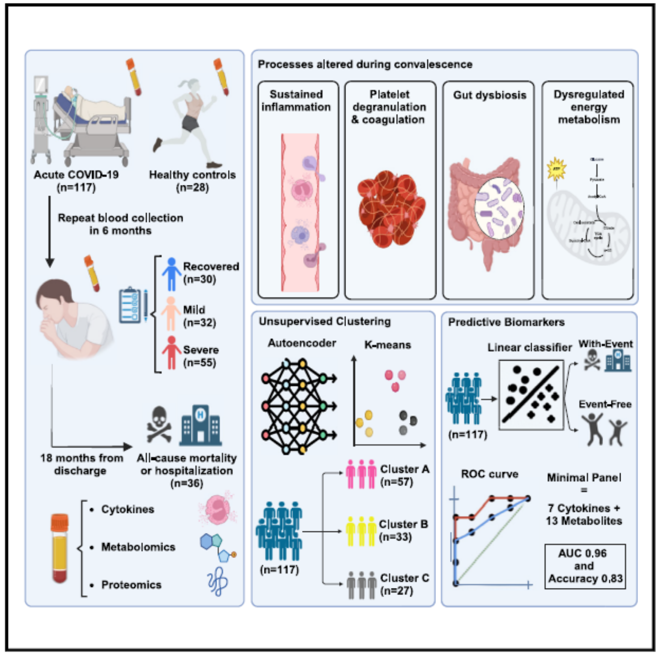
Multi-omics Case Study

Cell Reports
Medicine

Article

Sequential multi-omics analysis identifies clinical phenotypes and predictive biomarkers for long COVID

Graphical abstract



Authors

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Karthik Srinivasan, ..., David S. Wishart,
Vinay Prasad, Gavin Y. Oudit

Correspondence

gavin.oudit@ualberta.ca

In brief

Wang et al. conduct a comprehensive multi-omics analysis to identify pathways differentially altered during acute SARS-CoV-2 infection and convalescence. This study provides clues into the heterogeneity of the post-acute COVID-19 symptoms and unveils potential therapeutic targets for long COVID.

Highlights

- Sequential multi-omics profiling of plasma during acute infection and convalescence
- Inflammation, platelet degranulation, and metabolic perturbations at convalescence
- Three distinct disease phenotypes based on unsupervised clustering of omics profile

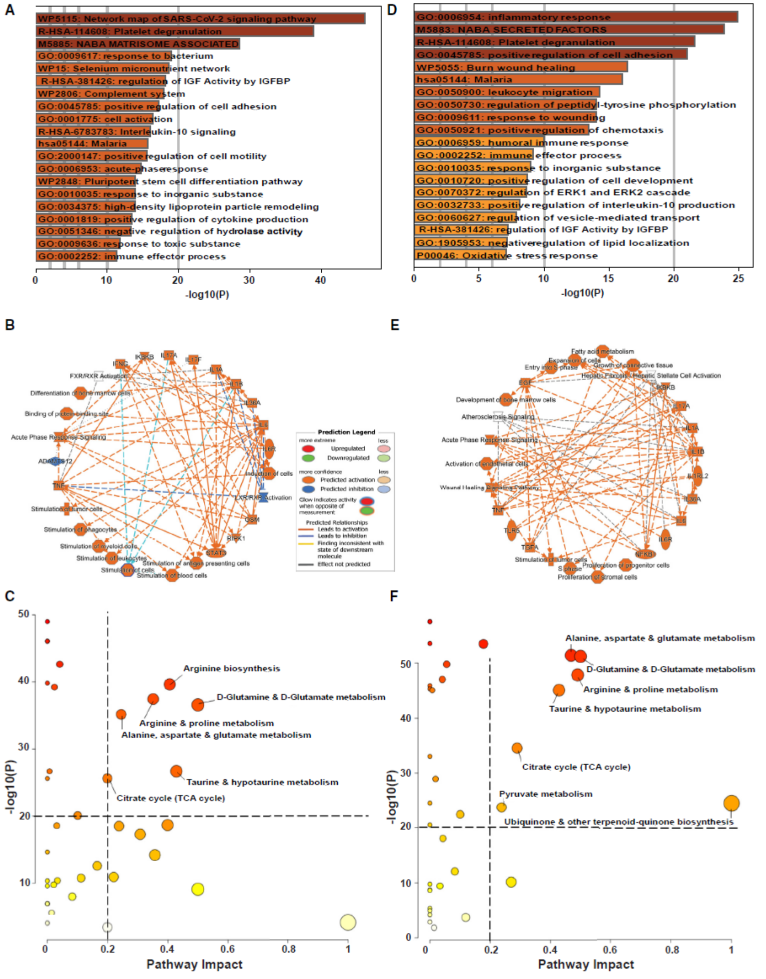


Figure 3. Pathways dysregulated during acute infection and convalescence

(A) Enriched Gene Ontology (GO) terms of differentially expressed proteins and cytokines on Metascape for acute COVID-19 compared to healthy controls, colored based on p values.

(B) Top regulatory effects of molecules and functions in acute COVID-19 based on Ingenuity Pathway Analysis (IPA).

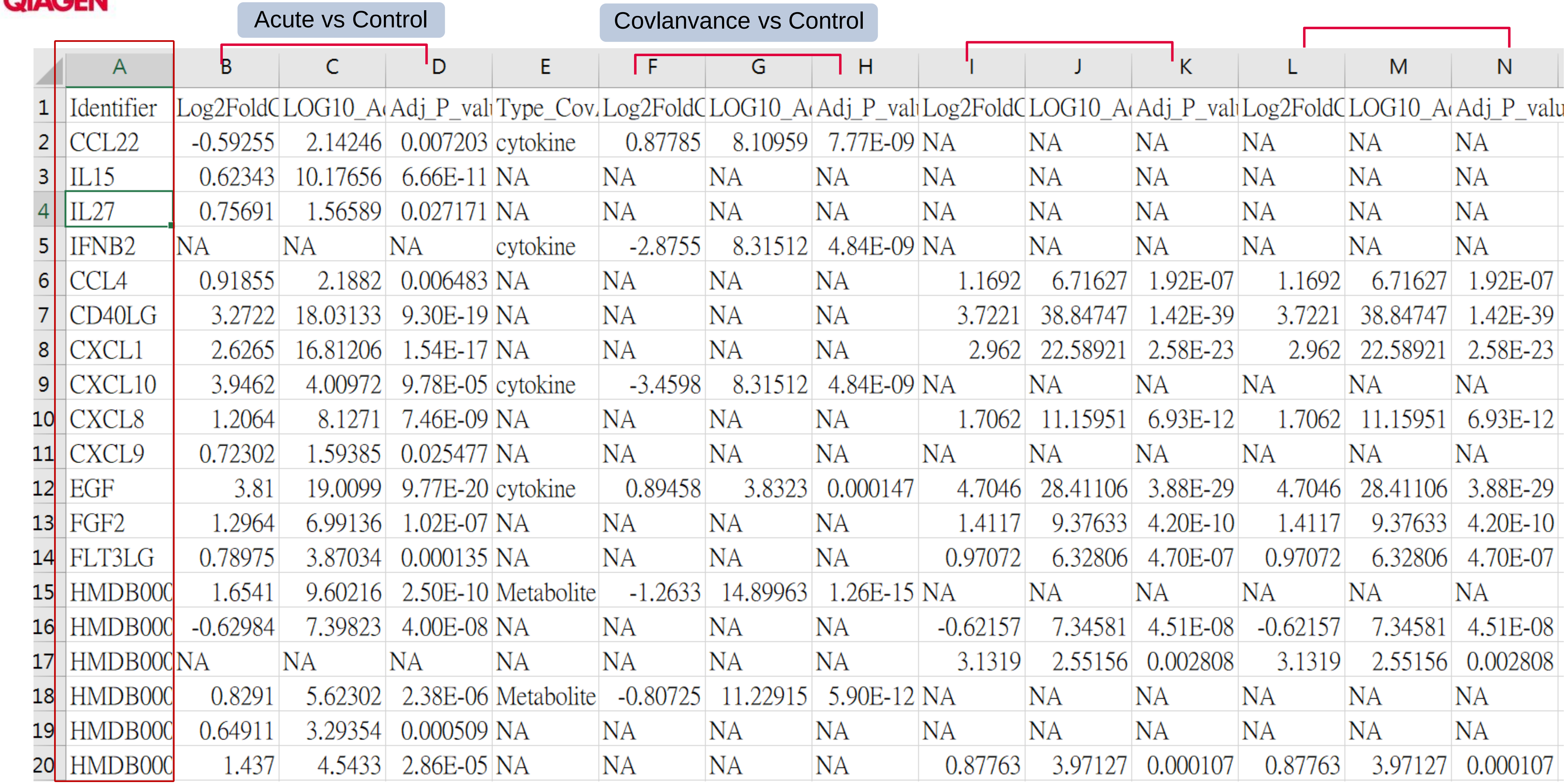
(C) Pathways associated with metabolic alterations in acute COVID-19 compared to healthy controls. Pathway impact indicates the sum of importance of the altered metabolites in the impacted pathway based on pathway topology; the −log(P) are test statistics for quantitative pathway enrichment analysis based on concentration differences between groups. Notable impacted pathways are above the dashed lines (impact >0.2 and −log(P) > 20).

(D) Enriched GO terms of differentially expressed proteins and cytokines on Metascape for convalescence phase compared to healthy controls, colored based on p values.

(E) Top regulatory effects of molecules and functions during convalescence based on Ingenuity Pathway Analysis (IPA).

(F) Pathways associated with metabolic alterations during convalescence compared to healthy controls.

Upload dataset protein

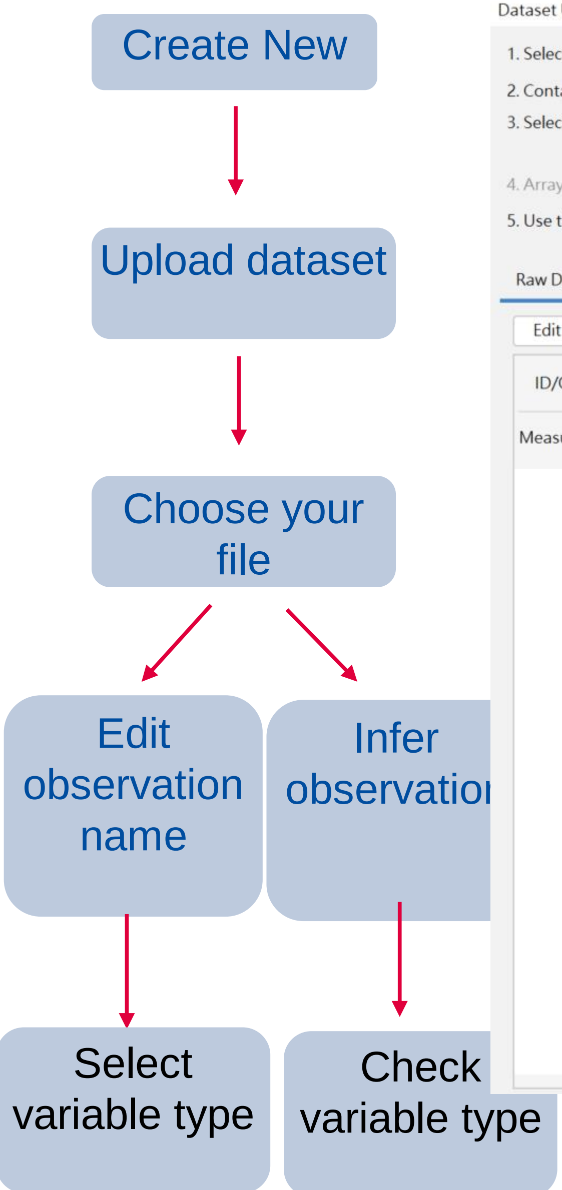


Acute vs Control

Covlanvance vs Control

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Identifier	Log2FoldC	LOG10_A	Adj_P_val	Type_Cov	Log2FoldC	LOG10_A	Adj_P_val	Log2FoldC	LOG10_A	Adj_P_val	Log2FoldC	LOG10_A	Adj_P_valu
2	CCL22	-0.59255	2.14246	0.007203	cytokine	0.87785	8.10959	7.77E-09	NA	NA	NA	NA	NA	NA
3	IL15	0.62343	10.17656	6.66E-11	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
4	IL27	0.75691	1.56589	0.027171	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
5	IFNB2	NA	NA	NA	cytokine	-2.8755	8.31512	4.84E-09	NA	NA	NA	NA	NA	NA
6	CCL4	0.91855	2.1882	0.006483	NA	NA	NA	NA	1.1692	6.71627	1.92E-07	1.1692	6.71627	1.92E-07
7	CD40LG	3.2722	18.03133	9.30E-19	NA	NA	NA	NA	3.7221	38.84747	1.42E-39	3.7221	38.84747	1.42E-39
8	CXCL1	2.6265	16.81206	1.54E-17	NA	NA	NA	NA	2.962	22.58921	2.58E-23	2.962	22.58921	2.58E-23
9	CXCL10	3.9462	4.00972	9.78E-05	cytokine	-3.4598	8.31512	4.84E-09	NA	NA	NA	NA	NA	NA
10	CXCL8	1.2064	8.1271	7.46E-09	NA	NA	NA	NA	1.7062	11.15951	6.93E-12	1.7062	11.15951	6.93E-12
11	CXCL9	0.72302	1.59385	0.025477	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
12	EGF	3.81	19.0099	9.77E-20	cytokine	0.89458	3.8323	0.000147	4.7046	28.41106	3.88E-29	4.7046	28.41106	3.88E-29
13	FGF2	1.2964	6.99136	1.02E-07	NA	NA	NA	NA	1.4117	9.37633	4.20E-10	1.4117	9.37633	4.20E-10
14	FLT3LG	0.78975	3.87034	0.000135	NA	NA	NA	NA	0.97072	6.32806	4.70E-07	0.97072	6.32806	4.70E-07
15	HMDB000	1.6541	9.60216	2.50E-10	Metabolite	-1.2633	14.89963	1.26E-15	NA	NA	NA	NA	NA	NA
16	HMDB000	-0.62984	7.39823	4.00E-08	NA	NA	NA	NA	-0.62157	7.34581	4.51E-08	-0.62157	7.34581	4.51E-08
17	HMDB000	NA	NA	NA	NA	NA	NA	NA	3.1319	2.55156	0.002808	3.1319	2.55156	0.002808
18	HMDB000	0.8291	5.62302	2.38E-06	Metabolite	-0.80725	11.22915	5.90E-12	NA	NA	NA	NA	NA	NA
19	HMDB000	0.64911	3.29354	0.000509	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
20	HMDB000	1.437	4.5433	2.86E-05	NA	NA	NA	NA	0.87763	3.97127	0.000107	0.87763	3.97127	0.000107

Upload dataset



Create New

Upload dataset

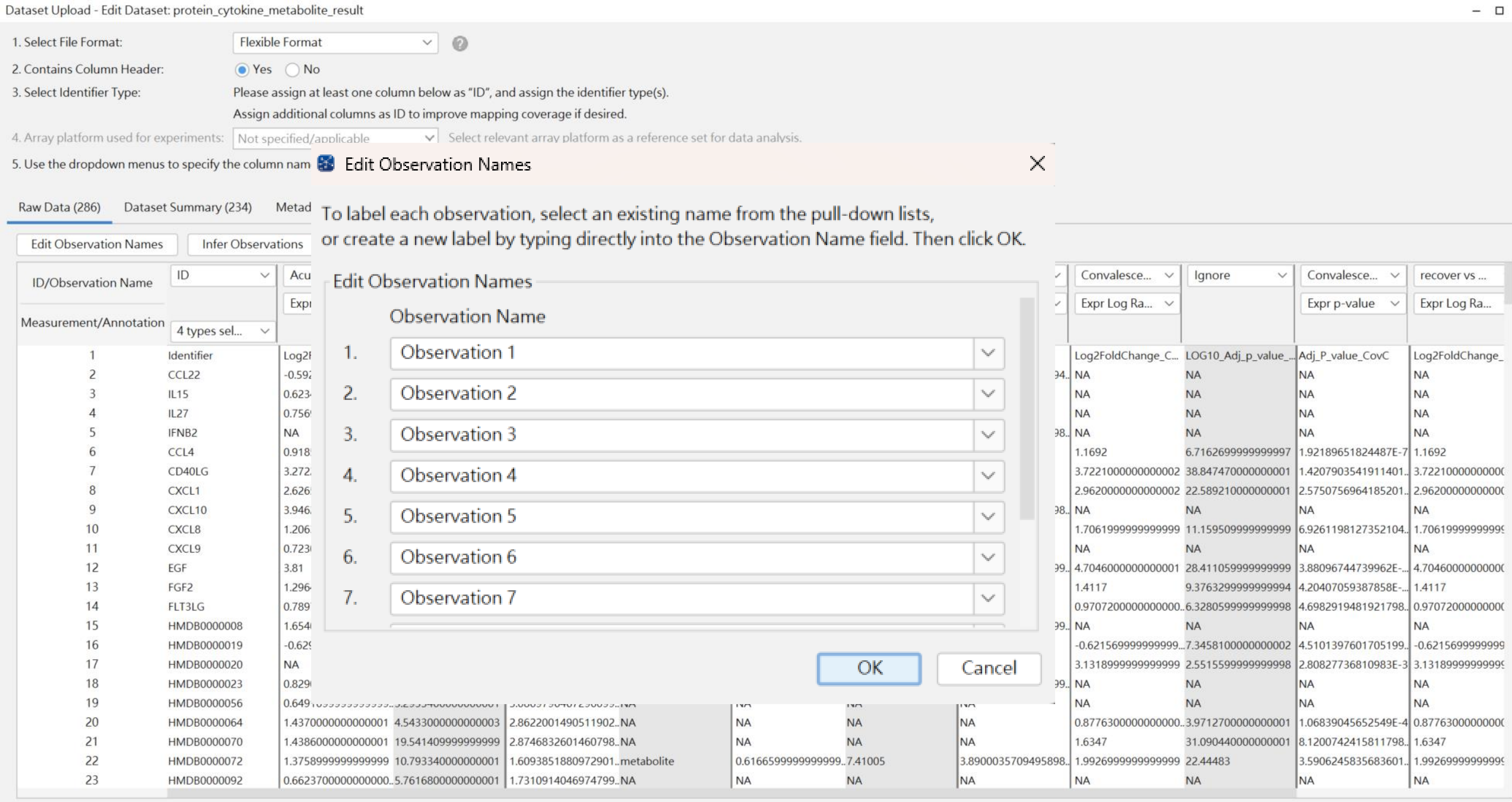
Choose your file

Edit observation name

Infer observation

Select variable type

Check variable type



Dataset Upload - Edit Dataset: protein_cytokine_metabolite_result

1. Select File Format: Flexible Format
2. Contains Column Header: ● Yes ○ No
3. Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
4. Array platform used for experiments: Not specified/applicable Select relevant array platform as a reference set for data analysis.
5. Use the dropdown menus to specify the column nam

ID/Observation Name	ID	Acu	Convalesce...	Ignore	Convalesce...	recover vs ...
Measurement/Annotation	4 types sel...	Expr	Expr Log Ra...		Expr p-value	Expr Log Ra...
1	Identifier	Log2F	Log2FoldChange_C...	LOG10_Adj_p_value_...	Adj_P_value_CovC	Log2FoldChange_
2	CCL22	-0.592	NA	NA	NA	NA
3	IL15	0.623	NA	NA	NA	NA
4	IL27	0.756	NA	NA	NA	NA
5	IFNB2	NA	NA	NA	NA	NA
6	CCL4	0.918	1.1692	6.7162699999999997	1.92189651824487E-7	1.1692
7	CD40LG	3.272	3.7221000000000002	38.847470000000001	1.4207903541911401..	3.722100000000000
8	CXCL1	2.626	2.9620000000000002	22.589210000000001	2.5750756964185201..	2.962000000000000
9	CXCL10	3.946	NA	NA	NA	NA
10	CXCL8	1.206	1.7061999999999999	11.159509999999999	6.9261198127352104..	1.706199999999999
11	CXCL9	0.723	NA	NA	NA	NA
12	EGF	3.81	4.7046000000000001	28.411059999999999	3.88096744739962E-...	4.704600000000000
13	FGF2	1.296	1.4117	9.3763299999999994	4.20407059387858E-...	1.4117
14	FLT3LG	0.789	0.97072000000000000..	6.3280599999999998	4.6982919481921798..	0.970720000000000
15	HMDB0000008	1.654	NA	NA	NA	NA
16	HMDB0000019	-0.629	-0.62156999999999999...	7.3458100000000002	4.5101397601705199..	-0.621569999999999
17	HMDB0000020	NA	3.1318999999999999	2.5515599999999998	2.80827736810983E-3	3.131899999999999
18	HMDB0000023	0.829	NA	NA	NA	NA
19	HMDB0000056	0.649	NA	NA	NA	NA
20	HMDB0000064	1.4370000000000001	0.87763000000000000..	3.9712700000000001	1.06839045652549E-4	0.877630000000000
21	HMDB0000070	1.4386000000000001	1.6347	31.090440000000001	8.1200742415811798..	1.6347
22	HMDB0000072	1.3758999999999999	1.9926999999999999	22.44483	3.5906245835683601..	1.992699999999999
23	HMDB0000092	0.66237000000000000..	NA	NA	NA	NA

Rows 20–23, further visible columns:

20	4.5433000000000003	2.8622001490511902..	NA	NA	NA	NA
21	19.541409999999999	2.8746832601460798..	NA	NA	NA	NA
22	10.793340000000001	1.6093851880972901..	metabolite	0.61665999999999999..	7.41005	3.8900035709495898..
23	5.7616800000000001	1.7310914046974799..	NA	NA	NA	NA

Edit Observation Names

To label each observation, select an existing name from the pull-down lists, or create a new label by typing directly into the Observation Name field. Then click OK.

Edit Observation Names

Observation Name

1. Observation 1
2. Observation 2
3. Observation 3
4. Observation 4
5. Observation 5
6. Observation 6
7. Observation 7

Core analysis

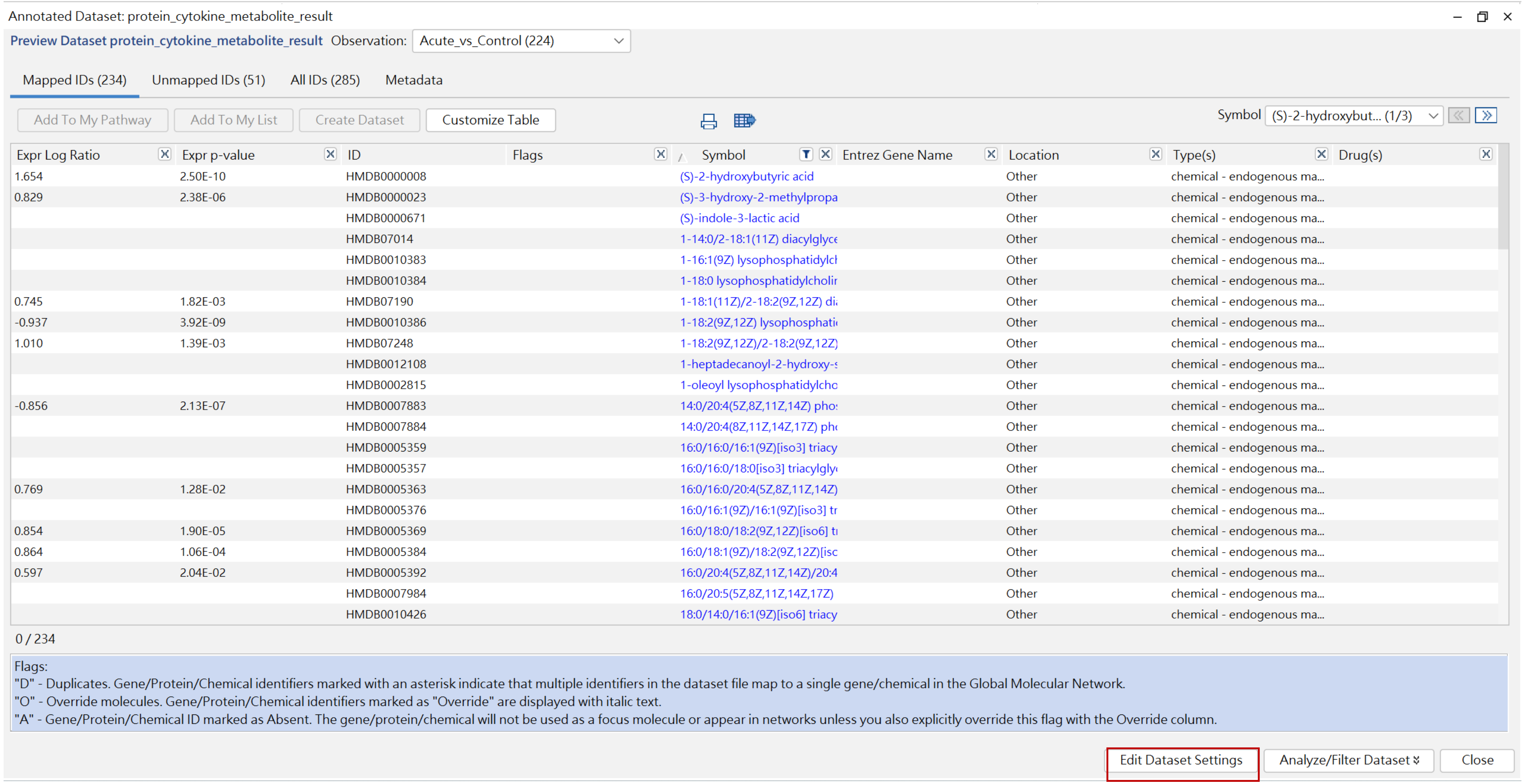
Analyze filter dataset

↓

Core analysis

↓

Set cut off



Annotated Dataset: protein_cytokine_metabolite_result

Preview Dataset protein_cytokine_metabolite_result Observation: Acute_vs_Control (224)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
1.654	2.50E-10	HMDB0000008		(S)-2-hydroxybutyric acid		Other	chemical - endogenous ma...	
0.829	2.38E-06	HMDB0000023		(S)-3-hydroxy-2-methylpropa		Other	chemical - endogenous ma...	
		HMDB0000671		(S)-indole-3-lactic acid		Other	chemical - endogenous ma...	
		HMDB07014		1-14:0/2-18:1(11Z) diacylglyce		Other	chemical - endogenous ma...	
		HMDB0010383		1-16:1(9Z) lysophosphatidylc		Other	chemical - endogenous ma...	
		HMDB0010384		1-18:0 lysophosphatidylcholi		Other	chemical - endogenous ma...	
0.745	1.82E-03	HMDB07190		1-18:1(11Z)/2-18:2(9Z,12Z) di		Other	chemical - endogenous ma...	
-0.937	3.92E-09	HMDB0010386		1-18:2(9Z,12Z) lysophosphati		Other	chemical - endogenous ma...	
1.010	1.39E-03	HMDB07248		1-18:2(9Z,12Z)/2-18:2(9Z,12Z)		Other	chemical - endogenous ma...	
		HMDB0012108		1-heptadecanoyl-2-hydroxy-		Other	chemical - endogenous ma...	
		HMDB0002815		1-oleoyl lysophosphatidylcho		Other	chemical - endogenous ma...	
-0.856	2.13E-07	HMDB0007883		14:0/20:4(5Z,8Z,11Z,14Z) pho		Other	chemical - endogenous ma...	
		HMDB0007884		14:0/20:4(8Z,11Z,14Z,17Z) ph		Other	chemical - endogenous ma...	
		HMDB0005359		16:0/16:0/16:1(9Z)[iso3] triacy		Other	chemical - endogenous ma...	
		HMDB0005357		16:0/16:0/18:0[iso3] triacylgly		Other	chemical - endogenous ma...	
0.769	1.28E-02	HMDB0005363		16:0/16:0/20:4(5Z,8Z,11Z,14Z)		Other	chemical - endogenous ma...	
		HMDB0005376		16:0/16:1(9Z)/16:1(9Z)[iso3] tr		Other	chemical - endogenous ma...	
0.854	1.90E-05	HMDB0005369		16:0/18:0/18:2(9Z,12Z)[iso6] t		Other	chemical - endogenous ma...	
0.864	1.06E-04	HMDB0005384		16:0/18:1(9Z)/18:2(9Z,12Z)[is		Other	chemical - endogenous ma...	
0.597	2.04E-02	HMDB0005392		16:0/20:4(5Z,8Z,11Z,14Z)/20:4		Other	chemical - endogenous ma...	
		HMDB0007984		16:0/20:5(5Z,8Z,11Z,14Z,17Z)		Other	chemical - endogenous ma...	
		HMDB0010426		18:0/14:0/16:1(9Z)[iso6] triacy		Other	chemical - endogenous ma...	

0 / 234

Flags:
"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.
"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with italic text.
"A" - Gene/Protein/Chemical ID marked as Absent. The gene/protein/chemical will not be used as a focus molecule or appear in networks unless you also explicitly override this flag with the Override column.

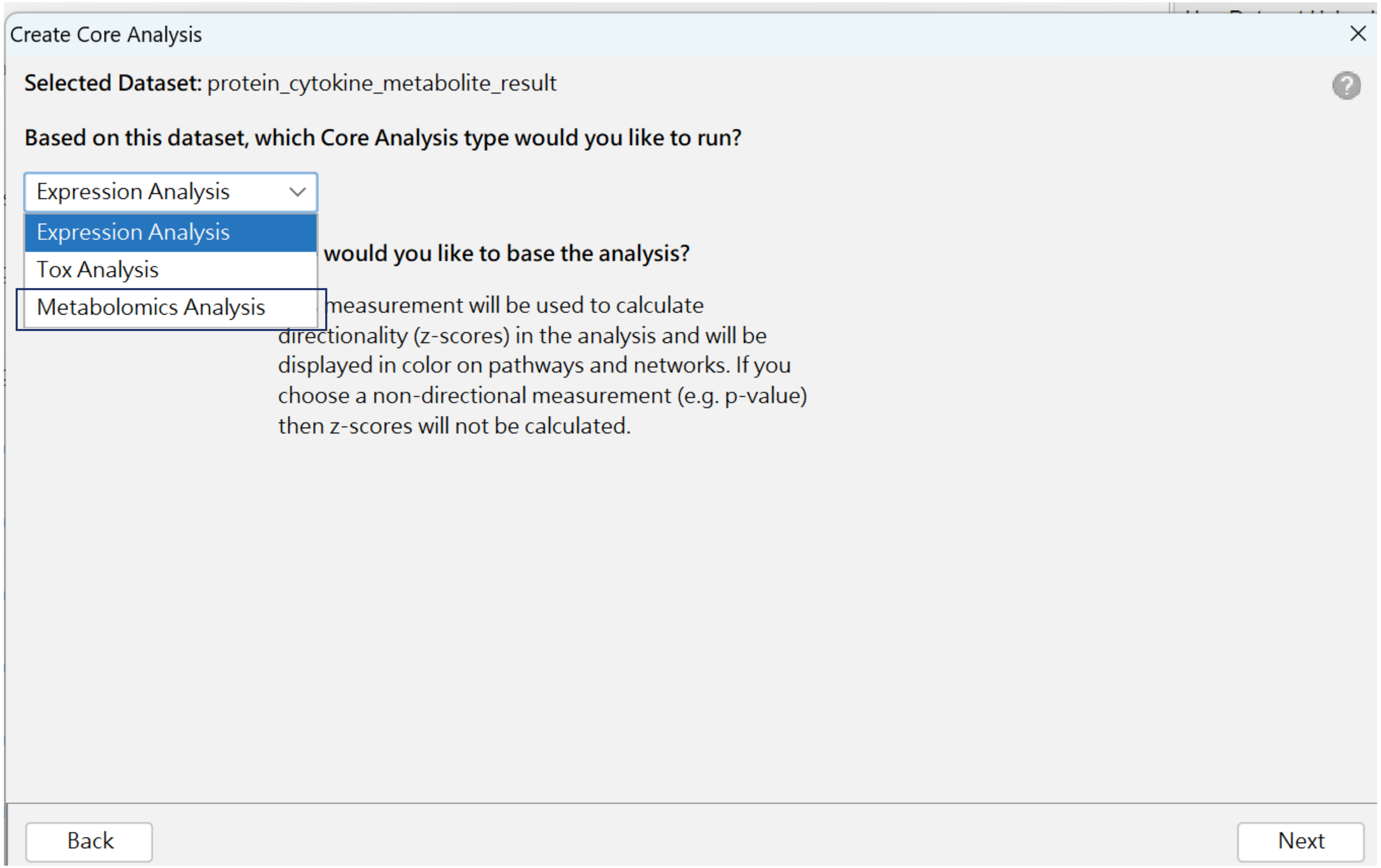
Choose which analysis do you want

Analyze filter dataset

Core analysis

Choose which analysis

Set cut off



Create Core Analysis

Selected Dataset: protein_cytokine_metabolite_result

Based on this dataset, which Core Analysis type would you like to run?

Expression Analysis

would you like to base the analysis?

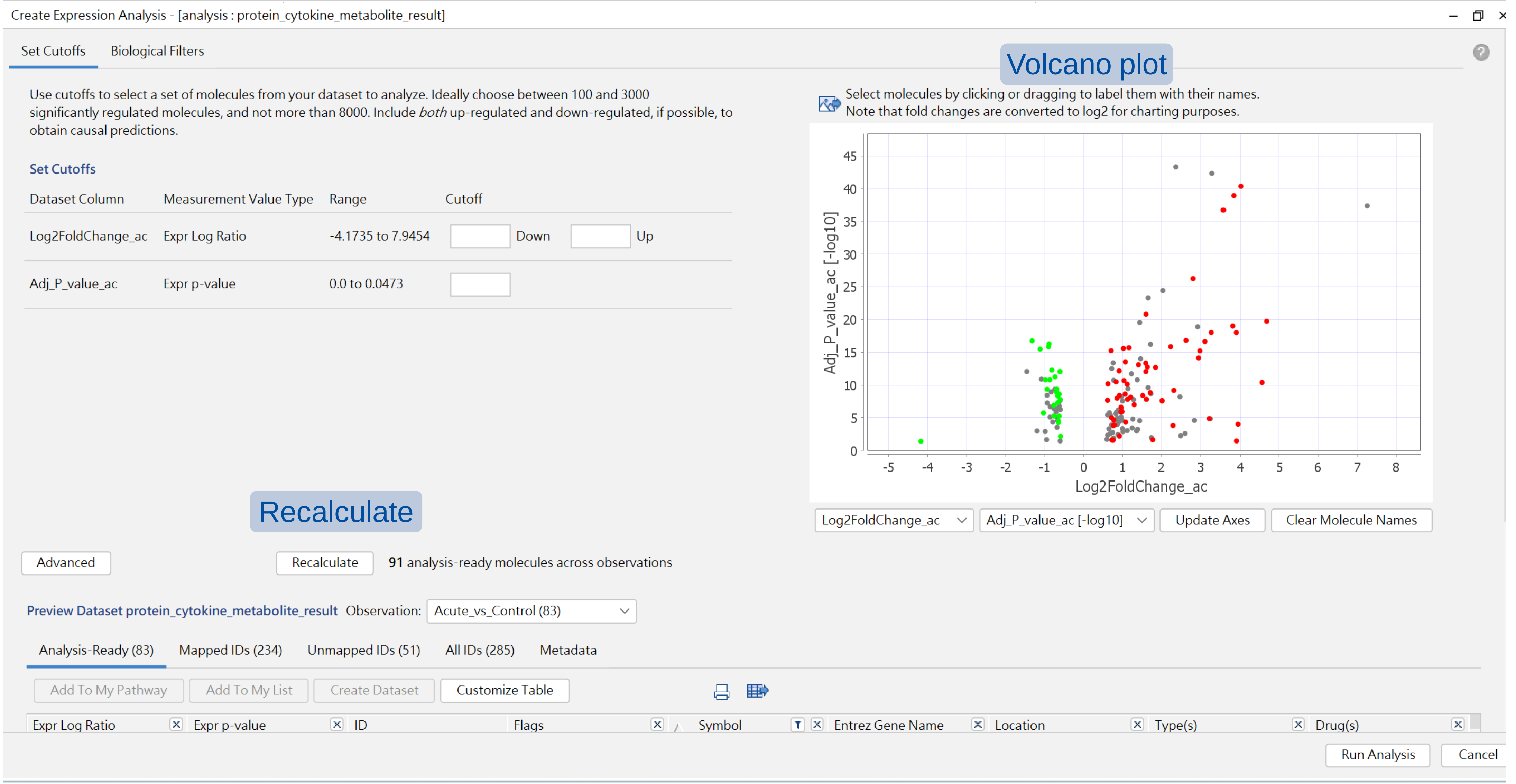
measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

Set Cutoff

Analyze filter dataset

Core analysis

Set cut off



Create Expression Analysis - [analysis : protein_cytokine_metabolite_result]

Set Cutoffs | Biological Filters

Use cutoffs to select a set of molecules from your dataset to analyze. Ideally choose between 100 and 3000 significantly regulated molecules, and not more than 8000. Include *both* up-regulated and down-regulated, if possible, to obtain causal predictions.

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff
Log2FoldChange_ac	Expr Log Ratio	-4.1735 to 7.9454	Down Up
Adj_P_value_ac	Expr p-value	0.0 to 0.0473	

Select molecules by clicking or dragging to label them with their names.
Note that fold changes are converted to log2 for charting purposes.

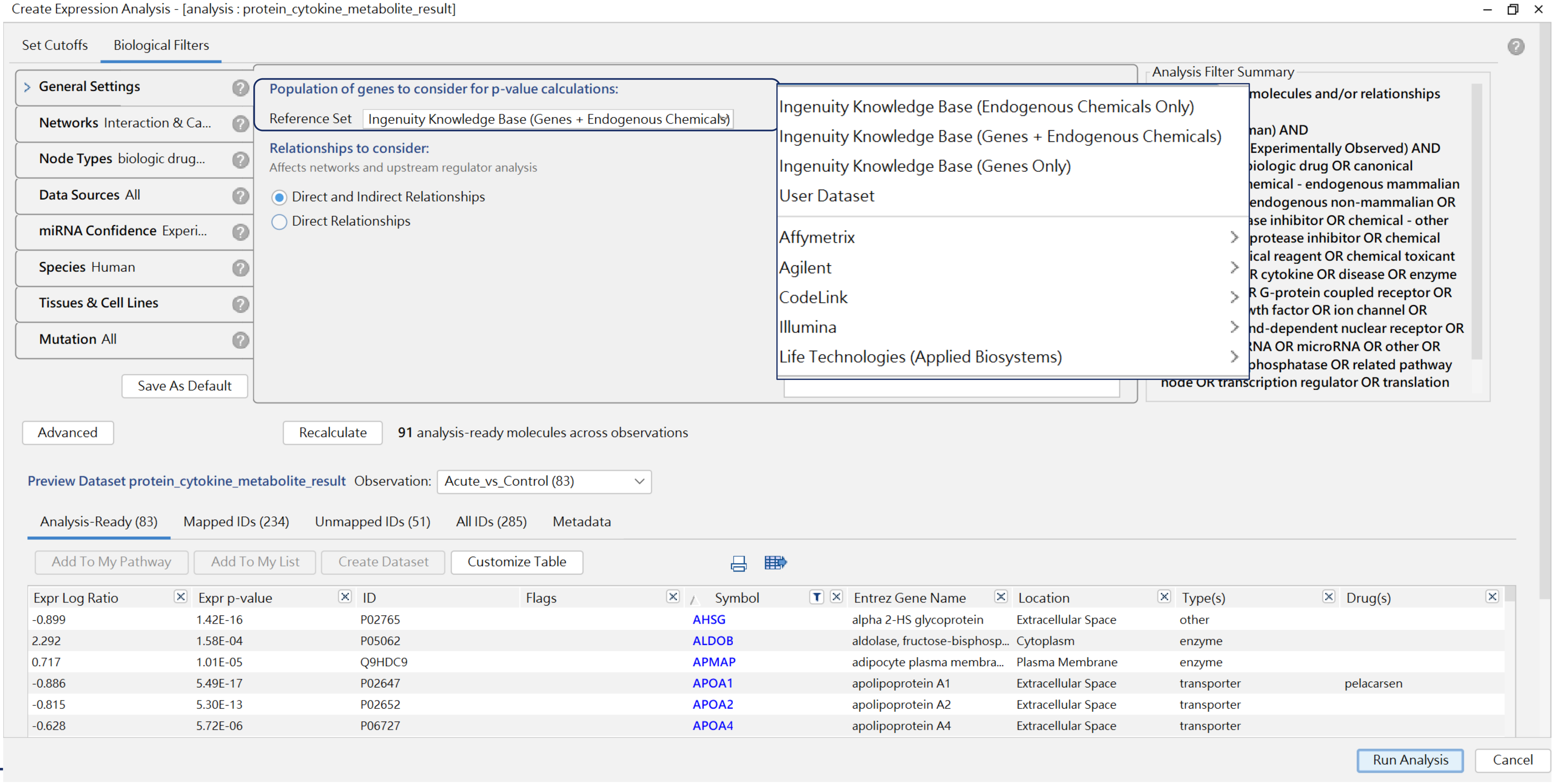
Volcano plot

Recalculate

91 analysis-ready molecules across observations

Preview Dataset protein_cytokine_metabolite_result Observation: Acute_vs_Control (83)

Biological Filter in Protein



Create Expression Analysis - [analysis : protein_cytokine_metabolite_result]

General Settings

Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species Human

Tissues & Cell Lines

Mutation All

Population of genes to consider for p-value calculations:

Reference Set: Ingenuity Knowledge Base (Genes + Endogenous Chemicals)

- Ingenuity Knowledge Base (Endogenous Chemicals Only)
- Ingenuity Knowledge Base (Genes + Endogenous Chemicals)
- Ingenuity Knowledge Base (Genes Only)
- User Dataset
- Affymetrix
- Agilent
- CodeLink
- Illumina
- Life Technologies (Applied Biosystems)

Relationships to consider:

Affects networks and upstream regulator analysis

● Direct and Indirect Relationships

○ Direct Relationships

Analysis Filter Summary

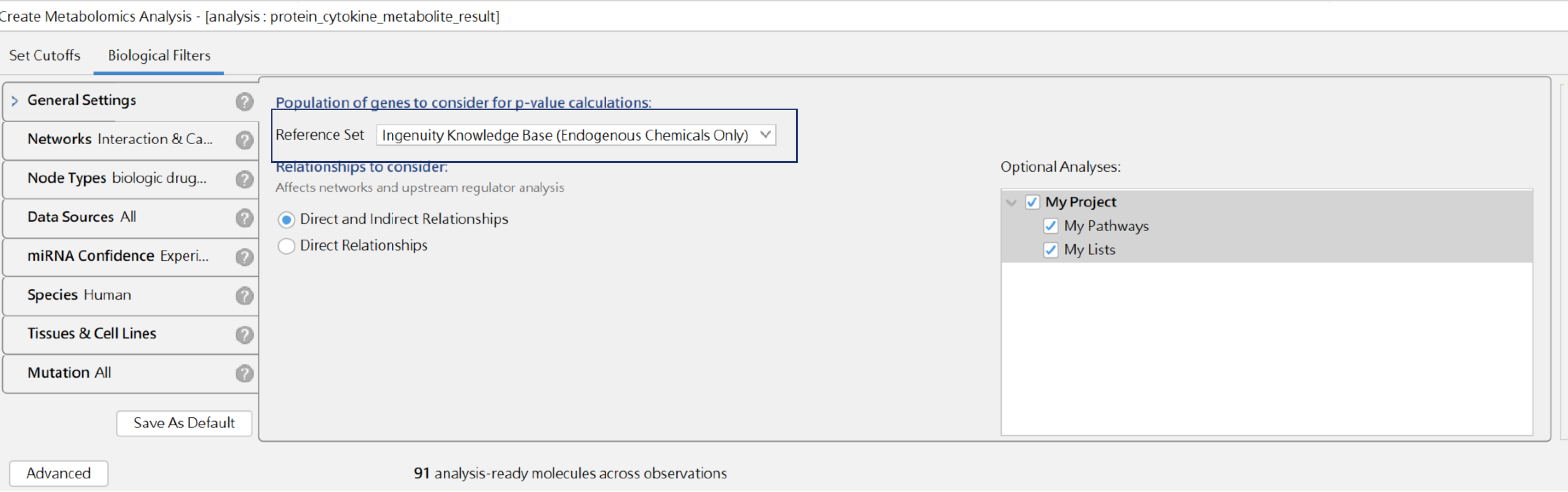
molecules and/or relationships
nan) AND
Experimentally Observed) AND
biologic drug OR canonical
hemical - endogenous mammalian
endogenous non-mammalian OR
ase inhibitor OR chemical - other
protease inhibitor OR chemical
ical reagent OR chemical toxicant
R cytokine OR disease OR enzyme
R G-protein coupled receptor OR
wth factor OR ion channel OR
nd-dependent nuclear receptor OR
RNA OR microRNA OR other OR
phosphatase OR related pathway
node OR transcription regulator OR translation

91 analysis-ready molecules across observations

Preview Dataset protein_cytokine_metabolite_result Observation: Acute_vs_Control (83)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-0.899	1.42E-16	P02765		AHSG	alpha 2-HS glycoprotein	Extracellular Space	other	
2.292	1.58E-04	P05062		ALDOB	aldolase, fructose-bisphosp...	Cytoplasm	enzyme	
0.717	1.01E-05	Q9HDC9		APMAP	adipocyte plasma membra...	Plasma Membrane	enzyme	
-0.886	5.49E-17	P02647		APOA1	apolipoprotein A1	Extracellular Space	transporter	pelacarsen
-0.815	5.30E-13	P02652		APOA2	apolipoprotein A2	Extracellular Space	transporter	
-0.628	5.72E-06	P06727		APOA4	apolipoprotein A4	Extracellular Space	transporter	

Biological Filter in metabolite



reate Metabolomics Analysis - [analysis : protein_cytokine_metabolite_result]

Population of genes to consider for p-value calculations:

Reference Set: Ingenuity Knowledge Base (Endogenous Chemicals Only)

Relationships to consider:

Affects networks and upstream regulator analysis

● Direct and Indirect Relationships

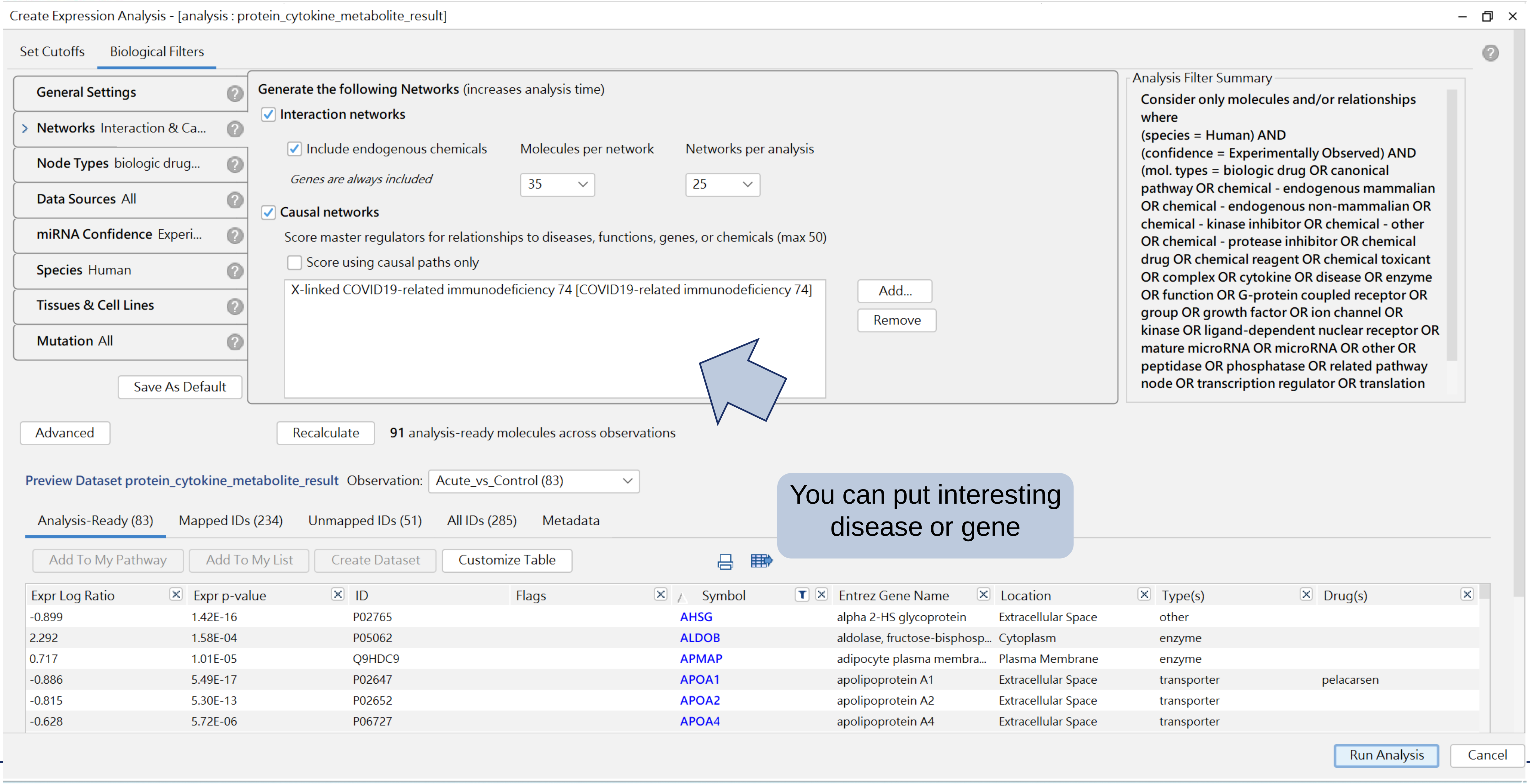
○ Direct Relationships

Optional Analyses:

- ☑ My Project
  - ☑ My Pathways
  - ☑ My Lists

91 analysis-ready molecules across observations

Casual network



Create Expression Analysis - [analysis : protein_cytokine_metabolite_result]

General Settings

Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species Human

Tissues & Cell Lines

Mutation All

Generate the following Networks (increases analysis time)

☑ **Interaction networks**

☑ Include endogenous chemicals

Genes are always included

Molecules per network: 35

Networks per analysis: 25

☑ **Causal networks**

Score master regulators for relationships to diseases, functions, genes, or chemicals (max 50)

☐ Score using causal paths only

X-linked COVID19-related immunodeficiency 74 [COVID19-related immunodeficiency 74]

Analysis Filter Summary

Consider only molecules and/or relationships where (species = Human) AND (confidence = Experimentally Observed) AND (mol. types = biologic drug OR canonical pathway OR chemical - endogenous mammalian OR chemical - endogenous non-mammalian OR chemical - kinase inhibitor OR chemical - other OR chemical - protease inhibitor OR chemical drug OR chemical reagent OR chemical toxicant OR complex OR cytokine OR disease OR enzyme OR function OR G-protein coupled receptor OR group OR growth factor OR ion channel OR kinase OR ligand-dependent nuclear receptor OR mature microRNA OR microRNA OR other OR peptidase OR phosphatase OR related pathway node OR transcription regulator OR translation

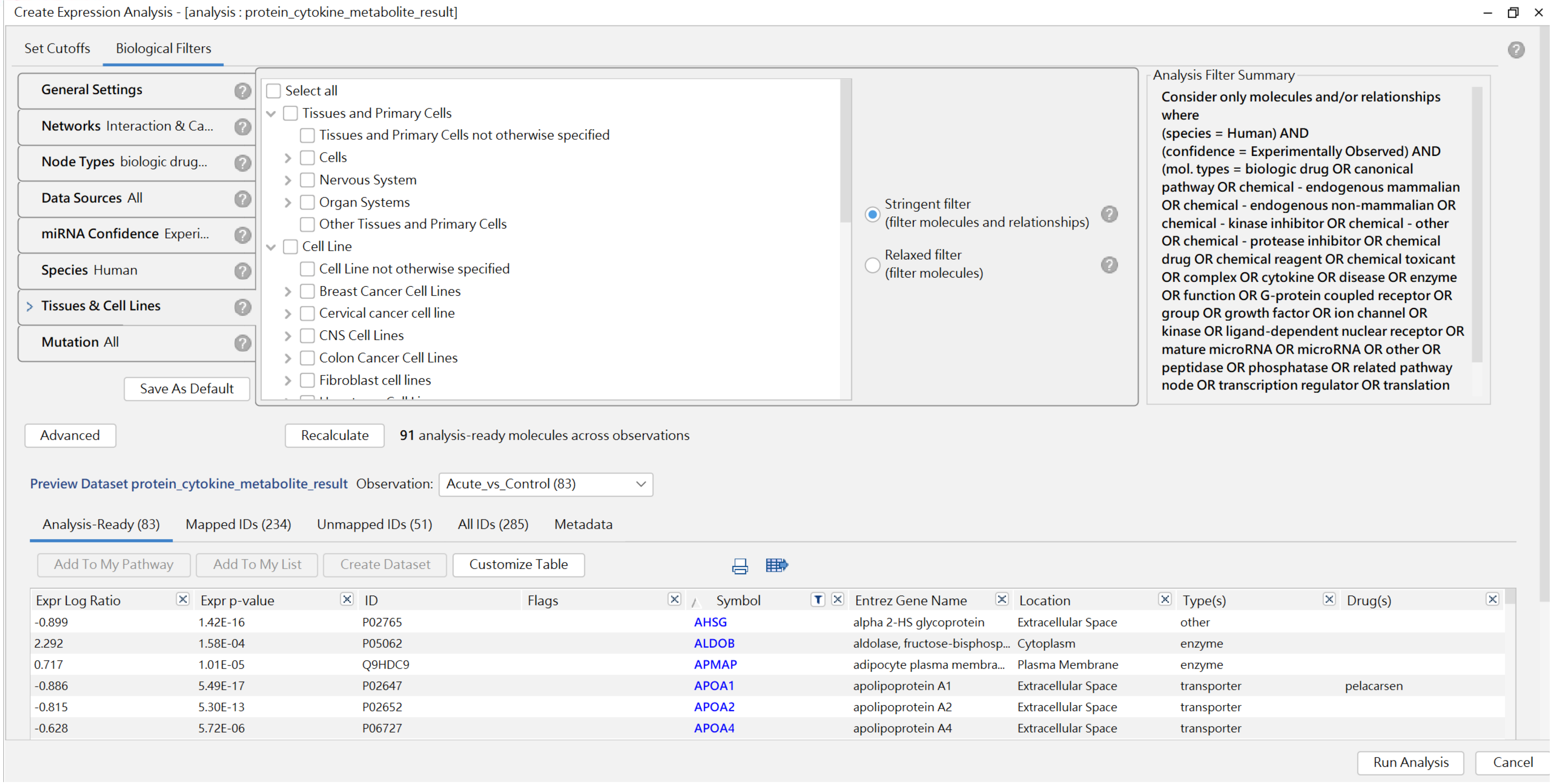
91 analysis-ready molecules across observations

Preview Dataset protein_cytokine_metabolite_result   Observation: Acute_vs_Control (83)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-0.899	1.42E-16	P02765		AHSG	alpha 2-HS glycoprotein	Extracellular Space	other	
2.292	1.58E-04	P05062		ALDOB	aldolase, fructose-bisphosp...	Cytoplasm	enzyme	
0.717	1.01E-05	Q9HDC9		APMAP	adipocyte plasma membra...	Plasma Membrane	enzyme	
-0.886	5.49E-17	P02647		APOA1	apolipoprotein A1	Extracellular Space	transporter	pelacarsen
-0.815	5.30E-13	P02652		APOA2	apolipoprotein A2	Extracellular Space	transporter	
-0.628	5.72E-06	P06727		APOA4	apolipoprotein A4	Extracellular Space	transporter	

You can put interesting disease or gene

Tissue and Cell lines



Create Expression Analysis - [analysis : protein_cytokine_metabolite_result]

General Settings
Networks Interaction & Ca...
Node Types biologic drug...
Data Sources All
miRNA Confidence Experi...
Species Human
Tissues & Cell Lines
Mutation All

- ☐ Select all
- ☐ Tissues and Primary Cells
  - ☐ Tissues and Primary Cells not otherwise specified
  - ☐ Cells
  - ☐ Nervous System
  - ☐ Organ Systems
  - ☐ Other Tissues and Primary Cells
- ☐ Cell Line
  - ☐ Cell Line not otherwise specified
  - ☐ Breast Cancer Cell Lines
  - ☐ Cervical cancer cell line
  - ☐ CNS Cell Lines
  - ☐ Colon Cancer Cell Lines
  - ☐ Fibroblast cell lines

● Stringent filter (filter molecules and relationships)

○ Relaxed filter (filter molecules)

Analysis Filter Summary

Consider only molecules and/or relationships where (species = Human) AND (confidence = Experimentally Observed) AND (mol. types = biologic drug OR canonical pathway OR chemical - endogenous mammalian OR chemical - endogenous non-mammalian OR chemical - kinase inhibitor OR chemical - other OR chemical - protease inhibitor OR chemical drug OR chemical reagent OR chemical toxicant OR complex OR cytokine OR disease OR enzyme OR function OR G-protein coupled receptor OR group OR growth factor OR ion channel OR kinase OR ligand-dependent nuclear receptor OR mature microRNA OR microRNA OR other OR peptidase OR phosphatase OR related pathway node OR transcription regulator OR translation

91 analysis-ready molecules across observations

Preview Dataset protein_cytokine_metabolite_result Observation: Acute_vs_Control (83)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-0.899	1.42E-16	P02765		AHSG	alpha 2-HS glycoprotein	Extracellular Space	other	
2.292	1.58E-04	P05062		ALDOB	aldolase, fructose-bisphosp...	Cytoplasm	enzyme	
0.717	1.01E-05	Q9HDC9		APMAP	adipocyte plasma membra...	Plasma Membrane	enzyme	
-0.886	5.49E-17	P02647		APOA1	apolipoprotein A1	Extracellular Space	transporter	pelacarsen
-0.815	5.30E-13	P02652		APOA2	apolipoprotein A2	Extracellular Space	transporter	
-0.628	5.72E-06	P06727		APOA4	apolipoprotein A4	Extracellular Space	transporter	

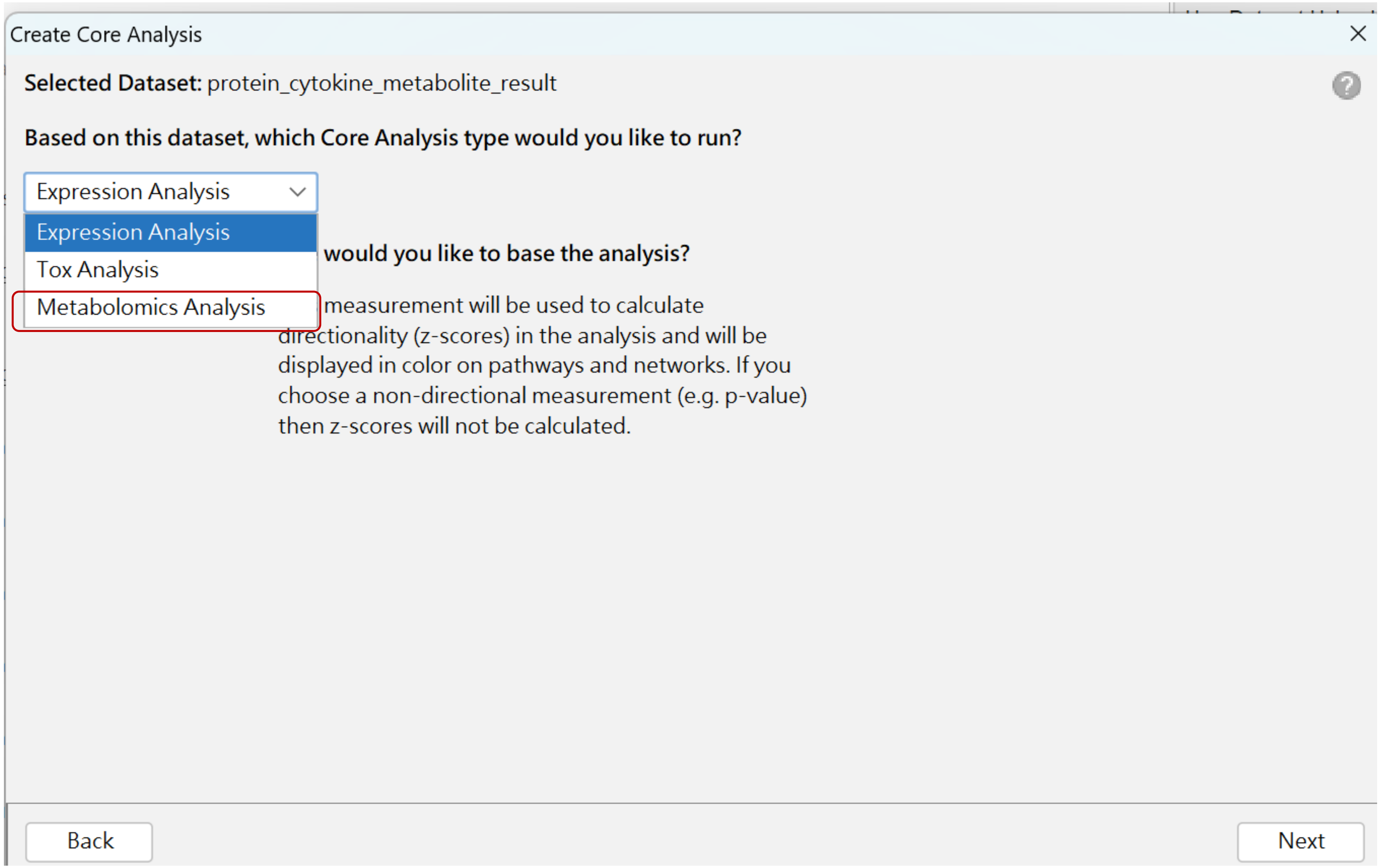
Choose which analysis do you want

Analyze filter dataset

Core analysis

Choose which analysis

Set cut off



Create Core Analysis

Selected Dataset: protein_cytokine_metabolite_result

Based on this dataset, which Core Analysis type would you like to run?

Expression Analysis

- Expression Analysis
- Tox Analysis
- Metabolomics Analysis

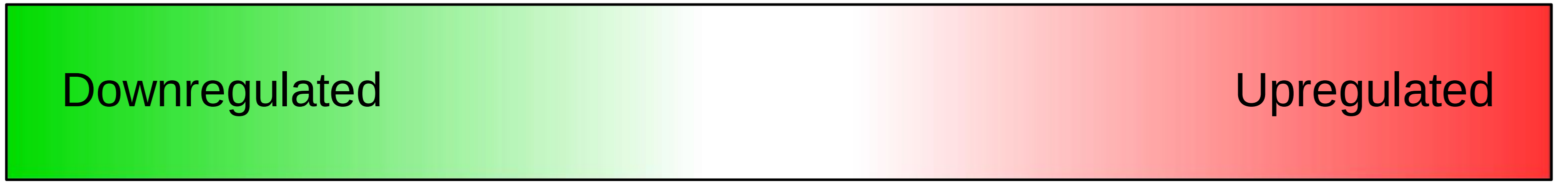
would you like to base the analysis?

measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

What do colors mean in IPA?

Pathway or gene activity predicted by IPA

Actual measurement of gene expression in your dataset

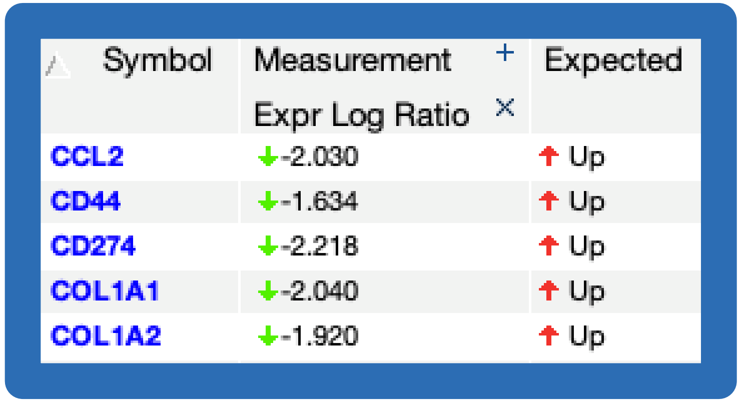


What do z-scores mean in IPA?

Actual dataset measurement

VS.

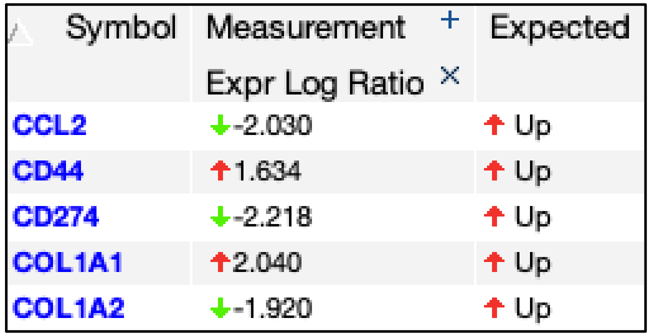
What IPA expects if pathway is activated



Symbol	Measurement Expr Log Ratio	Expected
CCL2	↓-2.030	↑ Up
CD44	↓-1.634	↑ Up
CD274	↓-2.218	↑ Up
COL1A1	↓-2.040	↑ Up
COL1A2	↓-1.920	↑ Up

Pathway inhibited

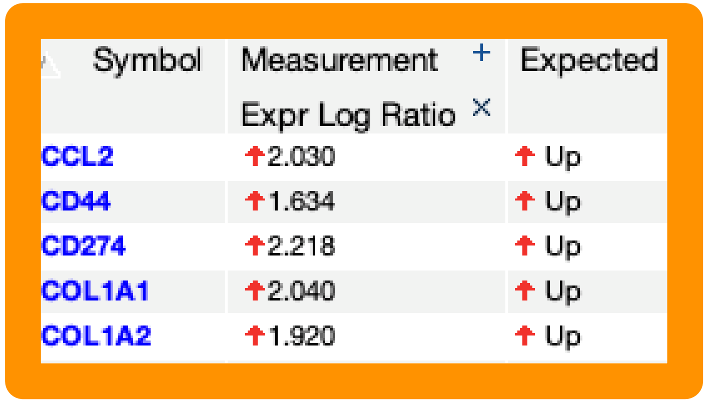
- Z score



Symbol	Measurement Expr Log Ratio	Expected
CCL2	↓-2.030	↑ Up
CD44	↑1.634	↑ Up
CD274	↓-2.218	↑ Up
COL1A1	↑2.040	↑ Up
COL1A2	↓-1.920	↑ Up

No clear signal for prediction

Z score = 0



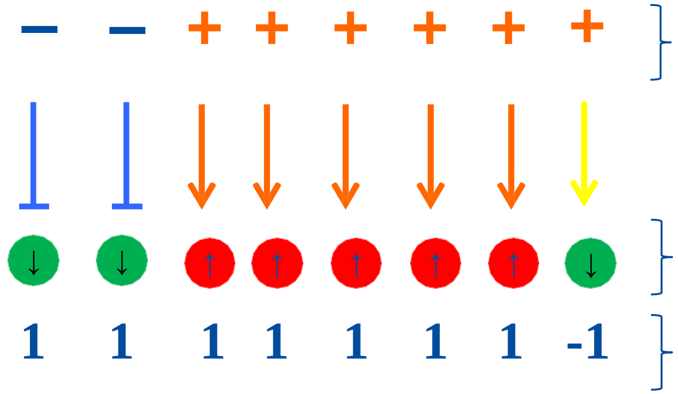
Symbol	Measurement Expr Log Ratio	Expected
CCL2	↑2.030	↑ Up
CD44	↑1.634	↑ Up
CD274	↑2.218	↑ Up
COL1A1	↑2.040	↑ Up
COL1A2	↑1.920	↑ Up

Pathway activated

+ Z score

How well do the actual measurements match the expected measurements?

z-score: Activation prediction



Gene expression from QIAGEN Knowledge Base (literature)

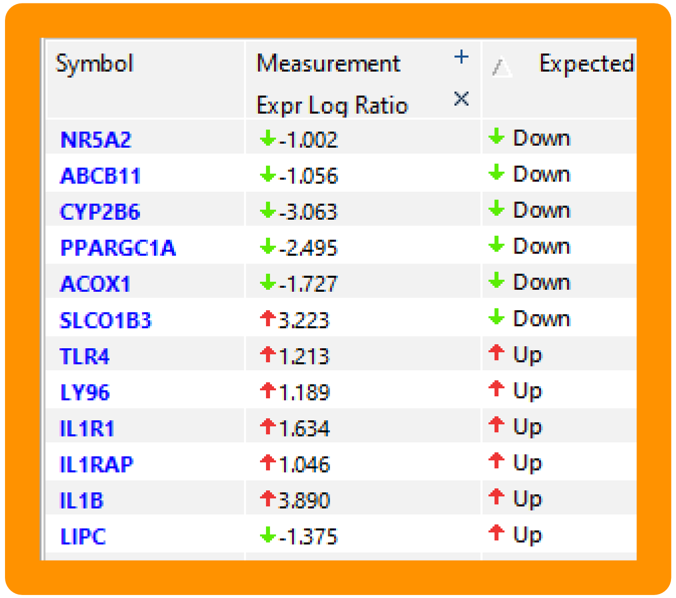
Gene expression in your dataset

+1 score for consistent relationships
and –1 for inconsistent relationships

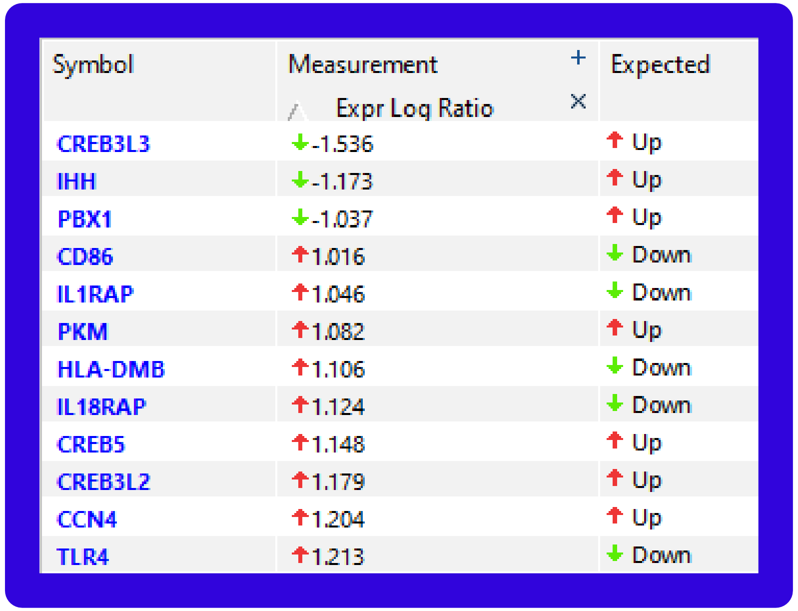
$$z = \frac{x}{\sigma_x} = \frac{\sum_i x_i}{\sqrt{N}} = \frac{N_+ - N_-}{\sqrt{N}} = (7-1)/\sqrt{8} = 2.12 \ (= \text{predicted activation})$$

- z-score is a statistical measure of the match between expected relationship direction and observed gene expression
- z-score greater than 2 or less than –2 is considered significant
- Note that the actual z-score is weighted by the underlying findings, the relationship bias and dataset bias

Examples of z-scores



Symbol	Measurement Expr Log Ratio	Expected
NR5A2	↓-1.002	↓ Down
ABCB11	↓-1.056	↓ Down
CYP2B6	↓-3.063	↓ Down
PPARGC1A	↓-2.495	↓ Down
ACOX1	↓-1.727	↓ Down
SLCO1B3	↑3.223	↓ Down
TLR4	↑1.213	↑ Up
LY96	↑1.189	↑ Up
IL1R1	↑1.634	↑ Up
IL1RAP	↑1.046	↑ Up
IL1B	↑3.890	↑ Up
LIPC	↓-1.375	↑ Up



Symbol	Measurement Expr Log Ratio	Expected
CREB3L3	↓-1.536	↑ Up
IHH	↓-1.173	↑ Up
PBX1	↓-1.037	↑ Up
CD86	↑1.016	↓ Down
IL1RAP	↑1.046	↓ Down
PKM	↑1.082	↑ Up
HLA-DMB	↑1.106	↓ Down
IL18RAP	↑1.124	↓ Down
CREB5	↑1.148	↑ Up
CREB3L2	↑1.179	↑ Up
CCN4	↑1.204	↑ Up
TLR4	↑1.213	↓ Down

Z-score = 2.4

10/12 measurements match expected

Mostly matching

Signal predominantly points to predicted activation

Z-score = -2.236

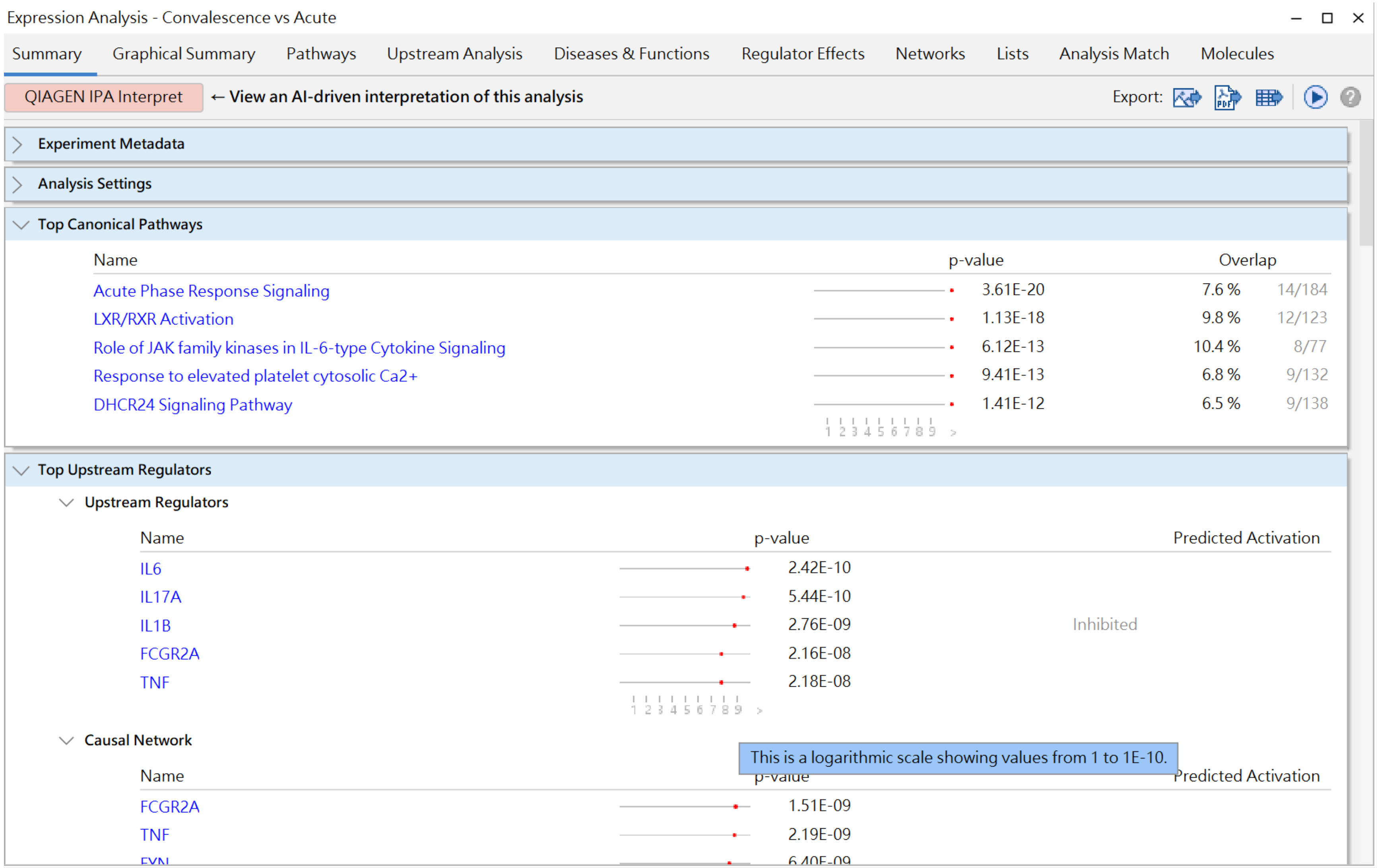
4/12 measurements match expected

Mostly anti-matching

Signal predominantly points to predicted inhibition

IPA Analysis Tabs

Summary Tab



← View an AI-driven interpretation of this analysis

Top Canonical Pathways

Name	p-value	Overlap	
Acute Phase Response Signaling	3.61E-20	7.6 %	14/184
LXR/RXR Activation	1.13E-18	9.8 %	12/123
Role of JAK family kinases in IL-6-type Cytokine Signaling	6.12E-13	10.4 %	8/77
Response to elevated platelet cytosolic Ca2+	9.41E-13	6.8 %	9/132
DHCR24 Signaling Pathway	1.41E-12	6.5 %	9/138

Top Upstream Regulators

Upstream Regulators

Name	p-value	Predicted Activation
IL6	2.42E-10	
IL17A	5.44E-10	
IL1B	2.76E-09	Inhibited
FCGR2A	2.16E-08	
TNF	2.18E-08	

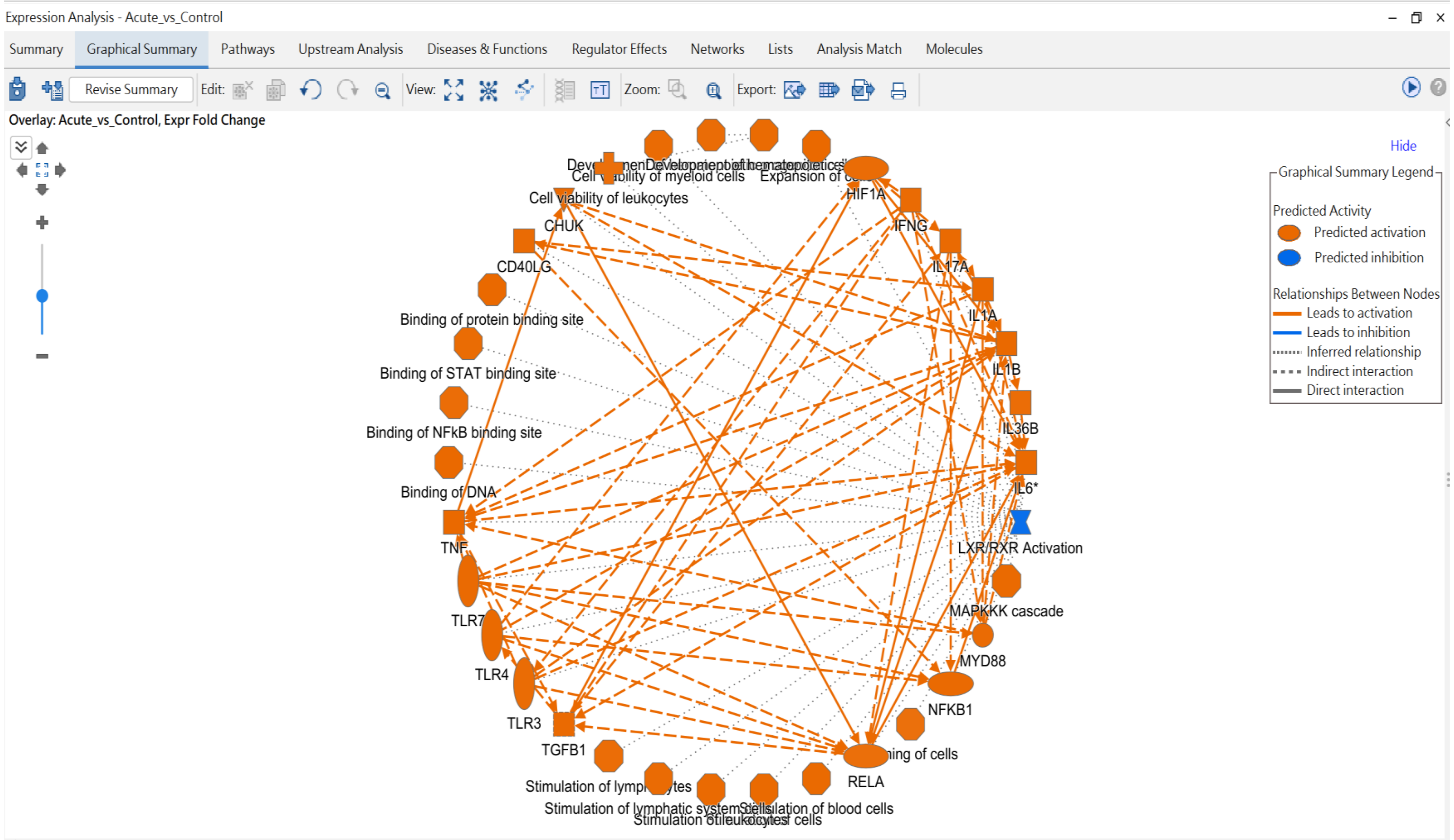
Causal Network

This is a logarithmic scale showing values from 1 to 1E-10.

Name	p-value	Predicted Activation
FCGR2A	1.51E-09	
TNF	2.19E-09	
FYN	6.40E-09	

Top 5 for all analysis modules and a quick high-level look at your data

Graphical Summary Tab



Graphical display of the top biological themes and features within your data with added AI inferences (dotted lines)

Pathways Tab

Change chart characteristics

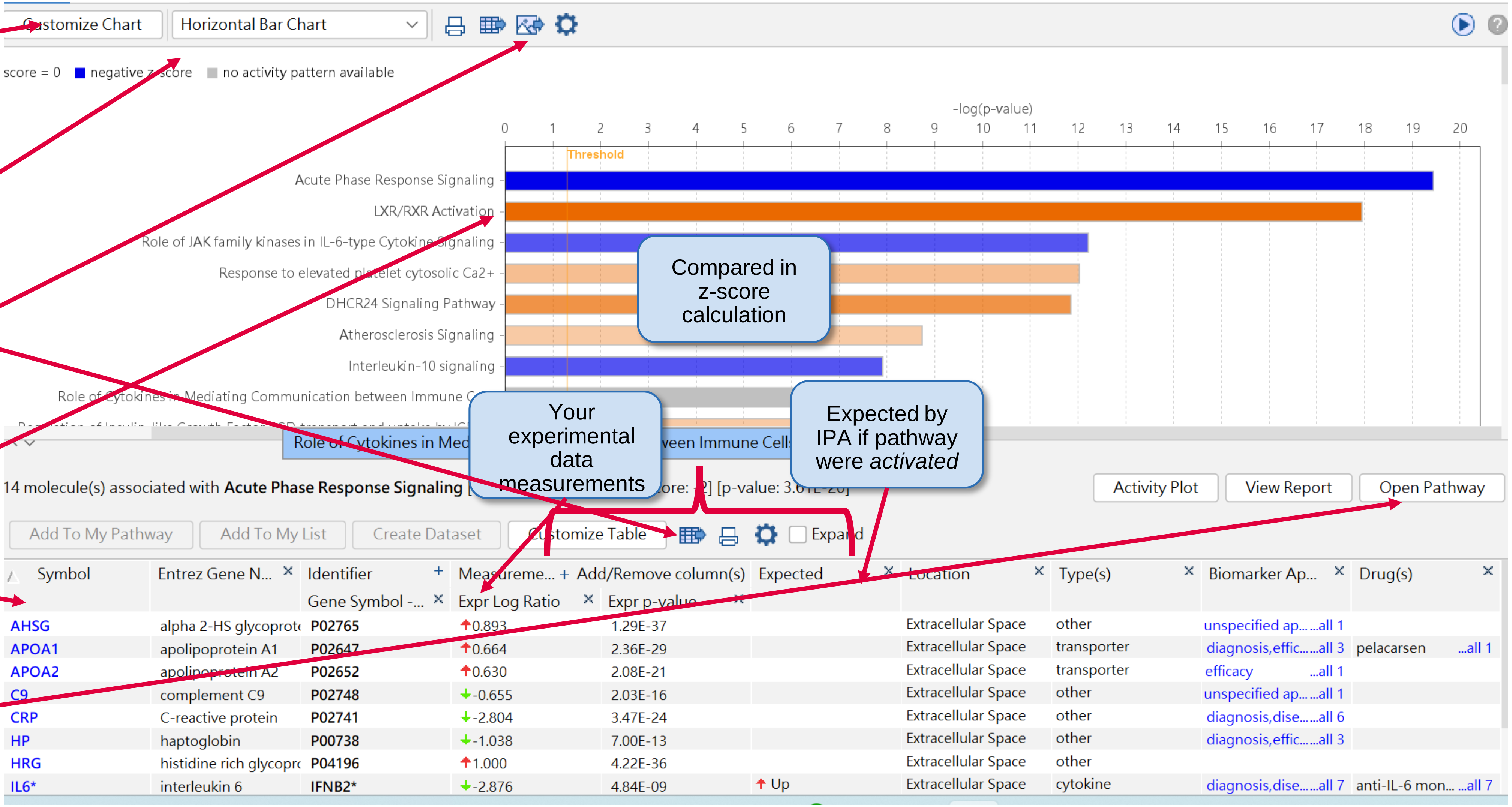
Change chart view

Export data or picture

Click on bar to display chart below

Genes in data set annotated to selected pathway

View network map of pathway



Compared in z-score calculation

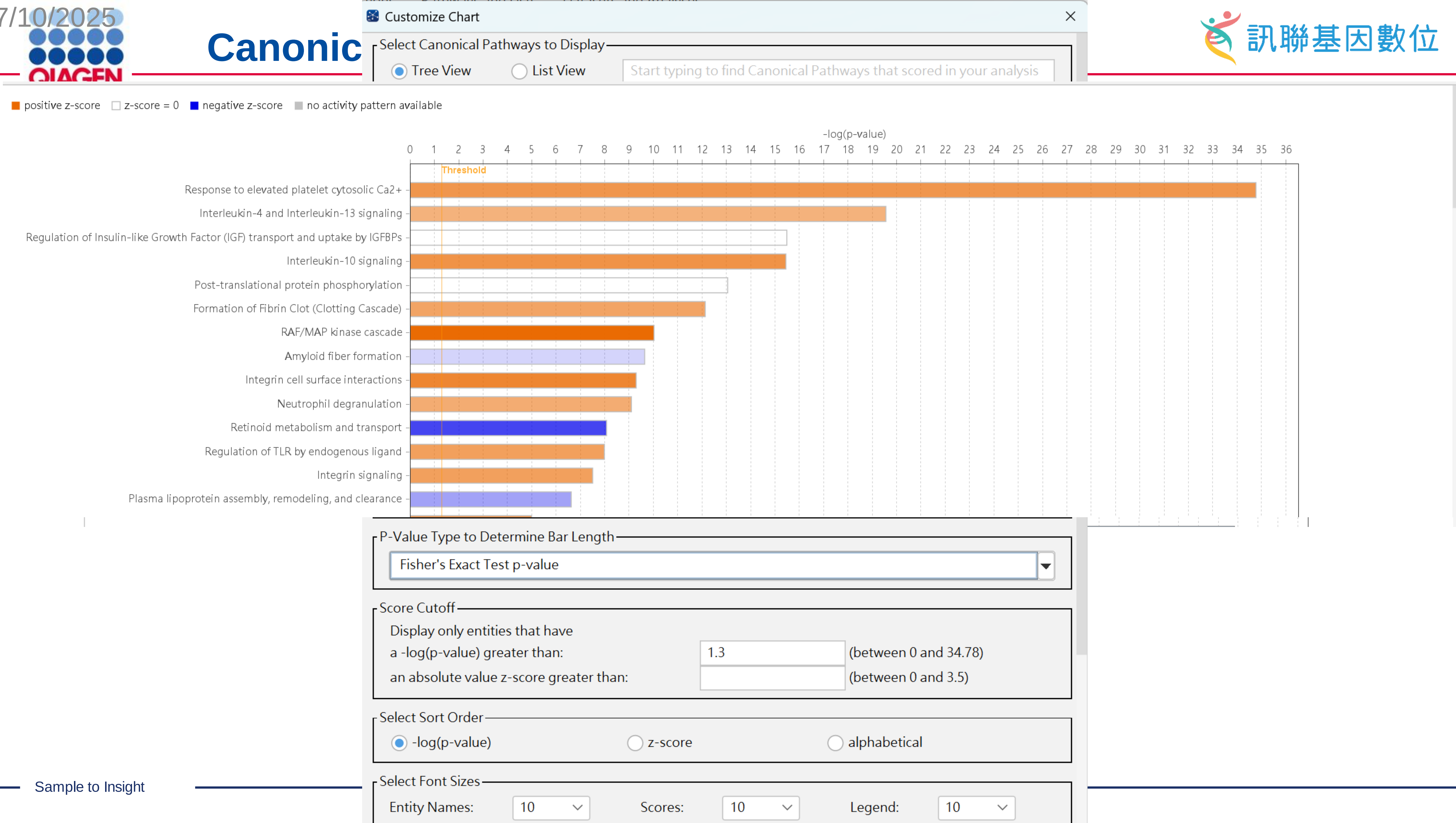
Your experimental data measurements

Expected by IPA if pathway were *activated*

Symbol	Entrez Gene N...	Identifier Gene Symbol -...	Measureme... Expr Log Ratio	Expr p-value	Expected	Location	Type(s)	Biomarker Ap...	Drug(s)
AHSG	alpha 2-HS glycoprote	P02765	↑0.893	1.29E-37		Extracellular Space	other	unspecified ap... ...all 1	
APOA1	apolipoprotein A1	P02647	↑0.664	2.36E-29		Extracellular Space	transporter	diagnosis,effic... ...all 3	pelacarsen ...all 1
APOA2	apolipoprotein A2	P02652	↑0.630	2.08E-21		Extracellular Space	transporter	efficacy ...all 1	
C9	complement C9	P02748	↓-0.655	2.03E-16		Extracellular Space	other	unspecified ap... ...all 1	
CRP	C-reactive protein	P02741	↓-2.804	3.47E-24		Extracellular Space	other	diagnosis,dise... ...all 6	
HP	haptoglobin	P00738	↓-1.038	7.00E-13		Extracellular Space	other	diagnosis,effic... ...all 3	
HRG	histidine rich glycopro	P04196	↑1.000	4.22E-36		Extracellular Space	other		
IL6*	interleukin 6	IFNB2*	↓-2.876	4.84E-09	↑ Up	Extracellular Space	cytokine	diagnosis,dise... ...all 7	anti-IL-6 mon... ...all 7

Metabolic and cell signaling pathways that are enriched in your data with activity prediction

Canonic



Customize Chart

Select Canonical Pathways to Display

● Tree View ○ List View

Start typing to find Canonical Pathways that scored in your analysis

P-Value Type to Determine Bar Length

Fisher's Exact Test p-value

Score Cutoff

Display only entities that have

a -log(p-value) greater than: 1.3 (between 0 and 34.78)

an absolute value z-score greater than: (between 0 and 3.5)

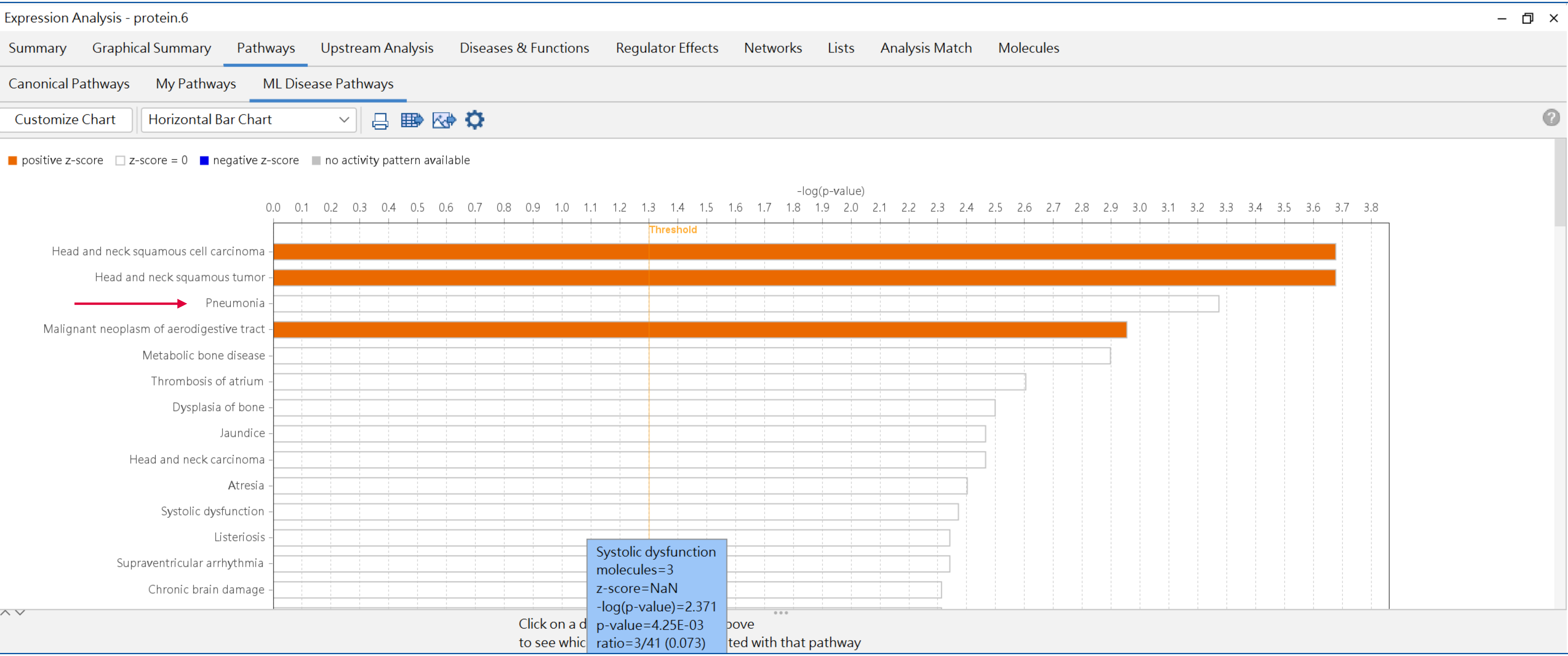
Select Sort Order

● -log(p-value) ○ z-score ○ alphabetical

Select Font Sizes

Entity Names: 10 Scores: 10 Legend: 10

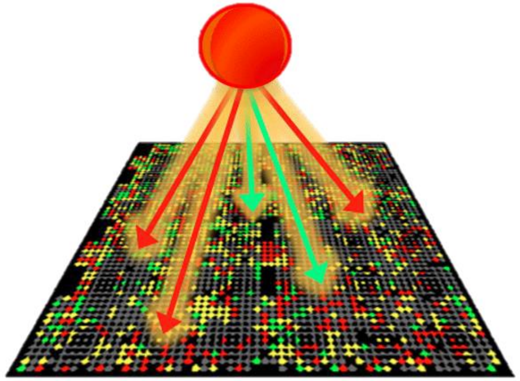
ML pathway



Systolic dysfunction
molecules=3
z-score=NaN
-log(p-value)=2.371
p-value=4.25E-03
ratio=3/41 (0.073)

Click on a d pove
to see whic ted with that pathway

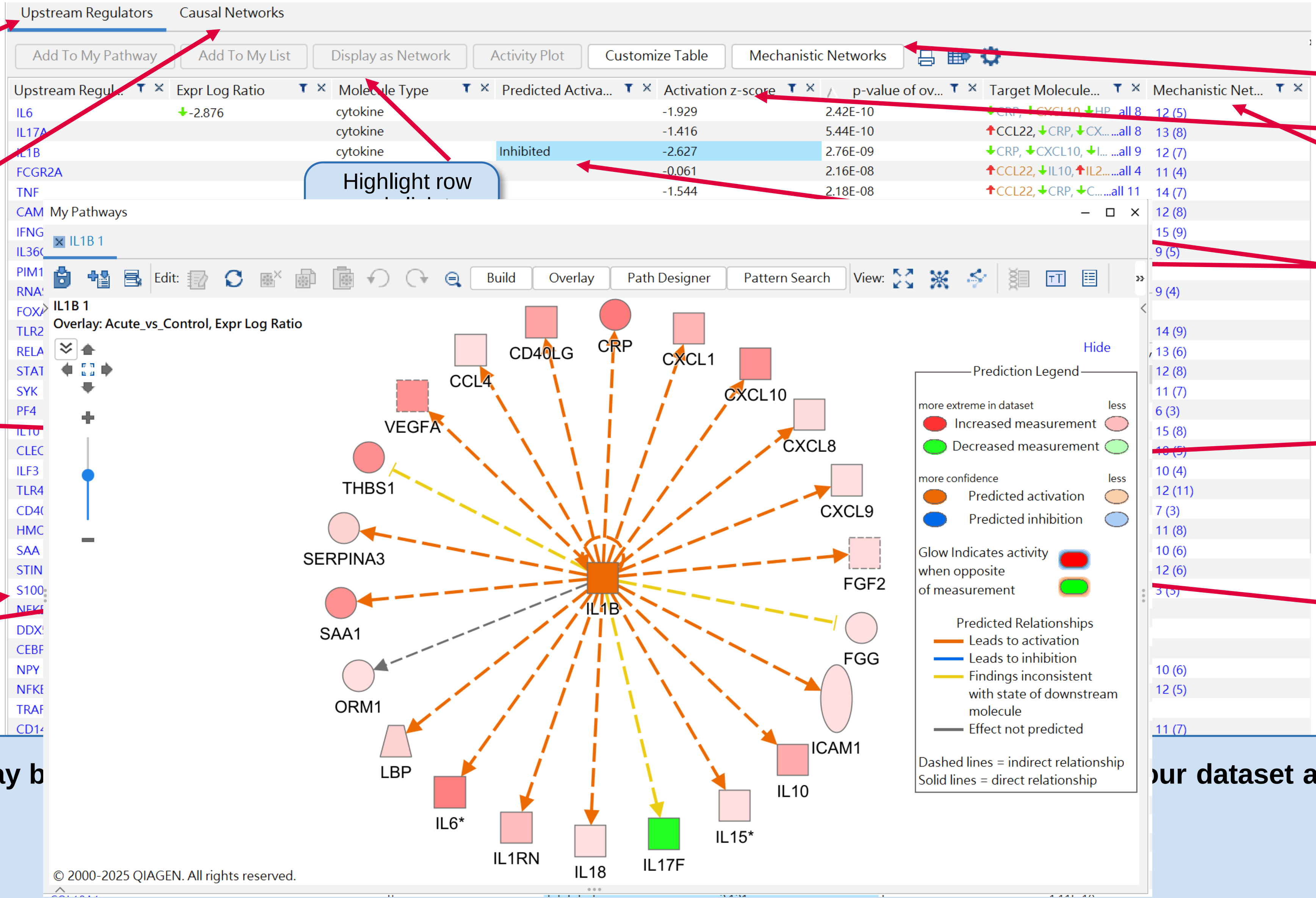
Upstream Regulator Analysis: *How does it work?*



- Use experimentally observed relationships (vs. Predicted event) between Upstream Regulators and genes to predict potential regulator and activation

- Predict activation or inhibition of regulator to explain the changes in gene expression in your dataset
- Calculates two complementary statistical measures:
  - ☐Activation z-score
  - ☐Overlap p-value

Upstream Analysis Tab



Upstream Regul...	Expr Log Ratio	Molecule Type	Predicted Activa...	Activation z-score	p-value of ov...	Target Molecule...	Mechanistic Net...
IL6	-2.876	cytokine		-1.929	2.42E-10	CRP, CXCL10, HP...all 8	12 (5)
IL17A		cytokine		-1.416	5.44E-10	CCL22, CRP, CX... ...all 8	13 (8)
IL1B		cytokine	Inhibited	-2.627	2.76E-09	CRP, CXCL10, I... ...all 9	12 (7)
FCGR2A				-0.061	2.16E-08	CCL22, IL10, IL2... ...all 4	11 (4)
TNF				-1.544	2.18E-08	CCL22, CRP, C... ...all 11	14 (7)

Immediately upstream of dataset genes regulators

One additional level upstream of regulatory networks

Measurement from your dataset for this regulator

Regulator predicted by IPA using patterns seen in your data (no measurement)

Highlight row

Export

Filter icons

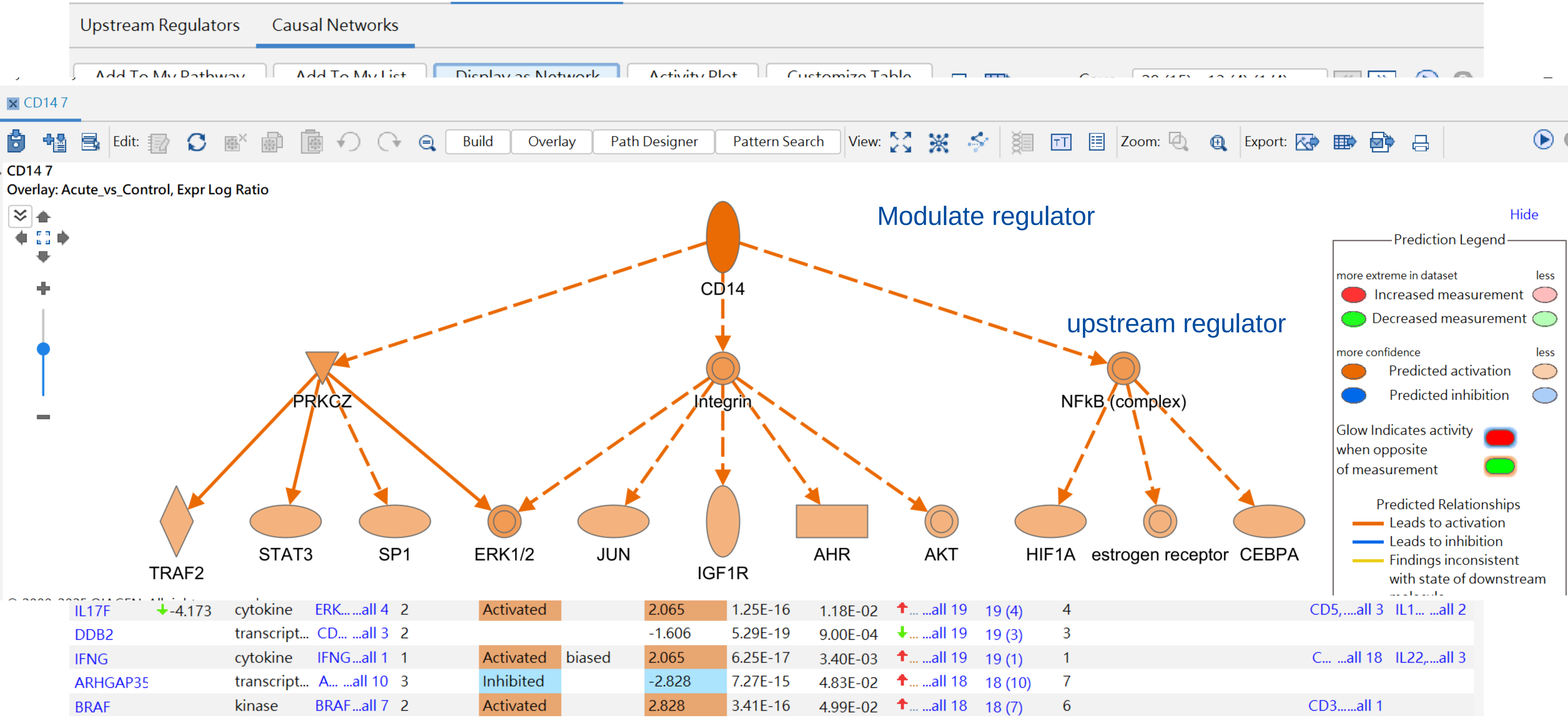
Activity prediction

Genes that this regulator targets present in your filtered dataset

P-value of significance

Regulators that may b **our dataset and some have**

Casual network



Modulate regulator

upstream regulator

IL17F	↓-4.173	cytokine	ERK... ...all 4	2	Activated		2.065	1.25E-16	1.18E-02	↑... ...all 19	19 (4)	4	CD5,....all 3	IL1... ...all 2
DDB2		transcript...	CD... ...all 3	2			-1.606	5.29E-19	9.00E-04	↓... ...all 19	19 (3)	3		
IFNG		cytokine	IFNG...all 1	1	Activated	biased	2.065	6.25E-17	3.40E-03	↑... ...all 19	19 (1)	1	C... ...all 18	IL22,...all 3
ARHGAP35		transcript...	A... ...all 10	3	Inhibited		-2.828	7.27E-15	4.83E-02	↑... ...all 18	18 (10)	7		
BRAF		kinase	BRAF...all 7	2	Activated		2.828	3.41E-16	4.99E-02	↑... ...all 18	18 (7)	6	CD3.....all 1	

Diseases & Functions Tab

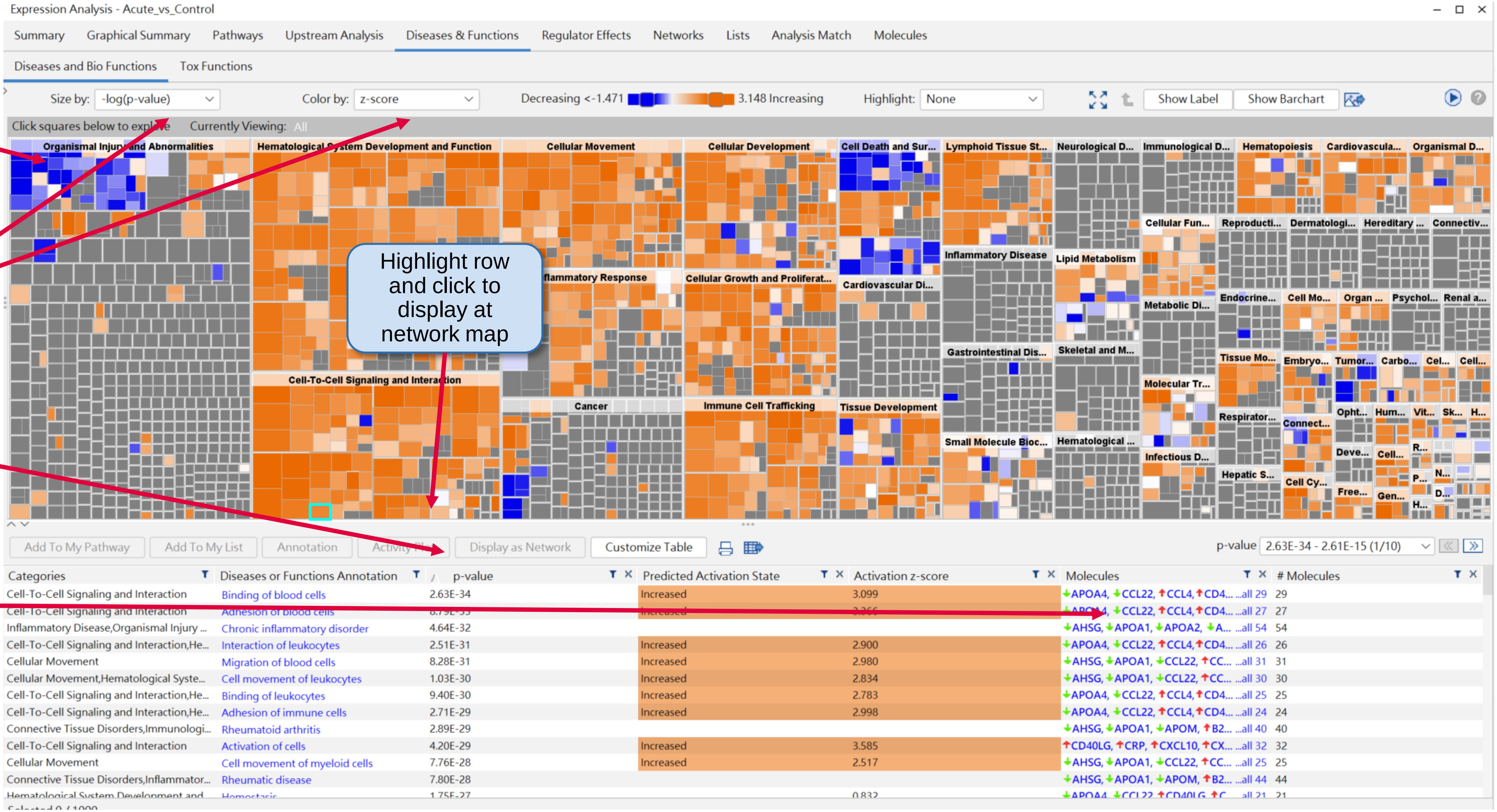
Color is activity prediction; size of square is p-value but can be changed

Organized by biological themes

Significance of enrichment

Genes from dataset involved in disease or function

Highlight row and click to display at network map

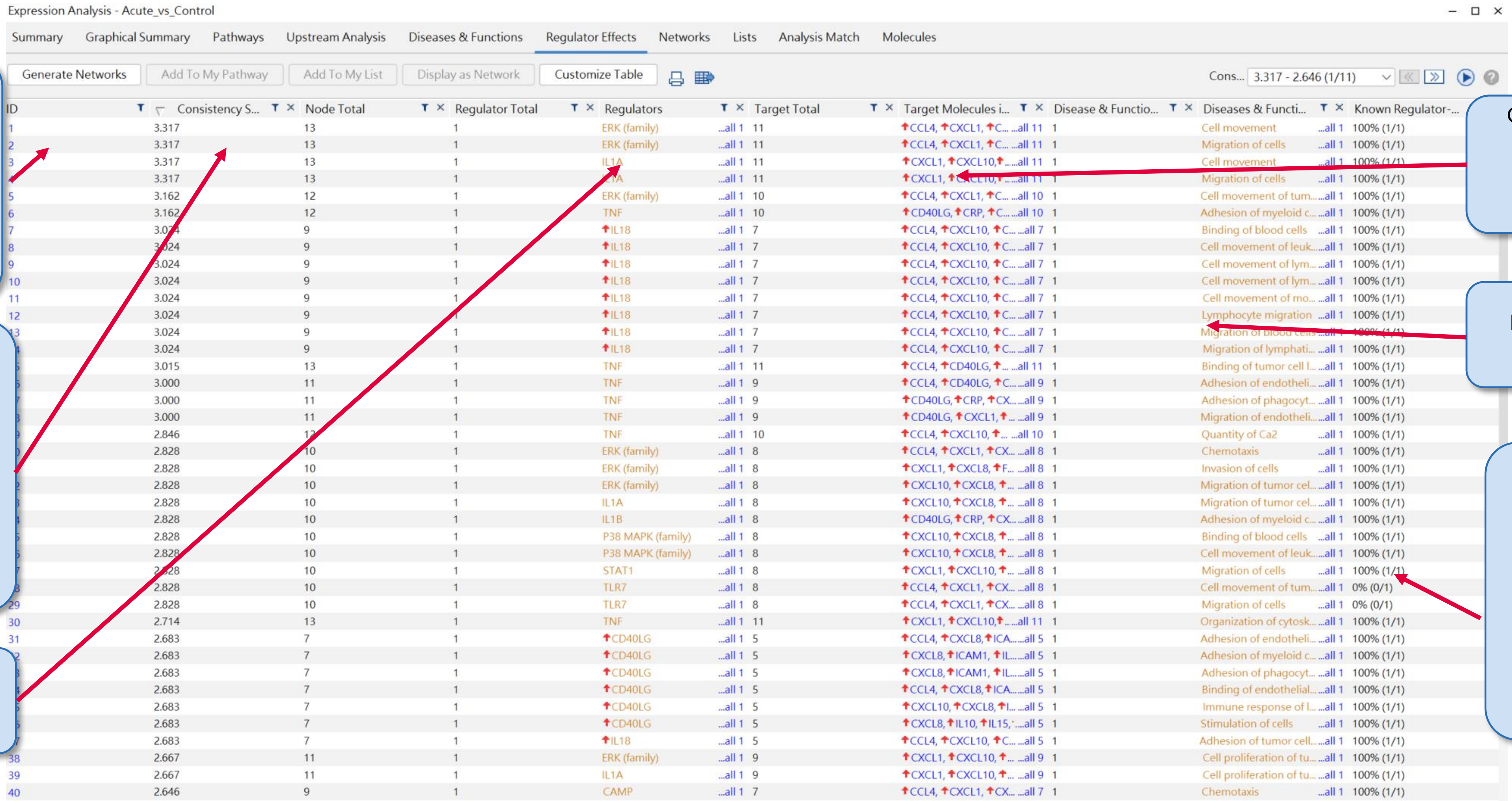


Categories	Diseases or Functions Annotation	p-value	Predicted Activation State	Activation z-score	Molecules	# Molecules
Cell-To-Cell Signaling and Interaction	Binding of blood cells	2.63E-34	Increased	3.099	↓APOA4, ↓CCL22, ↑CCL4, ↑CD4... ...all 29	29
Cell-To-Cell Signaling and Interaction	Adhesion of blood cells	8.79E-33	Increased	3.266	↓APOA4, ↓CCL22, ↑CCL4, ↑CD4... ...all 27	27
Inflammatory Disease,Organismal Injury ...	Chronic inflammatory disorder	4.64E-32			↓AHSG, ↓APOA1, ↓APOA2, ↓A... ...all 54	54
Cell-To-Cell Signaling and Interaction,He...	Interaction of leukocytes	2.51E-31	Increased	2.900	↓APOA4, ↓CCL22, ↑CCL4, ↑CD4... ...all 26	26
Cellular Movement	Migration of blood cells	8.28E-31	Increased	2.980	↓AHSG, ↓APOA1, ↓CCL22, ↑CC... ...all 31	31
Cellular Movement,Hematological Syste...	Cell movement of leukocytes	1.03E-30	Increased	2.834	↓AHSG, ↓APOA1, ↓CCL22, ↑CC... ...all 30	30
Cell-To-Cell Signaling and Interaction,He...	Binding of leukocytes	9.40E-30	Increased	2.783	↓APOA4, ↓CCL22, ↑CCL4, ↑CD4... ...all 25	25
Cell-To-Cell Signaling and Interaction,He...	Adhesion of immune cells	2.71E-29	Increased	2.998	↓APOA4, ↓CCL22, ↑CCL4, ↑CD4... ...all 24	24
Connective Tissue Disorders,Immunologi...	Rheumatoid arthritis	2.89E-29			↓AHSG, ↓APOA1, ↓APOM, ↑B2... ...all 40	40
Cell-To-Cell Signaling and Interaction	Activation of cells	4.20E-29	Increased	3.585	↑CD40LG, ↑CRP, ↑CXCL10, ↑CX... ...all 32	32
Cellular Movement	Cell movement of myeloid cells	7.76E-28	Increased	2.517	↓AHSG, ↓APOA1, ↓CCL22, ↑CC... ...all 25	25
Connective Tissue Disorders,Inflammator...	Rheumatic disease	7.80E-28			↓AHSG, ↓APOA1, ↓APOM, ↑B2... ...all 44	44
Hematological System Development and...	Hemostasis	1.75E-27		0.832	↓APOA4, ↓CCL22, ↑CD40LG, ↑C... ...all 21	21

Selected 0 / 1000

Diseases and functions that may be key to the biology in your experimental data based on patterns of expression observed

Regulator Effects Tab



Cons... 3.317 - 2.646 (1/11)

ID	Consistency S...	Node Total	Regulator Total	Regulators	Target Total	Target Molecules i...	Disease & Functio...	Diseases & Functi...	Known Regulator-...
1	3.317	13	1	ERK (family) ...all 1	11	↑CCL4, ↑CXCL1, ↑C... ...all 11	1	Cell movement ...all 1	100% (1/1)
2	3.317	13	1	ERK (family) ...all 1	11	↑CCL4, ↑CXCL1, ↑C... ...all 11	1	Migration of cells ...all 1	100% (1/1)
3	3.317	13	1	IL1A ...all 1	11	↑CXCL1, ↑CXCL10,↑... ...all 11	1	Cell movement ...all 1	100% (1/1)
4	3.317	13	1	IL1A ...all 1	11	↑CXCL1, ↑CXCL10,↑... ...all 11	1	Migration of cells ...all 1	100% (1/1)
5	3.162	12	1	ERK (family) ...all 1	10	↑CCL4, ↑CXCL1, ↑C... ...all 10	1	Cell movement of tum... ...all 1	100% (1/1)
6	3.162	12	1	TNF ...all 1	10	↑CD40LG, ↑CRP, ↑C... ...all 10	1	Adhesion of myeloid c... ...all 1	100% (1/1)
7	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Binding of blood cells ...all 1	100% (1/1)
8	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Cell movement of leuk... ...all 1	100% (1/1)
9	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Cell movement of lym... ...all 1	100% (1/1)
10	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Cell movement of lym... ...all 1	100% (1/1)
11	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Cell movement of mo... ...all 1	100% (1/1)
12	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Lymphocyte migration ...all 1	100% (1/1)
13	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Migration of blood cells ...all 1	100% (1/1)
4	3.024	9	1	↑IL18 ...all 1	7	↑CCL4, ↑CXCL10, ↑C... ...all 7	1	Migration of lymphati... ...all 1	100% (1/1)
5	3.015	13	1	TNF ...all 1	11	↑CCL4, ↑CD40LG, ↑... ...all 11	1	Binding of tumor cell l... ...all 1	100% (1/1)
6	3.000	11	1	TNF ...all 1	9	↑CCL4, ↑CD40LG, ↑C... ...all 9	1	Adhesion of endotheli... ...all 1	100% (1/1)
7	3.000	11	1	TNF ...all 1	9	↑CD40LG, ↑CRP, ↑CX... ...all 9	1	Adhesion of phagocyt... ...all 1	100% (1/1)
8	3.000	11	1	TNF ...all 1	9	↑CD40LG, ↑CXCL1, ↑... ...all 9	1	Migration of endotheli... ...all 1	100% (1/1)
9	2.846	12	1	TNF ...all 1	10	↑CCL4, ↑CXCL10, ↑... ...all 10	1	Quantity of Ca2 ...all 1	100% (1/1)
0	2.828	10	1	ERK (family) ...all 1	8	↑CCL4, ↑CXCL1, ↑CX... ...all 8	1	Chemotaxis ...all 1	100% (1/1)
	2.828	10	1	ERK (family) ...all 1	8	↑CXCL1, ↑CXCL8, ↑F... ...all 8	1	Invasion of cells ...all 1	100% (1/1)
2	2.828	10	1	ERK (family) ...all 1	8	↑CXCL10, ↑CXCL8, ↑... ...all 8	1	Migration of tumor cel... ...all 1	100% (1/1)
3	2.828	10	1	IL1A ...all 1	8	↑CXCL10, ↑CXCL8, ↑... ...all 8	1	Migration of tumor cel... ...all 1	100% (1/1)
4	2.828	10	1	IL1B ...all 1	8	↑CD40LG, ↑CRP, ↑CX... ...all 8	1	Adhesion of myeloid c... ...all 1	100% (1/1)
5	2.828	10	1	P38 MAPK (family) ...all 1	8	↑CXCL10, ↑CXCL8, ↑... ...all 8	1	Binding of blood cells ...all 1	100% (1/1)
6	2.828	10	1	P38 MAPK (family) ...all 1	8	↑CXCL10, ↑CXCL8, ↑... ...all 8	1	Cell movement of leuk... ...all 1	100% (1/1)
7	2.828	10	1	STAT1 ...all 1	8	↑CXCL1, ↑CXCL10, ↑... ...all 8	1	Migration of cells ...all 1	100% (1/1)
8	2.828	10	1	TLR7 ...all 1	8	↑CCL4, ↑CXCL1, ↑CX... ...all 8	1	Cell movement of tum... ...all 1	0% (0/1)
29	2.828	10	1	TLR7 ...all 1	8	↑CCL4, ↑CXCL1, ↑CX... ...all 8	1	Migration of cells ...all 1	0% (0/1)
30	2.714	13	1	TNF ...all 1	11	↑CXCL1, ↑CXCL10,↑... ...all 11	1	Organization of cytosk... ...all 1	100% (1/1)
31	2.683	7	1	↑CD40LG ...all 1	5	↑CCL4, ↑CXCL8, ↑ICA... ...all 5	1	Adhesion of endotheli... ...all 1	100% (1/1)
2	2.683	7	1	↑CD40LG ...all 1	5	↑CXCL8, ↑ICAM1, ↑IL... ...all 5	1	Adhesion of myeloid c... ...all 1	100% (1/1)
3	2.683	7	1	↑CD40LG ...all 1	5	↑CXCL8, ↑ICAM1, ↑IL... ...all 5	1	Adhesion of phagocyt... ...all 1	100% (1/1)
4	2.683	7	1	↑CD40LG ...all 1	5	↑CCL4, ↑CXCL8, ↑ICA... ...all 5	1	Binding of endothelial... ...all 1	100% (1/1)
5	2.683	7	1	↑CD40LG ...all 1	5	↑CXCL10, ↑CXCL8, ↑I... ...all 5	1	Immune response of l... ...all 1	100% (1/1)
6	2.683	7	1	↑CD40LG ...all 1	5	↑CXCL8, ↑IL10, ↑IL15, ...all 5	1	Stimulation of cells ...all 1	100% (1/1)
7	2.683	7	1	↑IL18 ...all 1	5	↑CCL4, ↑CXCL10, ↑C... ...all 5	1	Adhesion of tumor cell... ...all 1	100% (1/1)
38	2.667	11	1	ERK (family) ...all 1	9	↑CXCL1, ↑CXCL10, ↑... ...all 9	1	Cell proliferation of tu... ...all 1	100% (1/1)
39	2.667	11	1	IL1A ...all 1	9	↑CXCL1, ↑CXCL10, ↑... ...all 9	1	Cell proliferation of tu... ...all 1	100% (1/1)
40	2.646	9	1	CAMP ...all 1	7	↑CCL4, ↑CXCL1, ↑CX... ...all 7	1	Chemotaxis ...all 1	100% (1/1)

Network of molecules and regulators that are predicted to be involved in diseases & functions

How matching your data is with the expected directions in IPA for the diseases & functions they're predicted to effect

Regulators involved in network

Genes from dataset involved in disease or function

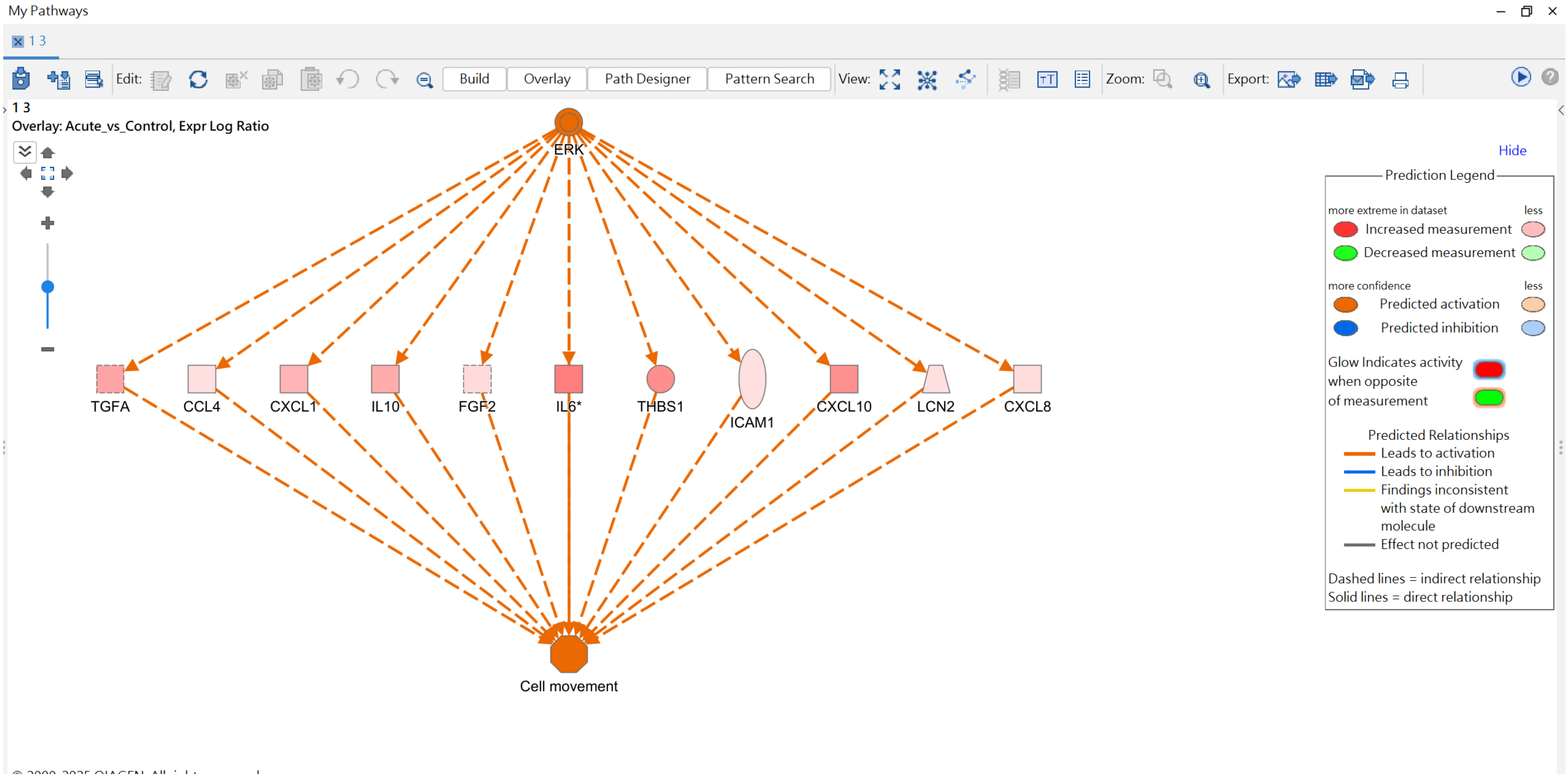
Disease or function

Known connections in IPA between regulator and disease & function- discover novel relationships

Ties dataset molecules and regulators to a predicted phenotypic outcome

Regulate Effect

訊聯基因數位



1 3

Overlay: Acute_vs_Control, Expr Log Ratio

Prediction Legend

more extreme in dataset		less
🔴	Increased measurement	●
🟢	Decreased measurement	●

more confidence		less
🟠	Predicted activation	●
🔵	Predicted inhibition	●

Glow Indicates activity when opposite of measurement

Predicted Relationships
- Leads to activation
- Leads to inhibition
- Findings inconsistent with state of downstream molecule
- Effect not predicted

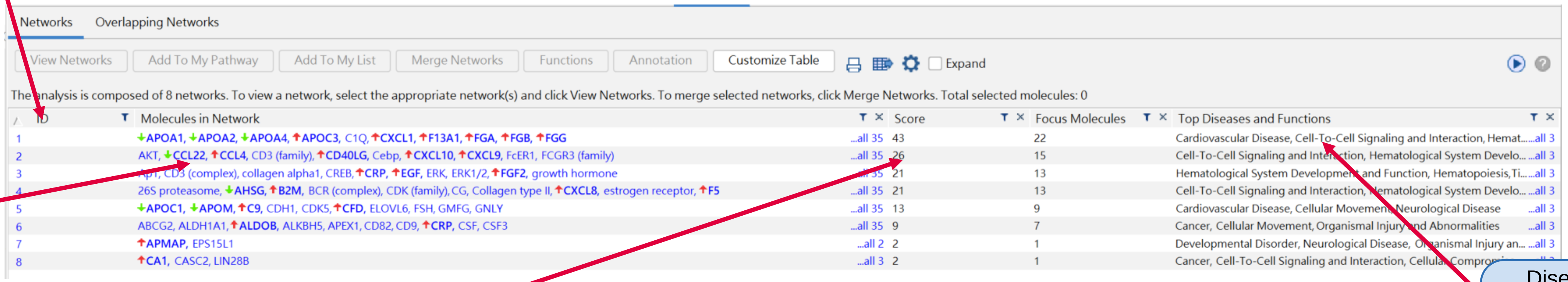
Dashed lines = indirect relationship
Solid lines = direct relationship

Networks Tab

Network of highly connected molecules, click to open network map

Molecule in **bold** is in your dataset; unbolded have been added to maximize connectivity

Based on a p-value calculation how likely molecules exist as part of a network than chance alone



The analysis is composed of 8 networks. To view a network, select the appropriate network(s) and click View Networks. To merge selected networks, click Merge Networks. Total selected molecules: 0

ID	Molecules in Network		Score	Focus Molecules	Top Diseases and Functions	
1	↓**APOA1**, ↓**APOA2**, ↓**APOA4**, ↑**APOC3**, C1Q, ↑**CXCL1**, ↑**F13A1**, ↑**FGA**, ↑**FGB**, ↑**FGG**	...all 35	43	22	Cardiovascular Disease, Cell-To-Cell Signaling and Interaction, Hemat...	...all 3
2	AKT, ↓**CCL22**, ↑**CCL4**, CD3 (family), ↑**CD40LG**, Cebp, ↑**CXCL10**, ↑**CXCL9**, FcER1, FCGR3 (family)	...all 35	26	15	Cell-To-Cell Signaling and Interaction, Hematological System Develo...	...all 3
3	Ap1, CD3 (complex), collagen alpha1, CREB, ↑**CRP**, ↑**EGF**, ERK, ERK1/2, ↑**FGF2**, growth hormone	...all 35	21	13	Hematological System Development and Function, Hematopoiesis, Ti...	...all 3
4	26S proteasome, ↓**AHSG**, ↑**B2M**, BCR (complex), CDK (family), CG, Collagen type II, ↑**CXCL8**, estrogen receptor, ↑**F5**	...all 35	21	13	Cell-To-Cell Signaling and Interaction, Hematological System Develo...	...all 3
5	↓**APOC1**, ↓**APOM**, ↑**C9**, CDH1, CDK5, ↑**CFD**, ELOVL6, FSH, GMFG, GNLY	...all 35	13	9	Cardiovascular Disease, Cellular Movement, Neurological Disease	...all 3
6	ABCG2, ALDH1A1, ↑**ALDOB**, ALKBH5, APEX1, CD82, CD9, ↑**CRP**, CSF, CSF3	...all 35	9	7	Cancer, Cellular Movement, Organismal Injury and Abnormalities	...all 3
7	↑**APMAP**, EPS15L1	...all 2	2	1	Developmental Disorder, Neurological Disease, Organismal Injury an...	...all 3
8	↑**CA1**, CASC2, LIN28B	...all 3	2	1	Cancer, Cell-To-Cell Signaling and Interaction, Cellular Comprom	

Disease or function predicted to be an outcome

Networks constructed from your dataset with level of connectivity prioritized

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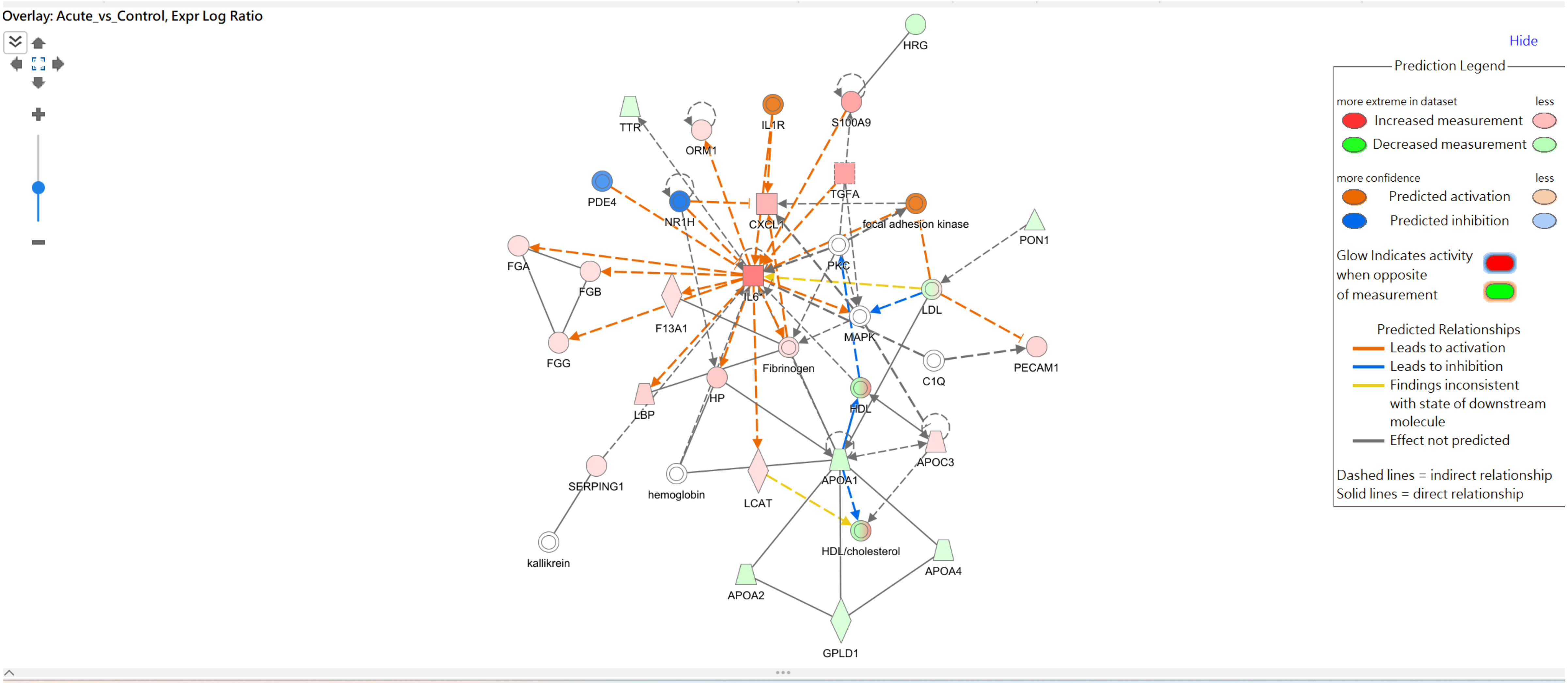
Network

訊聯基因數位



Overlay: Acute_vs_Control, Expr Log Ratio

Hide

Prediction Legend

more extreme in dataset — less

● Increased measurement ●

● Decreased measurement ●

more confidence — less

● Predicted activation ●

● Predicted inhibition ●

Glow Indicates activity when opposite of measurement ● ●

Predicted Relationships

— Leads to activation

— Leads to inhibition

— Findings inconsistent with state of downstream molecule

— Effect not predicted

Dashed lines = indirect relationship

Solid lines = direct relationship

Analysis Match

How signatures are created and compared

- ➢ Data source from Omicsoft datalands

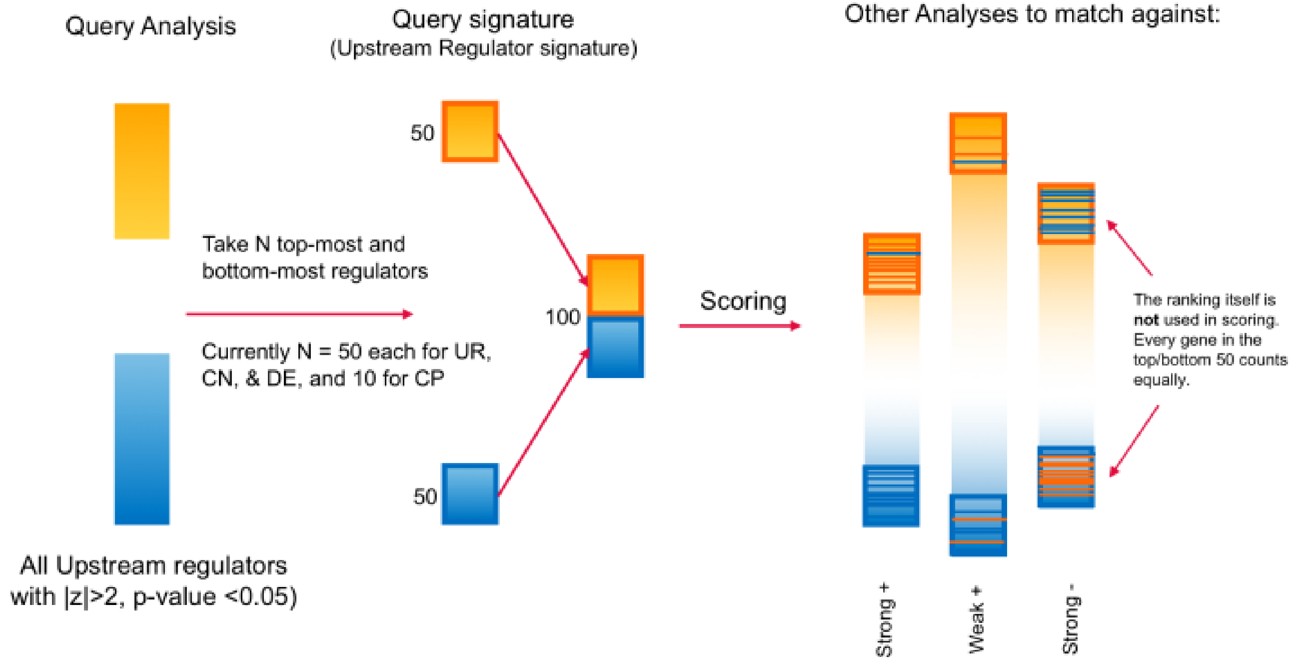
Canonical Pathways (up to 20 pathways)

Upstream Regulators (up to 100 regulators)

Causal Networks (up to 100 master regulators)

Diseases & Functions (up to 100 diseases or functions)

Example



Query Analysis

Query signature
(Upstream Regulator signature)

Other Analyses to match against:

Take N top-most and bottom-most regulators

Currently N = 50 each for UR, CN, & DE, and 10 for CP

All Upstream regulators with |z|>2, p-value <0.05)

Scoring

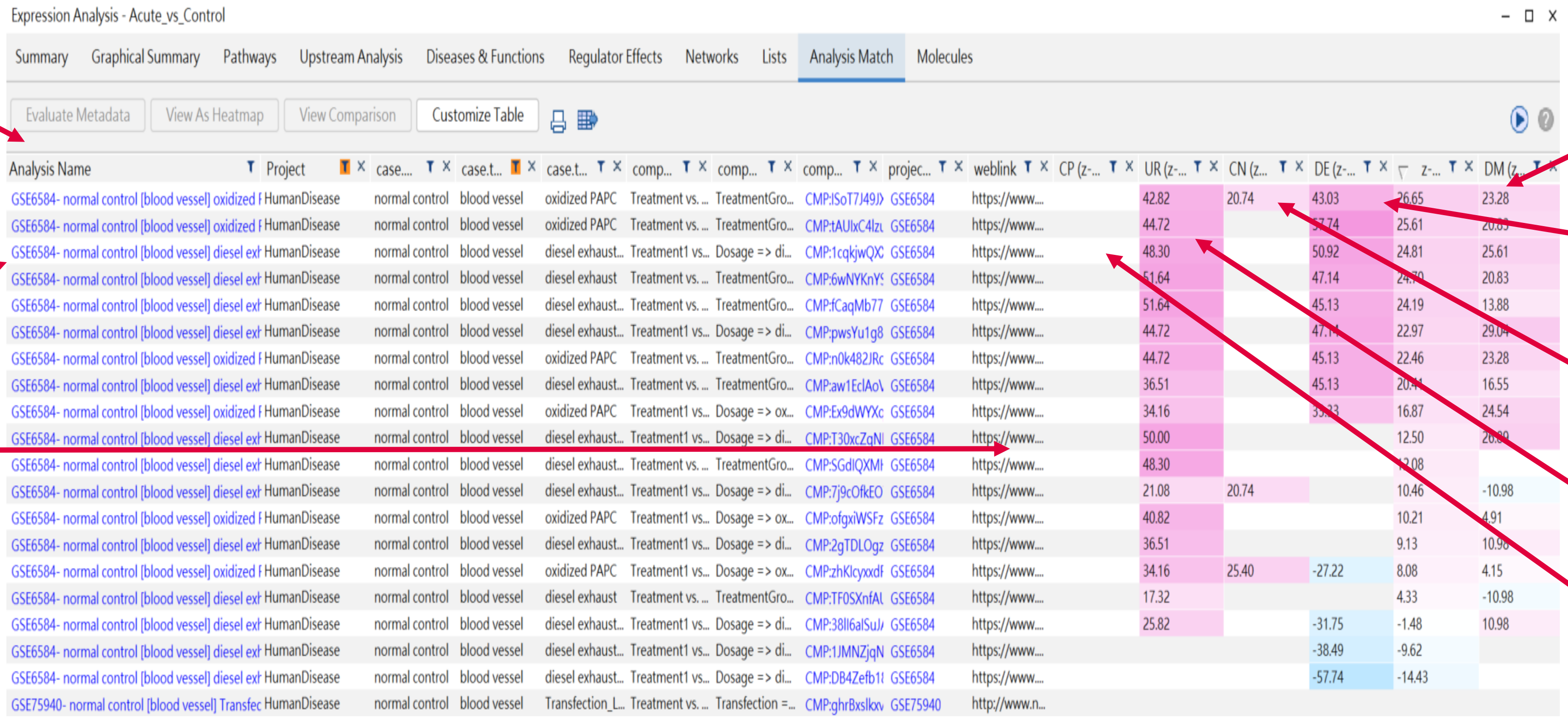
The ranking itself is **not** used in scoring. Every gene in the top/bottom 50 counts equally.

Analysis Match Tab

Public and previously run analyses with matching or antimatching results

Double click to open core analysis

Link to Land Explorer to view volcano plot of comparison



Analysis Name	Project	case....	case.t...	case.t...	comp...	comp...	comp...	projec...	weblink	CP (z-...	UR (z-...	CN (z...	DE (z-...	z-...	DM (z...
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment vs. ...	TreatmentGro...	CMP:ISoT7J49J›	GSE6584	https://www....		42.82	20.74	43.03	26.65	23.28
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment vs. ...	TreatmentGro...	CMP:tAUlxC4lzı	GSE6584	https://www....		44.72		57.74	25.61	20.83
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:1cqkjwQX	GSE6584	https://www....		48.30		50.92	24.81	25.61
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust	Treatment vs. ...	TreatmentGro...	CMP:6wNYKnY	GSE6584	https://www....		51.64		47.14	24.70	20.83
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment vs. ...	TreatmentGro...	CMP:fCaqMb77	GSE6584	https://www....		51.64		45.13	24.19	13.88
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:pwsYu1g8	GSE6584	https://www....		44.72		47.14	22.97	29.04
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment vs. ...	TreatmentGro...	CMP:n0k482JRc	GSE6584	https://www....		44.72		45.13	22.46	23.28
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment vs. ...	TreatmentGro...	CMP:aw1EclAo\	GSE6584	https://www....		36.51		45.13	20.41	16.55
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment1 vs...	Dosage => ox...	CMP:Ex9dWYXc	GSE6584	https://www....		34.16		35.23	16.87	24.54
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:T30xcZqNI	GSE6584	https://www....		50.00			12.50	20.89
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment vs. ...	TreatmentGro...	CMP:SGdlQXMI	GSE6584	https://www....		48.30			12.08	
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:7j9cOfkEO	GSE6584	https://www....		21.08	20.74		10.46	-10.98
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment1 vs...	Dosage => ox...	CMP:ofgxiWSFz	GSE6584	https://www....		40.82			10.21	4.91
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:2gTDLOgz	GSE6584	https://www....		36.51			9.13	10.98
GSE6584- normal control [blood vessel] oxidized F	HumanDisease	normal control	blood vessel	oxidized PAPC	Treatment1 vs...	Dosage => ox...	CMP:zhKlcyxxdF	GSE6584	https://www....		34.16	25.40	-27.22	8.08	4.15
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust	Treatment vs. ...	TreatmentGro...	CMP:TF0SXnfAl	GSE6584	https://www....		17.32			4.33	-10.98
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:38ll6alSuJ	GSE6584	https://www....		25.82		-31.75	-1.48	10.98
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:1JMNZjqN	GSE6584	https://www....				-38.49	-9.62	
GSE6584- normal control [blood vessel] diesel ext	HumanDisease	normal control	blood vessel	diesel exhaust...	Treatment1 vs...	Dosage => di...	CMP:DB4Zefb1	GSE6584	https://www....				-57.74	-14.43	
GSE75940- normal control [blood vessel] Transfec	HumanDisease	normal control	blood vessel	Transfection_L...	Treatment vs. ...	Transfection =...	CMP:ghrBxslkxv	GSE75940	http://www.n...						

Average z-score from all 4 analysis features

DE: Downstream effects (i.e. diseases and functions

CN: Causal Networks

UR: Upstream Regulators

CP: Canonical Pathways

Matches your core analysis against public datasets in IPA as well as previously run core analyses and returns similar and dissimilar datasets based on 4 core analysis features: CP, UR, CN, DE

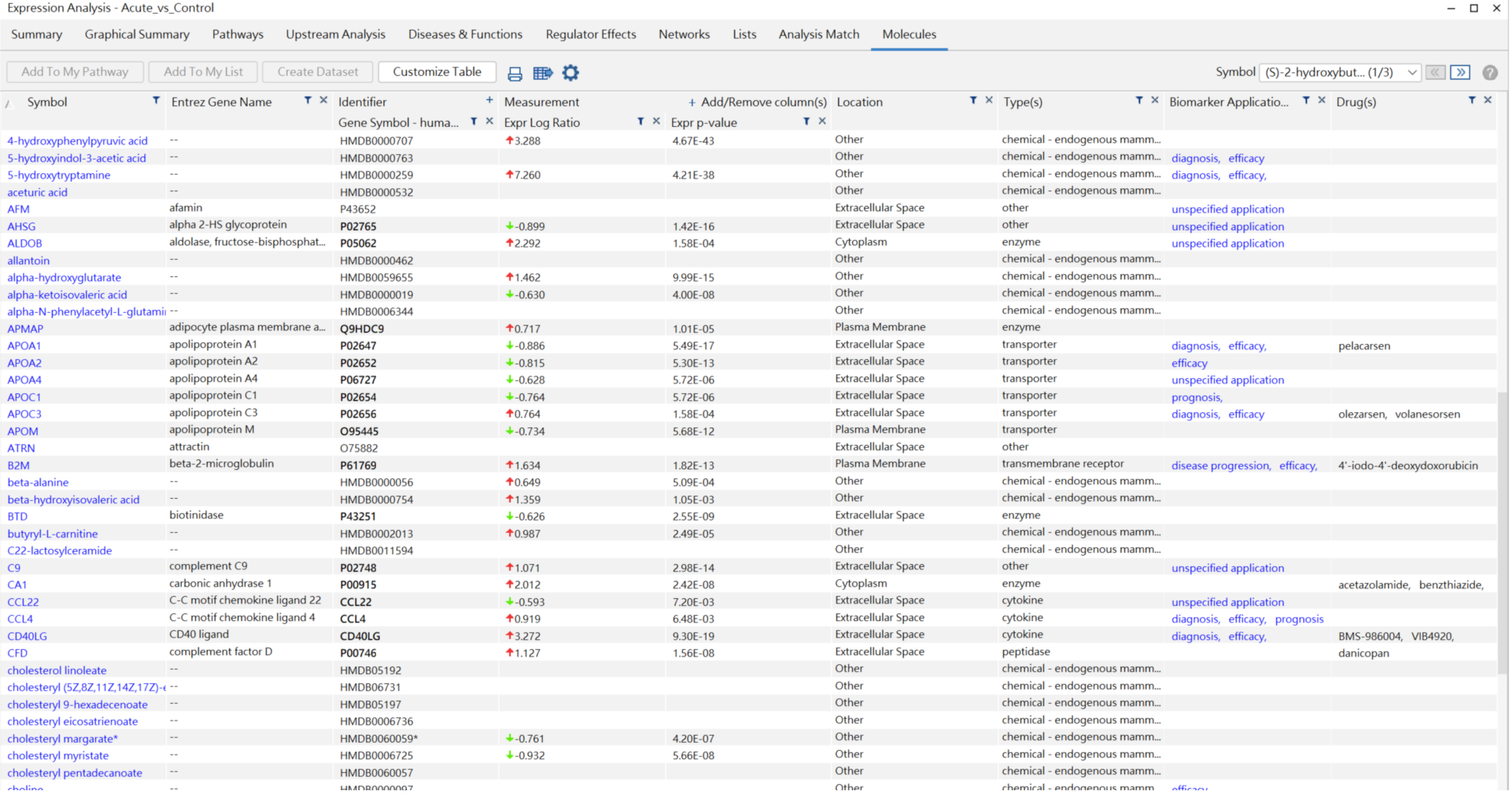
****All columns are filterable****

Positive z-score: Pink: matching ***Negative z-score: Blue: antimatching***

Molecules

Biomarker Application

Drug



Symbol	Entrez Gene Name	Identifier	Measurement	+ Add/Remove column(s)	Location	Type(s)	Biomarker Applicatio...	Drug(s)
		Gene Symbol - huma...	Expr Log Ratio	Expr p-value				
4-hydroxyphenylpyruvic acid	--	HMDB0000707	↑3.288	4.67E-43	Other	chemical - endogenous mamm...		
5-hydroxyindol-3-acetic acid	--	HMDB0000763			Other	chemical - endogenous mamm...	diagnosis, efficacy	
5-hydroxytryptamine	--	HMDB0000259	↑7.260	4.21E-38	Other	chemical - endogenous mamm...	diagnosis, efficacy,	
aceturic acid	--	HMDB0000532			Other	chemical - endogenous mamm...		
AFM	afamin	P43652			Extracellular Space	other	unspecified application	
AHSG	alpha 2-HS glycoprotein	P02765	↓-0.899	1.42E-16	Extracellular Space	other	unspecified application	
ALDOB	aldolase, fructose-bisphosphat...	P05062	↑2.292	1.58E-04	Cytoplasm	enzyme	unspecified application	
allantoin	--	HMDB0000462			Other	chemical - endogenous mamm...		
alpha-hydroxyglutarate	--	HMDB0059655	↑1.462	9.99E-15	Other	chemical - endogenous mamm...		
alpha-ketoisovaleric acid	--	HMDB0000019	↓-0.630	4.00E-08	Other	chemical - endogenous mamm...		
alpha-N-phenylacetyl-L-glutami	--	HMDB0006344			Other	chemical - endogenous mamm...		
APMAP	adipocyte plasma membrane a...	Q9HDC9	↑0.717	1.01E-05	Plasma Membrane	enzyme		
APOA1	apolipoprotein A1	P02647	↓-0.886	5.49E-17	Extracellular Space	transporter	diagnosis, efficacy,	pelacarsen
APOA2	apolipoprotein A2	P02652	↓-0.815	5.30E-13	Extracellular Space	transporter	efficacy	
APOA4	apolipoprotein A4	P06727	↓-0.628	5.72E-06	Extracellular Space	transporter	unspecified application	
APOC1	apolipoprotein C1	P02654	↓-0.764	5.72E-06	Extracellular Space	transporter	prognosis,	
APOC3	apolipoprotein C3	P02656	↑0.764	1.58E-04	Extracellular Space	transporter	diagnosis, efficacy	olezarsen, volanesorsen
APOM	apolipoprotein M	O95445	↓-0.734	5.68E-12	Plasma Membrane	transporter		
ATRN	attractin	O75882			Extracellular Space	other		
B2M	beta-2-microglobulin	P61769	↑1.634	1.82E-13	Plasma Membrane	transmembrane receptor	disease progression, efficacy,	4'-iodo-4'-deoxydoxorubicin
beta-alanine	--	HMDB0000056	↑0.649	5.09E-04	Other	chemical - endogenous mamm...		
beta-hydroxyisovaleric acid	--	HMDB0000754	↑1.359	1.05E-03	Other	chemical - endogenous mamm...		
BTD	biotinidase	P43251	↓-0.626	2.55E-09	Extracellular Space	enzyme		
butyryl-L-carnitine	--	HMDB0002013	↑0.987	2.49E-05	Other	chemical - endogenous mamm...		
C22-lactosylceramide	--	HMDB0011594			Other	chemical - endogenous mamm...		
C9	complement C9	P02748	↑1.071	2.98E-14	Extracellular Space	other	unspecified application	
CA1	carbonic anhydrase 1	P00915	↑2.012	2.42E-08	Cytoplasm	enzyme		acetazolamide, benzthiazide,
CCL22	C-C motif chemokine ligand 22	CCL22	↓-0.593	7.20E-03	Extracellular Space	cytokine	unspecified application	
CCL4	C-C motif chemokine ligand 4	CCL4	↑0.919	6.48E-03	Extracellular Space	cytokine	diagnosis, efficacy, prognosis	
CD40LG	CD40 ligand	CD40LG	↑3.272	9.30E-19	Extracellular Space	cytokine	diagnosis, efficacy,	BMS-986004, VIB4920,
CFD	complement factor D	P00746	↑1.127	1.56E-08	Extracellular Space	peptidase		danicopan
cholesterol linoleate	--	HMDB05192			Other	chemical - endogenous mamm...		
cholesteryl (5Z,8Z,11Z,14Z,17Z)-e	--	HMDB06731			Other	chemical - endogenous mamm...		
cholesteryl 9-hexadecenoate	--	HMDB05197			Other	chemical - endogenous mamm...		
cholesteryl eicosatrienoate	--	HMDB0006736			Other	chemical - endogenous mamm...		
cholesteryl margarate*	--	HMDB0060059*	↓-0.761	4.20E-07	Other	chemical - endogenous mamm...		
cholesteryl myristate	--	HMDB0006725	↓-0.932	5.66E-08	Other	chemical - endogenous mamm...		
cholesteryl pentadecanoate	--	HMDB0060057			Other	chemical - endogenous mamm...		
choline	--	HMDB0000097			Other	chemical - endogenous mamm	efficacy	

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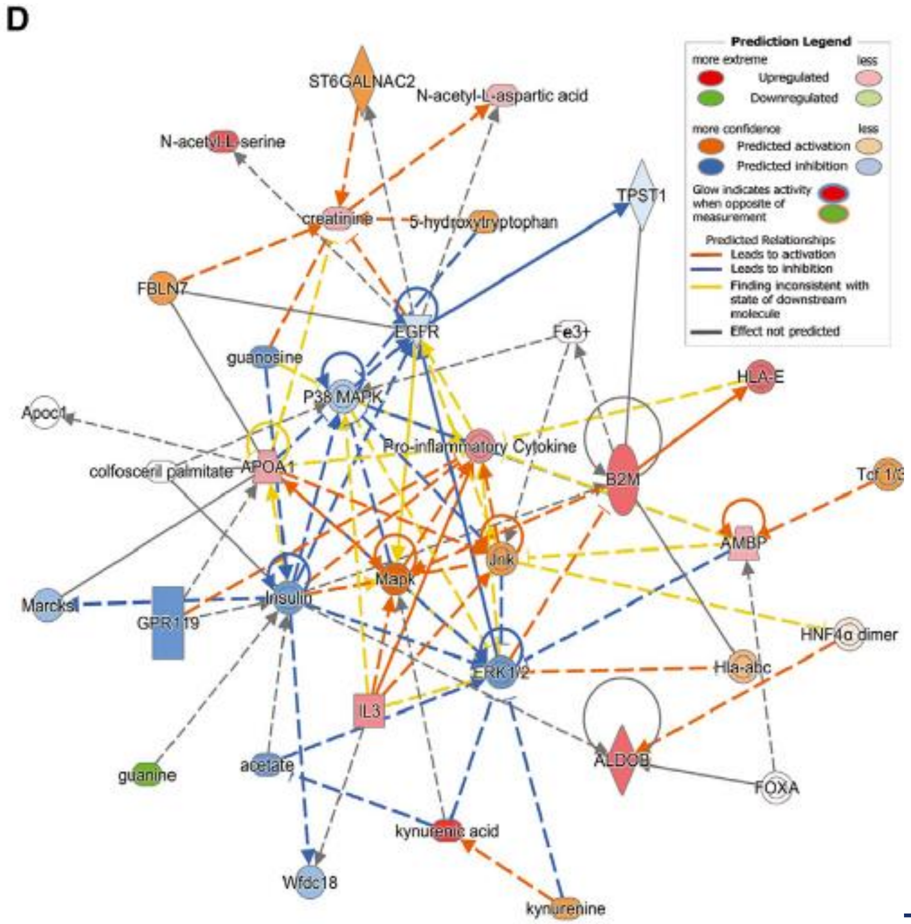
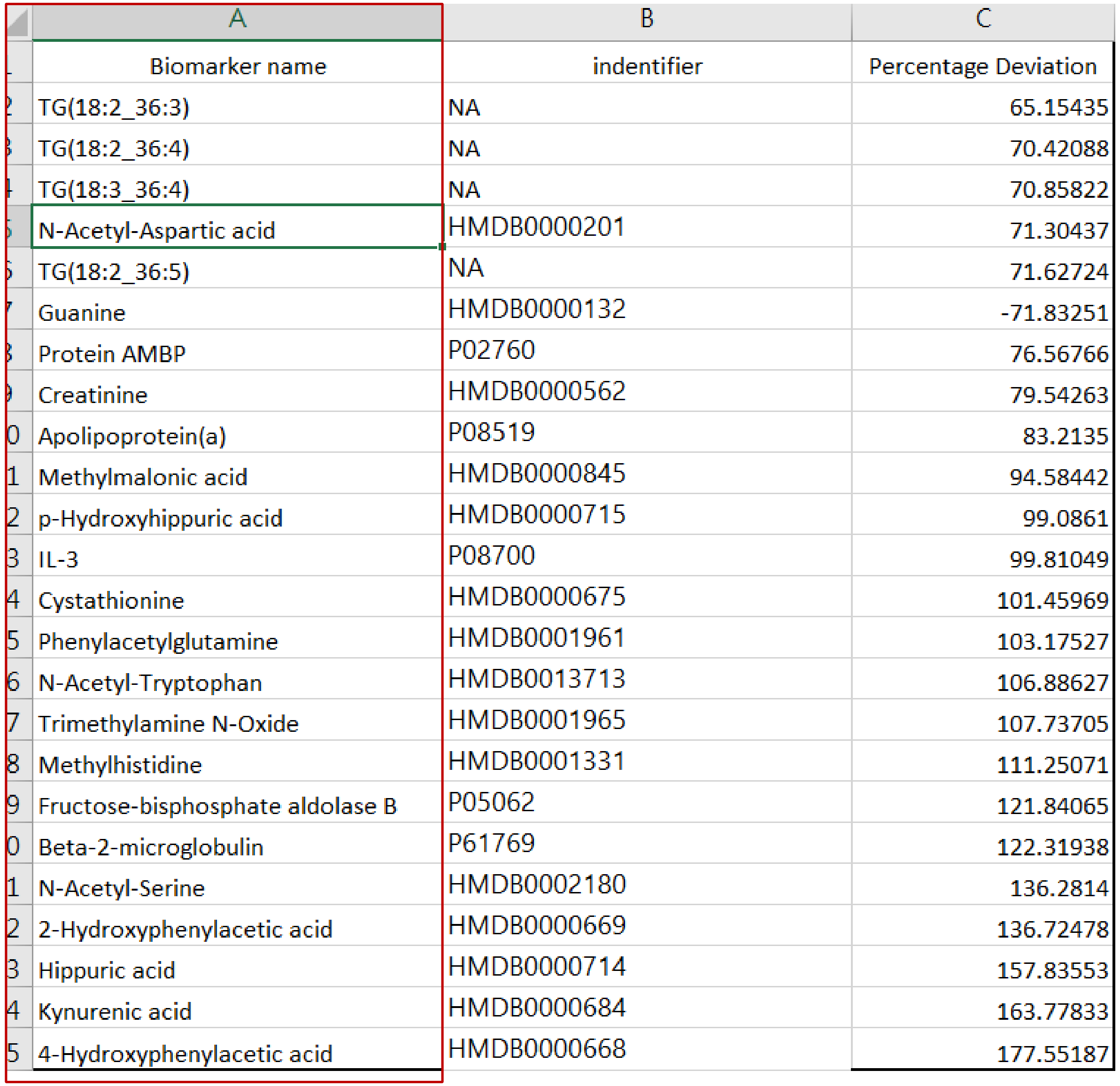
Constructed Gene/Metabolite network

訊聯基因數位

Unsupervised method
Separate COVID19 patients to 3 cluster
Cluster 3 poor status





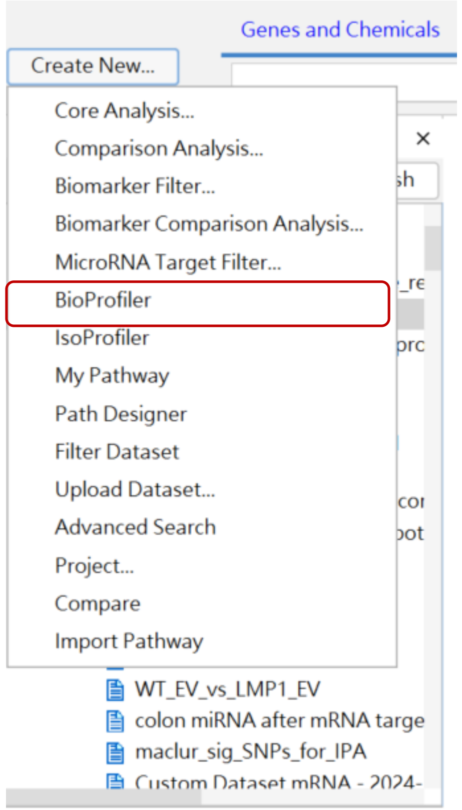
A	B	C
Biomarker name	indentifier	Percentage Deviation
TG(18:2_36:3)	NA	65.15435
TG(18:2_36:4)	NA	70.42088
TG(18:3_36:4)	NA	70.85822
N-Acetyl-Aspartic acid	HMDB0000201	71.30437
TG(18:2_36:5)	NA	71.62724
Guanine	HMDB0000132	-71.83251
Protein AMBP	P02760	76.56766
Creatinine	HMDB0000562	79.54263
Apolipoprotein(a)	P08519	83.2135
Methylmalonic acid	HMDB0000845	94.58442
p-Hydroxyhippuric acid	HMDB0000715	99.0861
IL-3	P08700	99.81049
Cystathionine	HMDB0000675	101.45969
Phenylacetylglutamine	HMDB0001961	103.17527
N-Acetyl-Tryptophan	HMDB0013713	106.88627
Trimethylamine N-Oxide	HMDB0001965	107.73705
Methylhistidine	HMDB0001331	111.25071
Fructose-bisphosphate aldolase B	P05062	121.84065
Beta-2-microglobulin	P61769	122.31938
N-Acetyl-Serine	HMDB0002180	136.2814
2-Hydroxyphenylacetic acid	HMDB0000669	136.72478
Hippuric acid	HMDB0000714	157.83553
Kynurenic acid	HMDB0000684	163.77833
4-Hydroxyphenylacetic acid	HMDB0000668	177.55187

Network

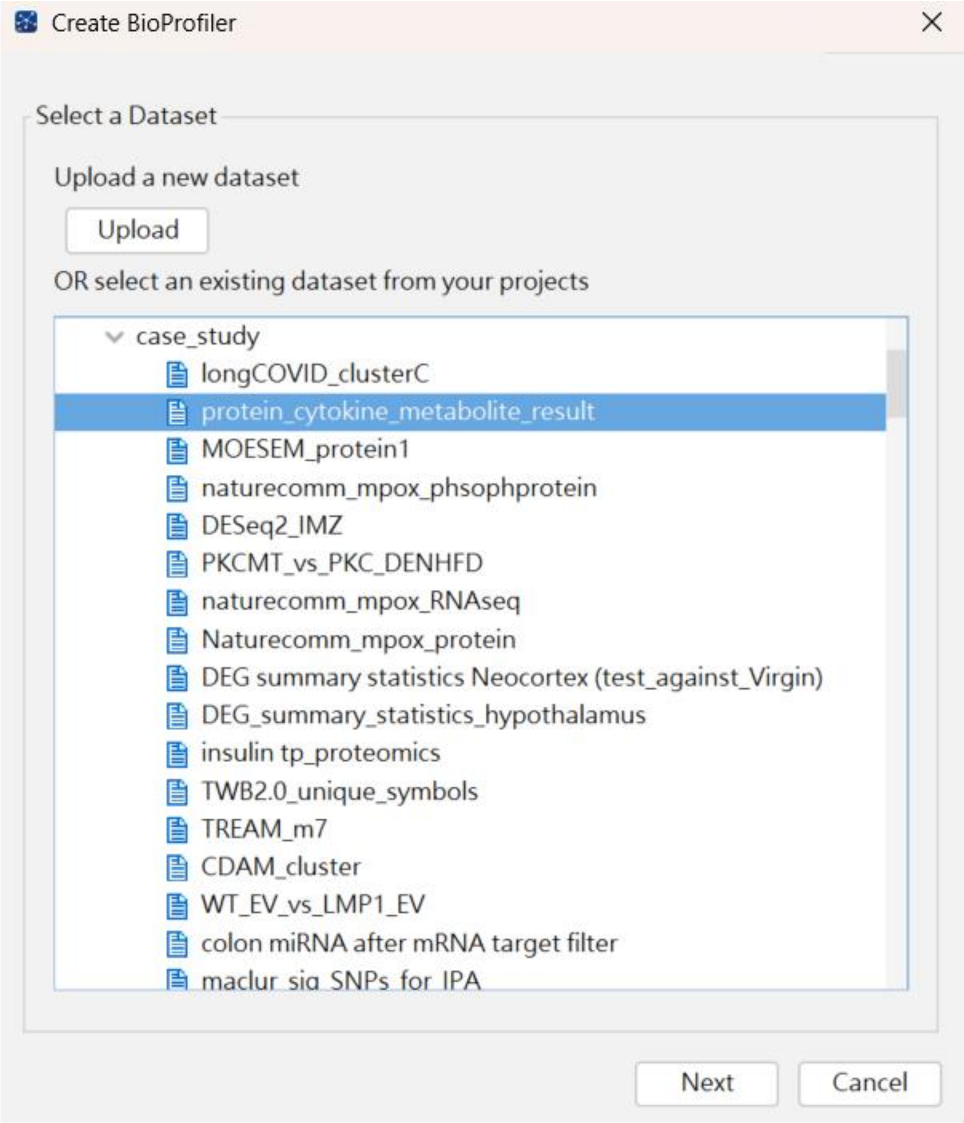
3 step

1. Constructed network
2. Overlap dataset

Bioprofilter



WT_EV_vs_LMP1_EV
colon miRNA after mRNA targe
maclur_sig_SNPs_for_IPA
Custom Dataset mRNA - 2024-



Select a Dataset

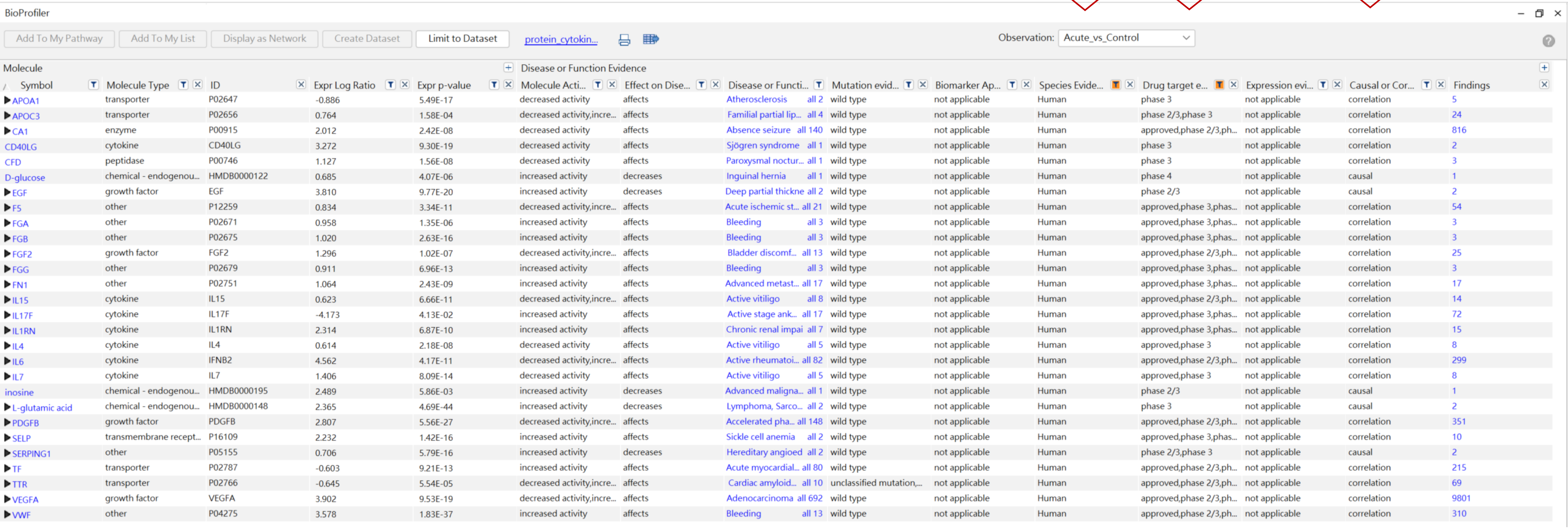
Upload a new dataset

OR select an existing dataset from your projects

- case_study
  - longCOVID_clusterC
  - protein_cytokine_metabolite_result
  - MOESEM_protein1
  - naturecomm_mpox_phsophprotein
  - DESeq2_IMZ
  - PKCMT_vs_PKC_DENHFD
  - naturecomm_mpox_RNAseq
  - Naturecomm_mpox_protein
  - DEG summary statistics Neocortex (test_against_Virgin)
  - DEG_summary_statistics_hypothalamus
  - insulin tp_proteomics
  - TWB2.0_unique_symbols
  - TREAM_m7
  - CDAM_cluster
  - WT_EV_vs_LMP1_EV
  - colon miRNA after mRNA target filter
  - maclur_sig_SNPs_for_IPA

Bioprofilter

Species Drug target Correlation/Causal



Observation: Acute_vs_Control

Molecule					Disease or Function Evidence									
Symbol	Molecule Type	ID	Expr Log Ratio	Expr p-value	Molecule Acti...	Effect on Dise...	Disease or Functi...	Mutation evid...	Biomarker Ap...	Species Evide...	Drug target e...	Expression evi...	Causal or Cor...	Findings
APOA1	transporter	P02647	-0.886	5.49E-17	decreased activity	affects	Atherosclerosis all 2	wild type	not applicable	Human	phase 3	not applicable	correlation	5
APOC3	transporter	P02656	0.764	1.58E-04	decreased activity,incre...	affects	Familial partial lip... all 4	wild type	not applicable	Human	phase 2/3,phase 3	not applicable	correlation	24
CA1	enzyme	P00915	2.012	2.42E-08	decreased activity	affects	Absence seizure all 140	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	816
CD40LG	cytokine	CD40LG	3.272	9.30E-19	decreased activity	affects	Sjögren syndrome all 1	wild type	not applicable	Human	phase 3	not applicable	correlation	2
CFD	peptidase	P00746	1.127	1.56E-08	decreased activity	affects	Paroxysmal noctur... all 1	wild type	not applicable	Human	phase 3	not applicable	correlation	3
D-glucose	chemical - endogenou...	HMDB0000122	0.685	4.07E-06	increased activity	decreases	Inguinal hernia all 1	wild type	not applicable	Human	phase 4	not applicable	causal	1
EGF	growth factor	EGF	3.810	9.77E-20	increased activity	decreases	Deep partial thickne all 2	wild type	not applicable	Human	phase 2/3	not applicable	causal	2
F5	other	P12259	0.834	3.34E-11	decreased activity,incre...	affects	Acute ischemic st... all 21	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	54
FGA	other	P02671	0.958	1.35E-06	increased activity	affects	Bleeding all 3	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	3
FGB	other	P02675	1.020	2.63E-16	increased activity	affects	Bleeding all 3	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	3
FGF2	growth factor	FGF2	1.296	1.02E-07	decreased activity,incre...	affects	Bladder discomf... all 13	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	25
FGG	other	P02679	0.911	6.96E-13	increased activity	affects	Bleeding all 3	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	3
FN1	other	P02751	1.064	2.43E-09	increased activity	affects	Advanced metast... all 17	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	17
IL15	cytokine	IL15	0.623	6.66E-11	decreased activity,incre...	affects	Active vitiligo all 8	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	14
IL17F	cytokine	IL17F	-4.173	4.13E-02	increased activity	affects	Active stage ank... all 17	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	72
IL1RN	cytokine	IL1RN	2.314	6.87E-10	increased activity	affects	Chronic renal impai all 7	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	15
IL4	cytokine	IL4	0.614	2.18E-08	decreased activity	affects	Active vitiligo all 5	wild type	not applicable	Human	approved,phase 3	not applicable	correlation	8
IL6	cytokine	IFNB2	4.562	4.17E-11	decreased activity,incre...	affects	Active rheumatoi... all 82	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	299
IL7	cytokine	IL7	1.406	8.09E-14	decreased activity	affects	Active vitiligo all 5	wild type	not applicable	Human	approved,phase 3	not applicable	correlation	8
inosine	chemical - endogenou...	HMDB0000195	2.489	5.86E-03	increased activity	decreases	Advanced maligna... all 1	wild type	not applicable	Human	phase 2/3	not applicable	causal	1
L-glutamic acid	chemical - endogenou...	HMDB0000148	2.365	4.69E-44	increased activity	decreases	Lymphoma, Sarco... all 2	wild type	not applicable	Human	phase 3	not applicable	causal	2
PDGFB	growth factor	PDGFB	2.807	5.56E-27	decreased activity,incre...	affects	Accelerated pha... all 148	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	351
SELP	transmembrane recept...	P16109	2.232	1.42E-16	increased activity	affects	Sickle cell anemia all 2	wild type	not applicable	Human	approved,phase 3,phas...	not applicable	correlation	10
SERPING1	other	P05155	0.706	5.79E-16	increased activity	decreases	Hereditary angioed all 2	wild type	not applicable	Human	phase 2/3,phase 3	not applicable	causal	2
TF	transporter	P02787	-0.603	9.21E-13	increased activity	affects	Acute myocardial... all 80	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	215
TTR	transporter	P02766	-0.645	5.54E-05	decreased activity,incre...	affects	Cardiac amyloid... all 10	unclassified mutation,...	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	69
VEGFA	growth factor	VEGFA	3.902	9.53E-19	decreased activity,incre...	affects	Adenocarcinoma all 692	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	9801
VWF	other	P04275	3.578	1.83E-37	increased activity	affects	Bleeding all 13	wild type	not applicable	Human	approved,phase 2/3,ph...	not applicable	correlation	310

Create New

↓

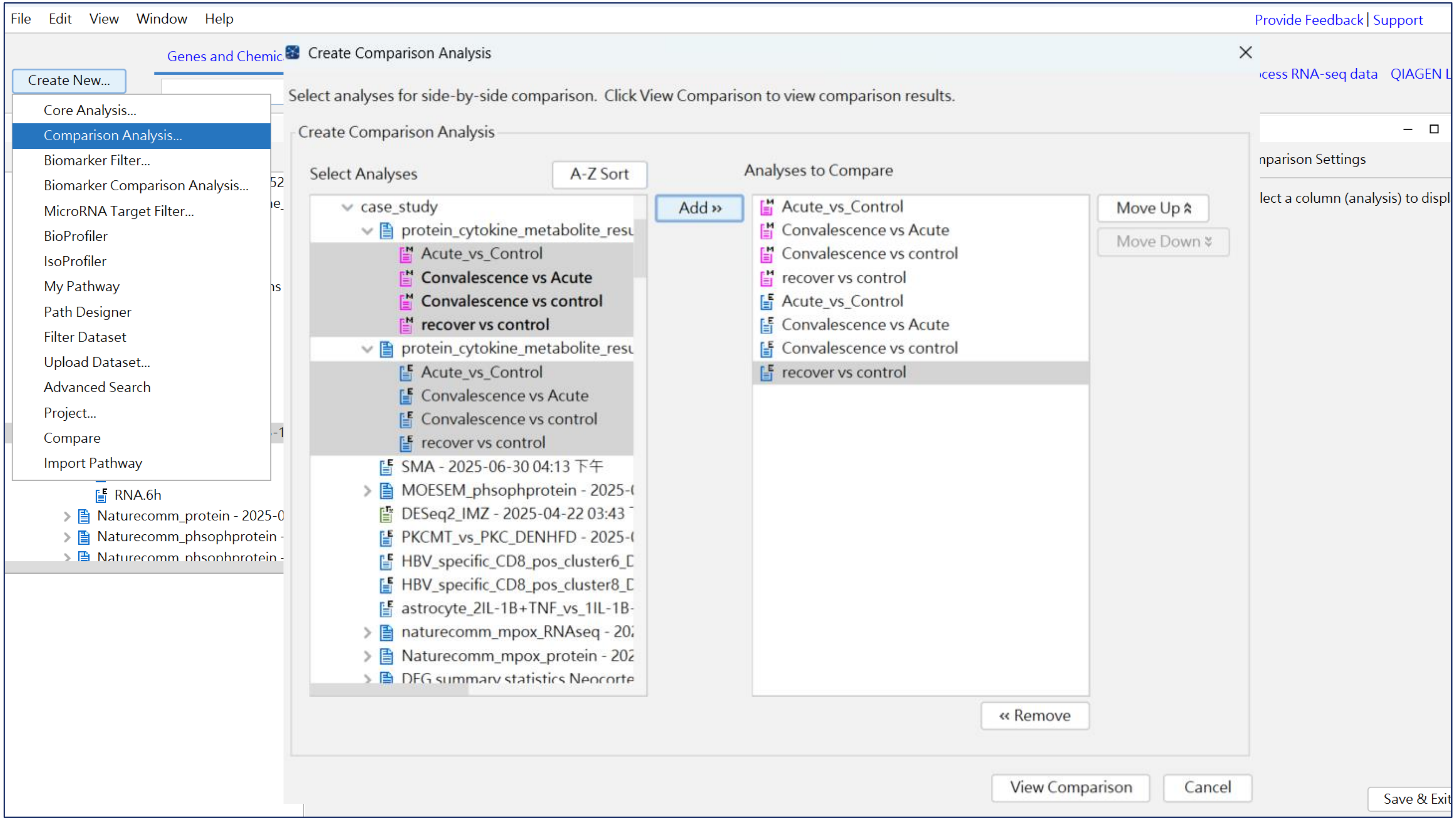
Comparison analysis

↓

View comparison

↓

Save and exit



Select analyses for side-by-side comparison. Click View Comparison to view comparison results.

Create Comparison Analysis

Select Analyses

- case_study
  - protein_cytokine_metabolite_resu
    - Acute_vs_Control
    - **Convalescence vs Acute**
    - **Convalescence vs control**
    - **recover vs control**
  - protein_cytokine_metabolite_resu
    - Acute_vs_Control
    - Convalescence vs Acute
    - Convalescence vs control
    - recover vs control
  - SMA - 2025-06-30 04:13 下午
  - MOESEM_phsophprotein - 2025-(
  - DESeq2_IMZ - 2025-04-22 03:43
  - PKCMT_vs_PKC_DENHFD - 2025-(
  - HBV_specific_CD8_pos_cluster6_D
  - HBV_specific_CD8_pos_cluster8_D
  - astrocyte_2IL-1B+TNF_vs_1IL-1B-
  - naturecomm_mpox_RNAseq - 202
  - Naturecomm_mpox_protein - 202
  - DEG summary statistics Neocorte

Analyses to Compare

- Acute_vs_Control
- Convalescence vs Acute
- Convalescence vs control
- recover vs control
- Acute_vs_Control
- Convalescence vs Acute
- Convalescence vs control
- recover vs control

Canonical pathway comparison

Measurement: Activation z-score -2.828 3.742

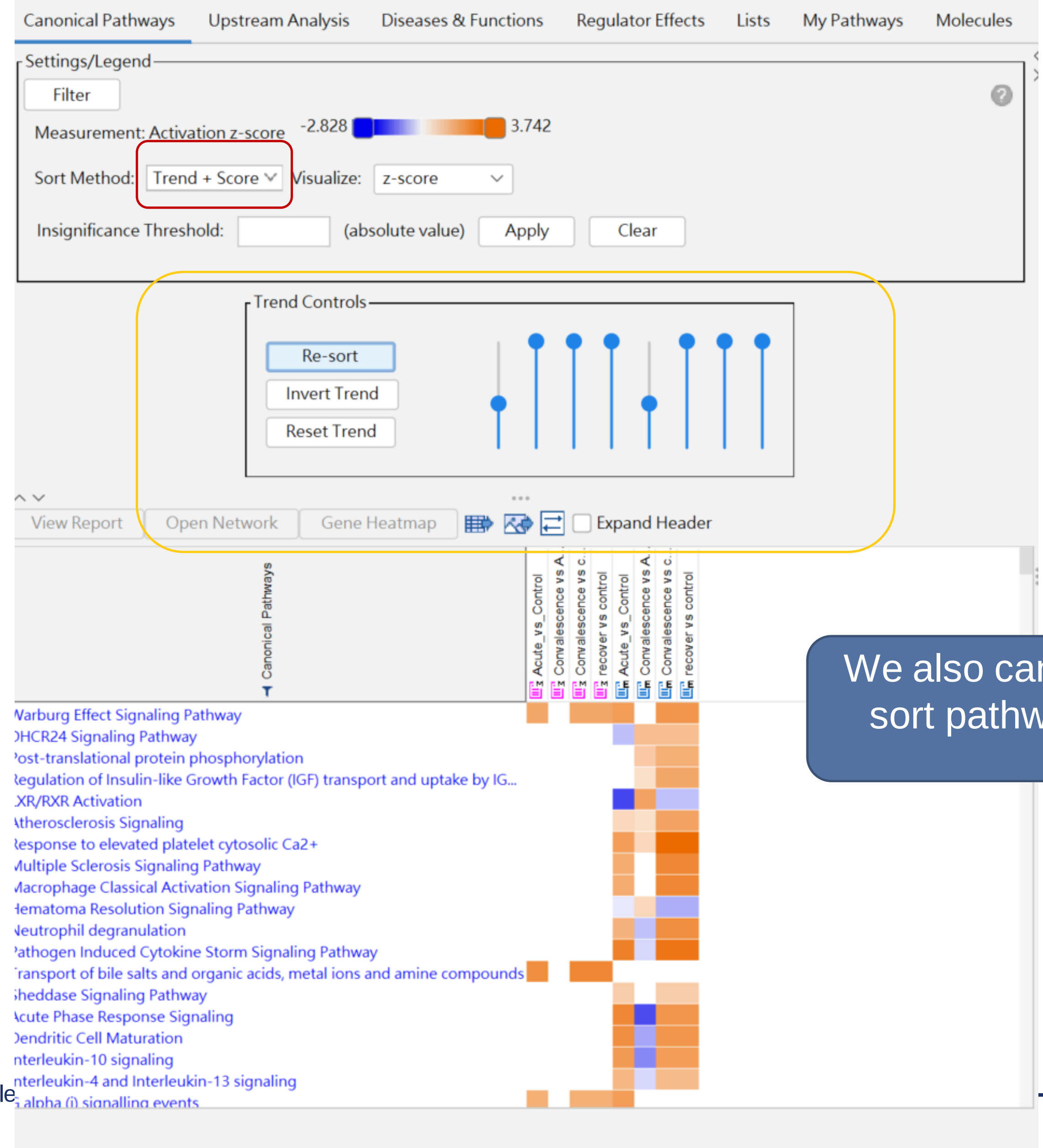
Sort Method: Score Visualize: z-score

Insignificance Threshold: (absolute value)

☐ Expand Header

Warburg Effect Signaling Pathway
Wound Healing Signaling Pathway
Response to elevated platelet cytosolic Ca2+
Pathogen Induced Cytokine Storm Signaling Pathway
Acute Phase Response Signaling
RAF/MAP kinase cascade
Tumor Microenvironment Pathway
Transport of inorganic cations/anions and amino acids/oligopeptides
Dendritic Cell Maturation
Cachexia Signaling Pathway
Pulmonary Fibrosis Idiopathic Signaling Pathway
Transport of bile salts and organic acids, metal ions and amine compounds
Communication between Innate and Adaptive Immune Cells
Interleukin-10 signaling
IL-17 Signaling
Role of Tissue Factor in Cancer
G alpha (i) signalling events
Irritable Bowel Syndrome Signaling Pathway
Glycation Signaling Pathway
Neutrophil degranulation
Hepatic Cholestasis
Hepatic Fibrosis Signaling Pathway
Autism Signaling Pathway
Multiple Sclerosis Signaling Pathway
Macrophage Classical Activation Signaling Pathway
Role of Osteoblasts in Rheumatoid Arthritis Signaling Pathway
Serotonin Receptor Signaling
Proteasomal PSMD10 Signaling Pathway

Filtered canonical pathway



Settings/Legend

Measurement: Activation z-score -2.828 3.742

Sort Method: Trend + Score Visualize: z-score

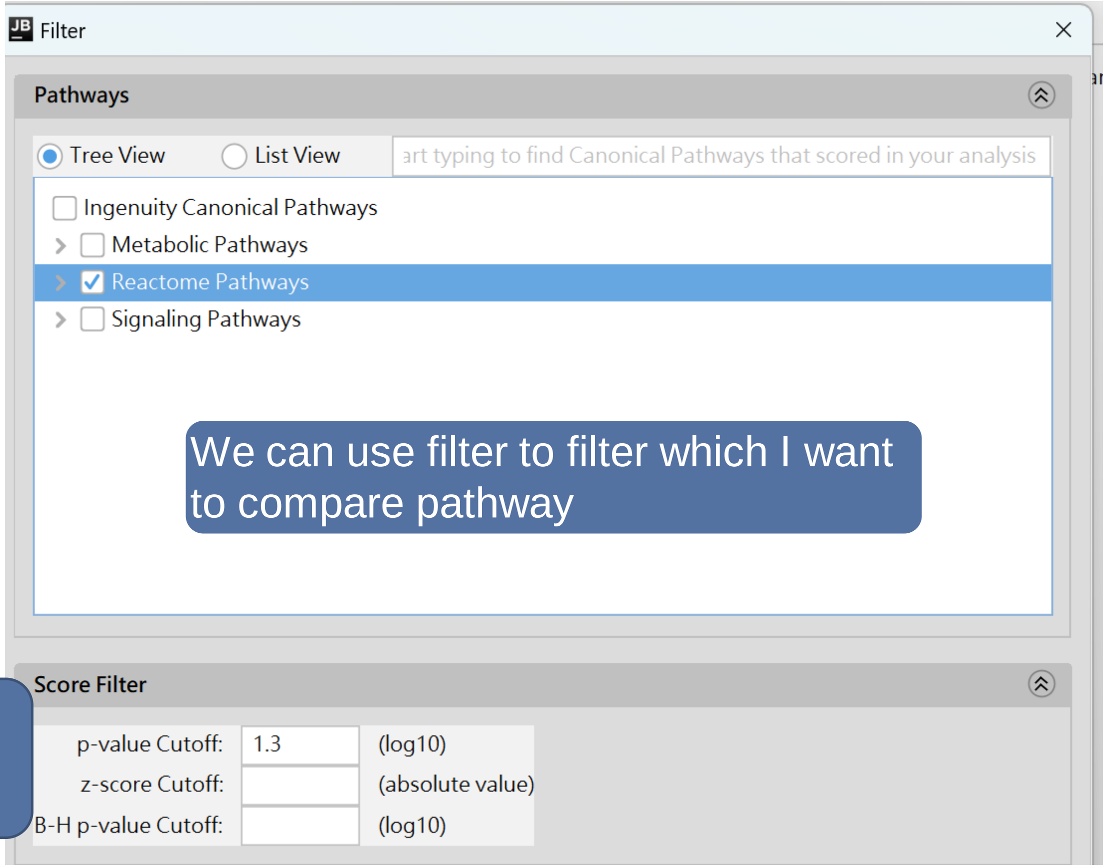
Insignificance Threshold: (absolute value) Apply Clear

Trend Controls

☐ Expand Header

Varburg Effect Signaling Pathway
)HCR24 Signaling Pathway
'ost-translational protein phosphorylation
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by IG...
XR/RXR Activation
Atherosclerosis Signaling
Response to elevated platelet cytosolic Ca2+
Multiple Sclerosis Signaling Pathway
Macrophage Classical Activation Signaling Pathway
Hematoma Resolution Signaling Pathway
Neutrophil degranulation
Pathogen Induced Cytokine Storm Signaling Pathway
Transport of bile salts and organic acids, metal ions and amine compounds
Sheddase Signaling Pathway
Acute Phase Response Signaling
Dendritic Cell Maturation
nterleukin-10 signaling
nterleukin-4 and Interleukin-13 signaling
alpha (i) signalling events

We also can re-sort pathway



Filter

Pathways

● Tree View ○ List View art typing to find Canonical Pathways that scored in your analysis

- ☐ Ingenuity Canonical Pathways
- ☐ Metabolic Pathways
- ☑ Reactome Pathways
- ☐ Signaling Pathways

We can use filter to filter which I want to compare pathway

Score Filter

p-value Cutoff: 1.3 (log10)

z-score Cutoff: (absolute value)

B-H p-value Cutoff: (log10)

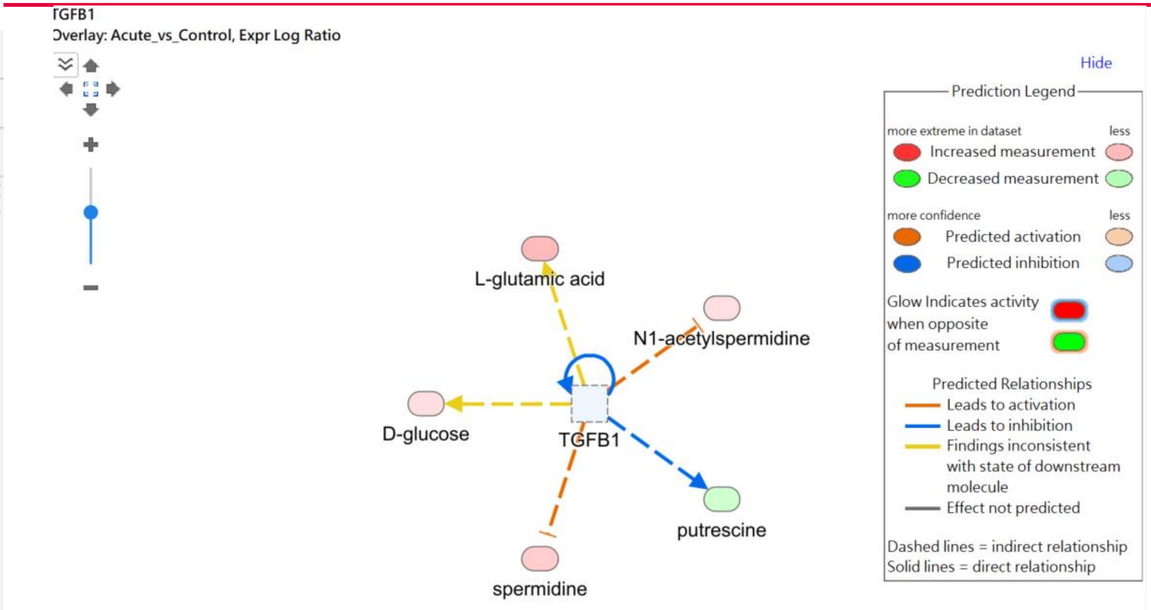
Upstream regulator comparison

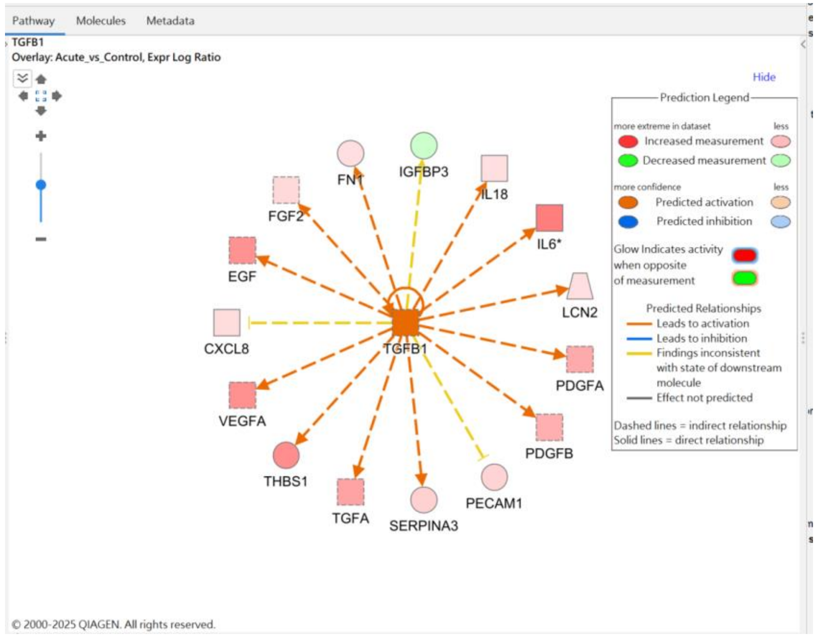
Measurement: Activation z-score -2.627 3.802

Sort Method: Trend + Score

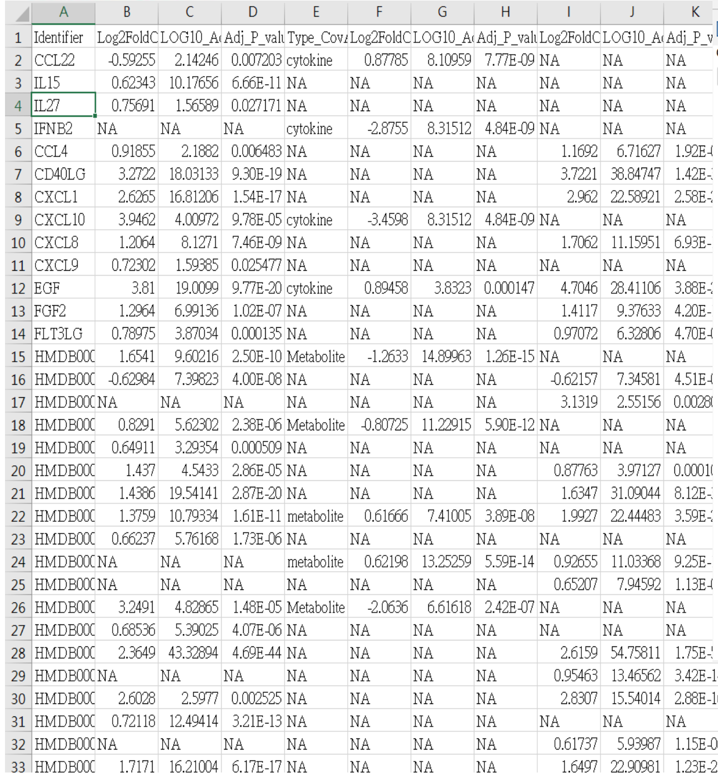
Visualize: z-score

Insignificance Threshold: ☐ (absolute value) Apply Clear

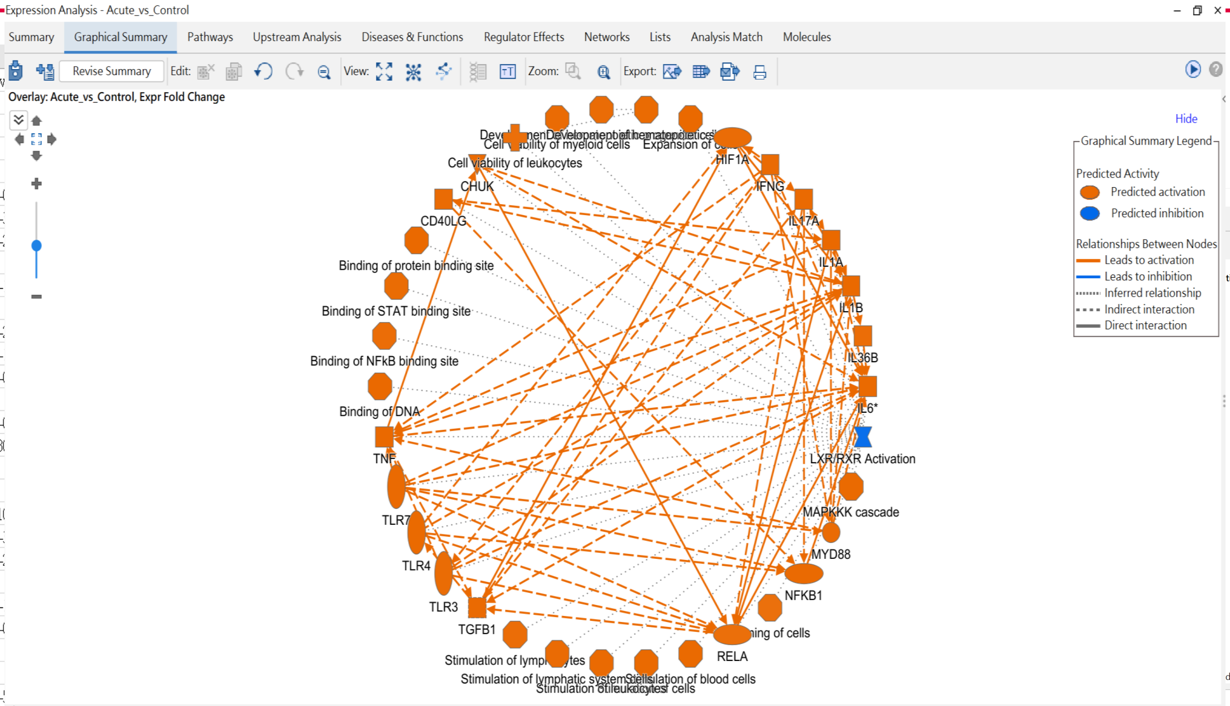




Summary: Evaluating your ’omics data using IPA

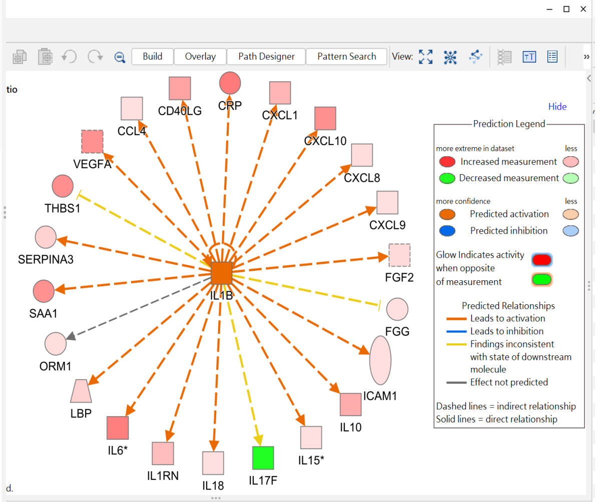


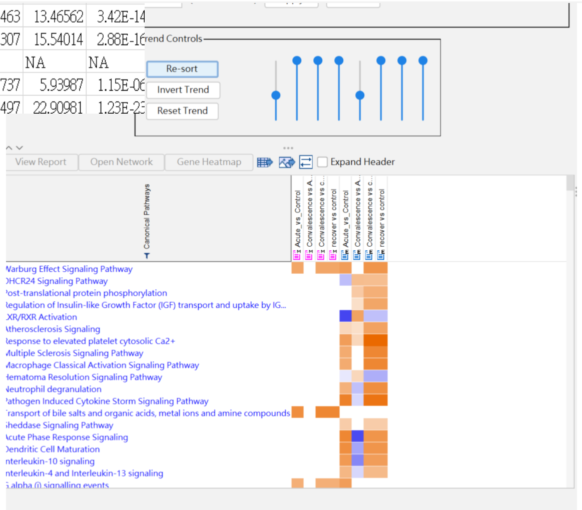
	A	B	C	D	E	F	G	H	I	J	K			
1	Identifier	Log2FoldC	LOG10_A	Adj_P_valu	Type_Cov	Log2FoldC	LOG10_A	Adj_P_valu	Log2FoldC	LOG10_A	Adj_P_v			
2	CCL22	-0.59255	2.14246	0.007203	cytokine	0.87785	8.10959	7.77E-09	NA	NA	NA			
3	IL15	0.62343	10.17656	6.66E-11	NA	NA	NA	NA	NA	NA	NA			
4	IL27	0.75691	1.56589	0.027171	NA	NA	NA	NA	NA	NA	NA			
5	IFNB2	NA	NA	NA	cytokine	-2.8755	8.31512	4.84E-09	NA	NA	NA			
6	CCL4	0.91855	2.1882	0.006483	NA	NA	NA	NA	1.1692	6.71627	1.92E-			
7	CD40LG	3.2722	18.03133	9.30E-19	NA	NA	NA	NA	3.7221	38.84747	1.42E-			
8	CXCL1	2.6265	16.81206	1.54E-17	NA	NA	NA	NA	2.962	22.58921	2.58E-			
9	CXCL10	3.9462	4.00972	9.78E-05	cytokine	-3.4598	8.31512	4.84E-09	NA	NA	NA			
10	CXCL8	1.2064	8.1271	7.46E-09	NA	NA	NA	NA	1.7062	11.15951	6.93E-			
11	CXCL9	0.72302	1.59385	0.025477	NA	NA	NA	NA	NA	NA	NA			
12	EGF	3.81	19.0099	9.77E-20	cytokine	0.89458	3.8323	0.000147	4.7046	28.41106	3.88E-			
13	FGF2	1.2964	6.99136	1.02E-07	NA	NA	NA	NA	1.4117	9.37633	4.20E-			
14	FLT3LG	0.78975	3.87034	0.000135	NA	NA	NA	NA	0.97072	6.32806	4.70E-			
15	HMDB000	1.6541	9.60216	2.50E-10	Metabolite	-1.2633	14.89963	1.26E-15	NA	NA	NA			
16	HMDB000	-0.62984	7.39823	4.00E-08	NA	NA	NA	NA	-0.62157	7.34581	4.51E-			
17	HMDB000	NA	NA	NA	NA	NA	NA	NA	3.1319	2.55156	0.0028			
18	HMDB000	0.8291	5.62302	2.38E-06	Metabolite	-0.80725	11.22915	5.90E-12	NA	NA	NA			
19	HMDB000	0.64911	3.29354	0.000509	NA	NA	NA	NA	NA	NA	NA			
20	HMDB000	1.437	4.5433	2.86E-05	NA	NA	NA	NA	0.87763	3.97127	0.0001			
21	HMDB000	1.4386	19.54141	2.87E-20	NA	NA	NA	NA	1.6347	31.09044	8.12E-			
22	HMDB000	1.3759	10.79334	1.61E-11	metabolite	0.61666	7.41005	3.89E-08	1.9927	22.44483	3.59E-			
23	HMDB000	0.66237	5.76168	1.73E-06	NA	NA	NA	NA	NA	NA	NA			
24	HMDB000	NA	NA	NA	metabolite	0.62198	13.25259	5.59E-14	0.92655	11.03368	9.25E-			
25	HMDB000	NA	NA	NA	NA	NA	NA	NA	0.65207	7.94592	1.13E-			
26	HMDB000	3.2491	4.82865	1.48E-05	Metabolite	-2.0636	6.61618	2.42E-07	NA	NA	NA			
27	HMDB000	0.68536	5.39025	4.07E-06	NA	NA	NA	NA	NA	NA	NA			
28	HMDB000	2.3649	43.32894	4.69E-44	NA	NA	NA	NA	2.6159	54.75811	1.75E-			
29	HMDB000	NA	NA	NA	NA	NA	NA	NA	0.95463	13.46562	3.42E-14	0.95463	13.46562	3.42E-14
30	HMDB000	2.6028	2.5977	0.002525	NA	NA	NA	NA	2.8307	15.54014	2.88E-16	2.8307	15.54014	2.88E-1
31	HMDB000	0.72118	12.49414	3.21E-13	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
32	HMDB000	NA	NA	NA	NA	NA	NA	NA	0.61737	5.93987	1.15E-06	0.61737	5.93987	1.15E-0
33	HMDB000	1.7171	16.21004	6.17E-17	NA	NA	NA	NA	1.6497	22.90981	1.23E-23	1.6497	22.90981	1.23E-2



Expression Analysis - Acute_vs_Control

Overlay: Acute_vs_Control, Expr Fold Change





Warburg Effect Signaling Pathway
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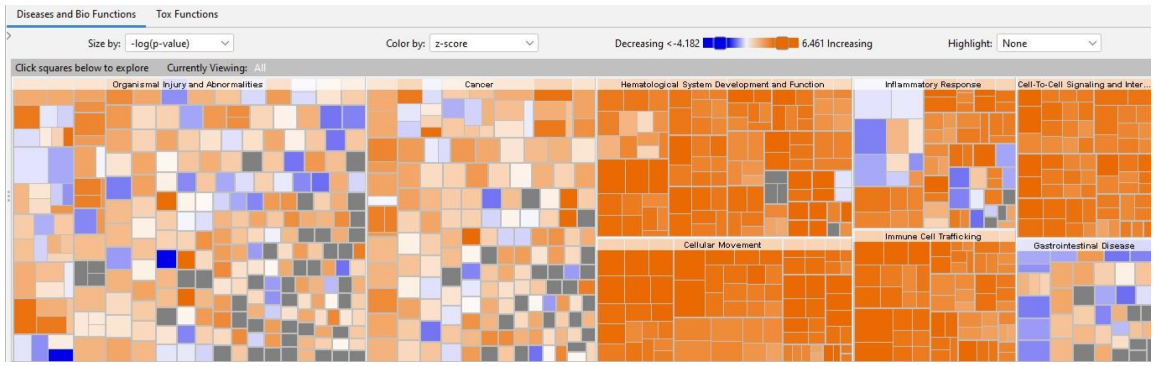
alpha (i) signalling events



Size by: -log(p-value)

Color by: z-score

Decreasing <-4.182 … 6.461 Increasing

Highlight: None

Click squares below to explore Currently Viewing: All

- Data upload and analysis setup
- Canonical pathways
- Upstream regulators
- Diseases and functions
- Comparison analysis

Better Care with Better Knowledge

若有需要進一步的資訊或在使用軟體上遇到問題歡迎聯繫以下窗口:
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Bioinfo@GGA.ASIA