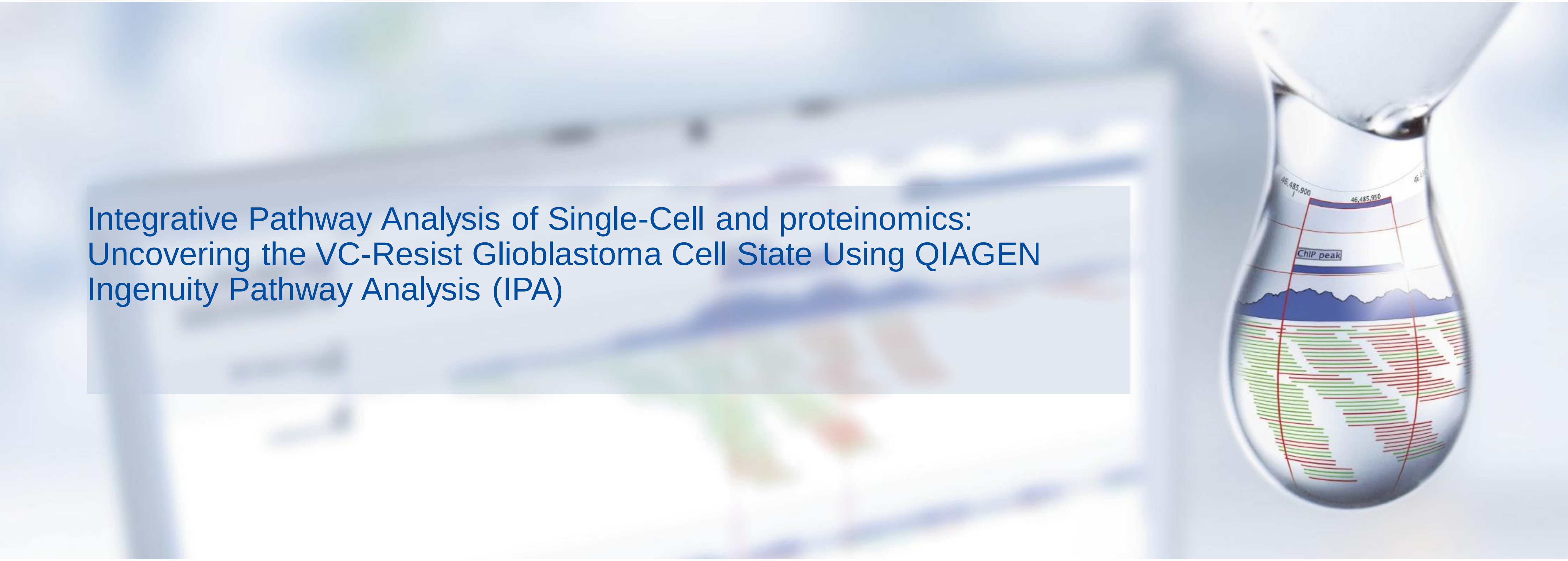
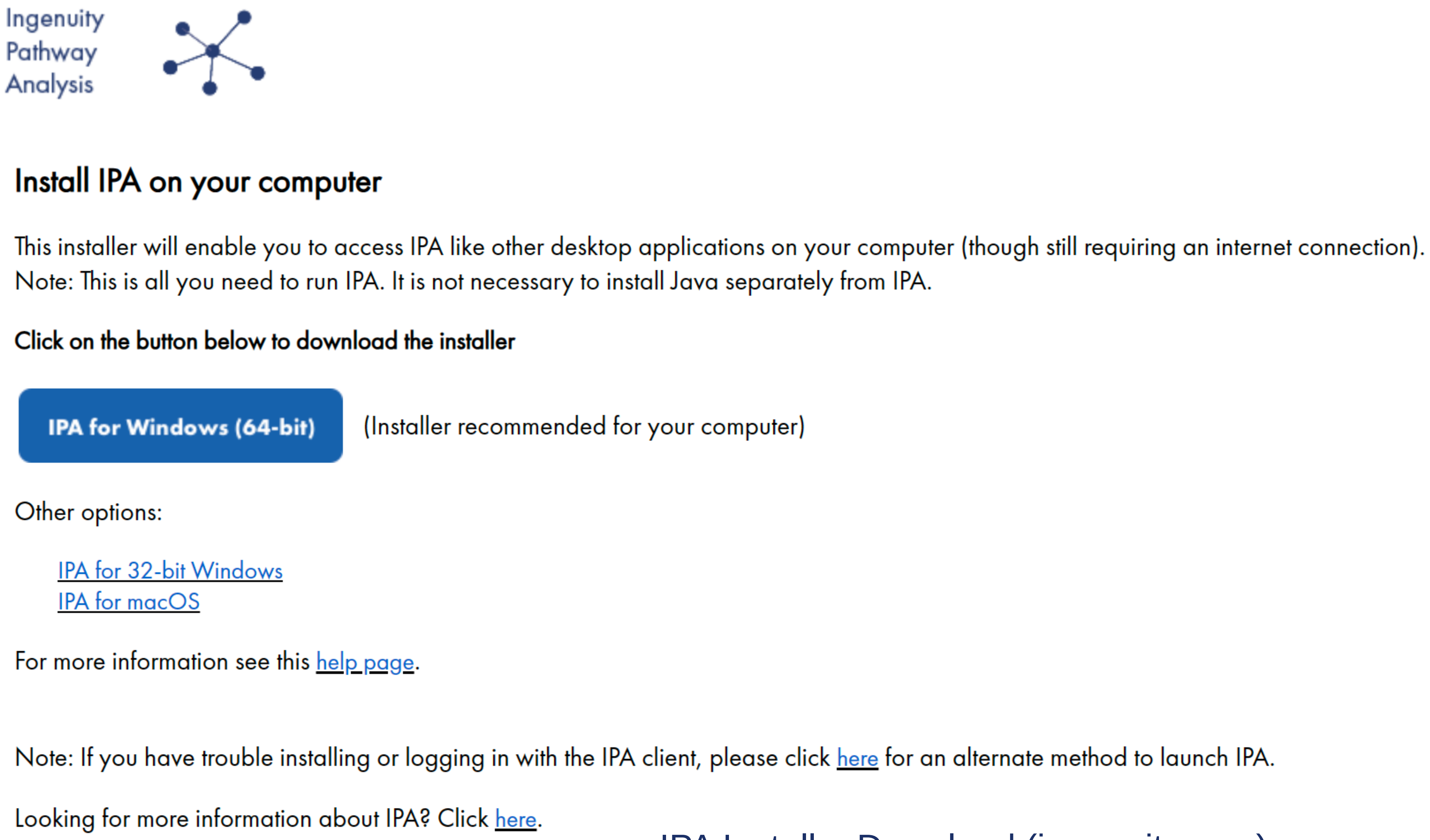


Integrative Pathway Analysis of Single-Cell and proteinomics: Uncovering the VC-Resist Glioblastoma Cell State Using QIAGEN Ingenuity Pathway Analysis (IPA)

Christine Hsiung 熊嘉妮 專案副理

HsinYi Huang 黃馨誼 專案副理 Bioinfo@GGA.ASIA

Choose your IPA installer



Ingenuity
Pathway
Analysis

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

IPA for Windows (64-bit) (Installer recommended for your computer)

Other options:

- IPA for 32-bit Windows
- IPA for macOS

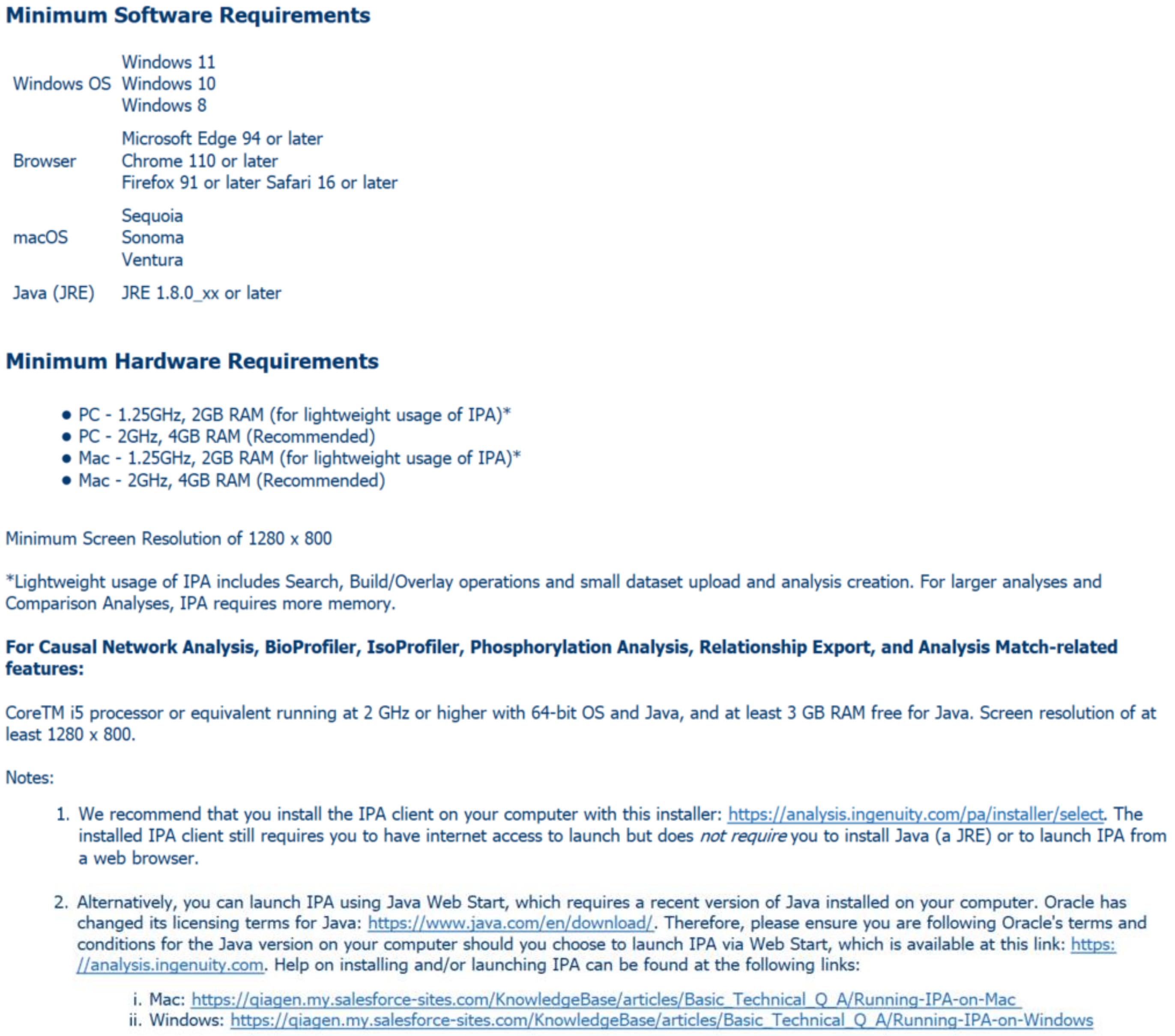
For more information see this help page.

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 and path designer

Machine Learning pathway

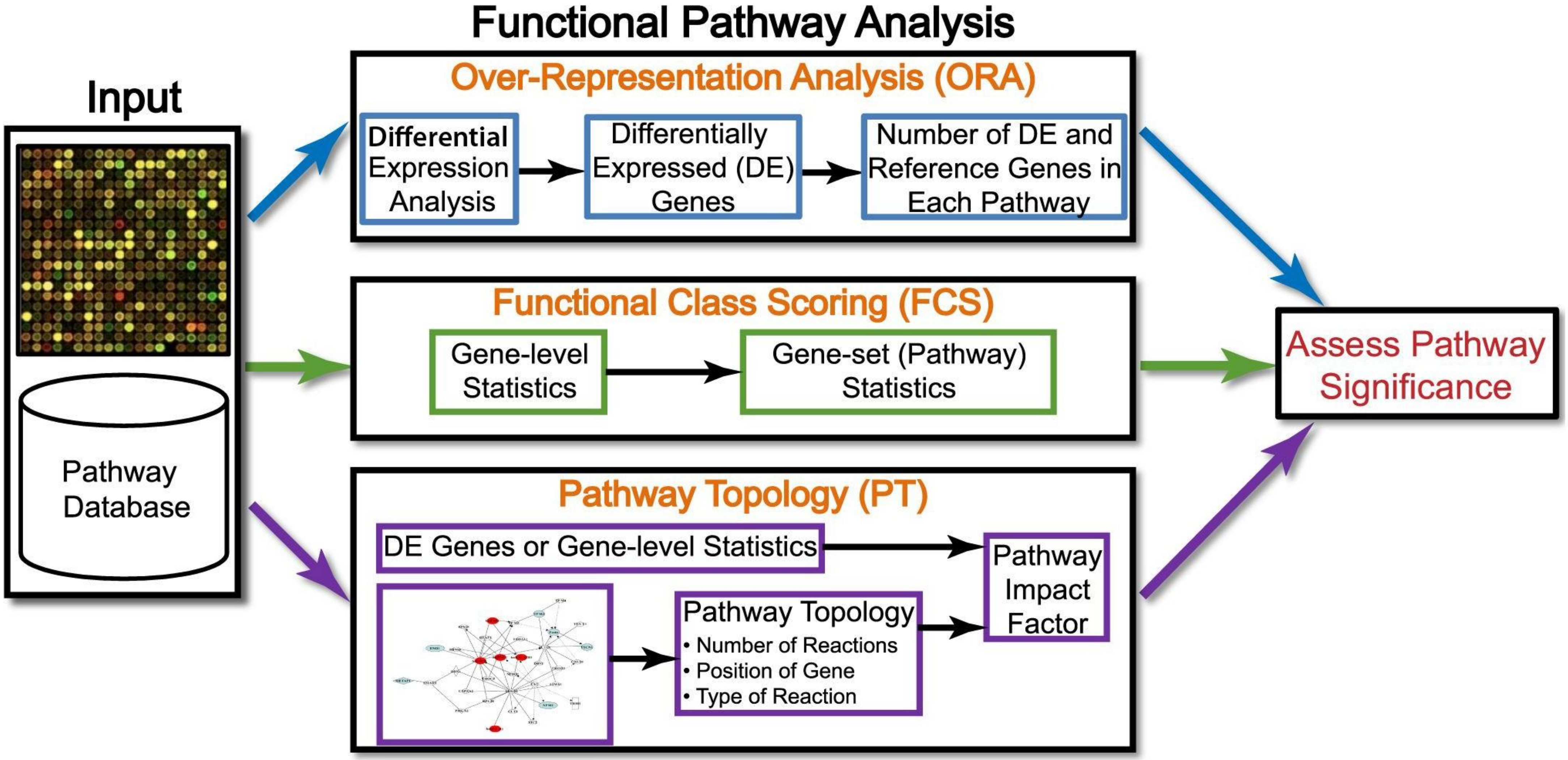
Interpreting your data using IPA

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

Comparison analysis and compare analysis

Summary

Introduction of pathway analysis



Functional Pathway Analysis

Input

Pathway Database

Over-Representation Analysis (ORA)

Differential Expression Analysis → Differentially Expressed (DE) Genes → Number of DE and Reference Genes in Each Pathway

Functional Class Scoring (FCS)

Gene-level Statistics → Gene-set (Pathway) Statistics

Pathway Topology (PT)

DE Genes or Gene-level Statistics → Pathway Impact Factor

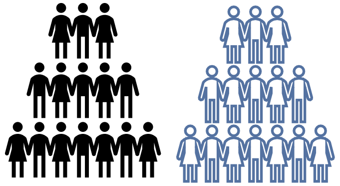
Pathway Topology
- Number of Reactions
- Position of Gene
- Type of Reaction

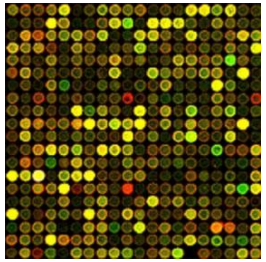
Assess Pathway Significance

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

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

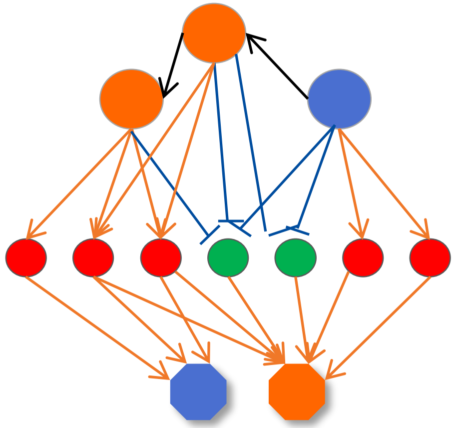
Function

Network

ORA/FCS/Topology Pathway Analysis

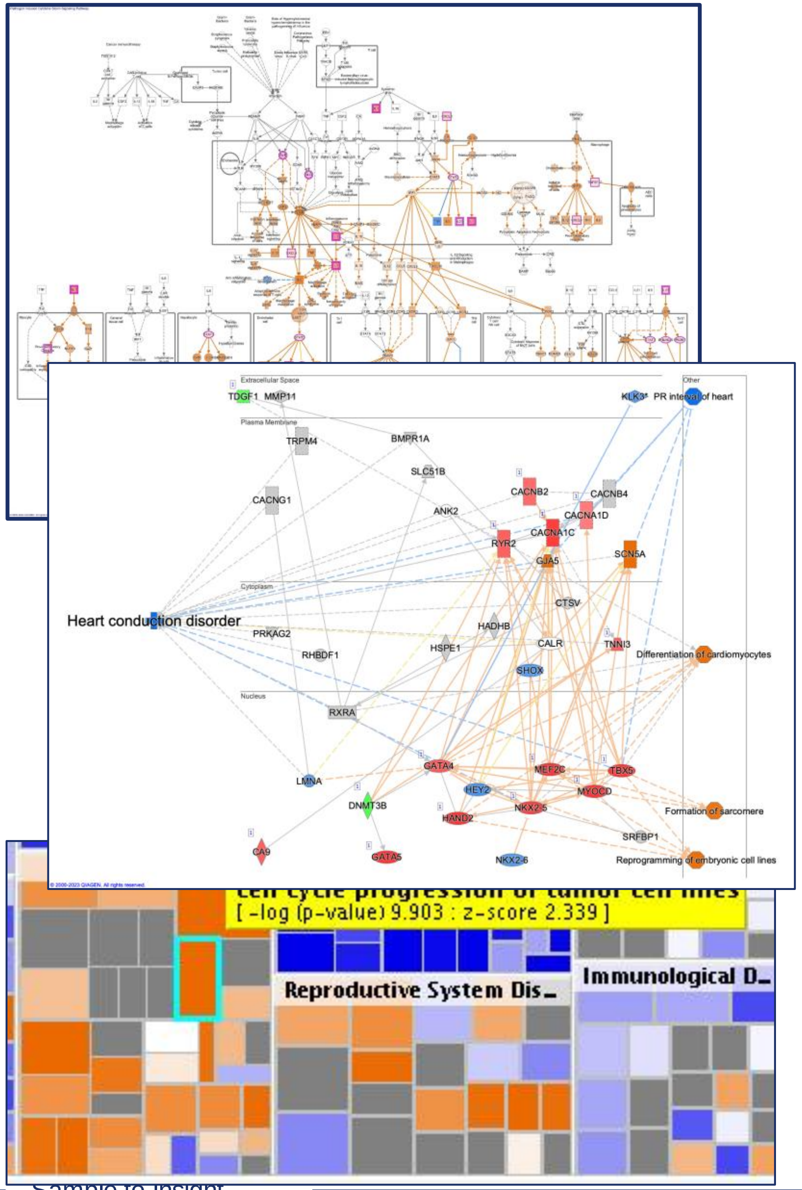
Machine learning

What do they relate to each other?

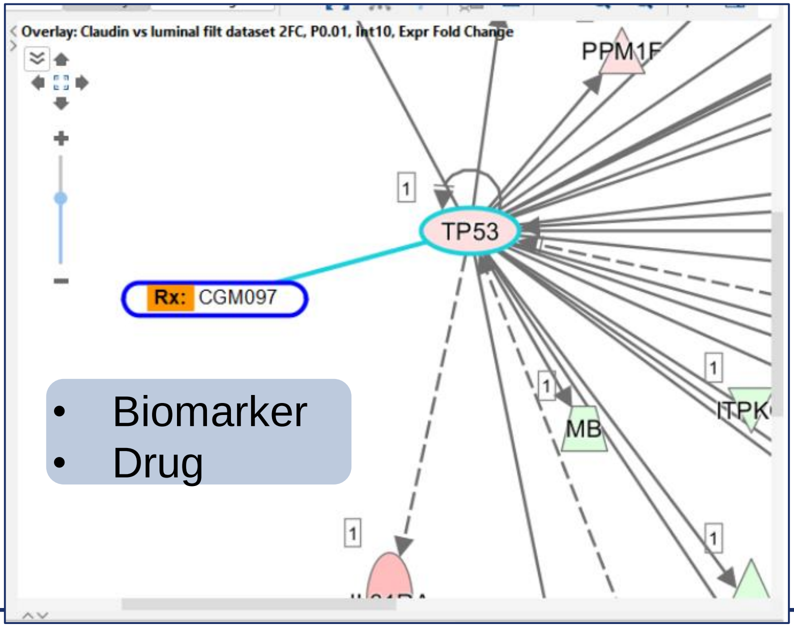


What are the relationship between each molecules?

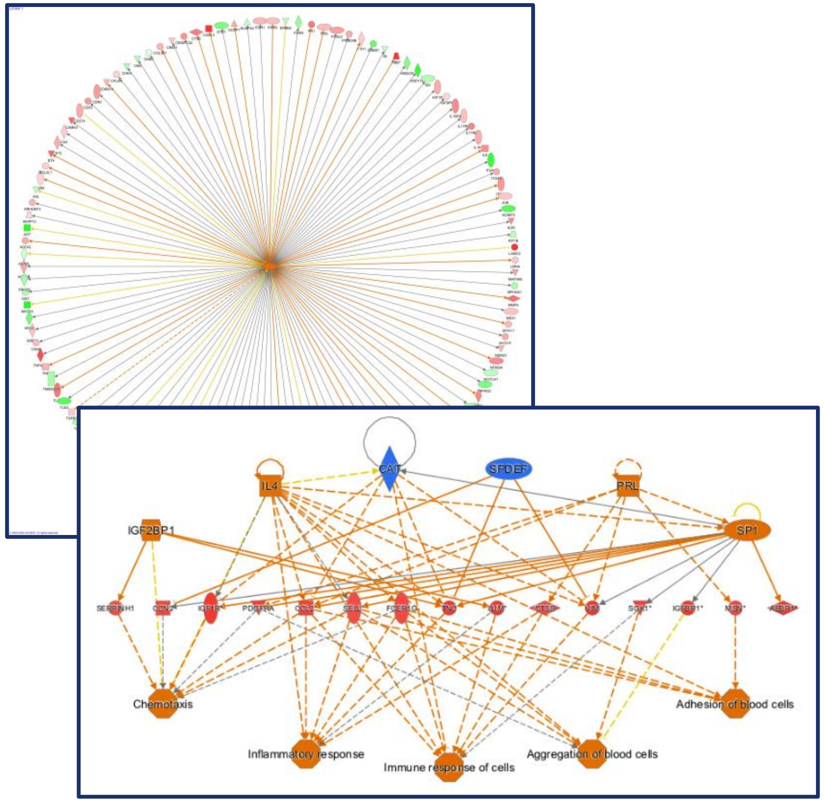
What Can We Achieve with IPA?

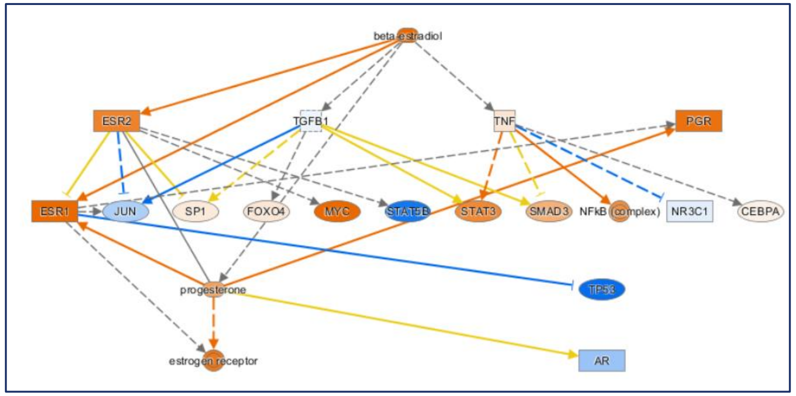


1. Canonical pathway
2. Machine Learning disease pathway
3. Disease and function
4. Upstream regulator
5. Regulate effect
6. Network


Overlay: Claudin vs luminal filt dataset 2FC, P0.01, Int10, Expr Fold Change

- Biomarker
- Drug





Publication using Qiagen Ingenuity Pathway Analysis

訊聯基因數位

From 2019-2025
2,127literatures

> 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

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

"ingenuity pathway analysis"

Search

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1,738 results Page 1 of 174

RESULTS BY YEAR

TEXT AVAILABILITY

☐ Clinical Trial
☐ Meta-Analysis
☐ Randomized Controlled Trial
☐ Review
☐ Systematic Review

☐ 1 Cite Share

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 Cite Share

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 Cite Share

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. ...

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

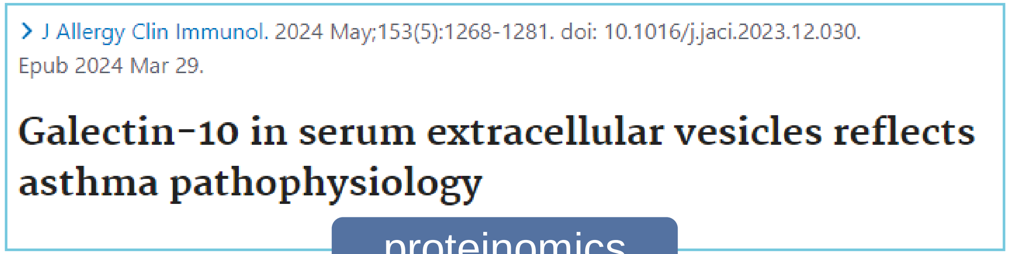
Deletion of Slc9a1 in Cx3cr1$^+$ cells stimulated microglial subcluster CREB1 signaling and microglia-oligodendrocyte crosstalk

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

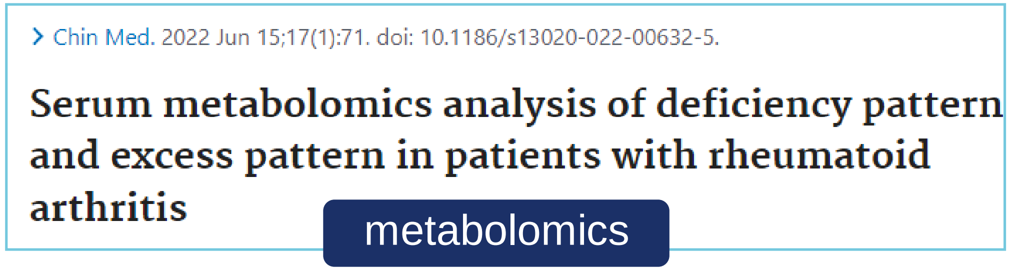
Single-cell RNA-seq



> 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

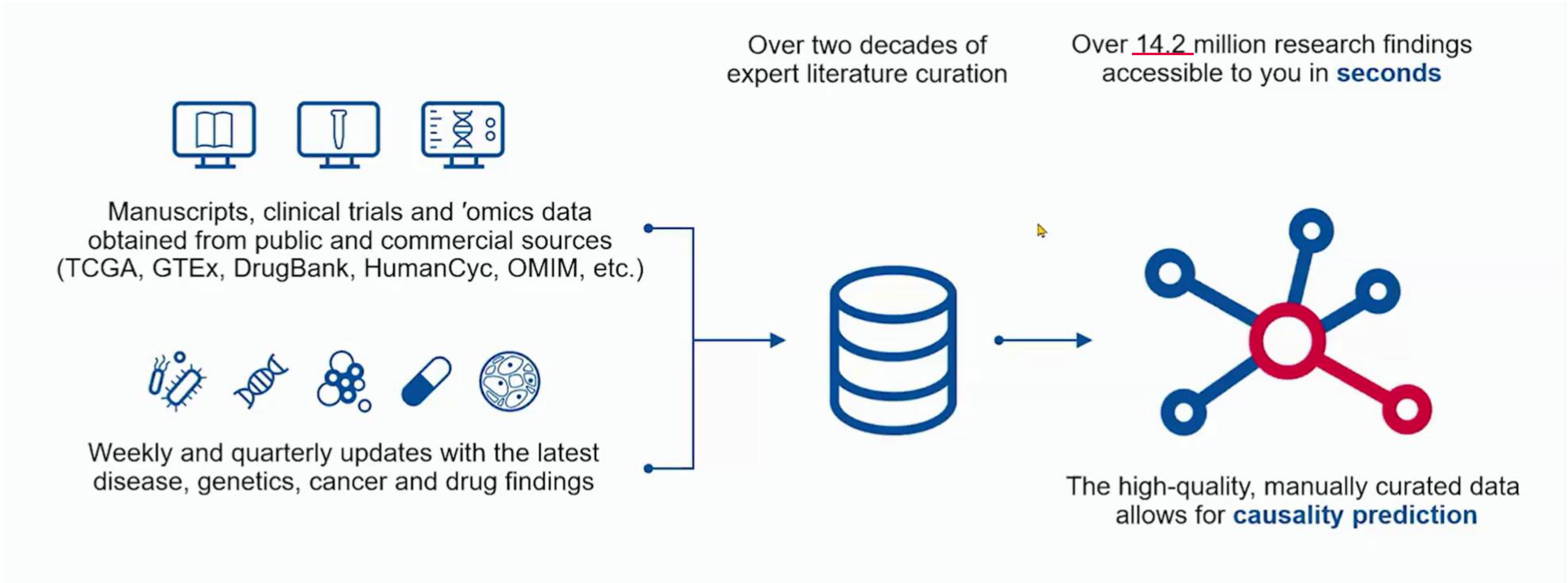


> Chin Med. 2022 Jun 15;17(1):71. doi: 10.1186/s13020-022-00632-5.

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

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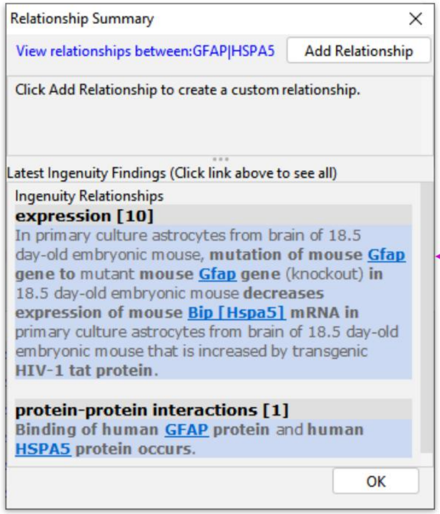
The high-quality, manually curated data allows for **causality prediction**

Every connection in IPA is backed by literature findings



Relationship Summary

View relationships between:GFAP|HSPA5 | Add Relationship

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

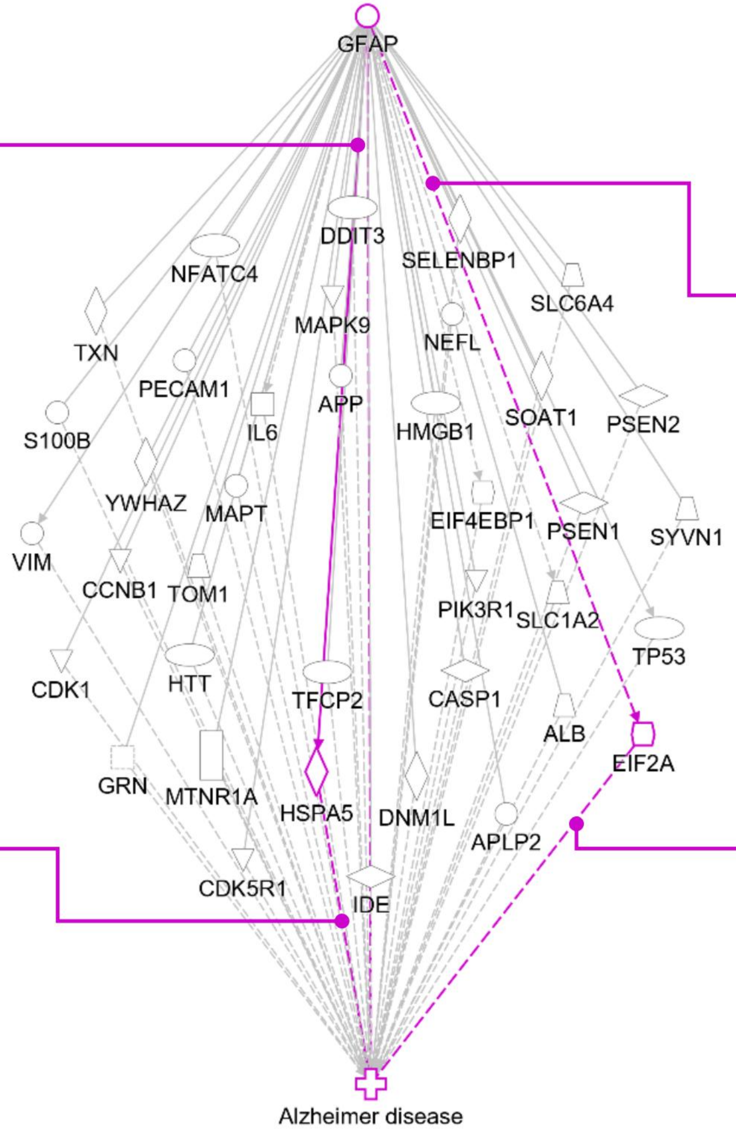
expression [10]

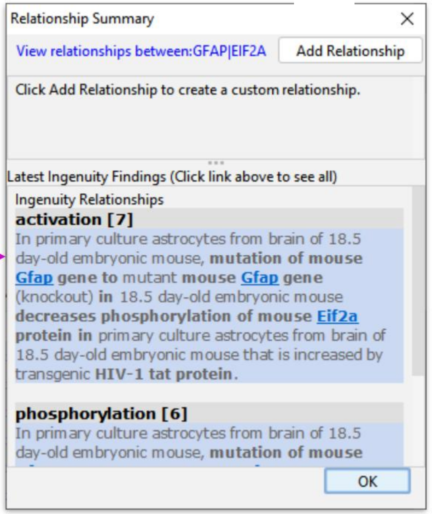
In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse Gfap gene to mutant mouse Gfap gene** (knockout) **in** 18.5 day-old embryonic mouse **decreases expression of mouse Bip [Hspa5] mRNA in** primary culture astrocytes from brain of 18.5 day-old embryonic mouse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

protein-protein interactions [1]

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

OK





Relationship Summary

View relationships between:GFAP|EIF2A | Add Relationship

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

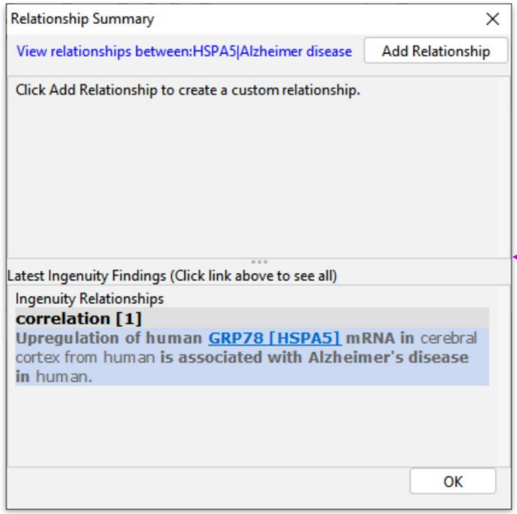
activation [7]

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**

OK



Relationship Summary

View relationships between:HSPA5|Alzheimer disease | Add Relationship

Click Add Relationship to create a custom relationship.

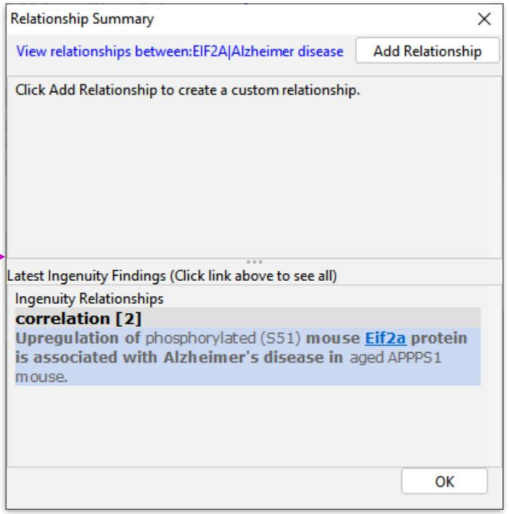
Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [1]

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

OK



Relationship Summary

View relationships between:EIF2A|Alzheimer disease | Add Relationship

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.

OK

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*)
- ✓ Domestic goat
- ✓ three-spined stickleback

Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

Supported Identifiers for Data Upload

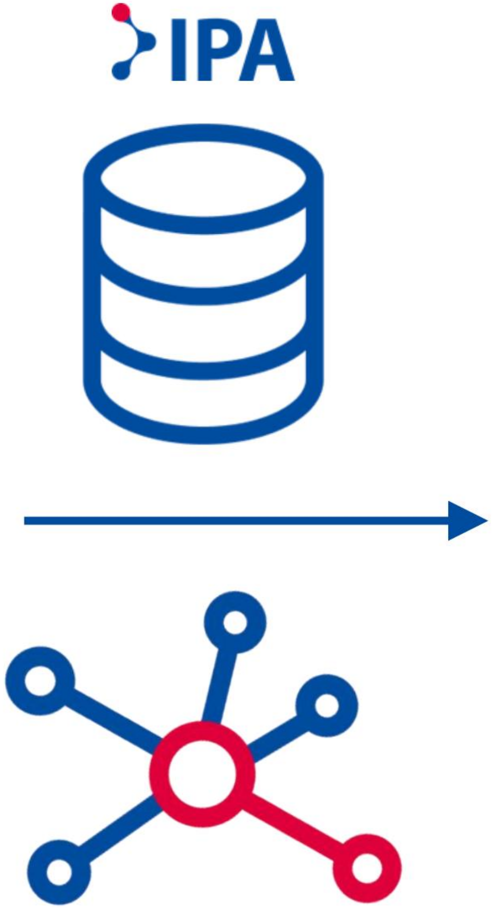
Get more complete mapping during dataset upload!

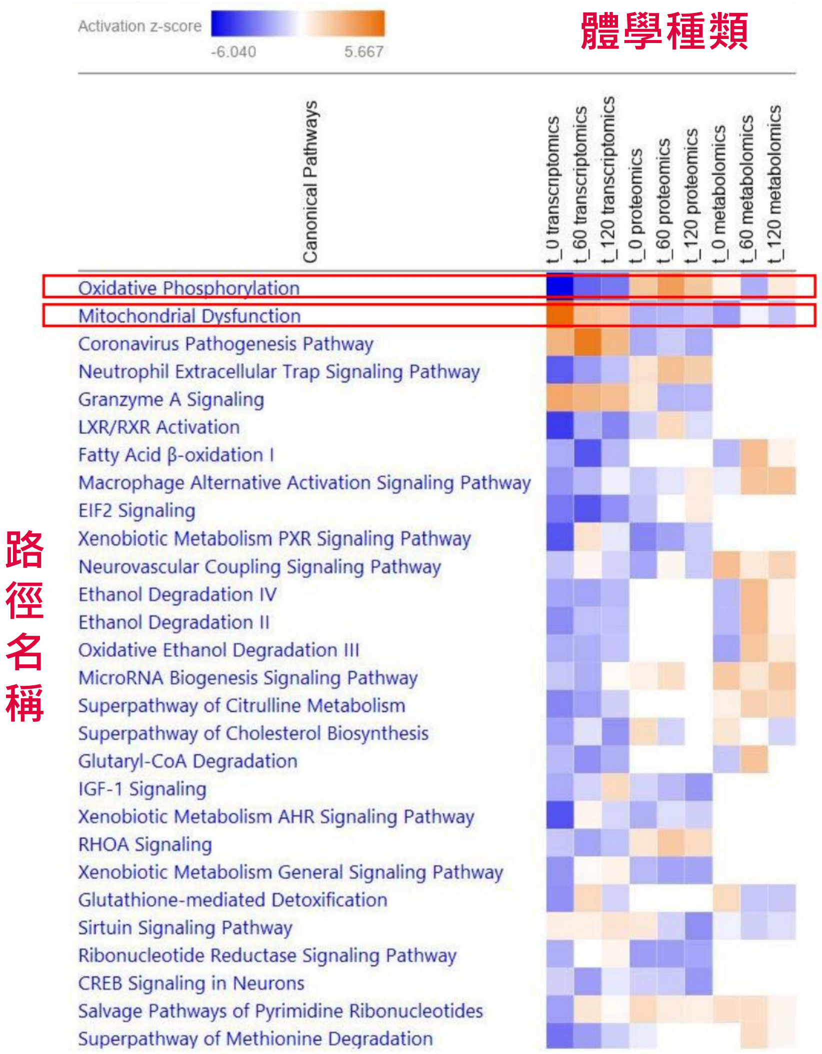
Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2023/8)	GenPept	Ensembl (110)	miRbase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (257)	International Protein Index (IPI)	RefSeq (human、mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human (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

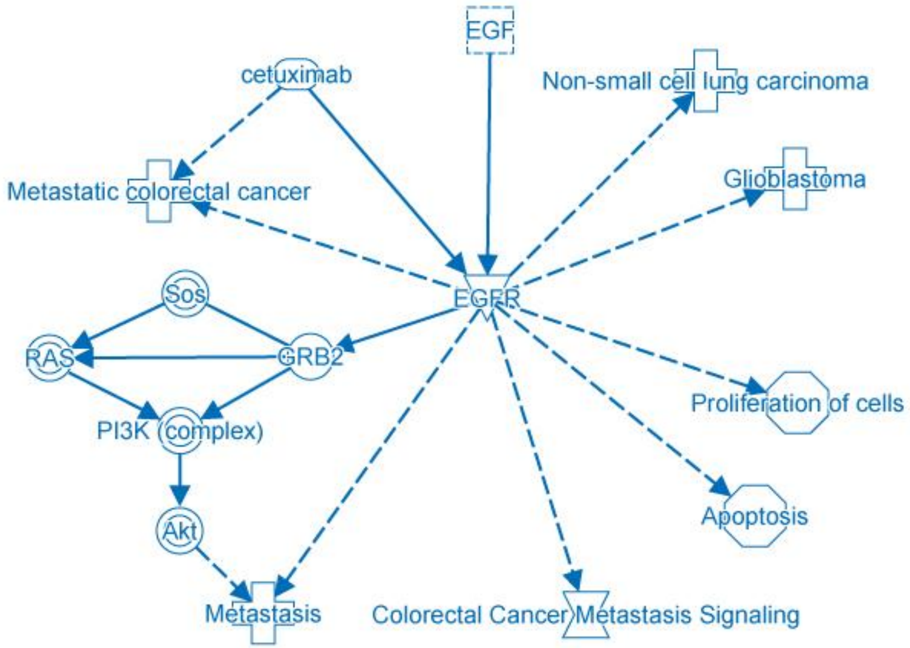
路徑名稱

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]

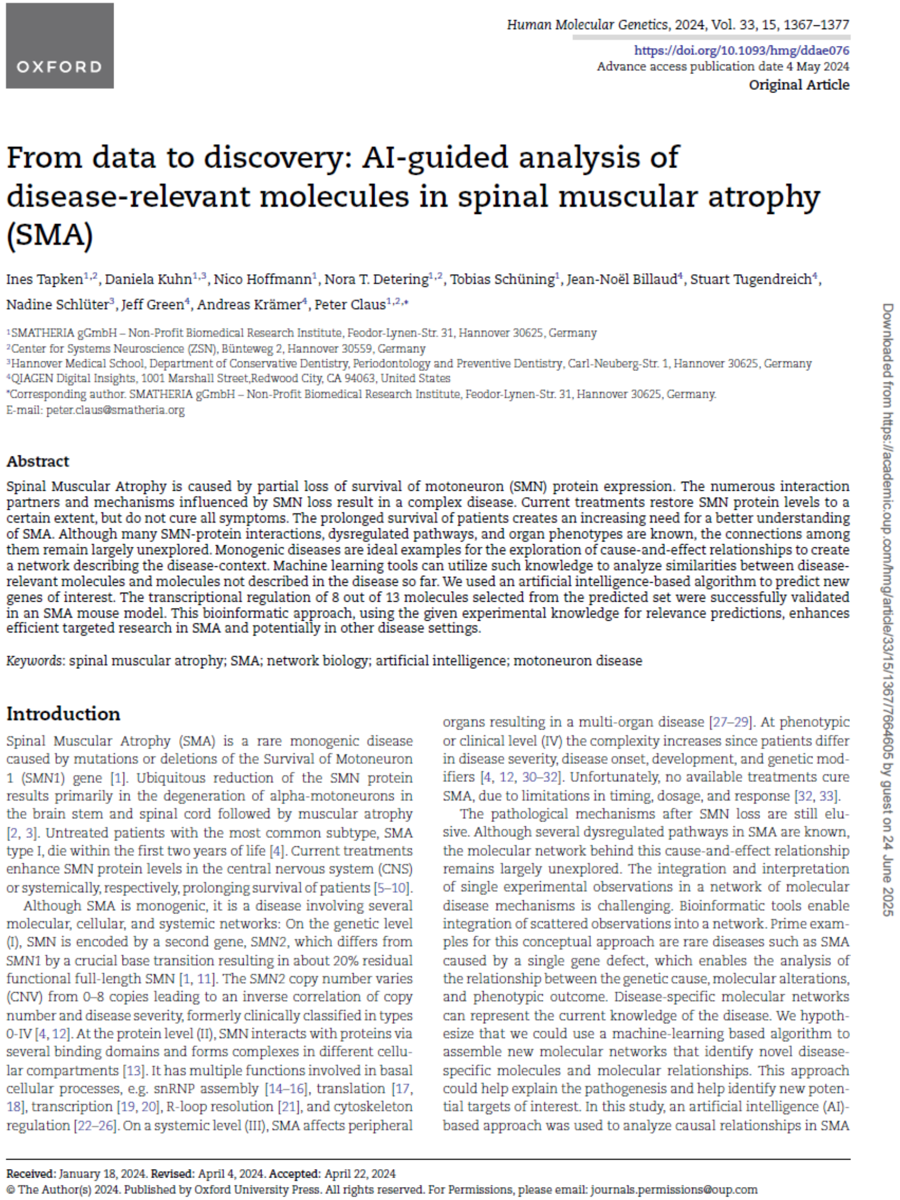
Type: causation
Direction: directional
Effect: increases
Tissue or primary cell: epithelial cells
Subcellular location: plasma membrane
Source: PubMed PMID: 22674072

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



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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[2]Center for Systems Neuroscience (ZSN), Bünteweg 2, Hannover 30559, Germany
[3]Hannover Medical School, Department of Conservative Dentistry, Periodontology and Preventive Dentistry, Carl-Neuberg-Str. 1, Hannover 30625, Germany
[4]QIAGEN Digital Insights, 1001 Marshall Street,Redwood City, CA 94063, United States
*Corresponding author. SMATHERIA gGmbH – Non-Profit Biomedical Research Institute, Feodor-Lynen-Str. 31, Hannover 30625, Germany.
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

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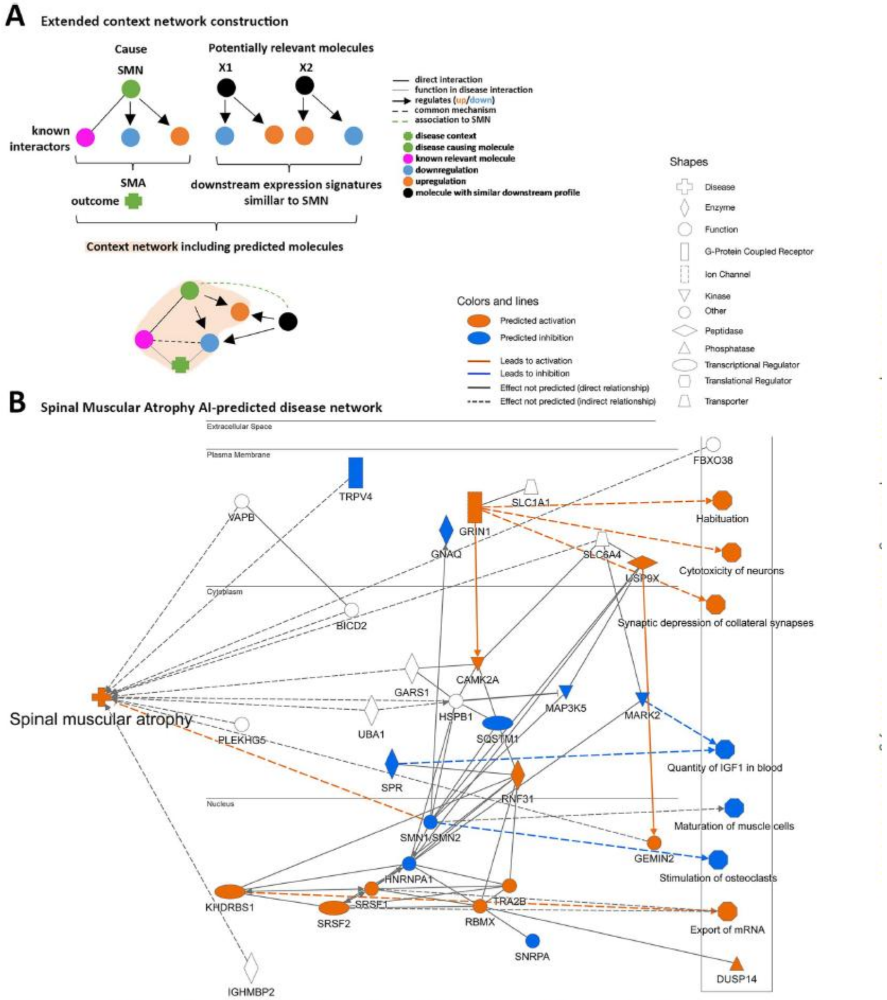
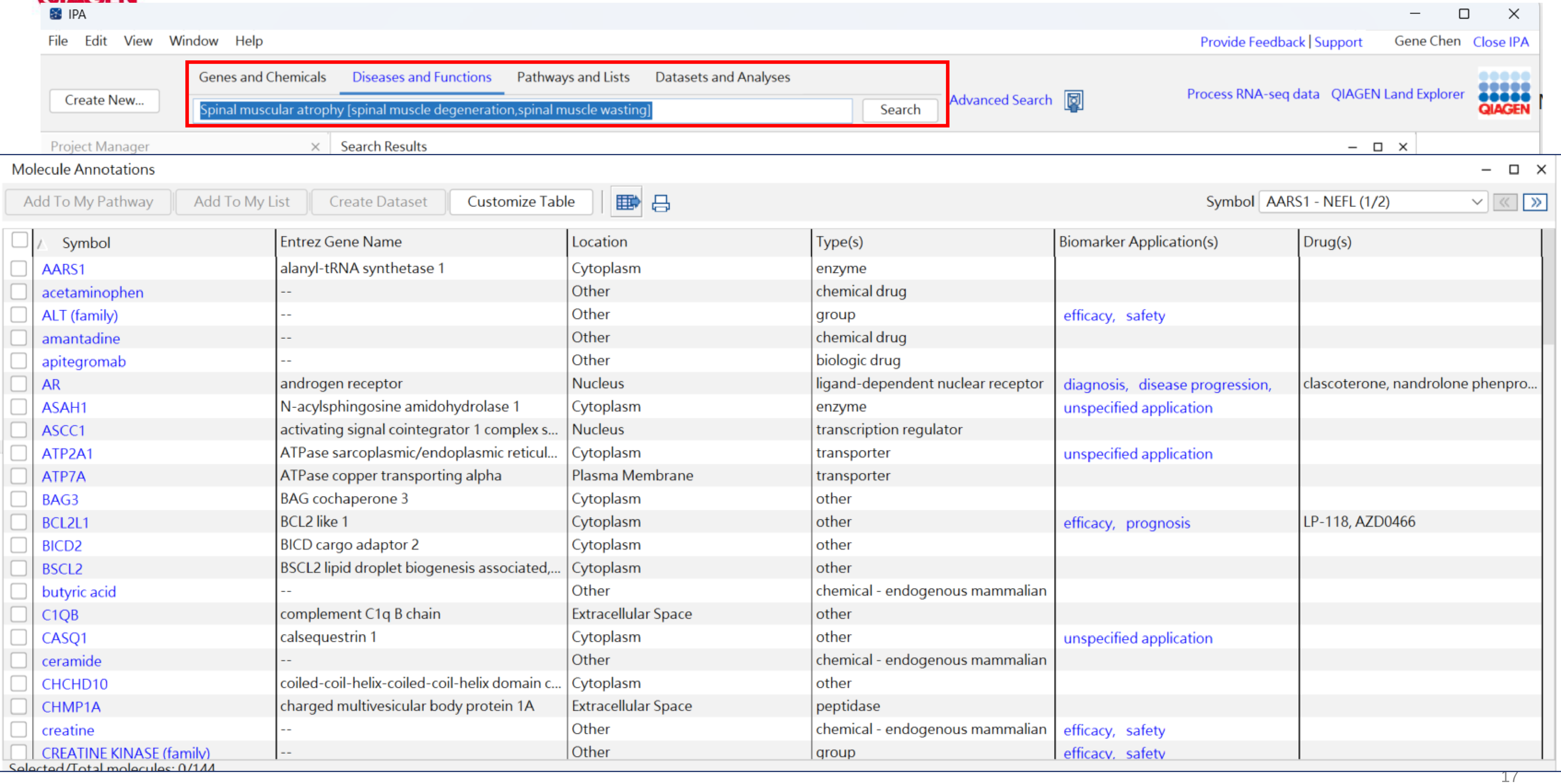


Figure 1. Artificial intelligence-predicted context network for spinal muscular atrophy. (A) Schematic representation of the AI-prediction algorithm and network construction. SMN (green circle) is the genetic cause and SMA (green cross) the disease outcome. In the QIAGEN Knowledge Base (QKB), interactors (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)

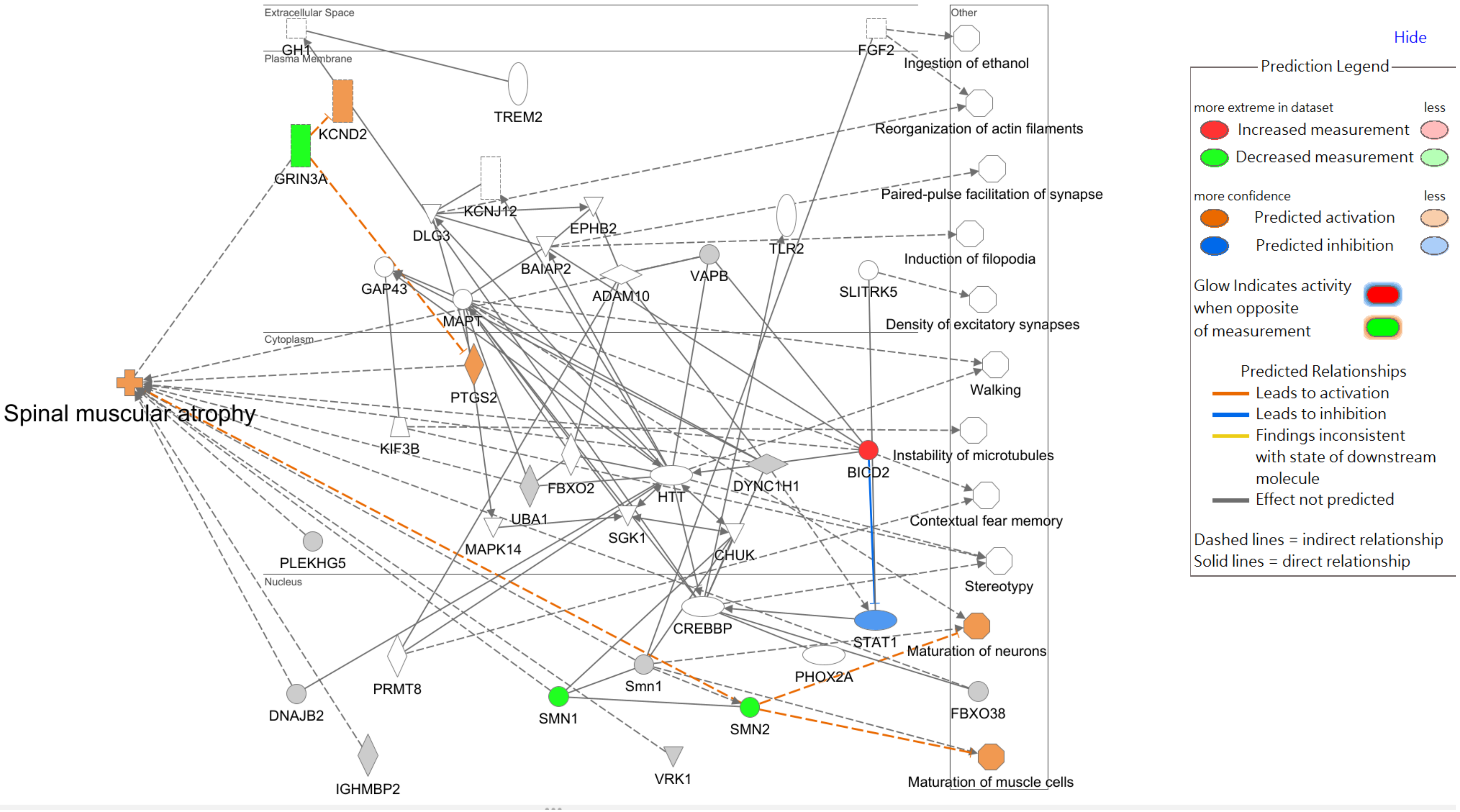
☐	Symbol	Entrez Gene Name	Location	Type(s)	Biomarker Application(s)	Drug(s)
☐	AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme		
☐	acetaminophen	--	Other	chemical drug		
☐	ALT (family)	--	Other	group	efficacy, safety	
☐	amantadine	--	Other	chemical drug		
☐	apitegromab	--	Other	biologic drug		
☐	AR	androgen 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

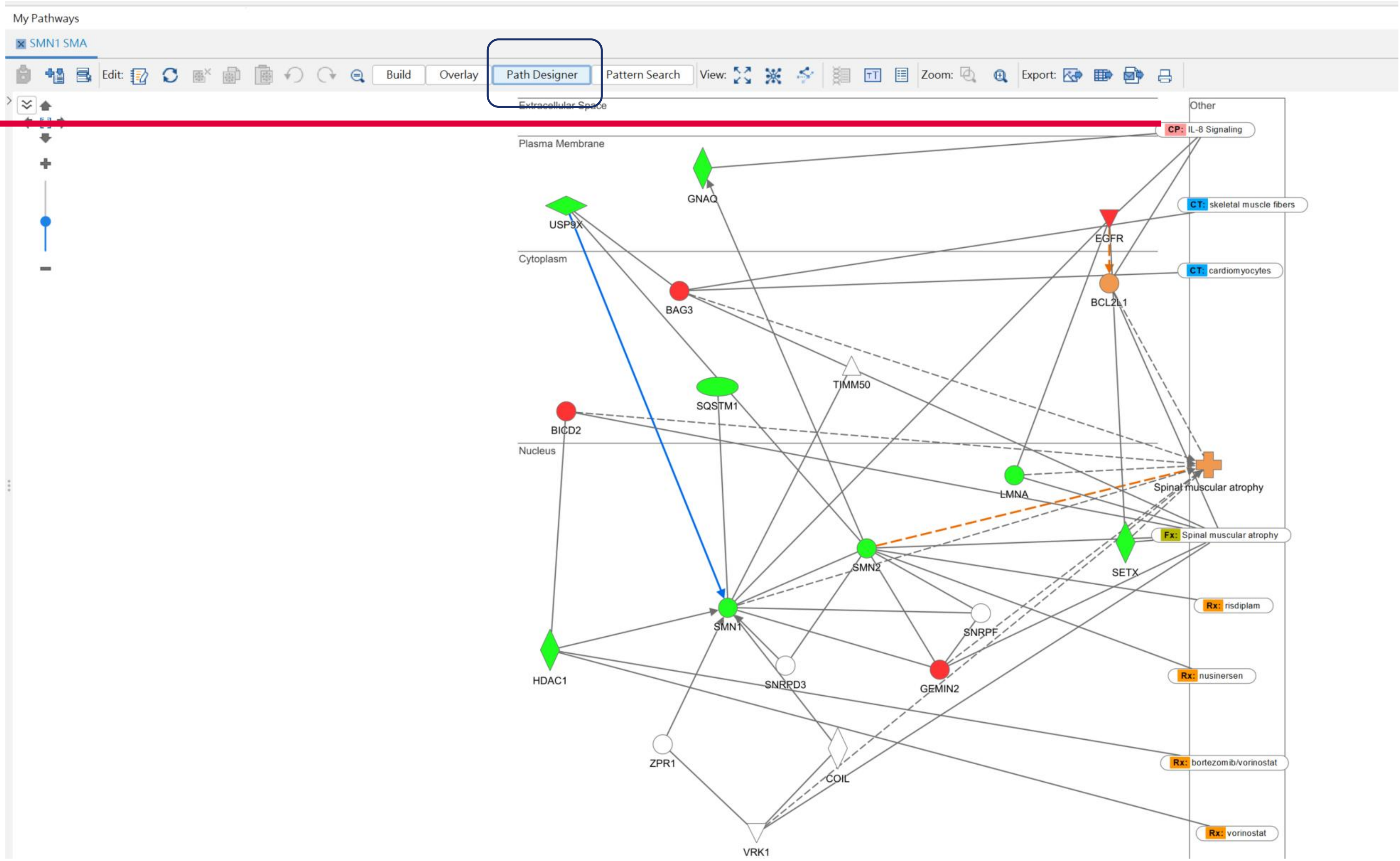
Machine learning pathway

Download the related Genes of disease

Upload dataset and Core analysis



Create networks from scratch and test activity in silico



<u>New feature:</u>
<u>Cells and Tissues overlay</u>

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

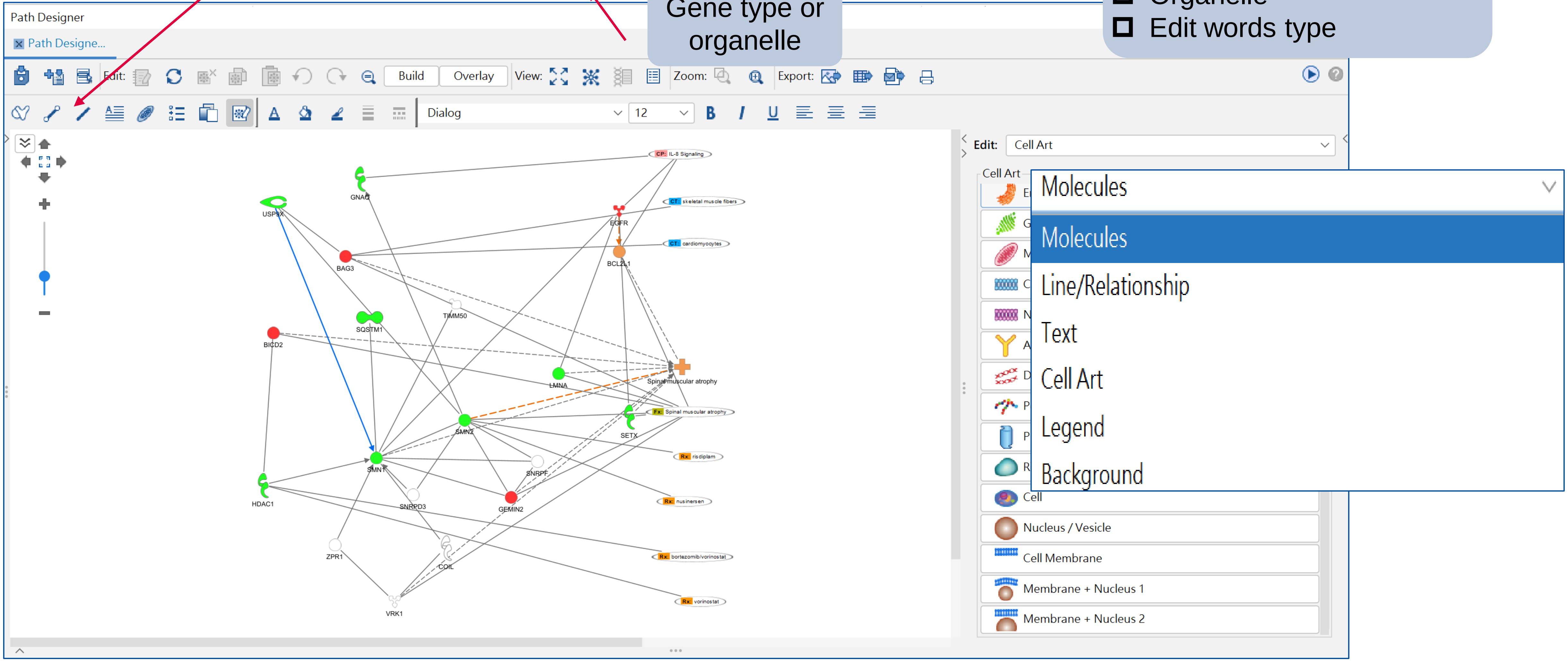
- Search for genes
- Build: grow (molecular or disease a function)
- Search for disease
- Path explore
- Overlay: Molecule activity predictor, Drug, Cells & Tissues
- Drug: IPA Chem View

Path Designer

Figure legend

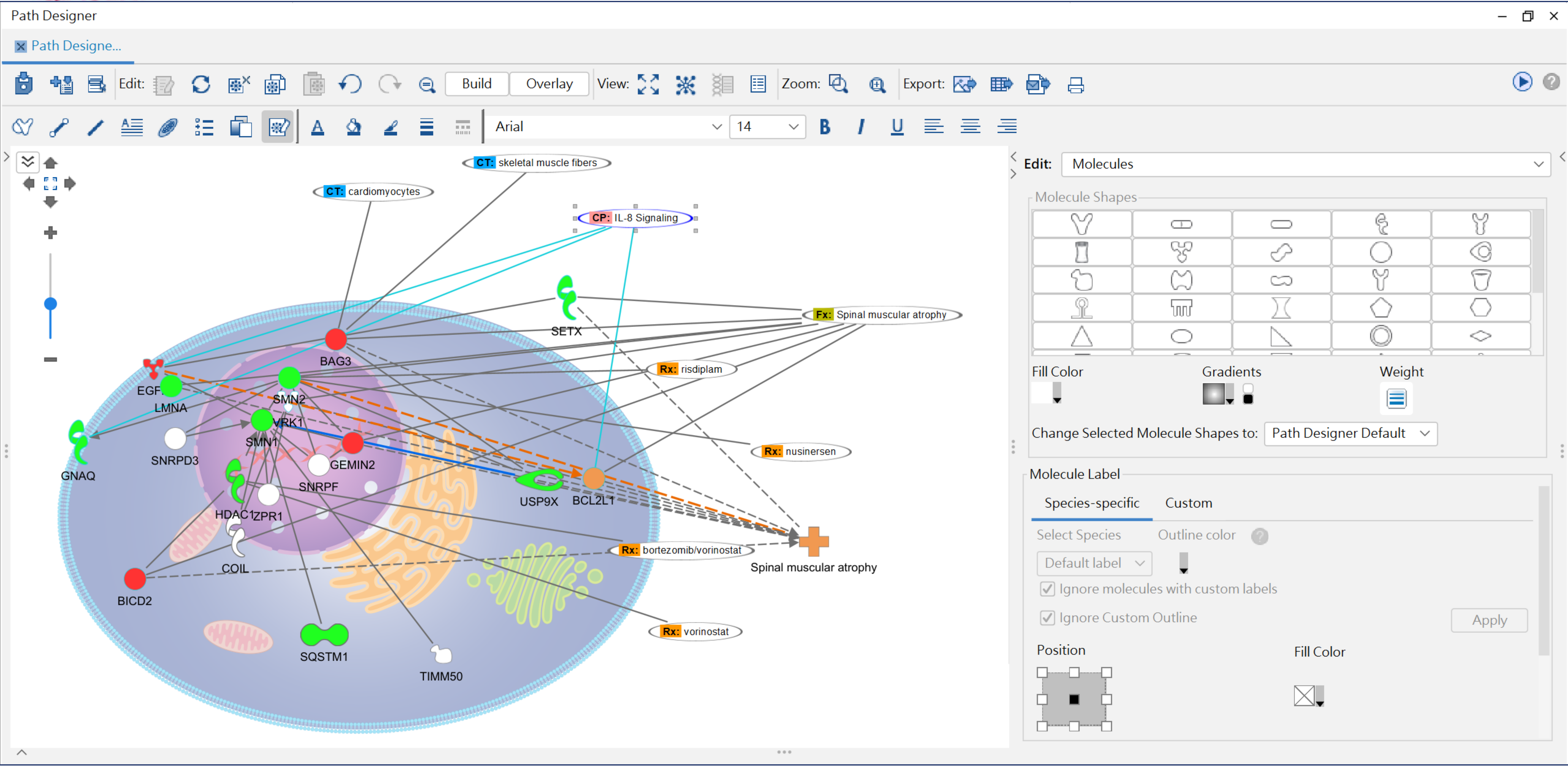
Gene type or organelle

We can add the
☐ molecules
☐ Organelle
☐ Edit words type



Edit: Cell Art

Path Designer



Font: Arial, 14

Edit: Molecules

Change Selected Molecule Shapes to: Path Designer Default

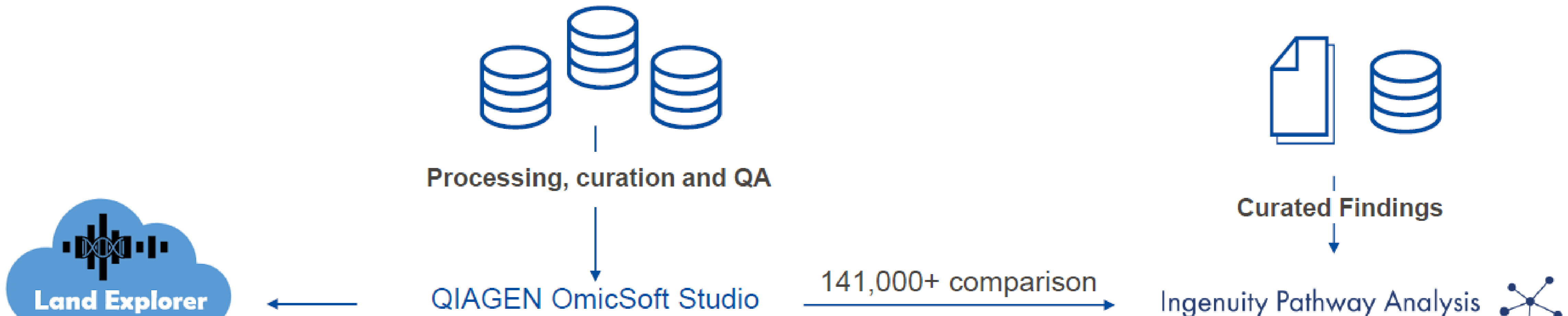
Select Species: Default label

Outline color

☑ Ignore molecules with custom labels

☑ Ignore Custom Outline

QIAGEN IPA Analysis Match and Land Explorer



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

Processing, curation and QA

QIAGEN OmicSoft Studio

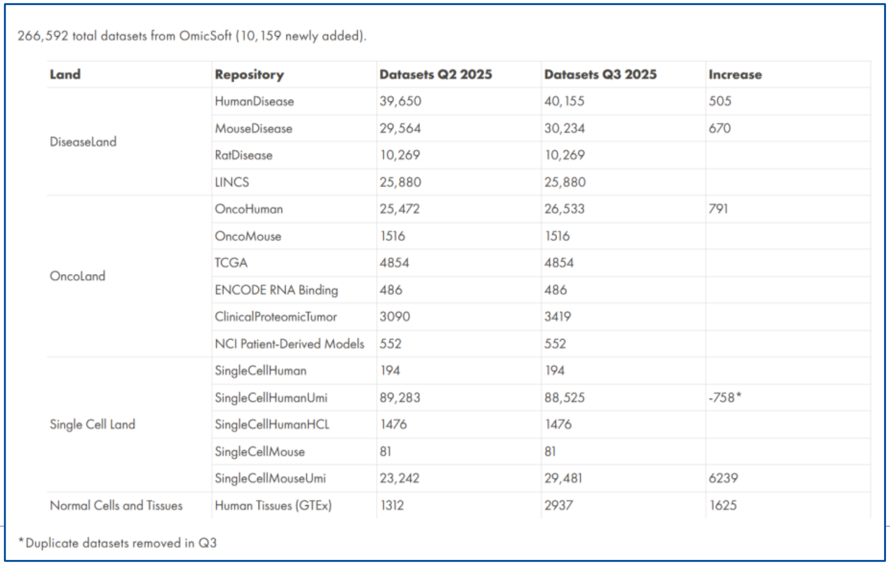
Land Explorer

141,000+ comparison

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

Curated Findings

Ingenuity Pathway Analysis



266,592 total datasets from OmicSoft (10,159 newly added).

Land	Repository	Datasets Q2 2025	Datasets Q3 2025	Increase
DiseaseLand	HumanDisease	39,650	40,155	505
	MouseDisease	29,564	30,234	670
	RatDisease	10,269	10,269	
	LINCS	25,880	25,880	
OncoLand	OncoHuman	25,472	26,533	791
	OncoMouse	1516	1516	
	TCGA	4854	4854	
	ENCODE RNA Binding	486	486	
	ClinicalProteomicTumor	3090	3419	
	NCI Patient-Derived Models	552	552	
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	89,283	88,525	-758*
	SingleCellHumanHCL	1476	1476	
	SingleCellMouse	81	81	
	SingleCellMouseUmi	23,242	29,481	6239
Normal Cells and Tissues	Human Tissues (GTEx)	1312	2937	1625

*Duplicate datasets removed in Q3

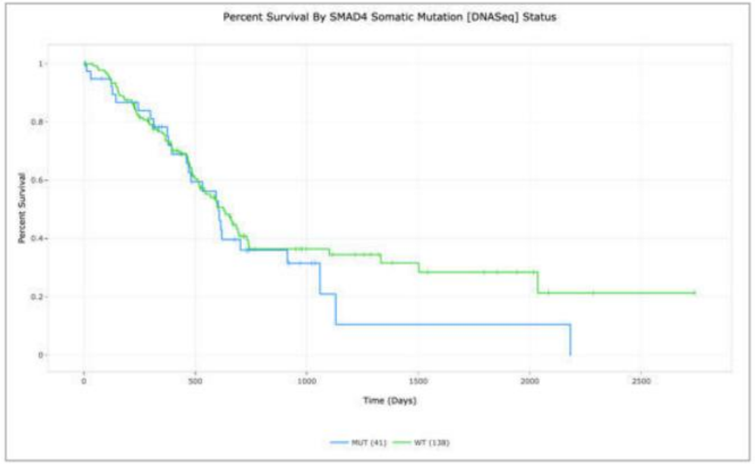
- Explore gene expression levels
- Determine where a target is differentially expressed
- Understand how ‘omics data influences survival
- Identify mutation status of a target

- 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

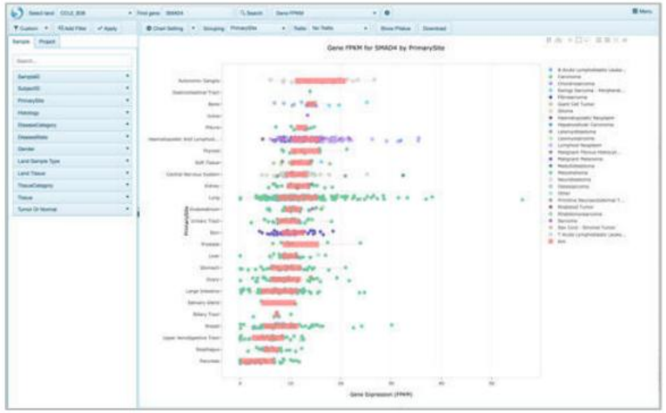
IPA with OmicSoft Land Explorer

Expression in Rat, Mouse, and Human Disease

Mutation frequency

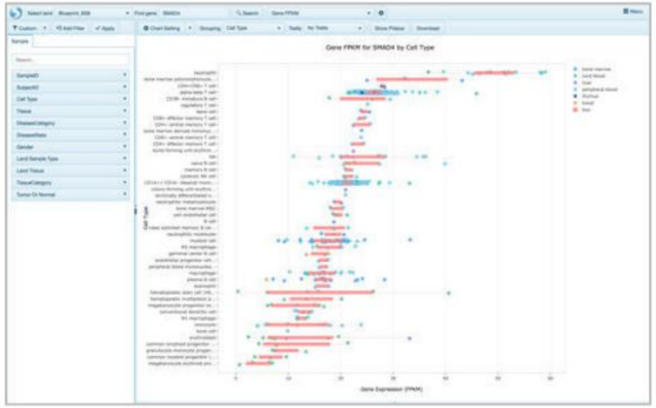


Survival plots



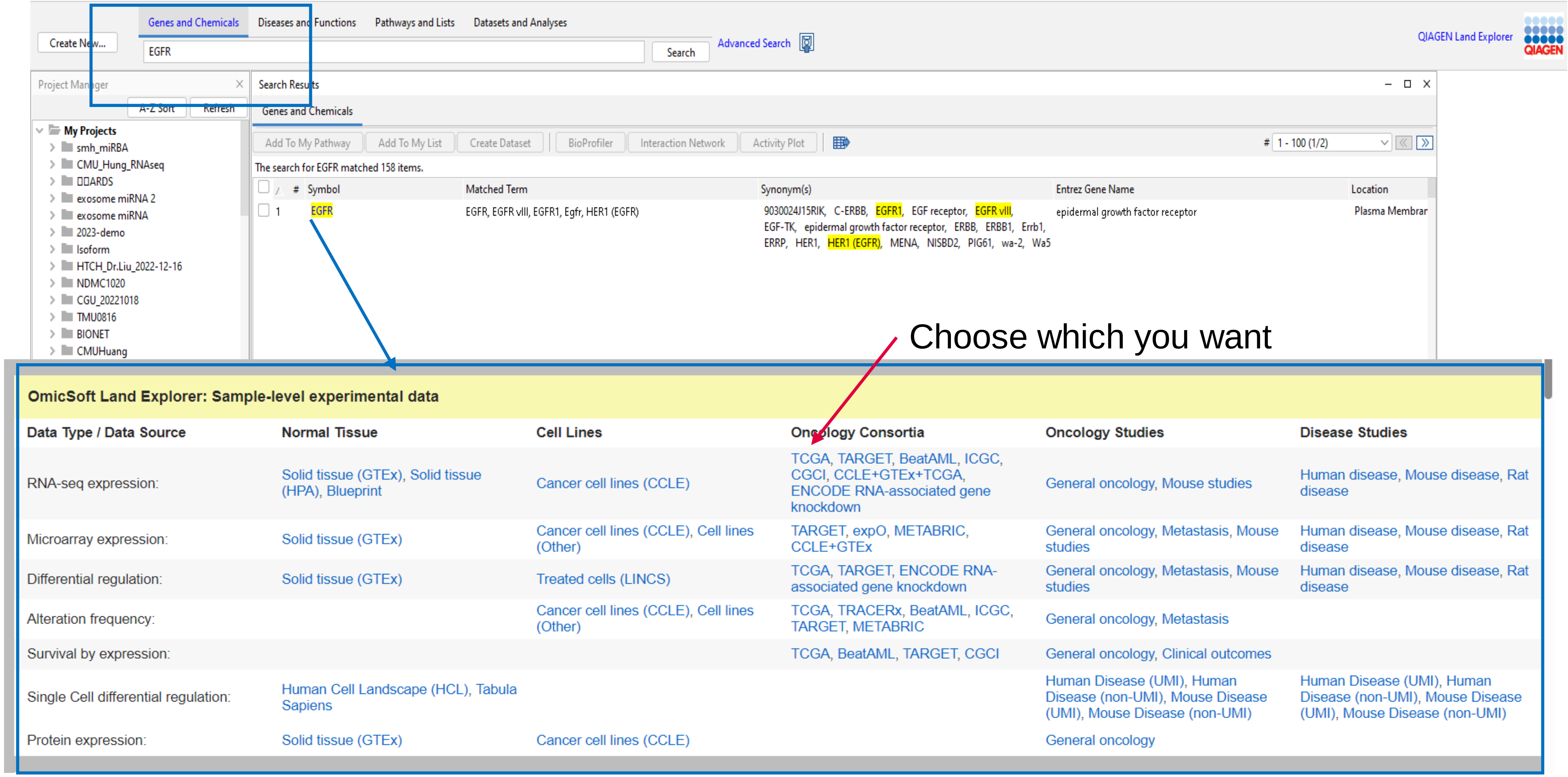
Cell line expression

Tumor expression



Hematopoietic expression (BluePrint)

IPA with OmicSoft Land Explorer



The search for EGFR matched 158 items.

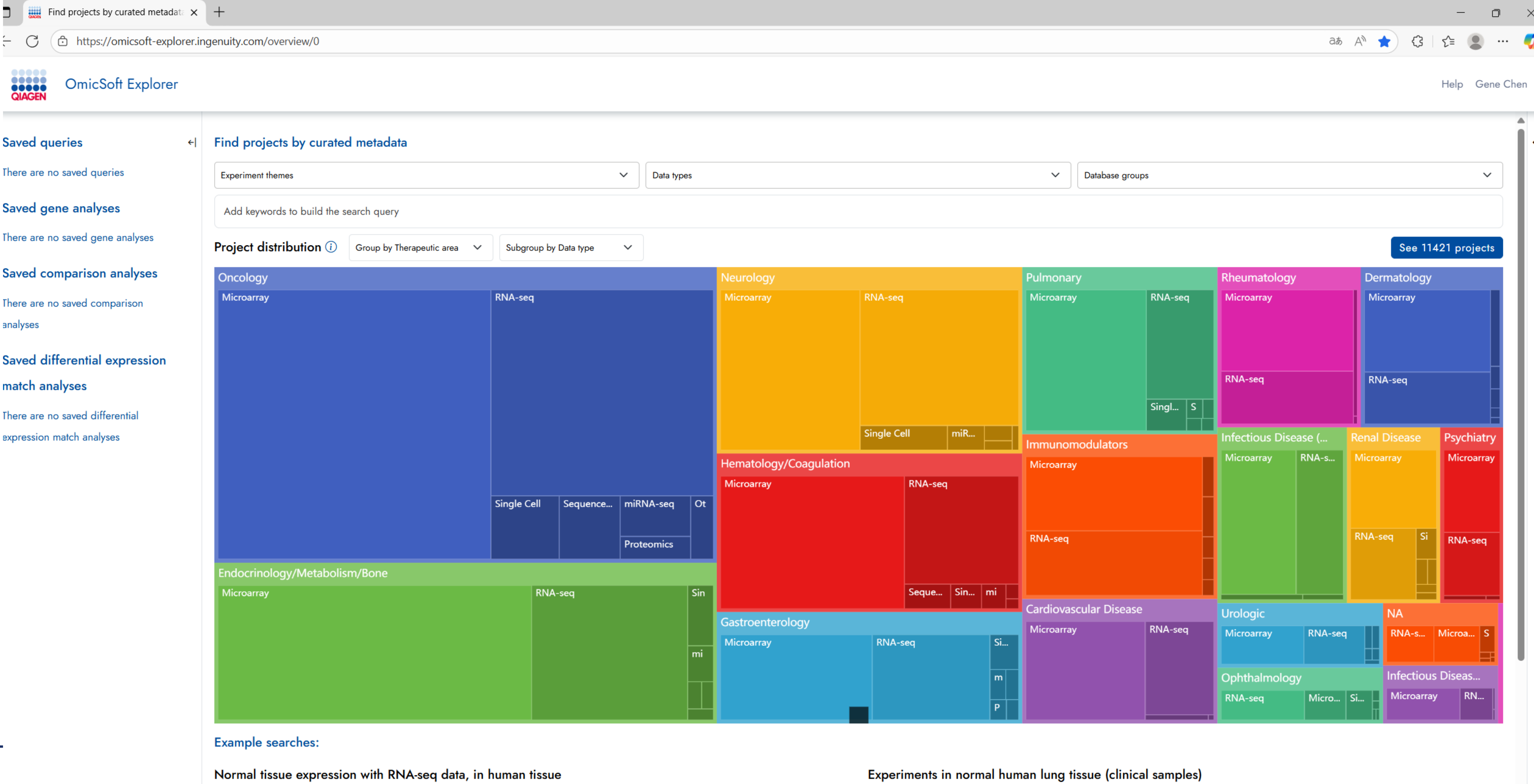
#	Symbol	Matched Term	Synonym(s)	Entrez Gene Name	Location
1	EGFR	EGFR, EGFR vIII, EGFR1, Egfr, HER1 (EGFR)	9030024J15RIK, C-ERBB, EGFR1, EGF receptor, EGFR vIII, EGF-TK, epidermal growth factor receptor, ERBB, ERBB1, Errb1, ERRP, HER1, HER1 (EGFR), MENA, NISBD2, PIG61, wa-2, Wa5	epidermal growth factor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



Find projects by curated metadat

https://omicsoft-explorer.ingenuity.com/overview/0

OmicSoft Explorer

Help Gene Chen

Saved queries

There are no saved queries

Saved gene analyses

There are no saved gene analyses

Saved comparison analyses

There are no saved comparison analyses

Saved differential expression match analyses

There are no saved differential expression match analyses

Find projects by curated metadata

Experiment themes

Data types

Database groups

Add keywords to build the search query

Project distribution

Group by Therapeutic area

Subgroup by Data type

See 11421 projects

Example searches:

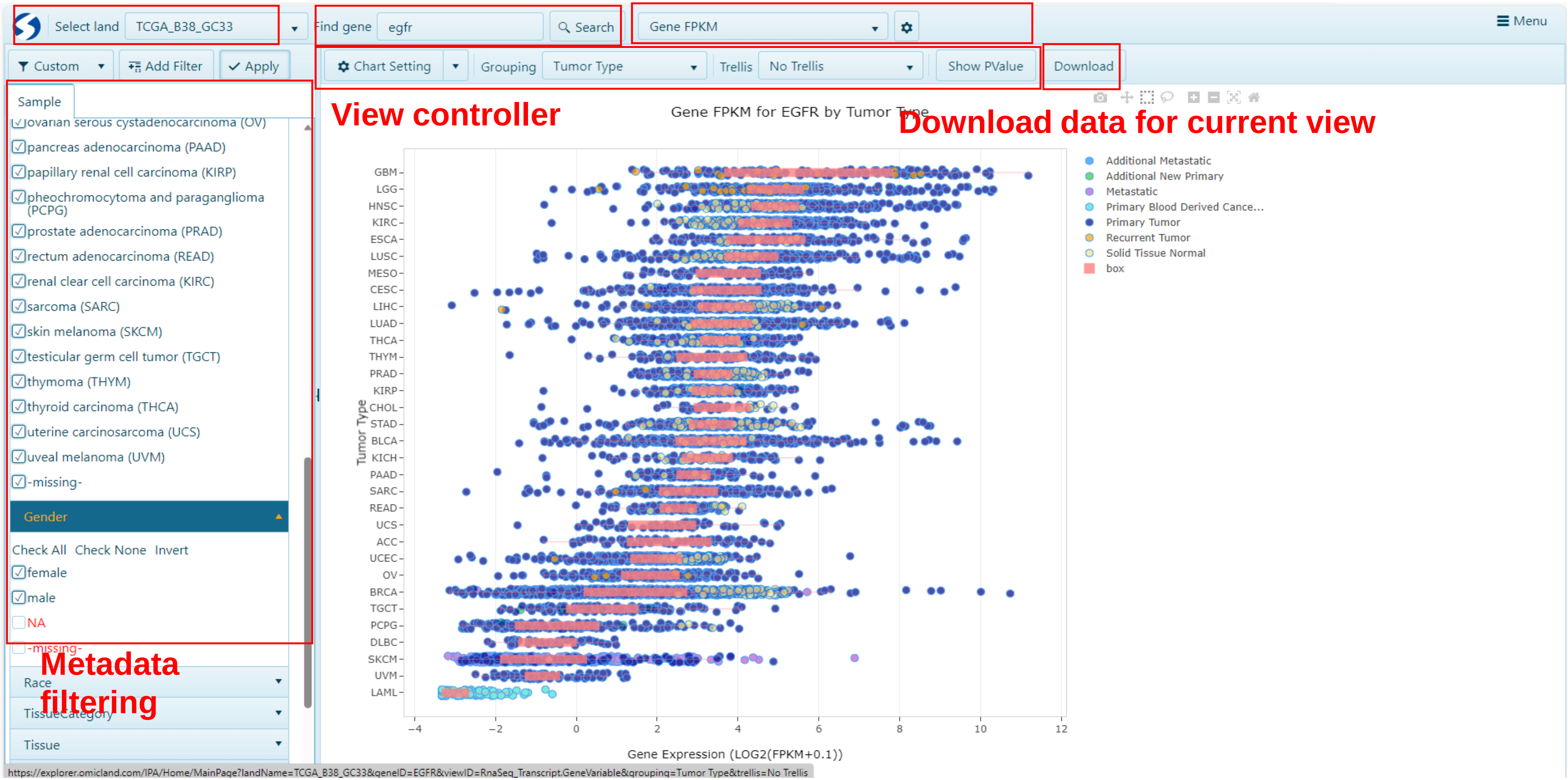
Normal tissue expression with RNA-seq data, in human tissue

Experiments in normal human lung tissue (clinical samples)

IPA with OmicSoft Land Explorer

- **TCGA-B38-G33**

Land selection **Search bar** **View selection**



View controller

Download data for current view

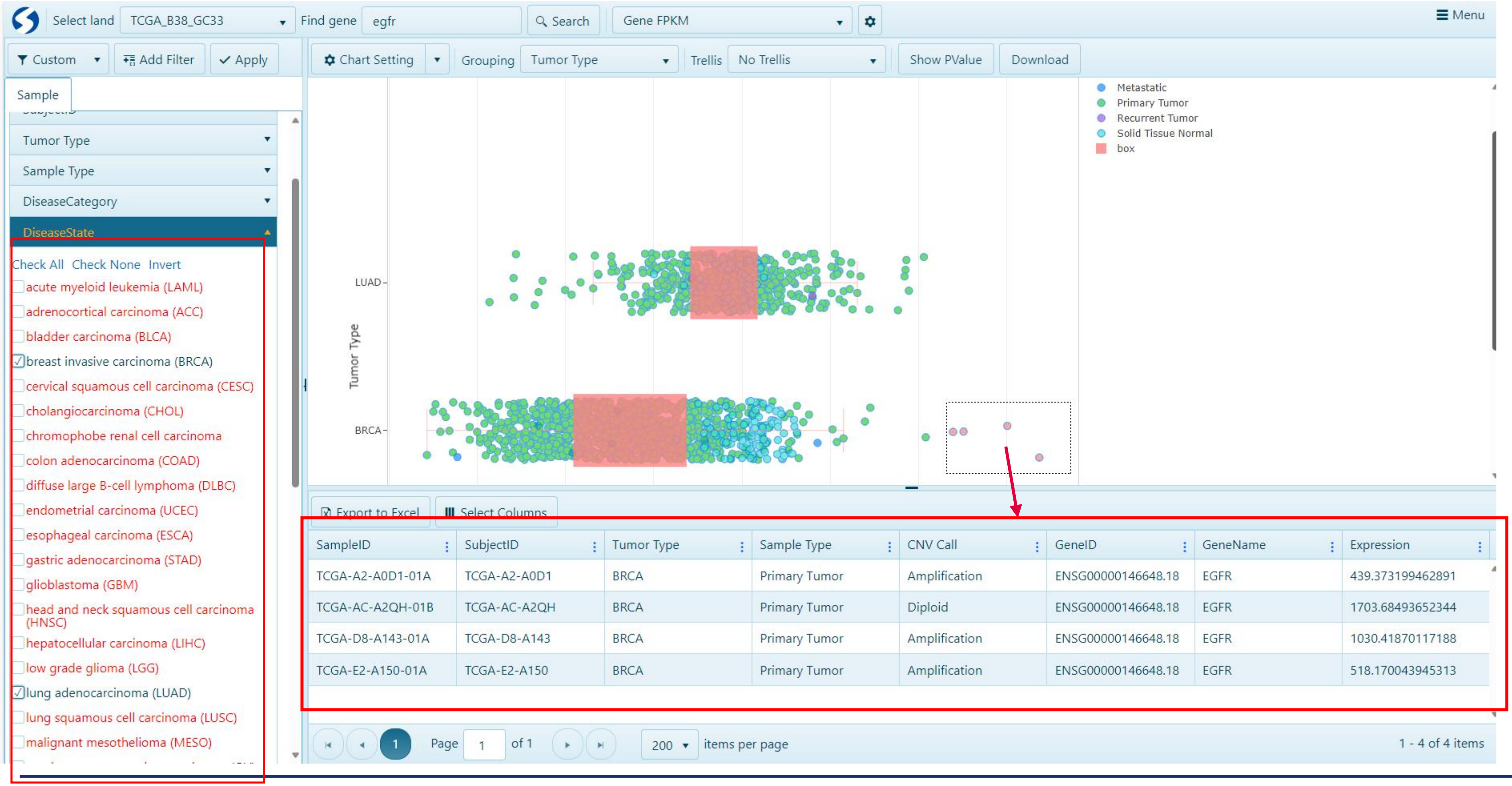
Metadata filtering

☑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-

☑female
☑male
☐NA
☐-missing-

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

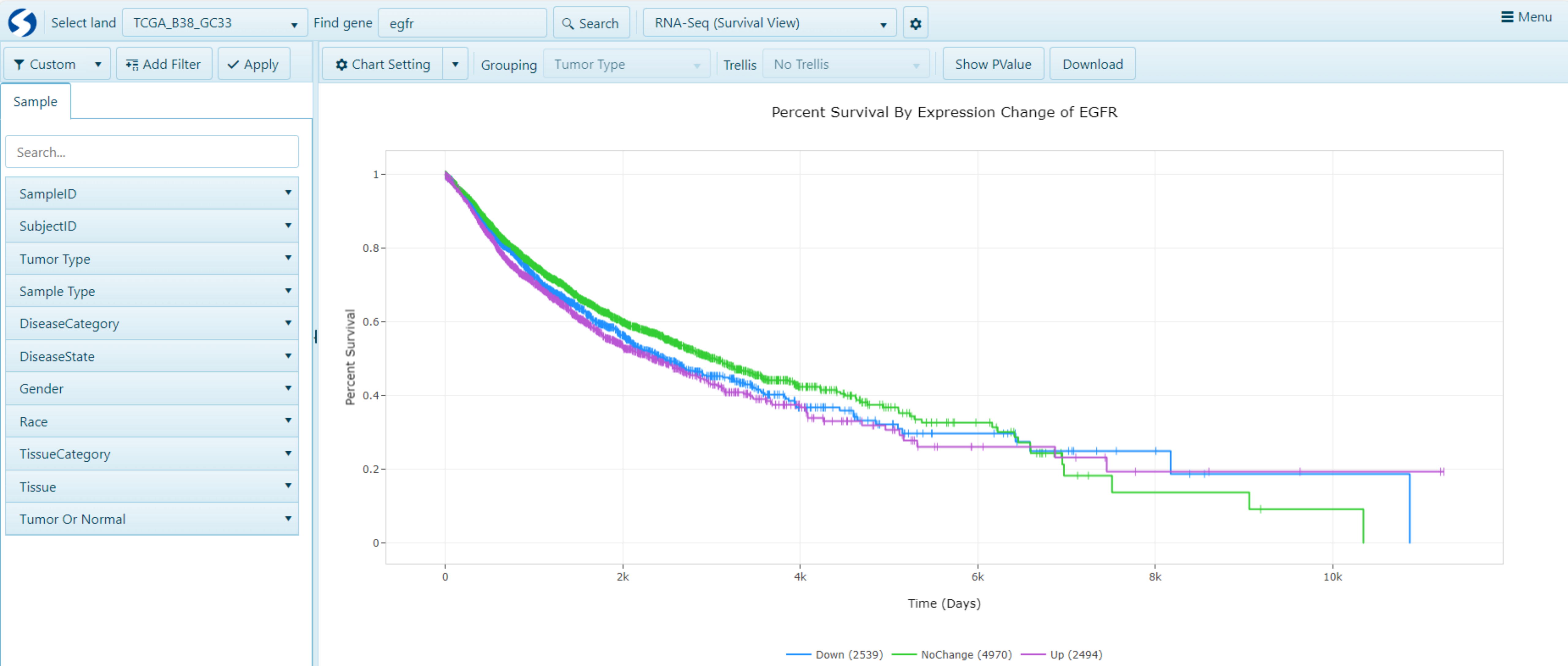
- ☐ acute myeloid leukemia (LAML)
- ☐ adrenocortical carcinoma (ACC)
- ☐ bladder carcinoma (BLCA)
- ☑ breast invasive carcinoma (BRCA)
- ☐ cervical squamous cell carcinoma (CESC)
- ☐ cholangiocarcinoma (CHOL)
- ☐ chromophobe renal cell carcinoma
- ☐ colon adenocarcinoma (COAD)
- ☐ diffuse large B-cell 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

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

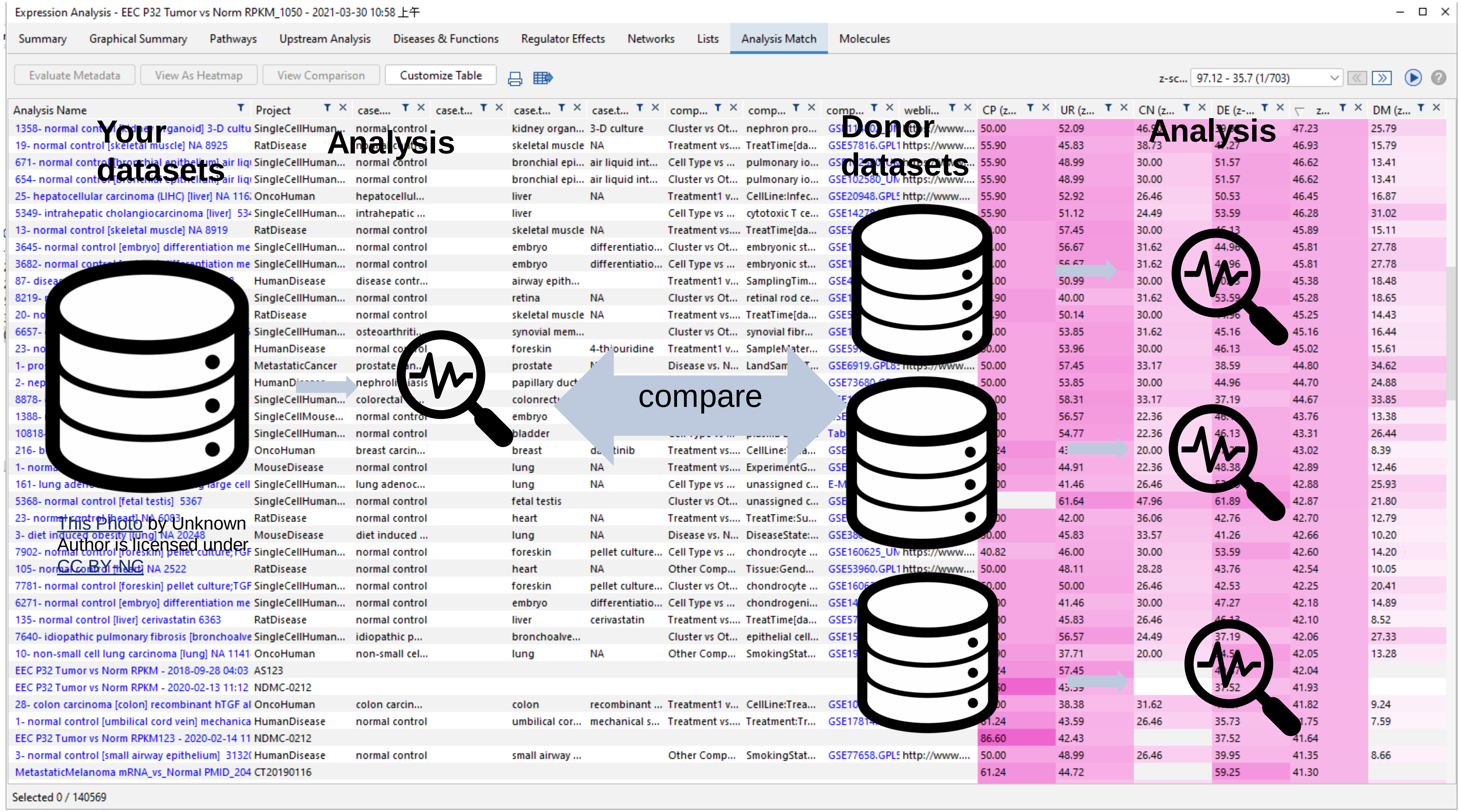
RNA-Seq (Survival View)

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 control [kidney organoid] 3-D cultu	SingleCellHuman...	normal control		kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GSE1[illegible]	https://www....	50.00	52.09	46.9	[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].27	46.93	15.79
671- normal control [bronchial epithelium] 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 control [bronchial epithelium] 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		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		.00	57.45	30.00	46.13	45.89	15.11
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control		embryo	differentiatio...	Cluster vs Ot...	embryonic st...	GSE1		.00	56.67	31.62	44.96	45.81	27.78
3682- normal cont[illegible]ifferentiation me	SingleCellHuman...	normal control		embryo	differentiatio...	Cell Type vs ...	embryonic st...	GSE1		.00	56.67	31.62	44.96	45.81	27.78
87- disea[illegible]	HumanDisease	disease contr...		airway epith...		Treatment1 v...	SamplingTim...	GSE4		.00	50.99	30.00	[illegible]	45.38	18.48
8219- [illegible]	SingleCellHuman...	normal control		retina	NA	Cluster vs Ot...	retinal rod ce...	GSE1		.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		.90	50.14	30.00	[illegible]	45.25	14.43
6657- [illegible]	SingleCellHuman...	osteoarthriti...		synovial mem...		Cluster vs Ot...	synovial fibr...	GSE1		.00	53.85	31.62	45.16	45.16	16.44
23- no[illegible]	HumanDisease	normal control		foreskin	4-thiouridine	Treatment1 v...	SampleMater...	GSE59		0.00	53.96	30.00	46.13	45.02	15.61
1- pro[illegible]	MetastaticCancer	prostate can...		prostate	N	Disease vs. N...	LandSam[illegible]	GSE6919.GPL8	https://www....	50.00	57.45	33.17	38.59	44.80	34.62
2- nep[illegible]	HumanD[illegible]	nephrolithiasis		papillary duct	[illegible]	[illegible]	[illegible]	GSE73680	[illegible]	50.00	53.85	30.00	44.96	44.70	24.88
8878- [illegible]	SingleCellHuman...	colorectal ...		colonrect	[illegible]	[illegible]	[illegible]	[illegible]		.00	58.31	33.17	37.19	44.67	33.85
1388- [illegible]	SingleCellMouse...	normal control		embryo	[illegible]	[illegible]	[illegible]	[illegible]		00	56.57	22.36	46.	43.76	13.38
10818- [illegible]	SingleCellHuman...	normal control		bladder	[illegible]	[illegible]	[illegible]	Tab		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		24	43	20.00	[illegible]	43.02	8.39
1- norma[illegible]	MouseDisease	normal control		lung	NA	Treatment vs....	ExperimentG...	GSE		90	44.91	22.36	48.38	42.89	12.46
161- lung aden[illegible]large cell	SingleCellHuman...	lung adenoc...		lung	NA	Cell Type vs ...	unassigned c...	E-M		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			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		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		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		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		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		00	45.83	26.46	46.13	42.10	8.52
7640- idiopathic pulmonary fibrosis [bronchoalve	SingleCellHuman...	idiopathic p...		bronchoalve...		Cluster vs Ot...	epithelial cell...	GSE15		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		90	37.71	20.00	[illegible]	42.05	13.28
EEC P32 Tumor vs Norm RPKM - 2018-09-28 04:03	AS123									24	57.45		[illegible]	42.04	
EEC P32 Tumor vs Norm RPKM - 2020-02-13 11:12	NDMC-0212									50	[illegible]		37.52	41.93	
28- colon carcinoma [colon] recombinant hTGF al	OncoHuman	colon carcin...		colon	recombinant ...	Treatment1 v...	CellLine:Trea...	GSE10		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		61.24	43.59	26.46	35.73	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

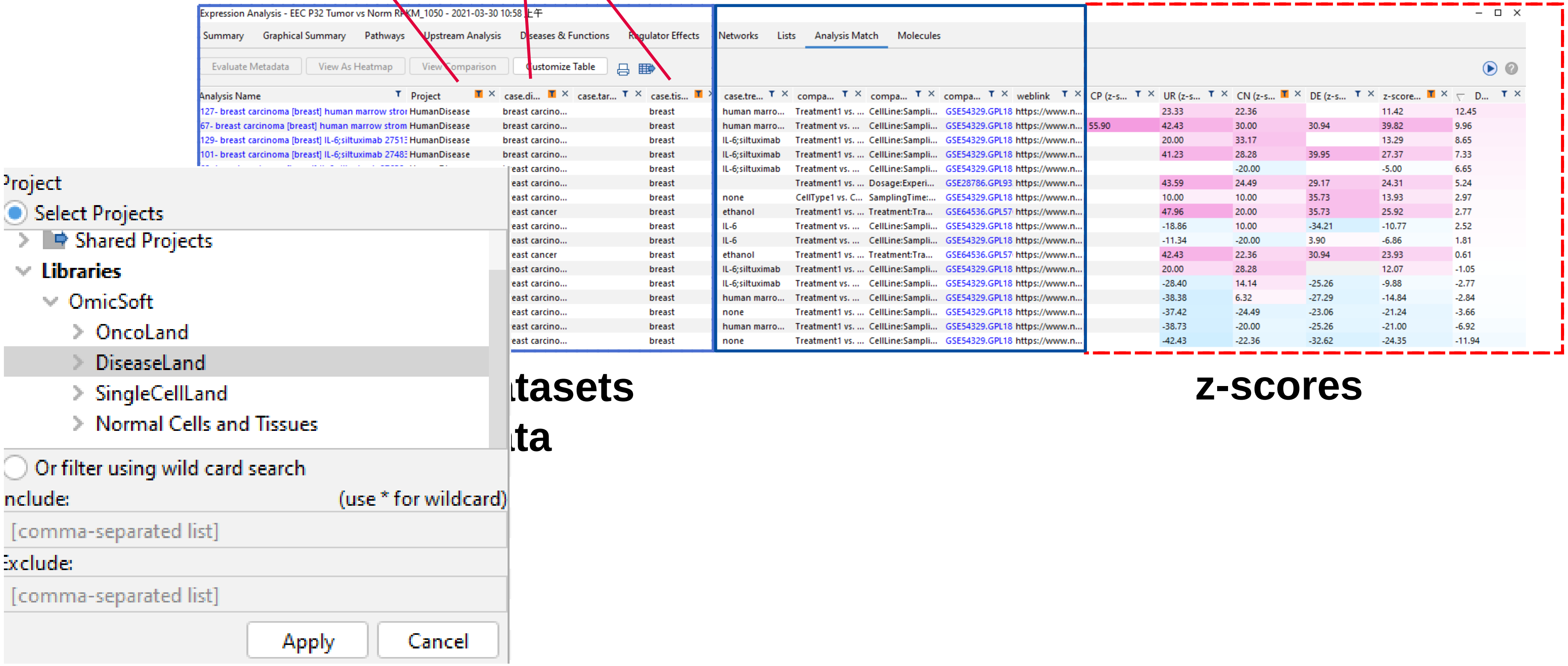
This Photo by Unknown Author is licensed under CC BY-NC

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]

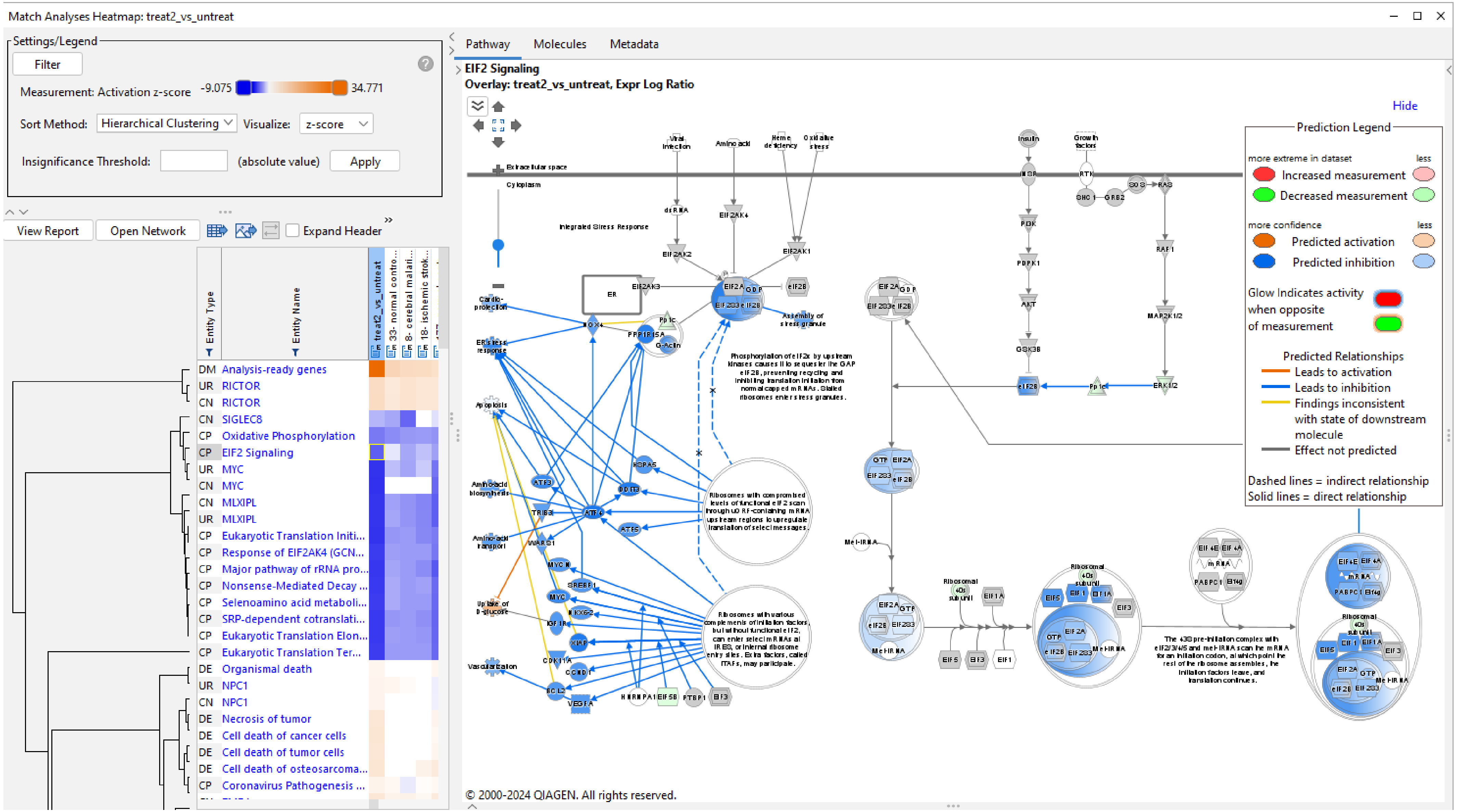
xclude:

[comma-separated list]

tasets
ta

z-scores

Analysis Match



Match Analyses Heatmap: treat2_vs_untreat

Settings/Legend

Filter

Measurement: Activation z-score -9.075 34.771

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value) Apply

View Report Open Network ☐ Expand Header

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 ...

Pathway Molecules Metadata

EIF2 Signaling
Overlay: treat2_vs_untreat, 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

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 scan 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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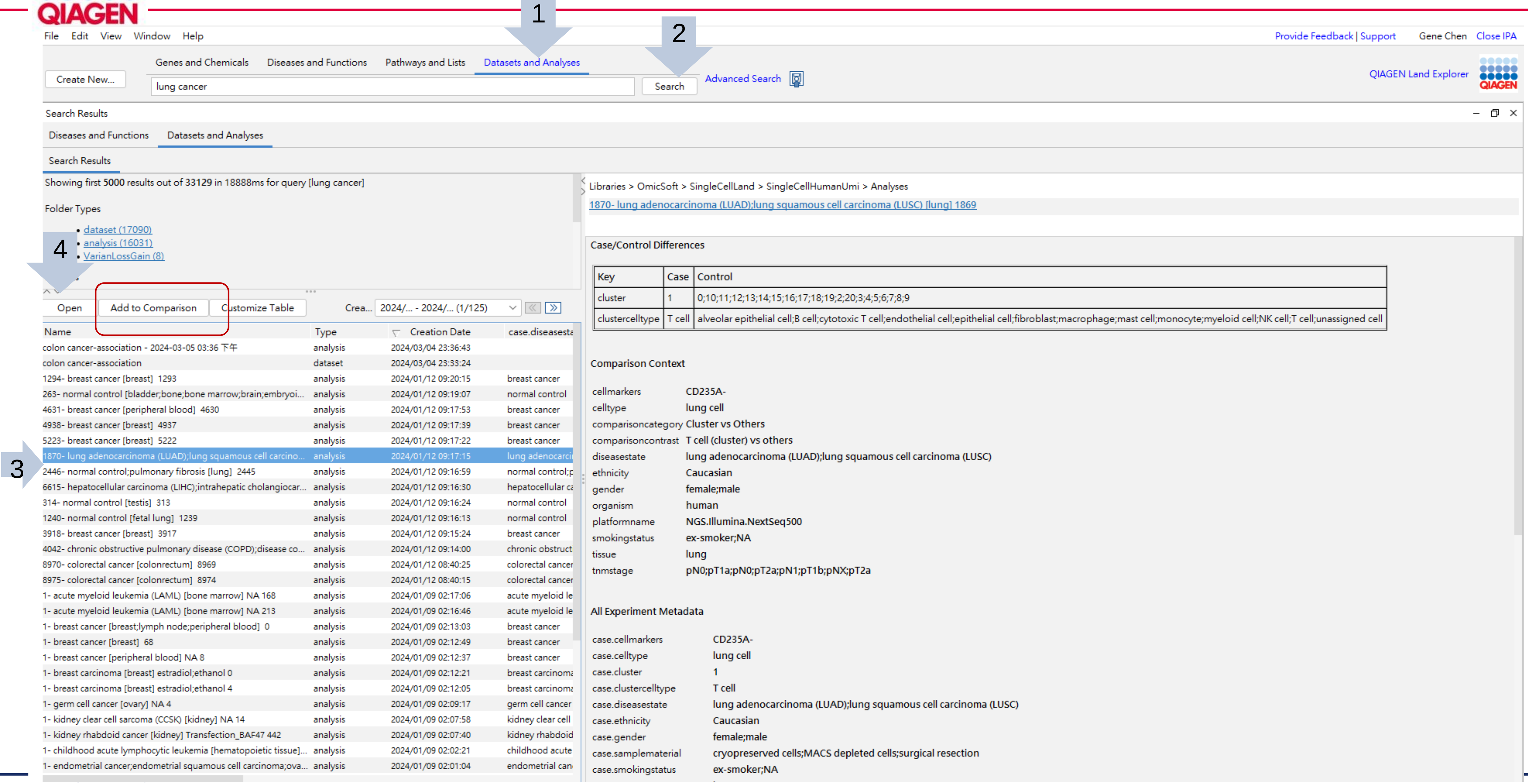
Dataset and analysis search



lung cancer

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

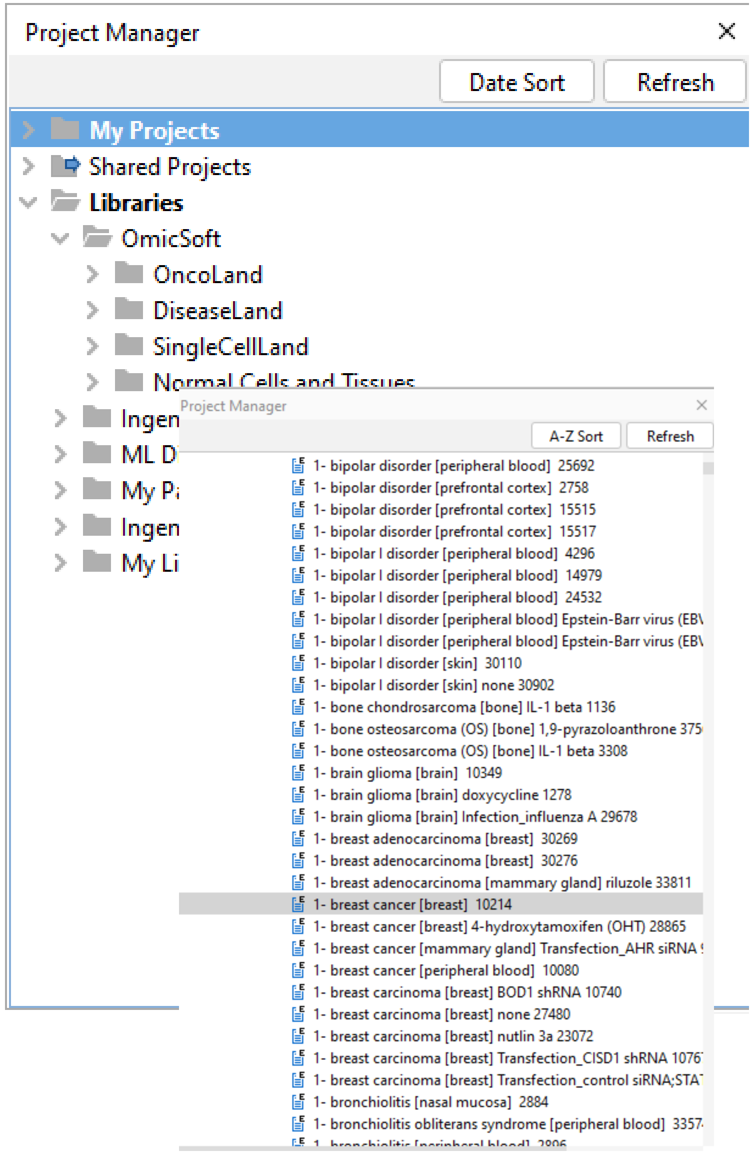
cellmarkers	CD235A-
celltype	lung cell
comparisoncategory	Cluster vs Others
comparisoncontrast	T cell (cluster) vs others
diseasestate	lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)
ethnicity	Caucasian
gender	female;male
organism	human
platformname	NGS.Illumina.NextSeq500
smokingstatus	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.



Project Manager

Date Sort | Refresh

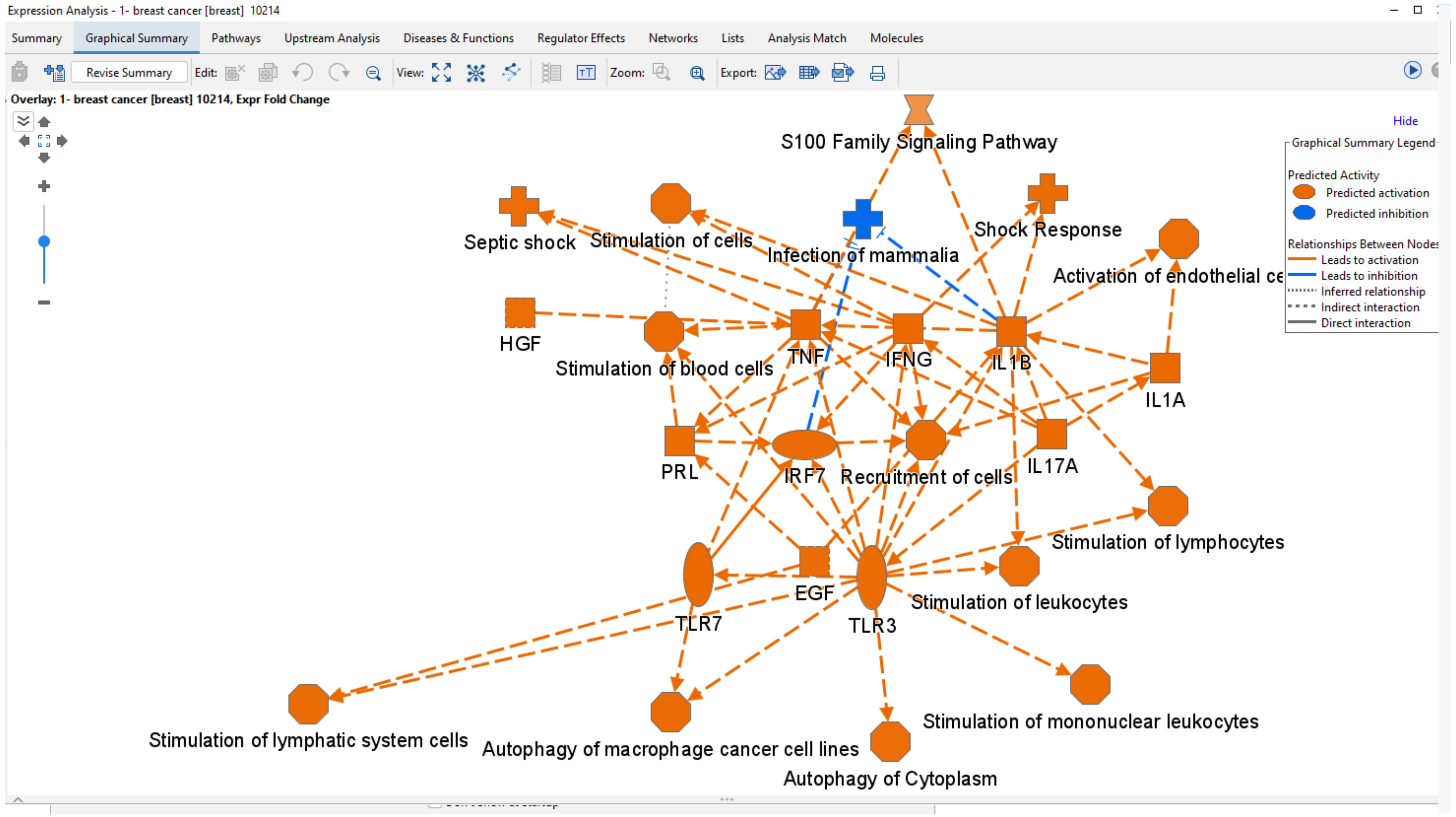
- My Projects
- Shared Projects
- Libraries
  - OmicSoft
    - OncoLand
    - DiseaseLand
    - SingleCellLand
    - Normal Cells and Tissues
  - Ingen
  - ML D
  - My P
  - Ingen
  - My Li

Project Manager

A-Z Sort | Refresh

- 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
- 1- bronchiolitis [peripheral blood] 2806

Graphical summary

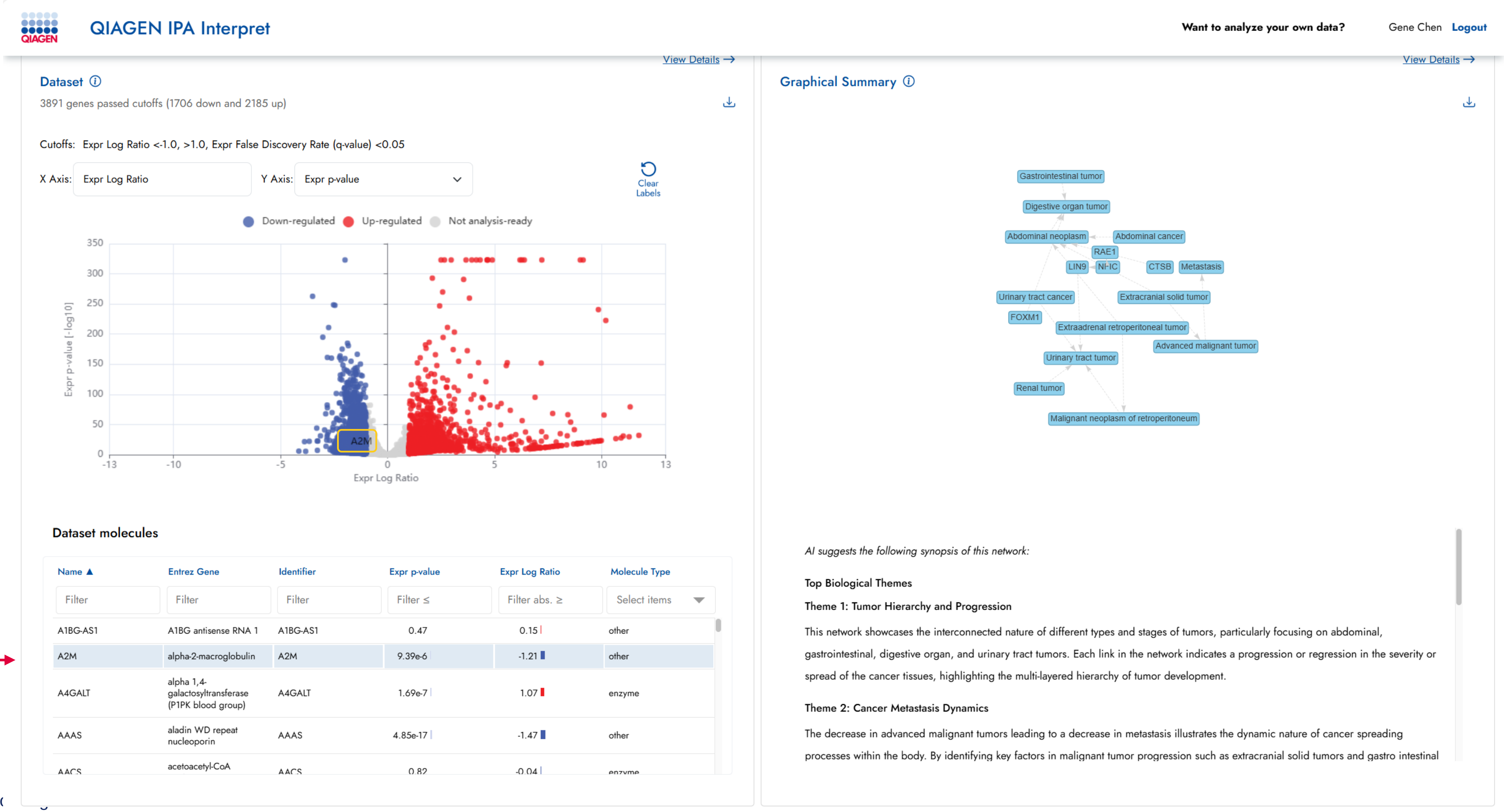


Expression Analysis - 1- breast cancer [breast] 10214

Overlay: 1- breast cancer [breast] 10214, Expr Fold Change

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

IPA interpret



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

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

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

Table | Bar Chart | **Bubble Chart**

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...

More filters

Figure Legend ON

Pathway type: 🟦 Signaling 🟨 Reactome 🟥 Metabolic

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)

IPA interpret

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

Dataset molecules for Cerebral Malformation Signaling Pathway

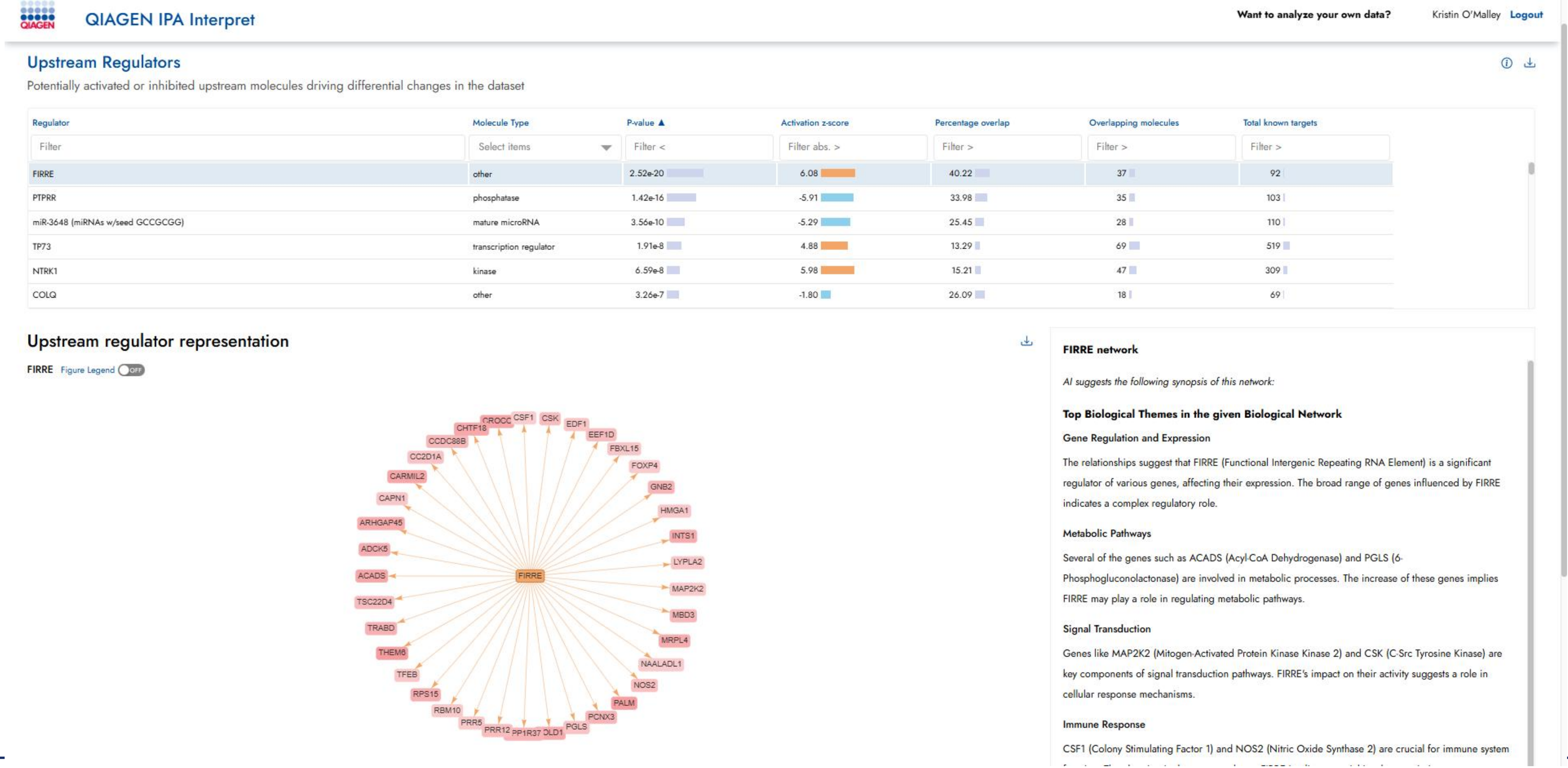
Showing all **19** molecules

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

Powered by QIAGEN Digital Insights

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

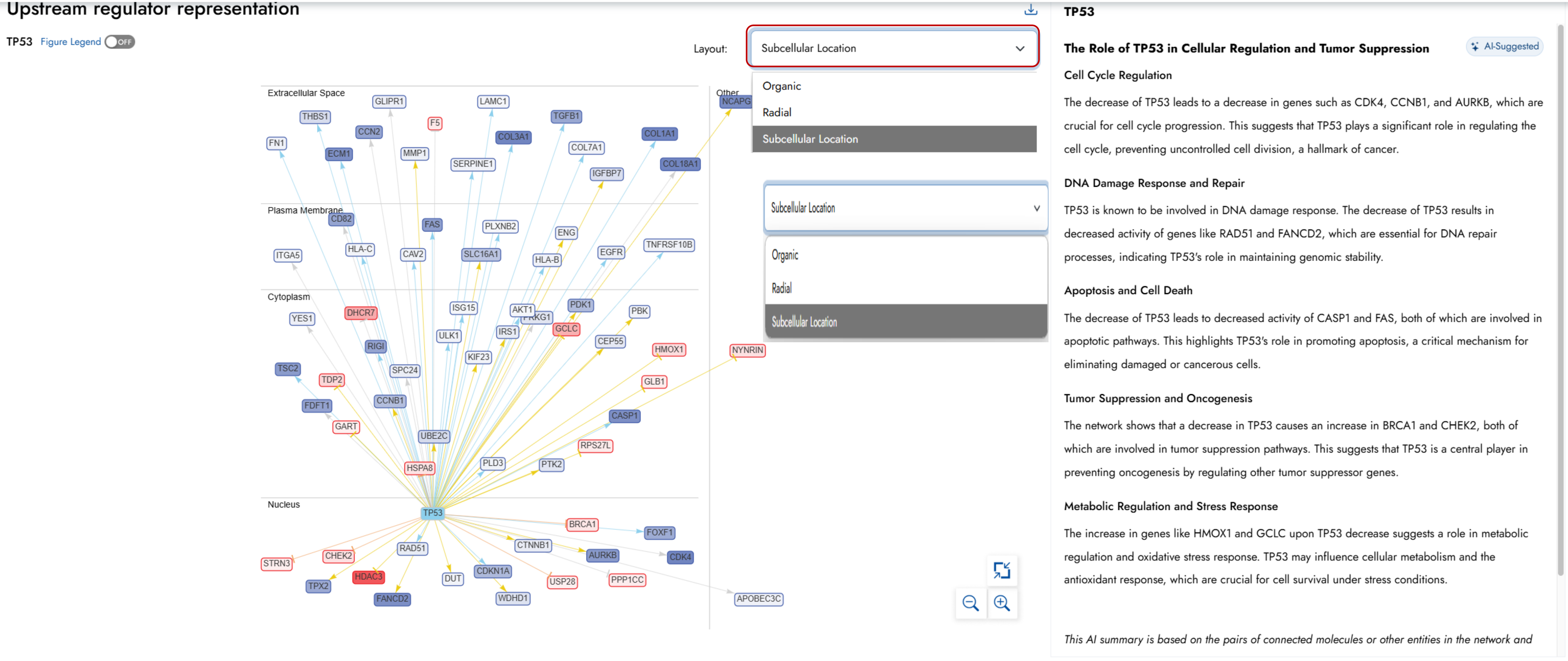
Genes like MAP2K2 (Mitogen-Activated Protein Kinase Kinase 2) and CSK (C-Src Tyrosine Kinase) are key components of signal transduction pathways. FIRRE's impact on their activity suggests a role in cellular response mechanisms.

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 in upstream regulator



Upstream regulator representation

TP53 Figure Legend OFF

Layout: Subcellular Location

TP53

The Role of TP53 in Cellular Regulation and Tumor Suppression AI-Suggested

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.

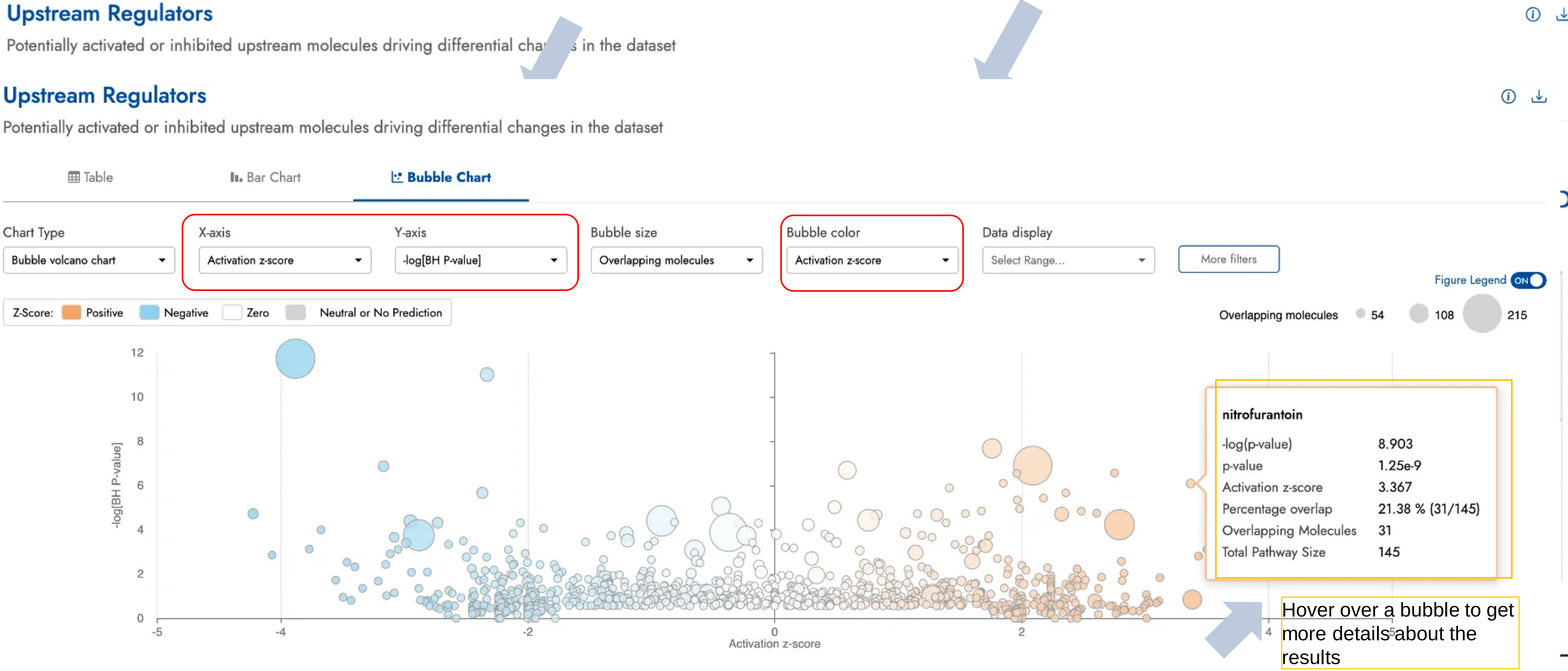
This AI summary is based on the pairs of connected molecules or other entities in the network and

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

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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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

Table | Bar Chart | **Bubble Chart**

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:

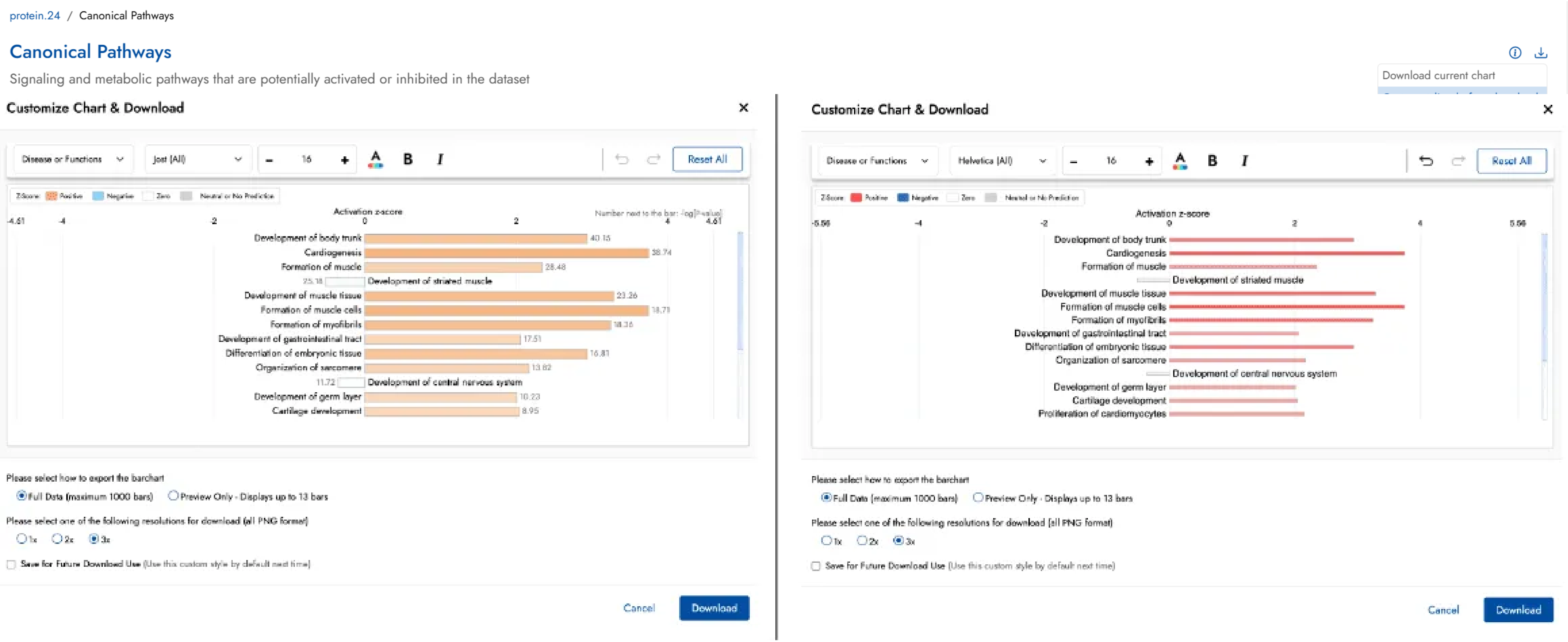
Diseases and Functions Display

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

☐ All Diseases and Functions (2761) Expand all Collapse all

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

Customize bar charts for image export



protein.24 / Canonical Pathways

Canonical Pathways

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

Download current chart

Customize Chart & Download

Disease or Functions | Jost (All) | 16 | Reset All

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)

Cancel | Download

Customize Chart & Download

Disease or Functions | Helvetica (All) | 16 | Reset All

Please select how to export the barchart

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

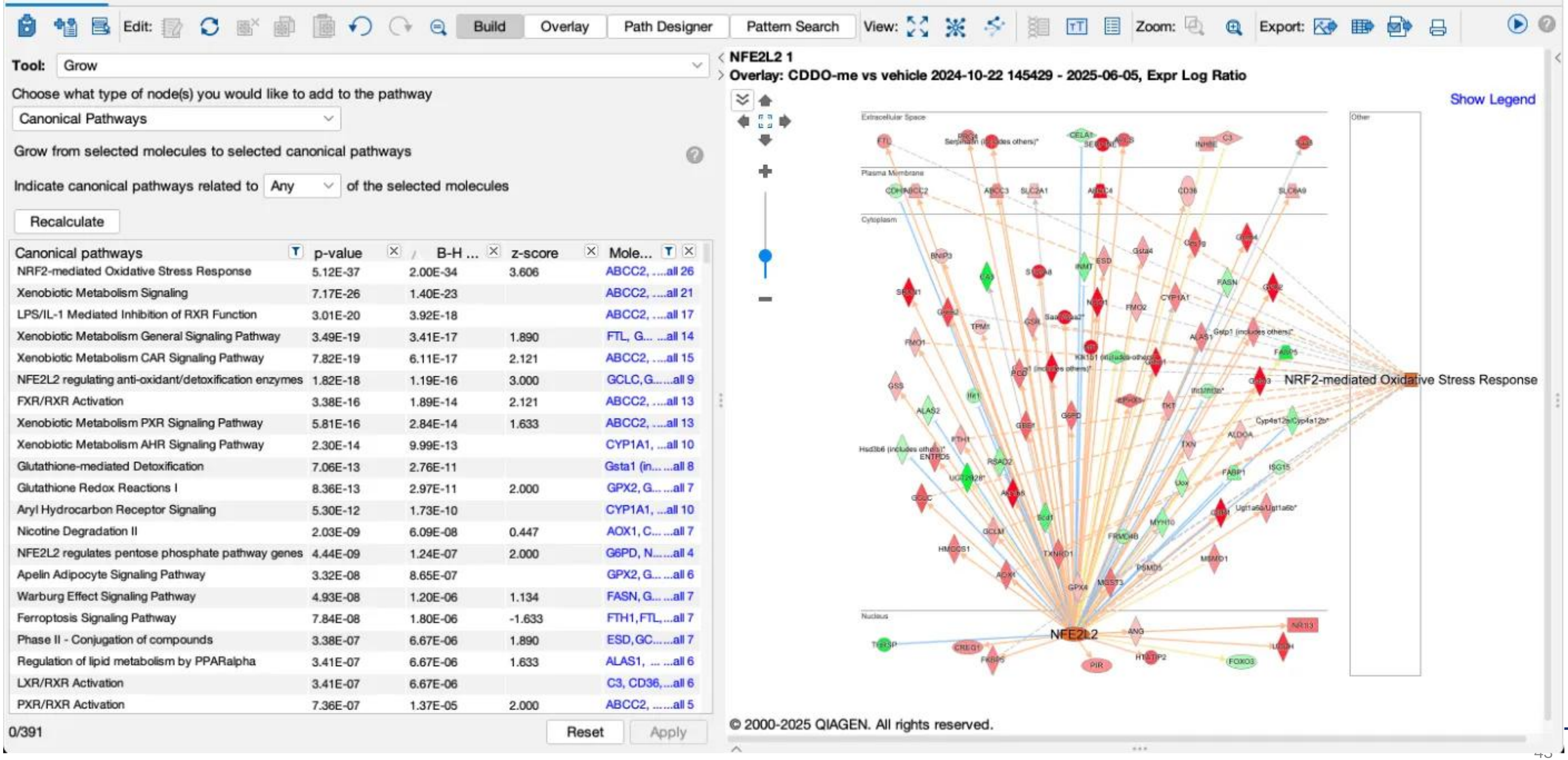
Please select one of the following resolutions for download (all PNG format)

○ 1x ○ 2x ● 3x

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

Cancel | Download

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

Recalculate

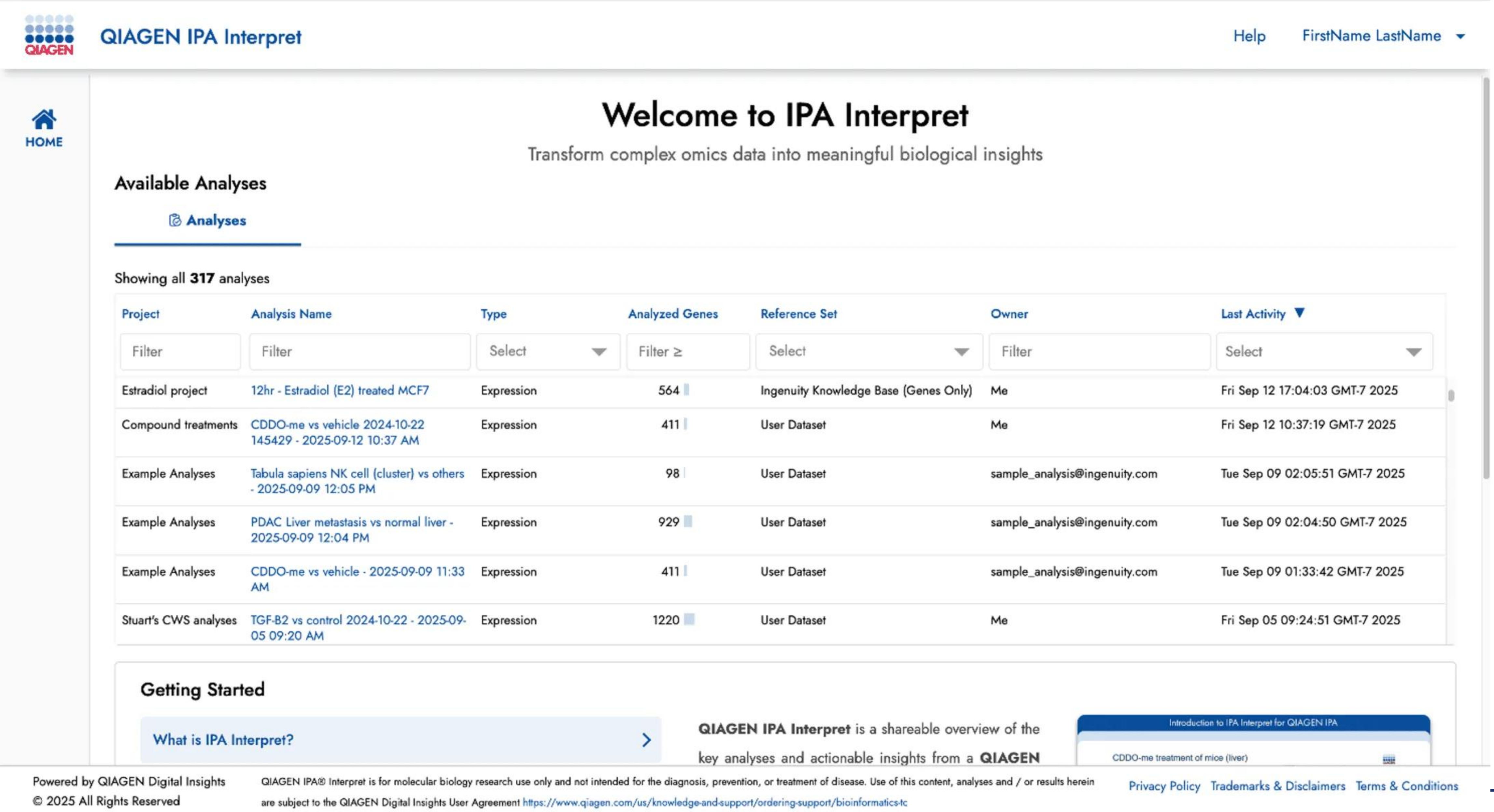
Canonical pathways	p-value	B-H ...	z-score	Mole...
NRF2-mediated Oxidative Stress Response	5.12E-37	2.00E-34	3.606	ABCC2, ...all 26
Xenobiotic Metabolism Signaling	7.17E-26	1.40E-23		ABCC2, ...all 21
LPS/IL-1 Mediated Inhibition of RXR Function	3.01E-20	3.92E-18		ABCC2, ...all 17
Xenobiotic Metabolism 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

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



QIAGEN IPA Interpret

Help FirstName LastName

HOME

Welcome to IPA Interpret

Transform complex omics data into meaningful biological insights

Available Analyses

Analyses

Showing all **317** analyses

Project	Analysis Name	Type	Analyzed Genes	Reference Set	Owner	Last Activity ▼
Filter	Filter	Select	Filter ≥	Select	Filter	Select
Estradiol project	12hr - Estradiol (E2) treated MCF7	Expression	564	Ingenuity Knowledge Base (Genes Only)	Me	Fri Sep 12 17:04:03 GMT-7 2025
Compound treatments	CDDO-me vs vehicle 2024-10-22 145429 - 2025-09-12 10:37 AM	Expression	411	User Dataset	Me	Fri Sep 12 10:37:19 GMT-7 2025
Example Analyses	Tabula sapiens NK cell (cluster) vs others - 2025-09-09 12:05 PM	Expression	98	User Dataset	sample_analysis@ingenuity.com	Tue Sep 09 02:05:51 GMT-7 2025
Example Analyses	PDAC Liver metastasis vs normal liver - 2025-09-09 12:04 PM	Expression	929	User Dataset	sample_analysis@ingenuity.com	Tue Sep 09 02:04:50 GMT-7 2025
Example Analyses	CDDO-me vs vehicle - 2025-09-09 11:33 AM	Expression	411	User Dataset	sample_analysis@ingenuity.com	Tue Sep 09 01:33:42 GMT-7 2025
Stuart's CWS analyses	TGF-B2 vs control 2024-10-22 - 2025-09-05 09:20 AM	Expression	1220	User Dataset	Me	Fri Sep 05 09:24:51 GMT-7 2025

Getting Started

What is IPA Interpret? ›

QIAGEN IPA Interpret is a shareable overview of the key analyses and actionable insights from a **QIAGEN**

Introduction to IPA Interpret for QIAGEN IPA

CDDO-me treatment of mice (liver)

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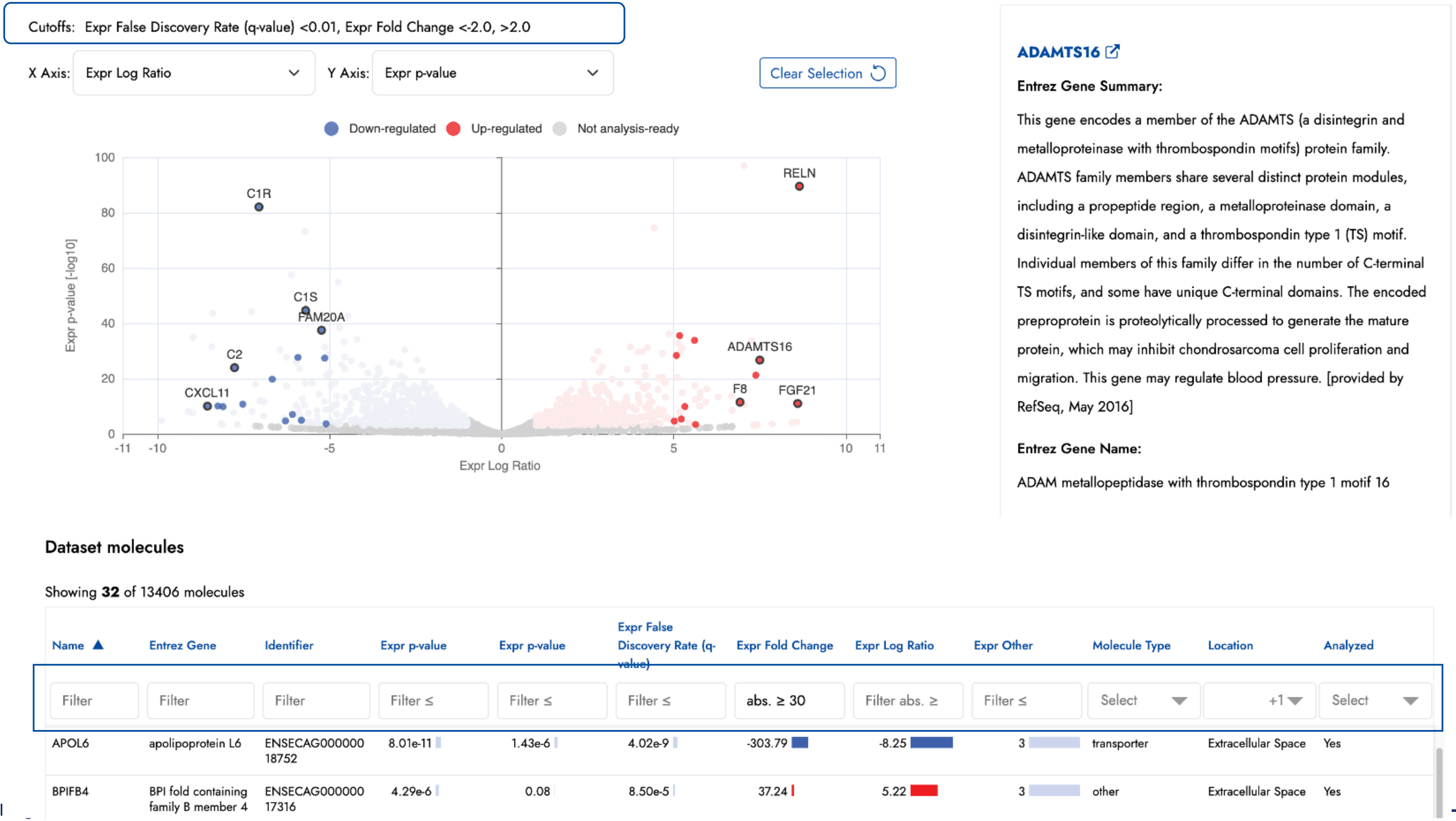
What’s new in the QIAGEN® Ingenuity Pathway Analysis Fall Release (2025)



Cutoffs: Expr False Discovery Rate (q-value) <0.01, Expr Fold Change <-2.0, >2.0

X Axis: Expr Log Ratio

Y Axis: Expr p-value

ADAMTS16

Entrez Gene Summary:

This gene encodes a member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) protein family. ADAMTS family members share several distinct protein modules, including a propeptide region, a metalloproteinase domain, a disintegrin-like domain, and a thrombospondin type 1 (TS) motif. Individual members of this family differ in the number of C-terminal TS motifs, and some have unique C-terminal domains. The encoded preproprotein is proteolytically processed to generate the mature protein, which may inhibit chondrosarcoma cell proliferation and migration. This gene may regulate blood pressure. [provided by RefSeq, May 2016]

Entrez Gene Name:

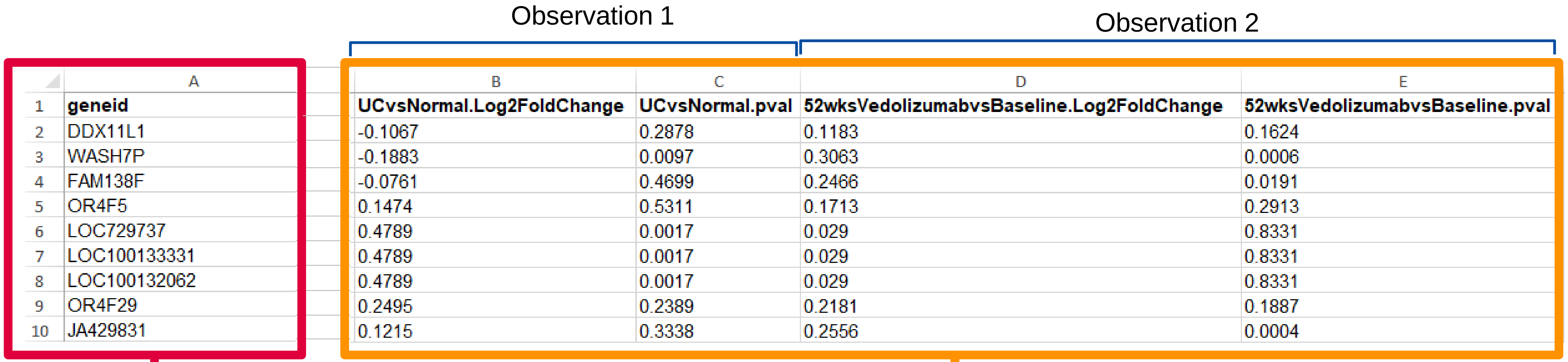
ADAM metallopeptidase with thrombospondin type 1 motif 16

Dataset molecules

Showing **32** of 13406 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	Analyzed
Filter	Filter	Filter	Filter ≤	Filter ≤	Filter ≤	abs. ≥ 30	Filter abs. ≥	Filter ≤	Select	+1	Select
APOL6	apolipoprotein L6	ENSECAG00000018752	8.01e-11	1.43e-6	4.02e-9	-303.79	-8.25	3	transporter	Extracellular Space	Yes
BPIFB4	BPI fold containing family B member 4	ENSECAG00000017316	4.29e-6	0.08	8.50e-5	37.24	5.22	3	other	Extracellular Space	Yes

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.

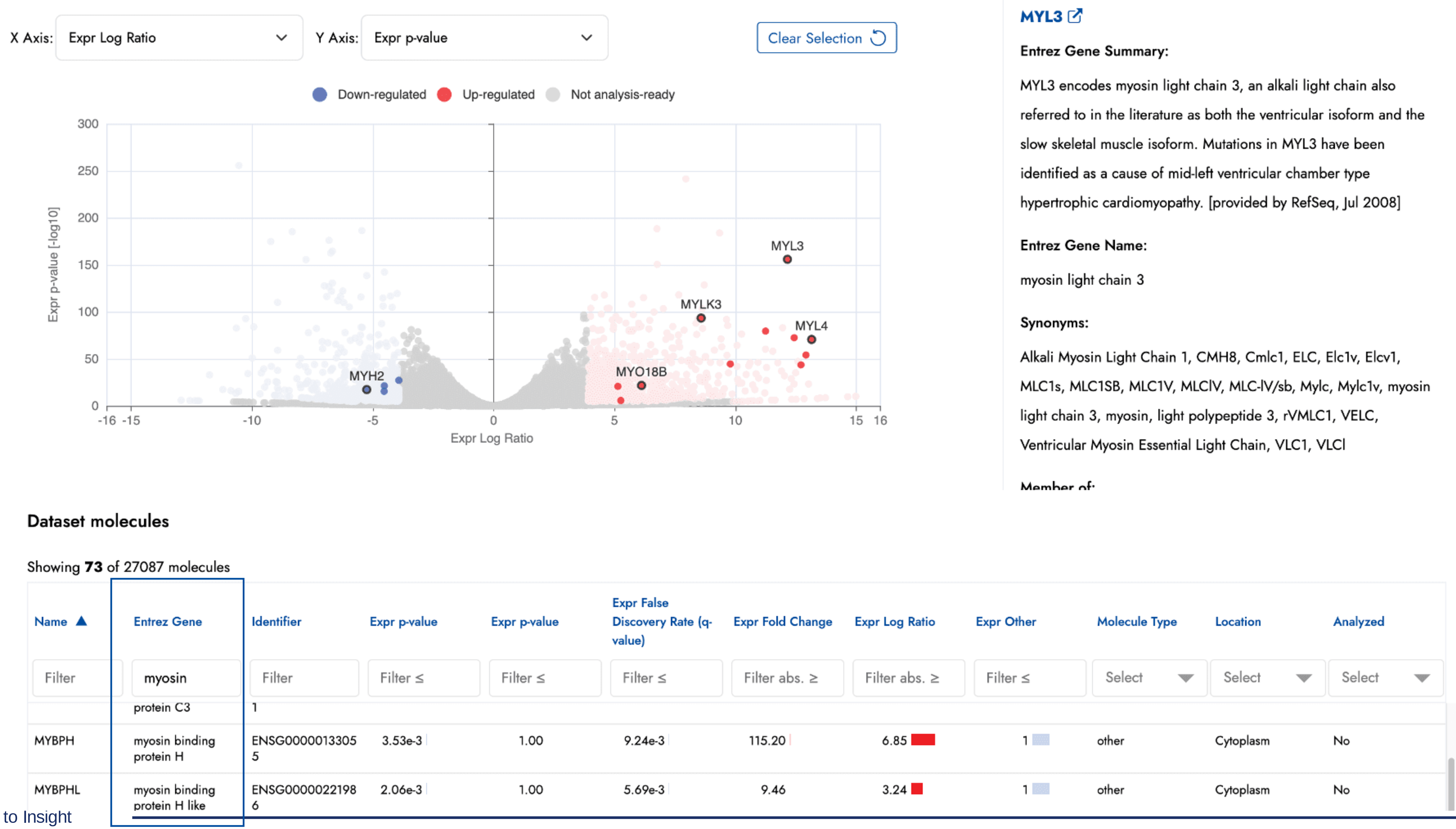
Significance values: P-values **optional but recommended to enable filtering for significance*

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

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



MYL3

Entrez Gene Summary:

MYL3 encodes myosin light chain 3, an alkali light chain also referred to in the literature as both the ventricular isoform and the slow skeletal muscle isoform. Mutations in MYL3 have been identified as a cause of mid-left ventricular chamber type hypertrophic cardiomyopathy. [provided by RefSeq, Jul 2008]

Entrez Gene Name:

myosin light chain 3

Synonyms:

Alkali Myosin Light Chain 1, CMH8, Cmlc1, ELC, Elc1v, Elcv1, MLC1s, MLC1SB, MLC1V, MLClV, MLC-lV/sb, Mylc, Mylc1v, myosin light chain 3, myosin, light polypeptide 3, rVMLC1, VELC, Ventricular Myosin Essential Light Chain, VLC1, VLCl

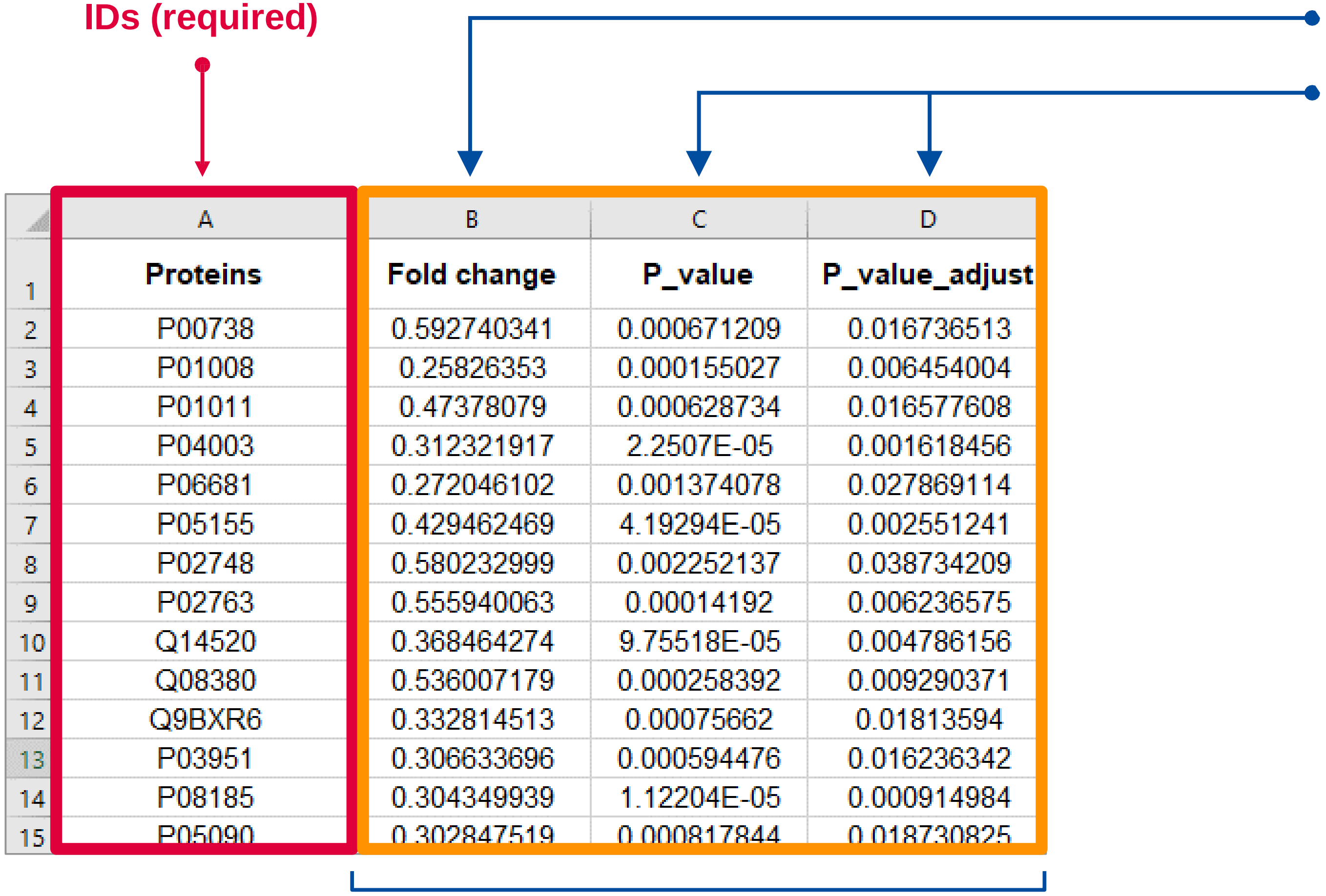
Member of:

Dataset molecules

Showing **73** of 27087 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	Analyzed
Filter	myosin	Filter	Filter ≤	Filter ≤	Filter ≤	Filter abs. ≥	Filter abs. ≥	Filter ≤	Select ▼	Select ▼	Select ▼
	protein C3	1									
MYBPH	myosin binding protein H	ENSG00000133055	3.53e-3	1.00	9.24e-3	115.20	6.85 🟥	1	other	Cytoplasm	No
MYBPHL	myosin binding protein H like	ENSG00000221986	2.06e-3	1.00	5.69e-3	9.46	3.24 🟥	1	other	Cytoplasm	No

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:

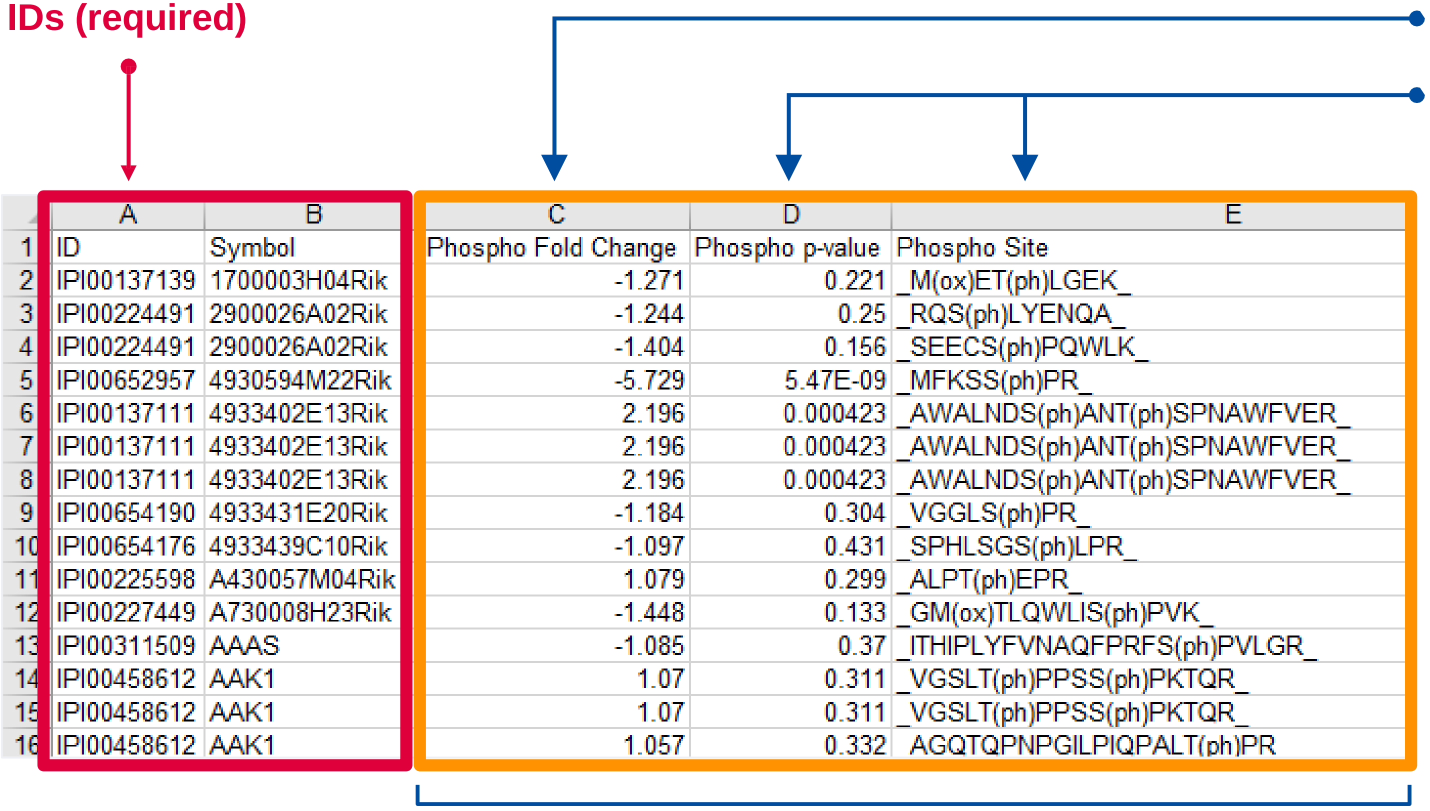
- https://www.uniprot.org/mapping/

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

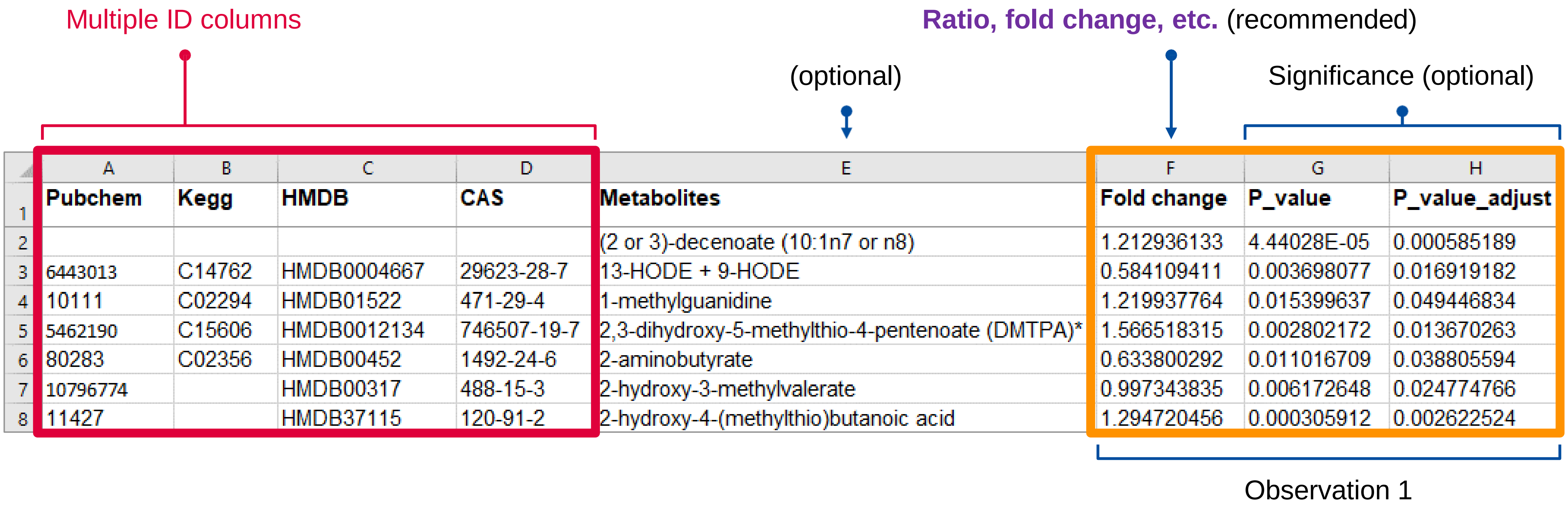
Common protein IDs

- 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)

Observation 1

	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

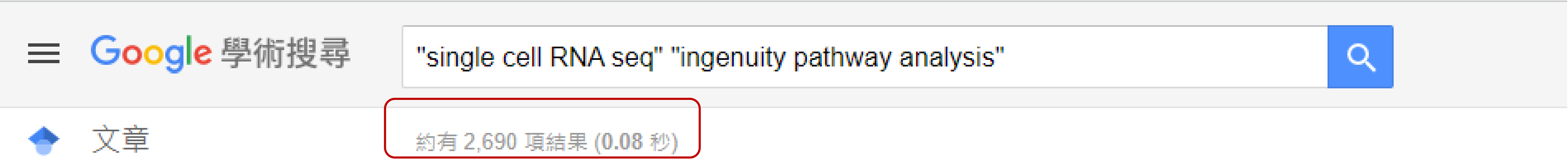
Common metabolite IDs

- 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

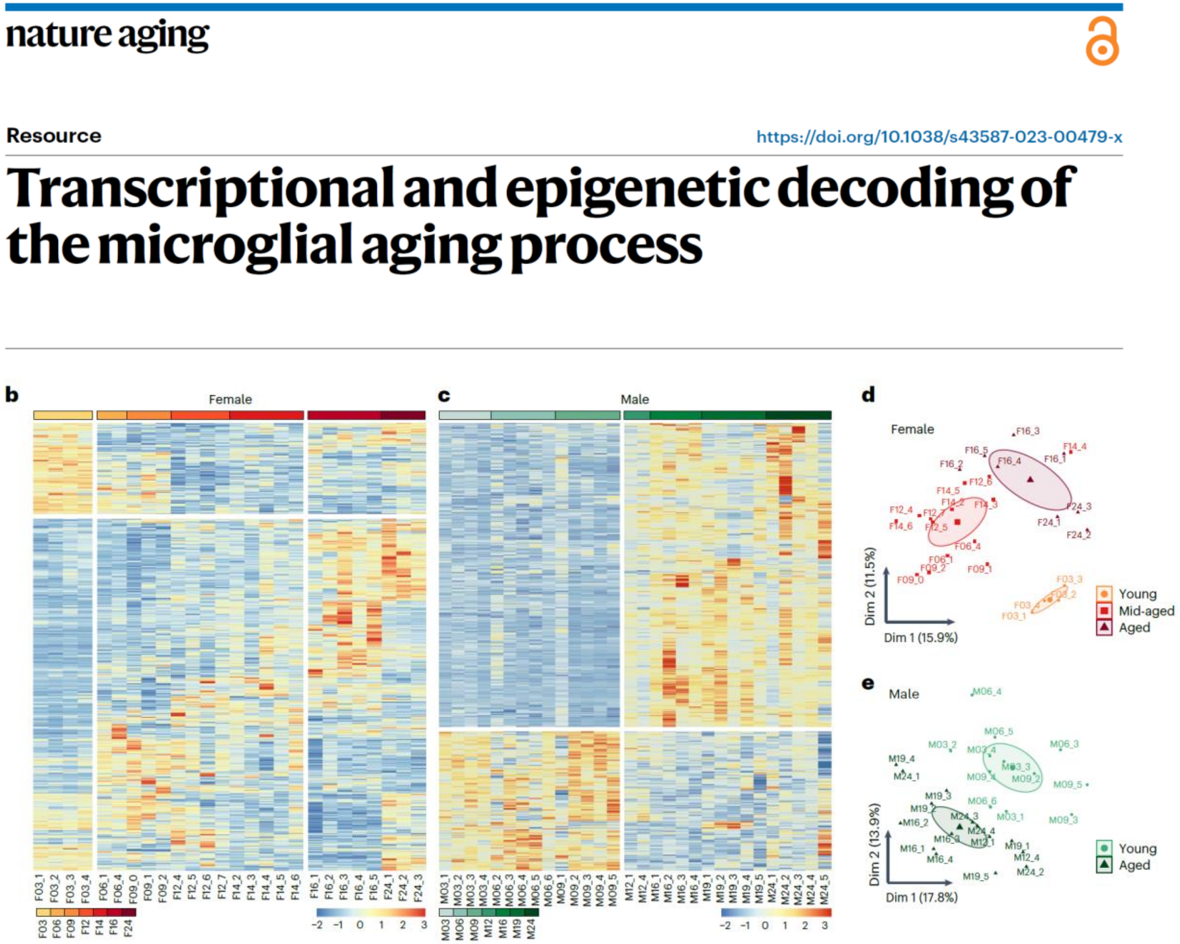
Publication of Single-cell RNA Seq and Qiagen IPA


Google 學術搜尋

"single cell RNA seq" "ingenuity pathway analysis"

文章

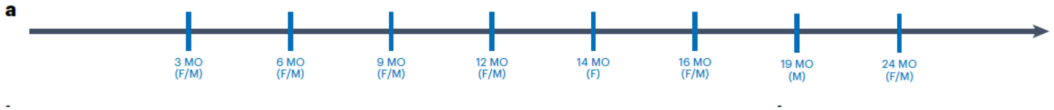
約有 2,690 項結果 (0.08 秒)

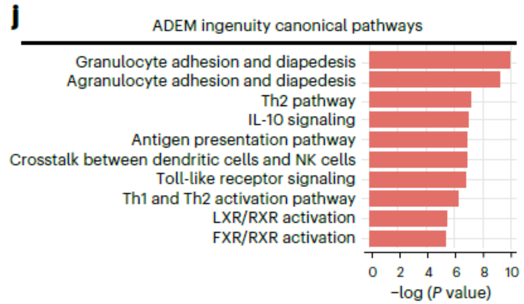

nature aging

Resource

https://doi.org/10.1038/s43587-023-00479-x

Transcriptional and epigenetic decoding of the microglial aging process

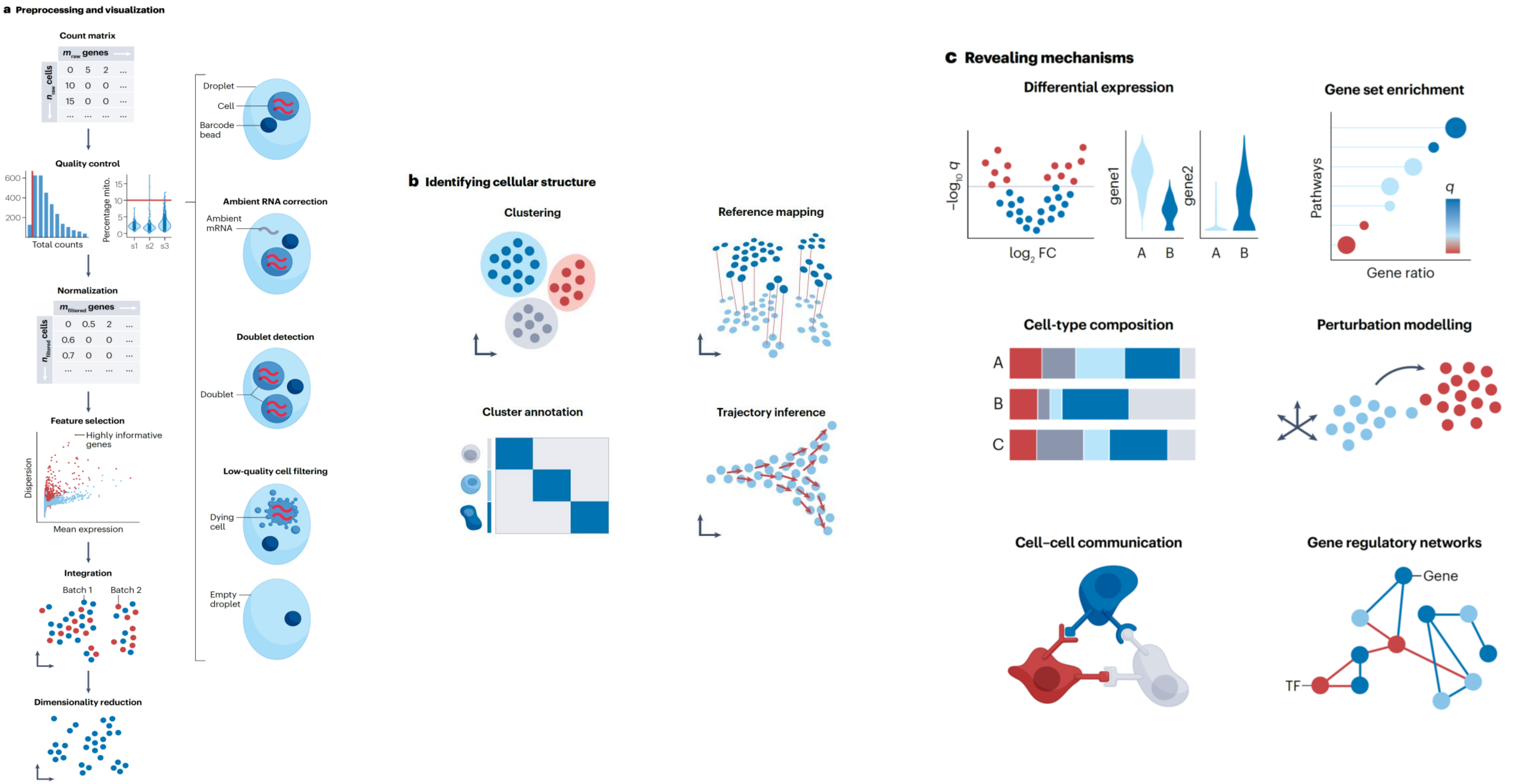




UCLA Health Jonsson Comprehensive Cancer center also use Qiagen IPA to interpreted spatial transcriptome

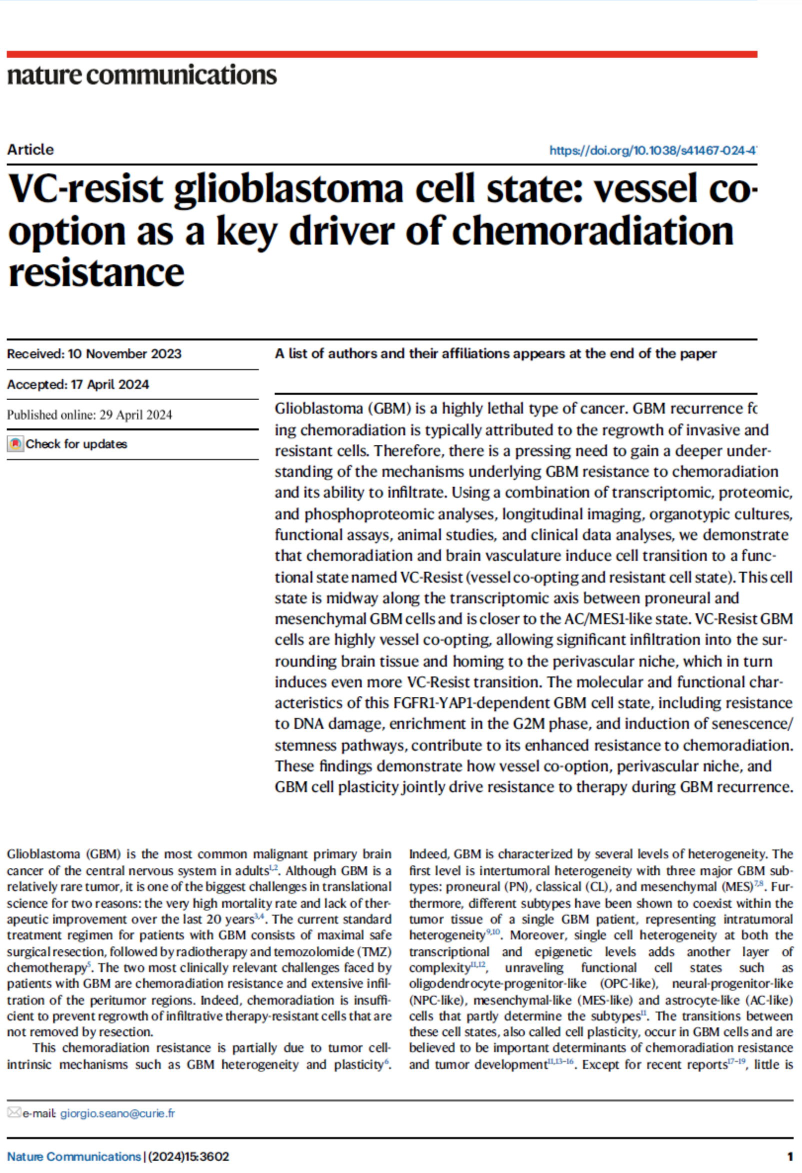
https://www.uclahealth.org/cancer/researchers/shared-resources/genomics

Overview of unimodal analysis steps for scRNA-seq



Heumos, L., Schaar, A.C., Lance, C. *et al.* Best practices for single-cell analysis across modalities. *Nat Rev Genet* **24**, 550–572 (2023). https://doi.org/10.1038/s41576-023-00586-w

Single-Cell RNA-seq case study



nature communications

Article https://doi.org/10.1038/s41467-024-4

VC-resist glioblastoma cell state: vessel co-option as a key driver of chemoradiation resistance

Received: 10 November 2023
Accepted: 17 April 2024

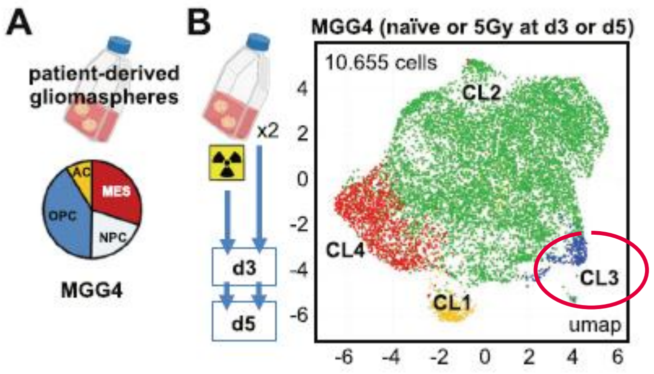
A list of authors and their affiliations appears at the end of the paper

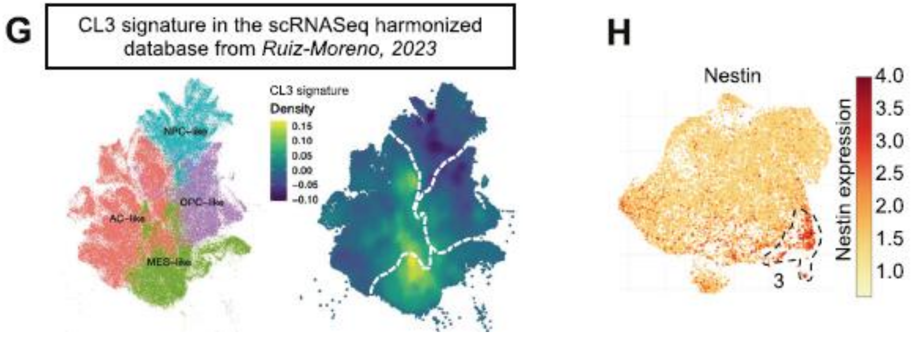
Glioblastoma (GBM) is a highly lethal type of cancer. GBM recurrence fc ing chemoradiation is typically attributed to the regrowth of invasive and resistant cells. Therefore, there is a pressing need to gain a deeper understanding of the mechanisms underlying GBM resistance to chemoradiation and its ability to infiltrate. Using a combination of transcriptomic, proteomic, and phosphoproteomic analyses, longitudinal imaging, organotypic cultures, functional assays, animal studies, and clinical data analyses, we demonstrate that chemoradiation and brain vasculature induce cell transition to a functional state named VC-Resist (vessel co-opting and resistant cell state). This cell state is midway along the transcriptomic axis between proneural and mesenchymal GBM cells and is closer to the AC/MES1-like state. VC-Resist GBM cells are highly vessel co-opting, allowing significant infiltration into the surrounding brain tissue and homing to the perivascular niche, which in turn induces even more VC-Resist transition. The molecular and functional characteristics of this FGFR1-YAP1-dependent GBM cell state, including resistance to DNA damage, enrichment in the G2M phase, and induction of senescence/stemness pathways, contribute to its enhanced resistance to chemoradiation. These findings demonstrate how vessel co-option, perivascular niche, and GBM cell plasticity jointly drive resistance to therapy during GBM recurrence.

Glioblastoma (GBM) is the most common malignant primary brain cancer of the central nervous system in adults[1,2]. Although GBM is a relatively rare tumor, it is one of the biggest challenges in translational science for two reasons: the very high mortality rate and lack of therapeutic improvement over the last 20 years[3,4]. The current standard treatment regimen for patients with GBM consists of maximal safe surgical resection, followed by radiotherapy and temozolomide (TMZ) chemotherapy[5]. The two most clinically relevant challenges faced by patients with GBM are chemoradiation resistance and extensive infiltration of the peritumor regions. Indeed, chemoradiation is insufficient to prevent regrowth of infiltrative therapy-resistant cells that are not removed by resection.

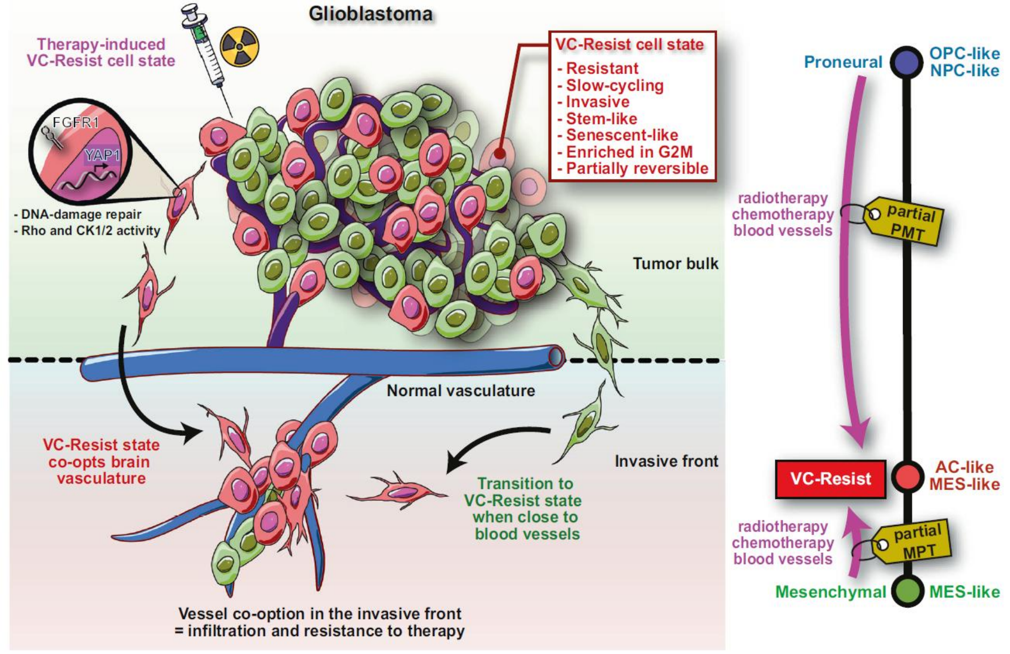
This chemoradiation resistance is partially due to tumor cell-intrinsic mechanisms such as GBM heterogeneity and plasticity[6]. Indeed, GBM is characterized by several levels of heterogeneity. The first level is intertumoral heterogeneity with three major GBM subtypes: proneural (PN), classical (CL), and mesenchymal (MES)[7,8]. Furthermore, different subtypes have been shown to coexist within the tumor tissue of a single GBM patient, representing intratumoral heterogeneity[9,10]. Moreover, single cell heterogeneity at both the transcriptional and epigenetic levels adds another layer of complexity[11,12], unraveling functional cell states such as oligodendrocyte-progenitor-like (OPC-like), neural-progenitor-like (NPC-like), mesenchymal-like (MES-like) and astrocyte-like (AC-like) cells that partly determine the subtypes[11]. The transitions between these cell states, also called cell plasticity, occur in GBM cells and are believed to be important determinants of chemoradiation resistance and tumor development[11,13–16]. Except for recent reports[17–19], little is

e-mail: giorgio.seano@curie.fr





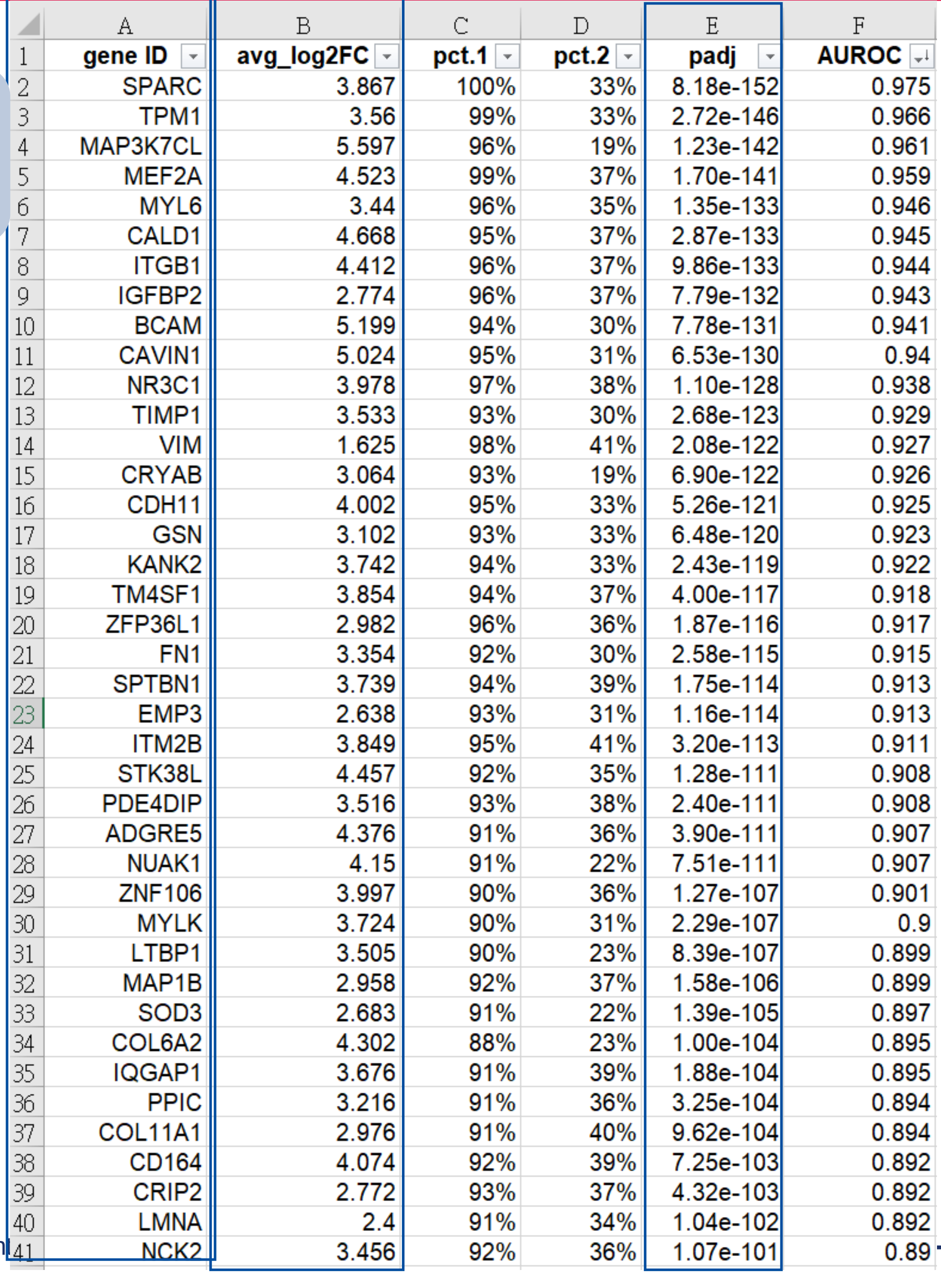
CL3 more stem cell like and highly Nestin



ig. 10 | **Here we show a cell state called VC-Resist that, even if already present ı naïve tumors at different levels, is strongly induced by chemoradiation and ngiocrine factors from the brain blood vessels.** The VC-Resist cells are interıediate in the PMT and are highly resistant to therapy, vessel co-opting, senescentke and slow-cycling. Considering our discoveries, we propose a model wherein chemoradiation leads to vessel co-option and resistance to therapy via reprogramming of GBM cells into the VC-Resist cell state. This creates a self-perpetuating cycle, as increased resistance and vessel co-option contribute to the recurrence of GBM.

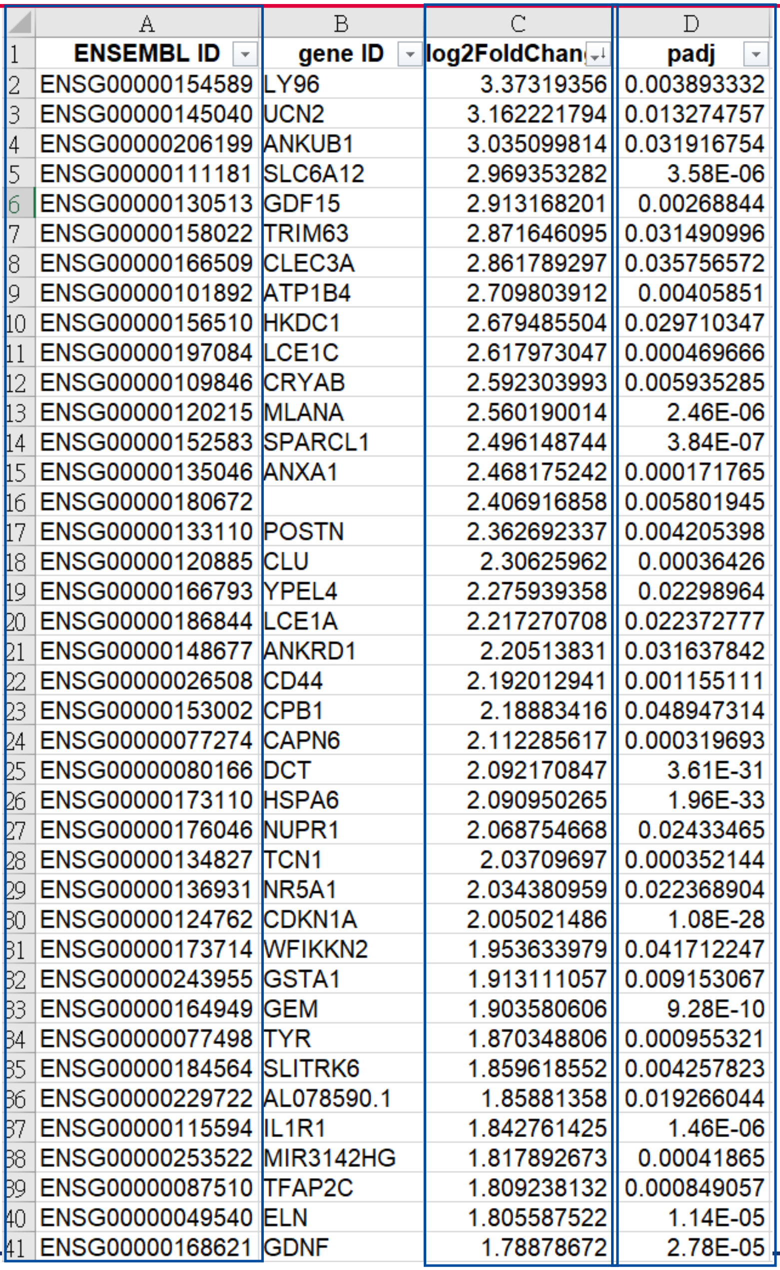
scRNA upload data

CL3 Differential Expression

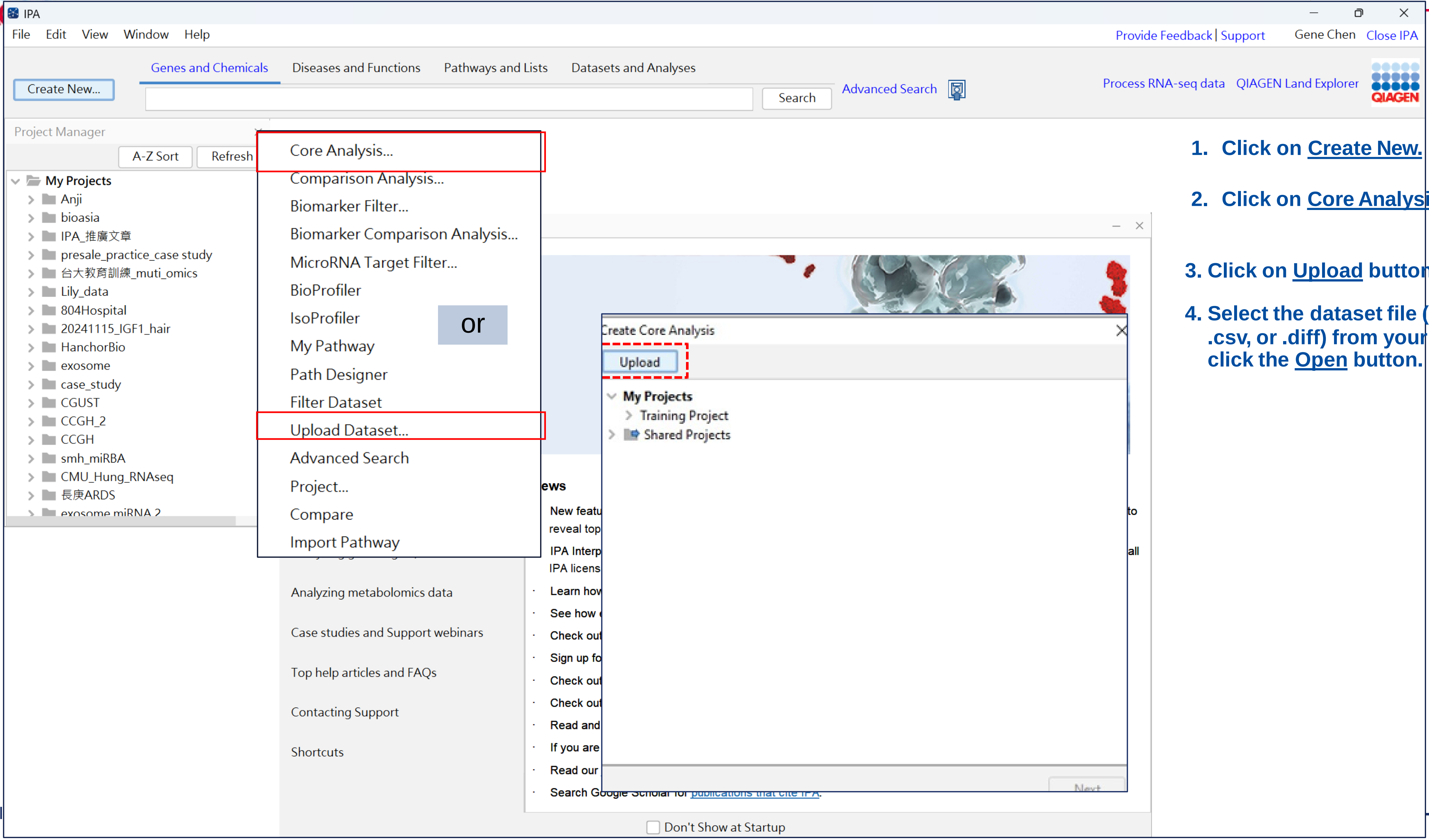


	A	B	C	D	E	F
1	gene ID	avg_log2FC	pct.1	pct.2	padj	AUROC
2	SPARC	3.867	100%	33%	8.18e-152	0.975
3	TPM1	3.56	99%	33%	2.72e-146	0.966
4	MAP3K7CL	5.597	96%	19%	1.23e-142	0.961
5	MEF2A	4.523	99%	37%	1.70e-141	0.959
6	MYL6	3.44	96%	35%	1.35e-133	0.946
7	CALD1	4.668	95%	37%	2.87e-133	0.945
8	ITGB1	4.412	96%	37%	9.86e-133	0.944
9	IGFBP2	2.774	96%	37%	7.79e-132	0.943
10	BCAM	5.199	94%	30%	7.78e-131	0.941
11	CAVIN1	5.024	95%	31%	6.53e-130	0.94
12	NR3C1	3.978	97%	38%	1.10e-128	0.938
13	TIMP1	3.533	93%	30%	2.68e-123	0.929
14	VIM	1.625	98%	41%	2.08e-122	0.927
15	CRYAB	3.064	93%	19%	6.90e-122	0.926
16	CDH11	4.002	95%	33%	5.26e-121	0.925
17	GSN	3.102	93%	33%	6.48e-120	0.923
18	KANK2	3.742	94%	33%	2.43e-119	0.922
19	TM4SF1	3.854	94%	37%	4.00e-117	0.918
20	ZFP36L1	2.982	96%	36%	1.87e-116	0.917
21	FN1	3.354	92%	30%	2.58e-115	0.915
22	SPTBN1	3.739	94%	39%	1.75e-114	0.913
23	EMP3	2.638	93%	31%	1.16e-114	0.913
24	ITM2B	3.849	95%	41%	3.20e-113	0.911
25	STK38L	4.457	92%	35%	1.28e-111	0.908
26	PDE4DIP	3.516	93%	38%	2.40e-111	0.908
27	ADGRE5	4.376	91%	36%	3.90e-111	0.907
28	NUAK1	4.15	91%	22%	7.51e-111	0.907
29	ZNF106	3.997	90%	36%	1.27e-107	0.901
30	MYLK	3.724	90%	31%	2.29e-107	0.9
31	LTBP1	3.505	90%	23%	8.39e-107	0.899
32	MAP1B	2.958	92%	37%	1.58e-106	0.899
33	SOD3	2.683	91%	22%	1.39e-105	0.897
34	COL6A2	4.302	88%	23%	1.00e-104	0.895
35	IQGAP1	3.676	91%	39%	1.88e-104	0.895
36	PPIC	3.216	91%	36%	3.25e-104	0.894
37	COL11A1	2.976	91%	40%	9.62e-104	0.894
38	CD164	4.074	92%	39%	7.25e-103	0.892
39	CRIP2	2.772	93%	37%	4.32e-103	0.892
40	LMNA	2.4	91%	34%	1.04e-102	0.892
41	NCK2	3.456	92%	36%	1.07e-101	0.89

MGG4 Nestin high



	A	B	C	D
1	ENSEMBL ID	gene ID	log2FoldChan	padj
2	ENSG00000154589	LY96	3.37319356	0.003893332
3	ENSG00000145040	UCN2	3.162221794	0.013274757
4	ENSG00000206199	ANKUB1	3.035099814	0.031916754
5	ENSG00000111181	SLC6A12	2.969353282	3.58E-06
6	ENSG00000130513	GDF15	2.913168201	0.00268844
7	ENSG00000158022	TRIM63	2.871646095	0.031490996
8	ENSG00000166509	CLEC3A	2.861789297	0.035756572
9	ENSG00000101892	ATP1B4	2.709803912	0.00405851
10	ENSG00000156510	HKDC1	2.679485504	0.029710347
11	ENSG00000197084	LCE1C	2.617973047	0.000469666
12	ENSG00000109846	CRYAB	2.592303993	0.005935285
13	ENSG00000120215	MLANA	2.560190014	2.46E-06
14	ENSG00000152583	SPARCL1	2.496148744	3.84E-07
15	ENSG00000135046	ANXA1	2.468175242	0.000171765
16	ENSG00000180672		2.406916858	0.005801945
17	ENSG00000133110	POSTN	2.362692337	0.004205398
18	ENSG00000120885	CLU	2.30625962	0.00036426
19	ENSG00000166793	YPEL4	2.275939358	0.02298964
20	ENSG00000186844	LCE1A	2.217270708	0.022372777
21	ENSG00000148677	ANKRD1	2.20513831	0.031637842
22	ENSG00000026508	CD44	2.192012941	0.001155111
23	ENSG00000153002	CPB1	2.18883416	0.048947314
24	ENSG00000077274	CAPN6	2.112285617	0.000319693
25	ENSG00000080166	DCT	2.092170847	3.61E-31
26	ENSG00000173110	HSPA6	2.090950265	1.96E-33
27	ENSG00000176046	NUPR1	2.068754668	0.02433465
28	ENSG00000134827	TCN1	2.03709697	0.000352144
29	ENSG00000136931	NR5A1	2.034380959	0.022368904
30	ENSG00000124762	CDKN1A	2.005021486	1.08E-28
31	ENSG00000173714	WFIKKN2	1.953633979	0.041712247
32	ENSG00000243955	GSTA1	1.913111057	0.009153067
33	ENSG00000164949	GEM	1.903580606	9.28E-10
34	ENSG00000077498	TYR	1.870348806	0.000955321
35	ENSG00000184564	SLITRK6	1.859618552	0.004257823
36	ENSG00000229722	AL078590.1	1.85881358	0.019266044
37	ENSG00000115594	IL1R1	1.842761425	1.46E-06
38	ENSG00000253522	MIR3142HG	1.817892673	0.00041865
39	ENSG00000087510	TFAP2C	1.809238132	0.000849057
40	ENSG00000049540	ELN	1.805587522	1.14E-05
41	ENSG00000168621	GDNF	1.78878672	2.78E-05



1. **Click on Create New.**

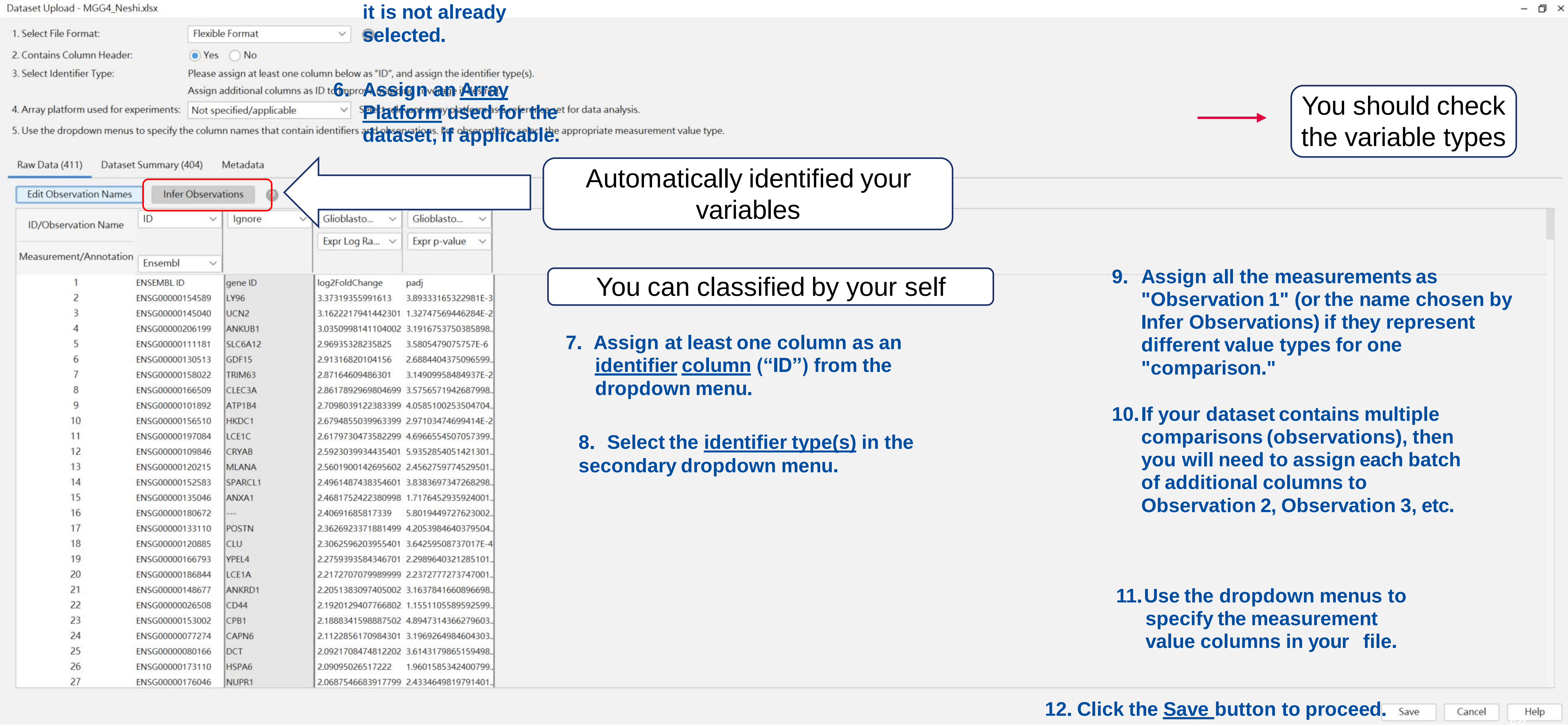
2. **Click on Core Analysis.**

3. **Click on Upload button.**

4. **Select the dataset file (.txt, .xls, .xlsx .csv, or .diff) from your computer an click the Open button.**

Identified your variable in your dataset

5. Select **Flexible Format** for the file format from the dropdown menu if it is not already selected.



Dataset Upload - MGG4_Neshi.xlsx

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 platforms as reference set for data analysis.
5. Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appropriate measurement value type.

6. Assign an **Array Platform** used for the dataset, if applicable.

You should check the variable types

Automatically identified your variables

You can classified by your self

ID/Observation Name	ID	Ignore	Glioblasto...	Glioblasto...
Measurement/Annotation	Ensembl		Expr Log Ra...	Expr p-value
1	ENSEMBL ID	gene ID	log2FoldChange	padj
2	ENSG00000154589	LY96	3.37319355991613	3.89333165322981E-3
3	ENSG00000145040	UCN2	3.1622217941442301	1.32747569446284E-2
4	ENSG00000206199	ANKUB1	3.0350998141104002	3.1916753750385898..
5	ENSG00000111181	SLC6A12	2.96935328235825	3.5805479075757E-6
6	ENSG00000130513	GDF15	2.91316820104156	2.6884404375096599..
7	ENSG00000158022	TRIM63	2.87164609486301	3.14909958484937E-2
8	ENSG00000166509	CLEC3A	2.8617892969804699	3.5756571942687998..
9	ENSG00000101892	ATP1B4	2.7098039122383399	4.0585100253504704..
10	ENSG00000156510	HKDC1	2.6794855039963399	2.97103474699414E-2
11	ENSG00000197084	LCE1C	2.6179730473582299	4.6966554507057399..
12	ENSG00000109846	CRYAB	2.5923039934435401	5.9352854051421301..
13	ENSG00000120215	MLANA	2.5601900142695602	2.4562759774529501..
14	ENSG00000152583	SPARCL1	2.4961487438354601	3.8383697347268298..
15	ENSG00000135046	ANXA1	2.4681752422380998	1.7176452935924001..
16	ENSG00000180672	---	2.40691685817339	5.8019449727623002..
17	ENSG00000133110	POSTN	2.3626923371881499	4.2053984640379504..
18	ENSG00000120885	CLU	2.3062596203955401	3.64259508737017E-4
19	ENSG00000166793	YPEL4	2.2759393584346701	2.2989640321285101..
20	ENSG00000186844	LCE1A	2.2172707079989999	2.2372777273747001..
21	ENSG00000148677	ANKRD1	2.2051383097405002	3.1637841660896698..
22	ENSG00000026508	CD44	2.1920129407766802	1.1551105589592599..
23	ENSG00000153002	CPB1	2.1888341598887502	4.8947314366279603..
24	ENSG00000077274	CAPN6	2.1122856170984301	3.1969264984604303..
25	ENSG00000080166	DCT	2.0921708474812202	3.6143179865159498..
26	ENSG00000173110	HSPA6	2.09095026517222	1.9601585342400799..
27	ENSG00000176046	NUPR1	2.0687546683917799	2.4334649819791401..

7. Assign at least one column as an **identifier column** ("ID") from the dropdown menu.

8. Select the **identifier type(s)** in the secondary dropdown menu.

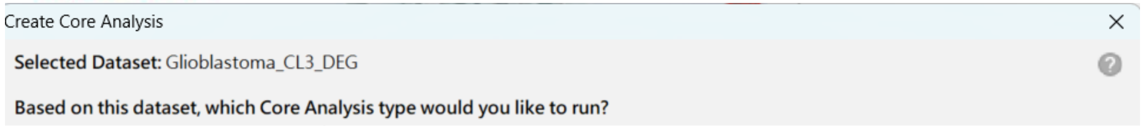
9. Assign all the measurements as "Observation 1" (or the name chosen by Infer Observations) if they represent different value types for one "comparison."

10. If your dataset contains multiple comparisons (observations), then you will need to assign each batch of additional columns to Observation 2, Observation 3, etc.

11. Use the dropdown menus to specify the measurement value columns in your file.

12. Click the **Save** button to proceed.

Setup Cut off and Biological filter

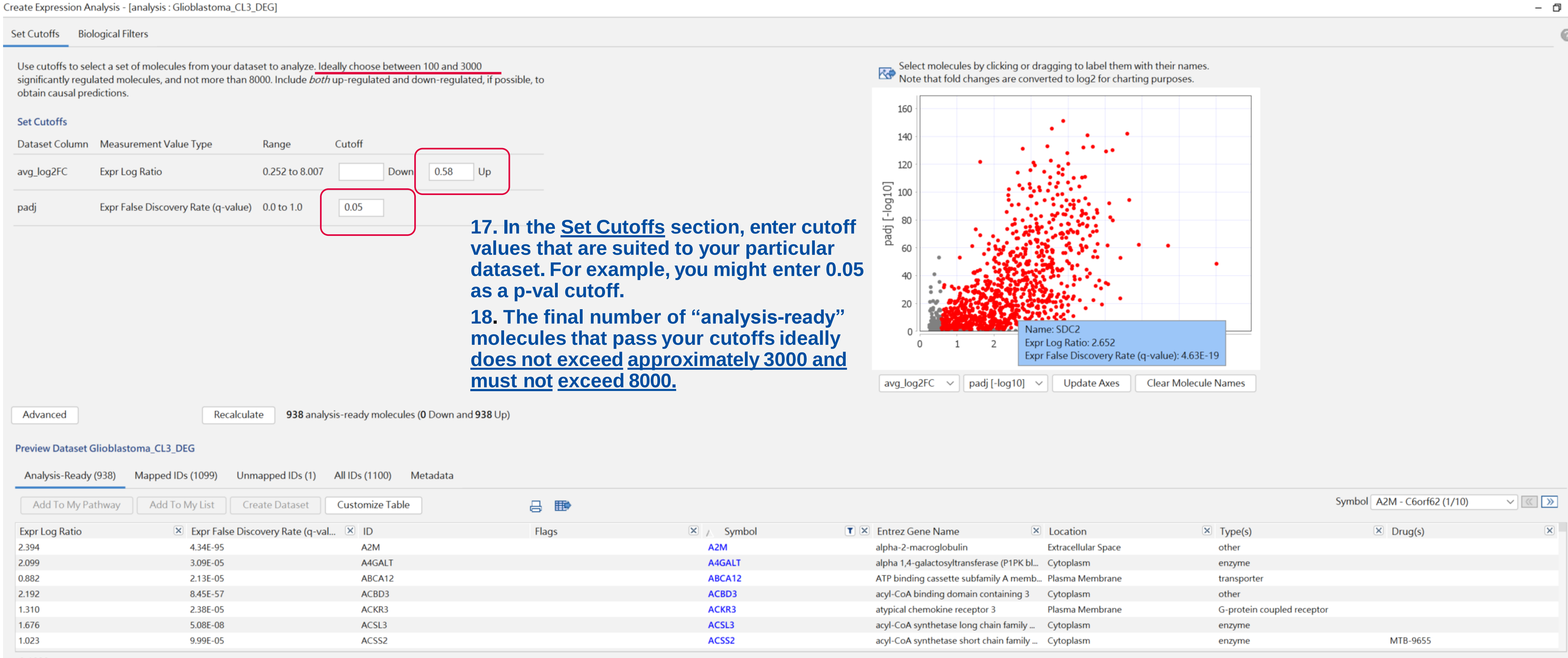


Create Core Analysis

Selected Dataset: Glioblastoma_CL3_DEG

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

16. **Specify the desired type of analysis to apply and measurement type to base it**



Create Expression Analysis - [analysis : Glioblastoma_CL3_DEG]

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			
avg_log2FC	Expr Log Ratio	0.252 to 8.007		Down	0.58	Up
padj	Expr False Discovery Rate (q-value)	0.0 to 1.0	0.05			

17. In the Set Cutoffs section, enter cutoff values that are suited to your particular dataset. For example, you might enter 0.05 as a p-val cutoff.

18. The final number of "analysis-ready" molecules that pass your cutoffs ideally does not exceed approximately 3000 and must not exceed 8000.

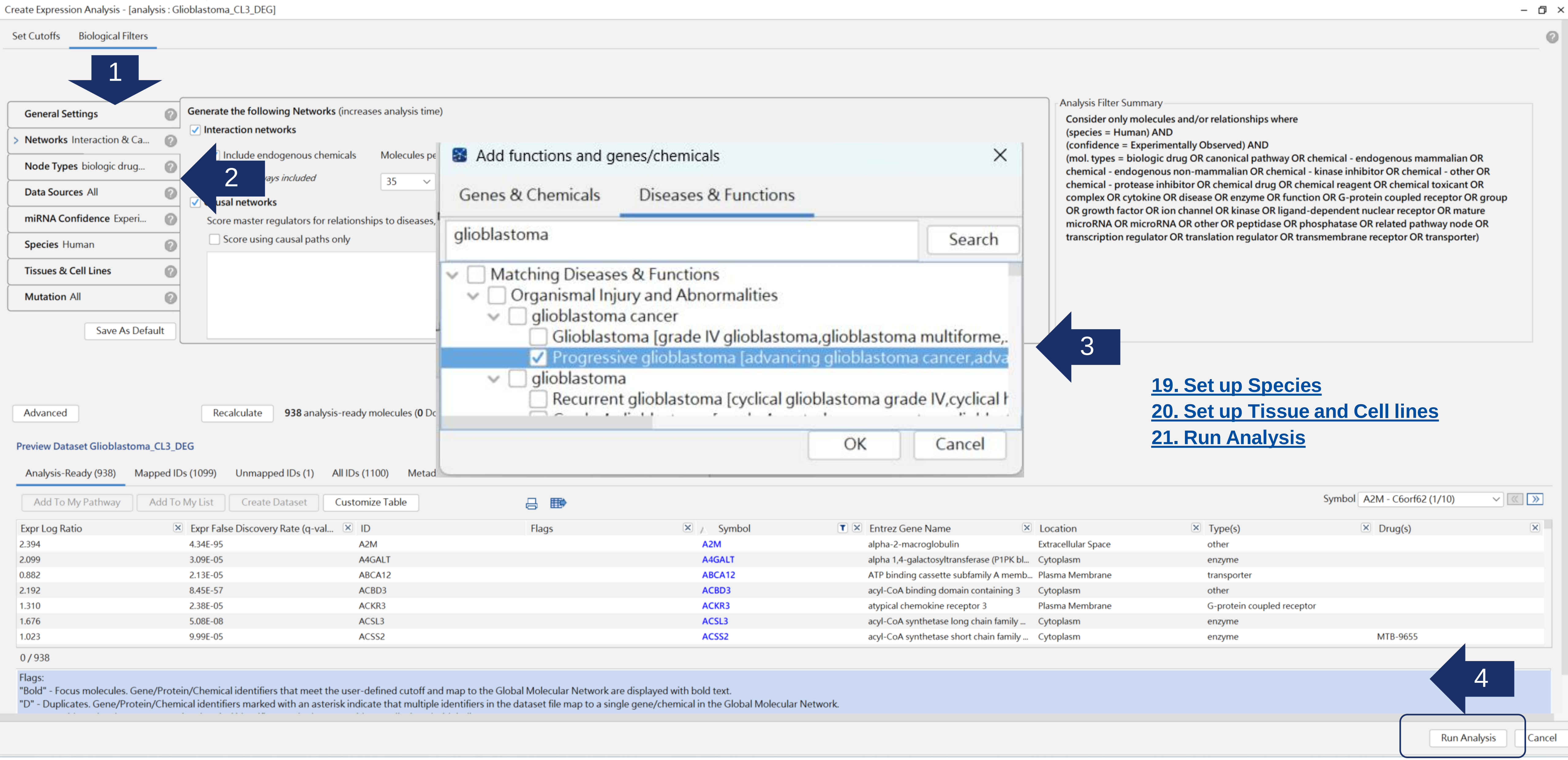
Select molecules by clicking or dragging to label them with their names. Note that fold changes are converted to log2 for charting purposes.

938 analysis-ready molecules (**0** Down and **938** Up)

Preview Dataset Glioblastoma_CL3_DEG

Expr Log Ratio	Expr False Discovery Rate (q-val...	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
2.394	4.34E-95	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	other	
2.099	3.09E-05	A4GALT		A4GALT	alpha 1,4-galactosyltransferase (P1PK bl...	Cytoplasm	enzyme	
0.882	2.13E-05	ABCA12		ABCA12	ATP binding cassette subfamily A memb...	Plasma Membrane	transporter	
2.192	8.45E-57	ACBD3		ACBD3	acyl-CoA binding domain containing 3	Cytoplasm	other	
1.310	2.38E-05	ACKR3		ACKR3	atypical chemokine receptor 3	Plasma Membrane	G-protein coupled receptor	
1.676	5.08E-08	ACSL3		ACSL3	acyl-CoA synthetase long chain family ...	Cytoplasm	enzyme	
1.023	9.99E-05	ACSS2		ACSS2	acyl-CoA synthetase short chain family ...	Cytoplasm	enzyme	MTB-9655

0 / 938



Create Expression Analysis - [analysis : Glioblastoma_CL3_DEG]

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 — Molecules pe

ays included — 35

☑ usal networks

Score master regulators for relationships to diseases,

☐ Score using causal paths only

Add functions and genes/chemicals

glioblastoma

- ☐ Matching Diseases & Functions
  - ☐ Organismal Injury and Abnormalities
    - ☐ glioblastoma cancer
      - ☐ Glioblastoma [grade IV glioblastoma,glioblastoma multiforme,.
      - ☑ Progressive glioblastoma [advancing glioblastoma cancer,adva
    - ☐ glioblastoma
      - ☐ Recurrent glioblastoma [cyclical glioblastoma grade IV,cyclical I

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 regulator OR transmembrane receptor OR transporter)

[19. Set up Species](#)
[20. Set up Tissue and Cell lines](#)
[21. Run Analysis](#)

938 analysis-ready molecules (0 Dc

Preview Dataset Glioblastoma_CL3_DEG

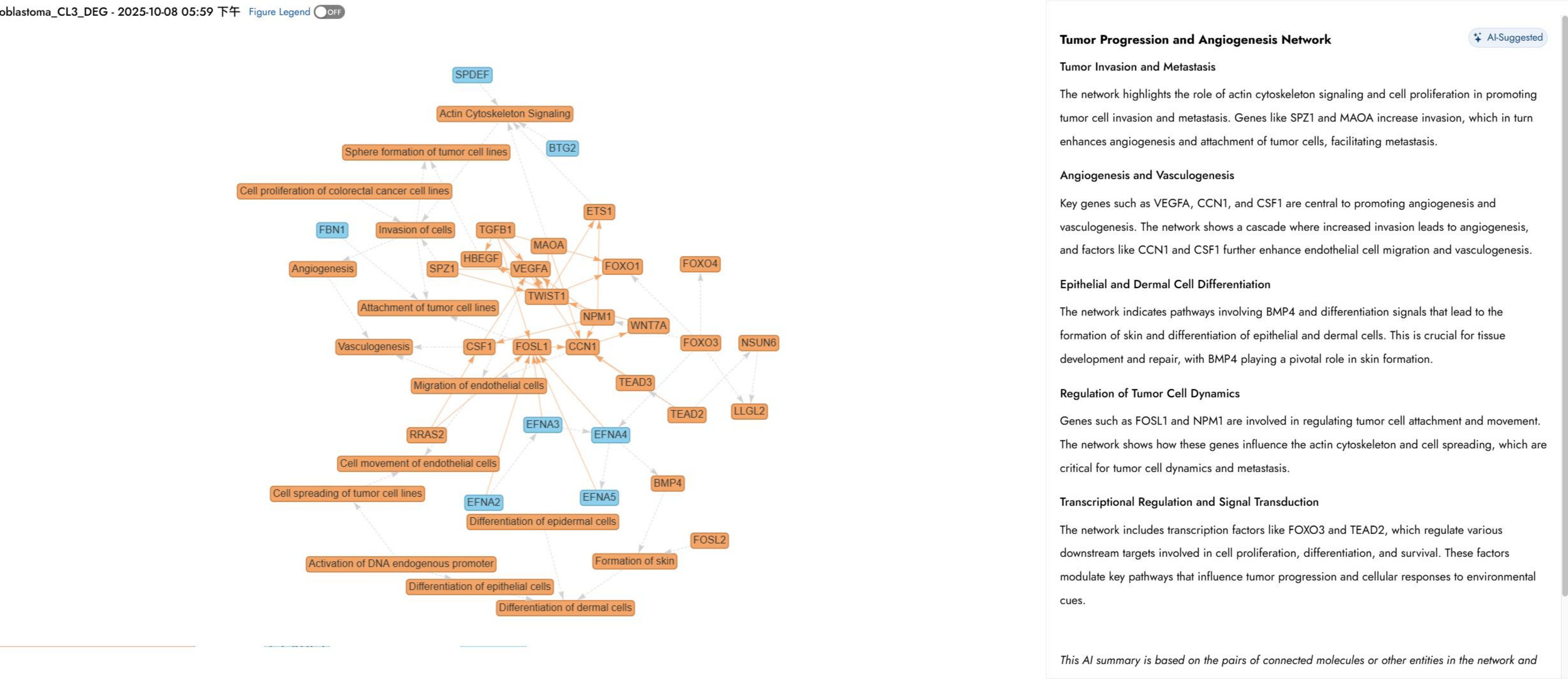
Symbol A2M - C6orf62 (1/10)

Expr Log Ratio	Expr False Discovery Rate (q-val...	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
2.394	4.34E-95	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	other	
2.099	3.09E-05	A4GALT		A4GALT	alpha 1,4-galactosyltransferase (P1PK bl...	Cytoplasm	enzyme	
0.882	2.13E-05	ABCA12		ABCA12	ATP binding cassette subfamily A memb...	Plasma Membrane	transporter	
2.192	8.45E-57	ACBD3		ACBD3	acyl-CoA binding domain containing 3	Cytoplasm	other	
1.310	2.38E-05	ACKR3		ACKR3	atypical chemokine receptor 3	Plasma Membrane	G-protein coupled receptor	
1.676	5.08E-08	ACSL3		ACSL3	acyl-CoA synthetase long chain family ...	Cytoplasm	enzyme	
1.023	9.99E-05	ACSS2		ACSS2	acyl-CoA synthetase short chain family ...	Cytoplasm	enzyme	MTB-9655

0 / 938

Flags:
"Bold" - Focus molecules. Gene/Protein/Chemical identifiers that meet the user-defined cutoff and map to the Global Molecular Network are displayed with bold text.
"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.

Graphical summary



oblastoma_CL3_DEG - 2025-10-08 05:59 下午

Tumor Progression and Angiogenesis Network

Tumor Invasion and Metastasis

The network highlights the role of actin cytoskeleton signaling and cell proliferation in promoting tumor cell invasion and metastasis. Genes like SPZ1 and MAOA increase invasion, which in turn enhances angiogenesis and attachment of tumor cells, facilitating metastasis.

Angiogenesis and Vasculogenesis

Key genes such as VEGFA, CCN1, and CSF1 are central to promoting angiogenesis and vasculogenesis. The network shows a cascade where increased invasion leads to angiogenesis, and factors like CCN1 and CSF1 further enhance endothelial cell migration and vasculogenesis.

Epithelial and Dermal Cell Differentiation

The network indicates pathways involving BMP4 and differentiation signals that lead to the formation of skin and differentiation of epithelial and dermal cells. This is crucial for tissue development and repair, with BMP4 playing a pivotal role in skin formation.

Regulation of Tumor Cell Dynamics

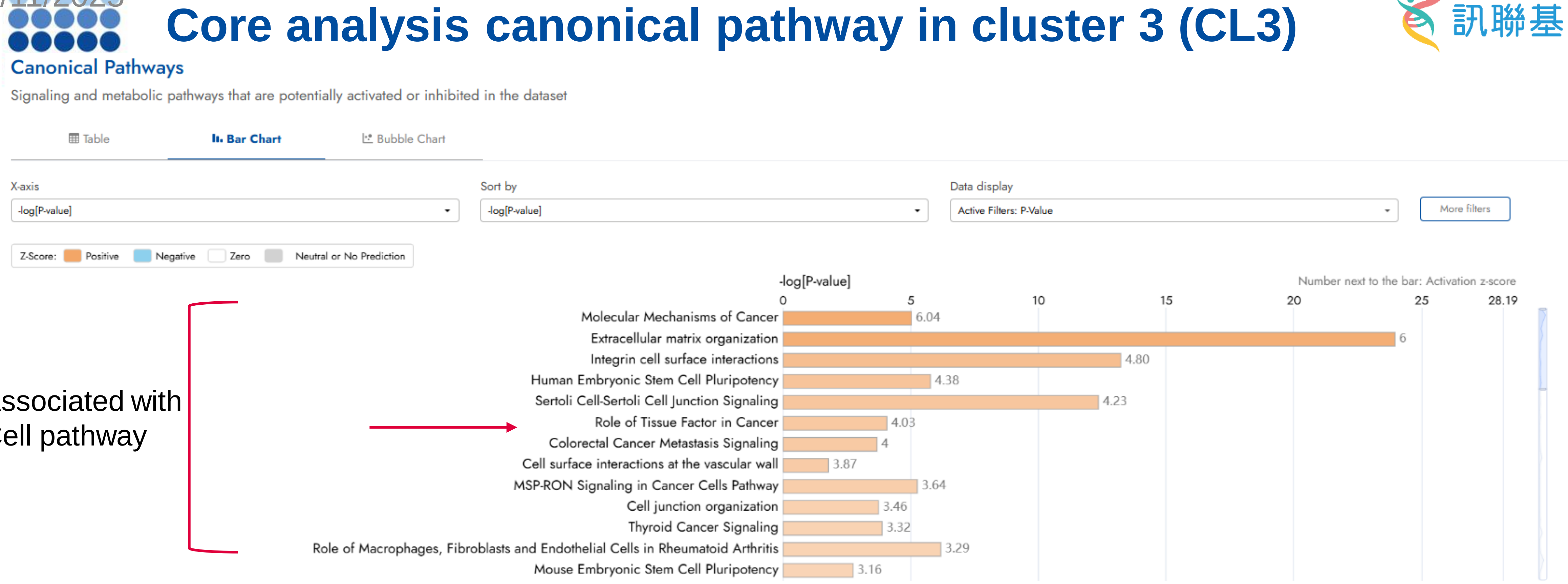
Genes such as FOSL1 and NPM1 are involved in regulating tumor cell attachment and movement. The network shows how these genes influence the actin cytoskeleton and cell spreading, which are critical for tumor cell dynamics and metastasis.

Transcriptional Regulation and Signal Transduction

The network includes transcription factors like FOXO3 and TEAD2, which regulate various downstream targets involved in cell proliferation, differentiation, and survival. These factors modulate key pathways that influence tumor progression and cellular responses to environmental cues.

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

Core analysis canonical pathway in cluster 3 (CL3)



Canonical Pathways

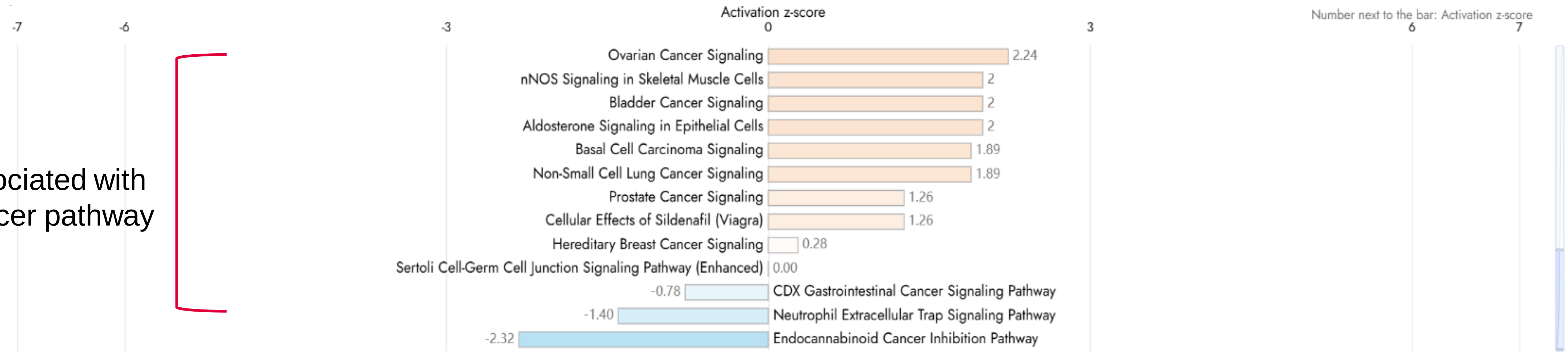
Signaling and metabolic pathways that are potentially activated or inhibited in the dataset

X-axis
-log[P-value]

Sort by
-log[P-value]

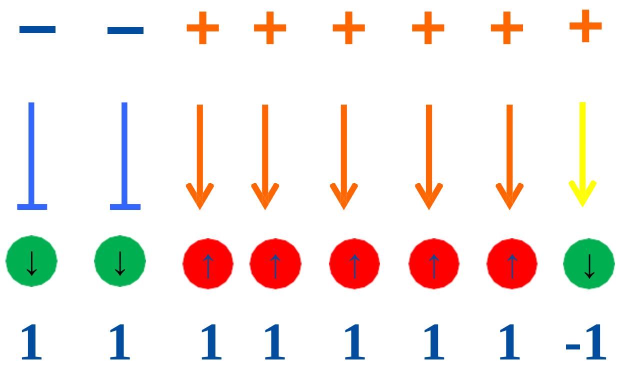
Data display
Active Filters: P-Value

Associated with Cell pathway



Associated with Cancer pathway

z-score: Activation prediction



Gene expression from QIAGEN Knowledge Base (literature)

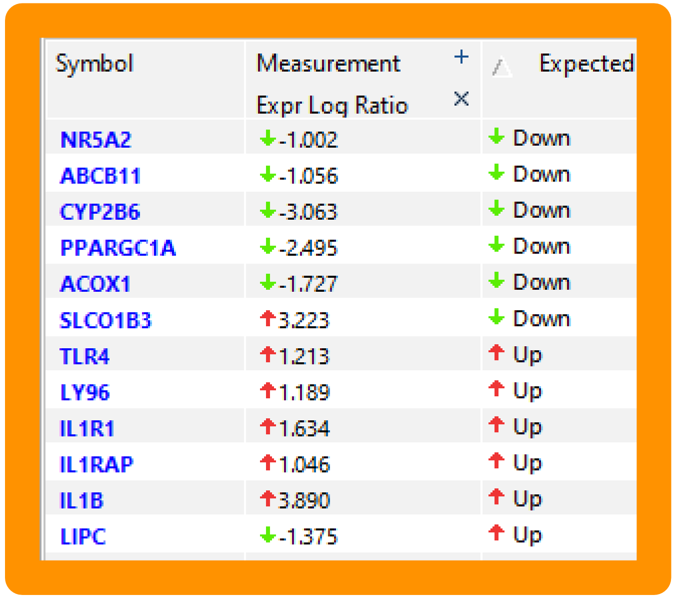
Gene expression in your dataset

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

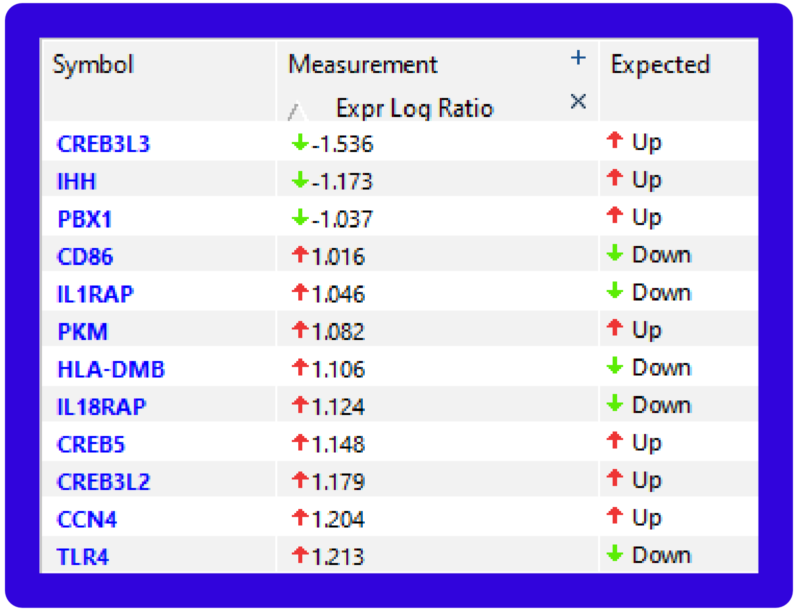
$$z = \frac{x}{\sigma_x} = \frac{\sum_i x_i}{\sqrt{N}} = \frac{N_+ - N_-}{\sqrt{N}} = (7\text{-}1)/\sqrt{8} = 2.12 \ (= \text{predicted activation})$$

- 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

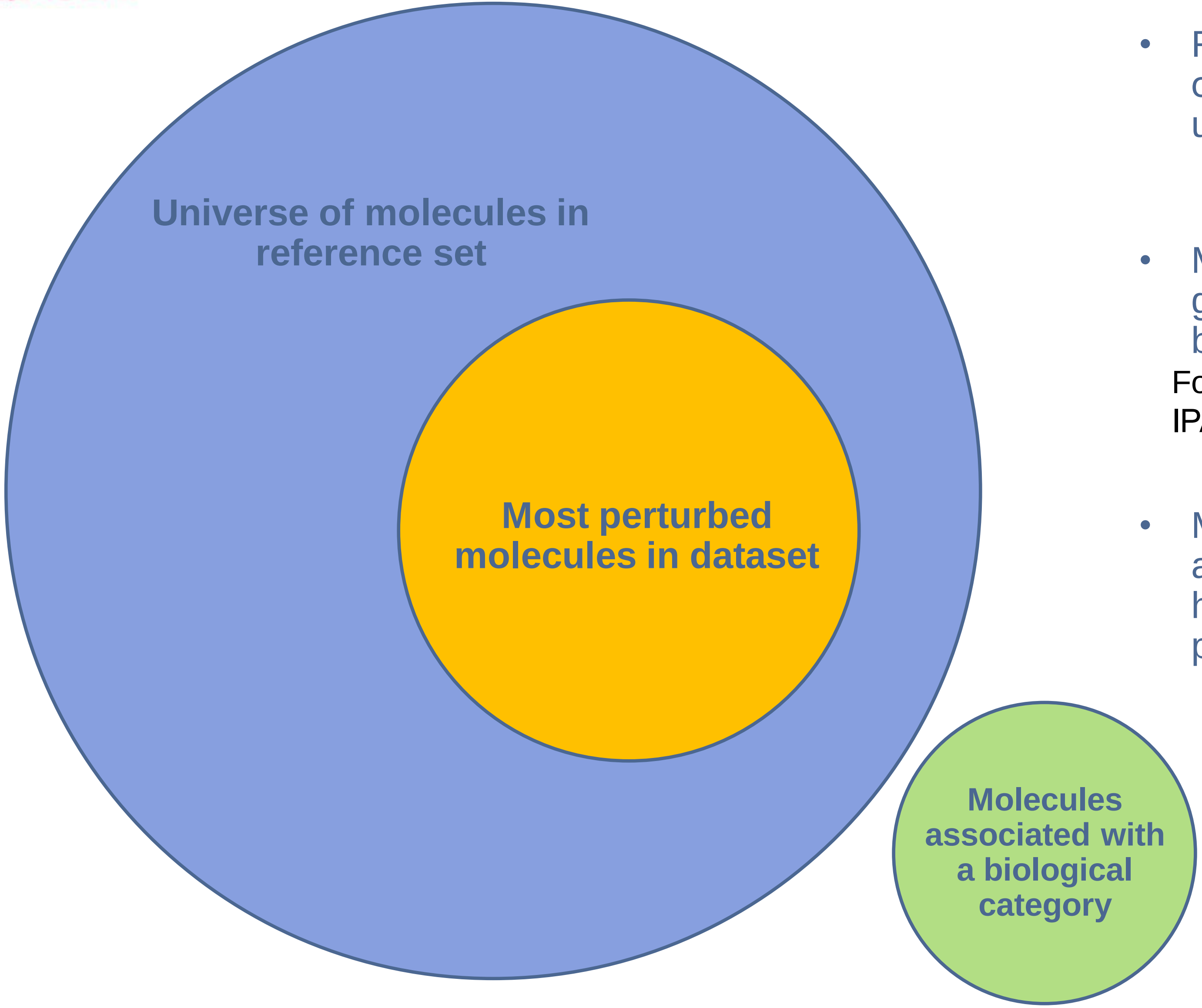
4/12 measurements match expected

Mostly anti-matching

Signal predominantly points to predicted inhibition

Enrichment in IPA

Pathway enrichment: P-value of overlap



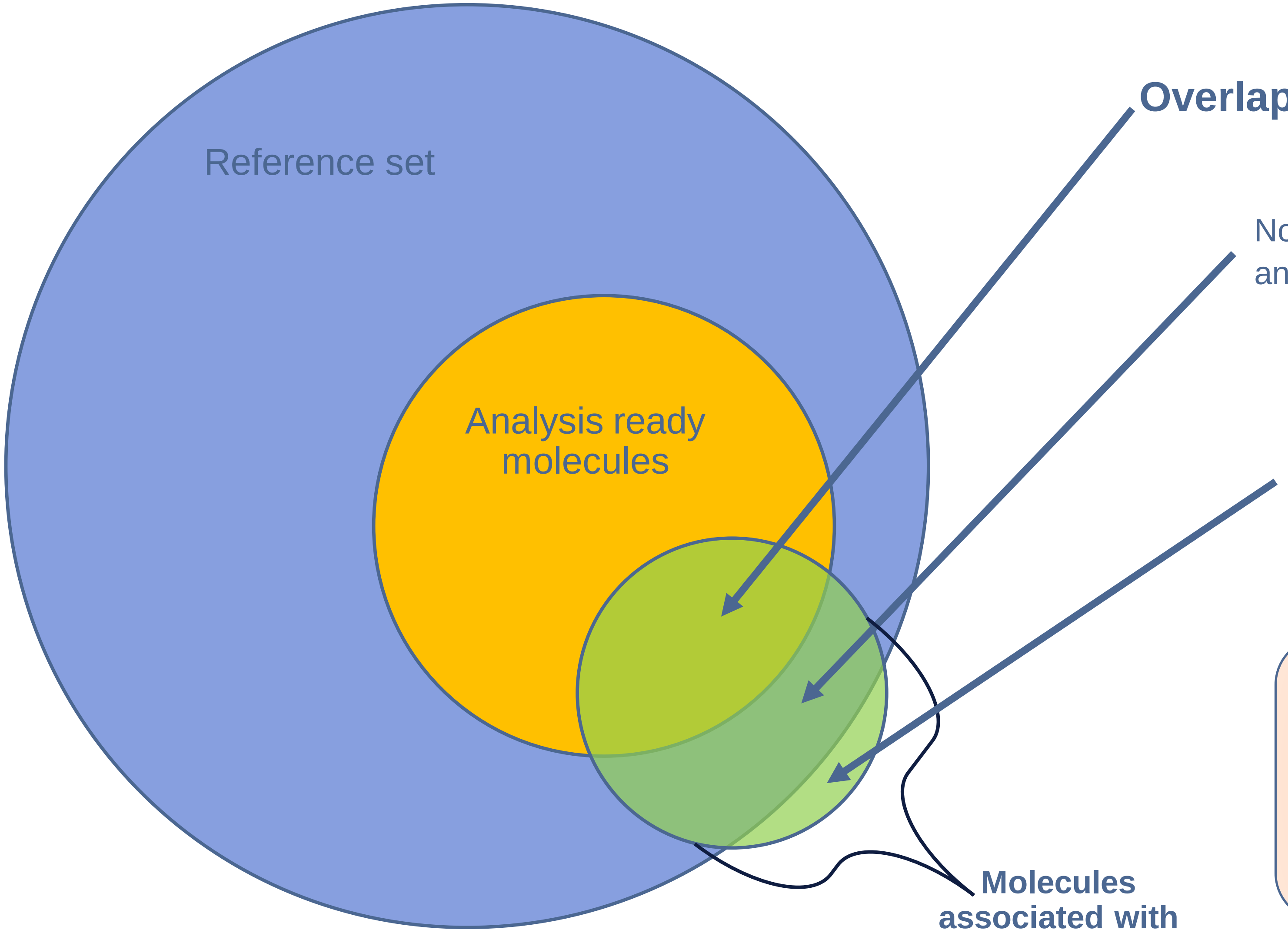
- Reference set is typically all genes or proteins that can be reliably detected by the ‘omics technology used

- Most perturbed is a subset of measured genes/proteins that were significantly different between experimental groups

Fold change cut offs and p-value cut offs used
IPA calls these “Analysis-ready molecules”

- Molecules associated with a biological category are a set of genes/proteins that the IPA knowledgebase has annotated to be important for a biological pathway, function, or disease.

Testing for Enrichment using the Fisher's Exact Test



Overlapping molecules

Non-analysis-ready molecules that have been annotated to a biological category

i.e. genes that did not pass cut offs

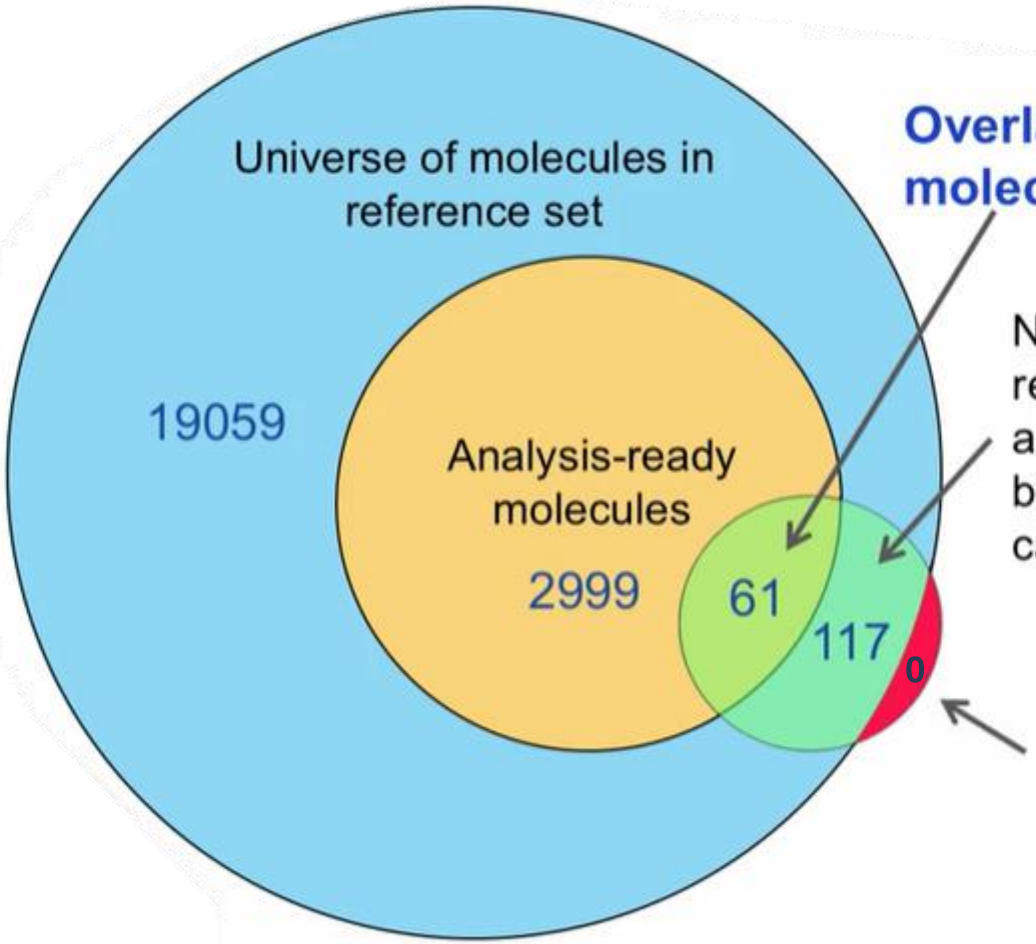
Genes not detected by the technology used and are annotated to a biological category

Molecules associated with a biological category

Is this overlap larger than expected by random sampling?

P-Value from the Right-tailed Fisher's Exact Test

p-value: the probability of observing a result as extreme or more extreme, if the null hypothesis is true



Overlapping molecules

Non-analysis-ready molecules associated with biological category

Molecules in category but not in reference set

**RNAseq theoretically can detect all molecules*

H_o = Overlap of molecules for a particular biological category is due to chance

α (significance level) = 0.05

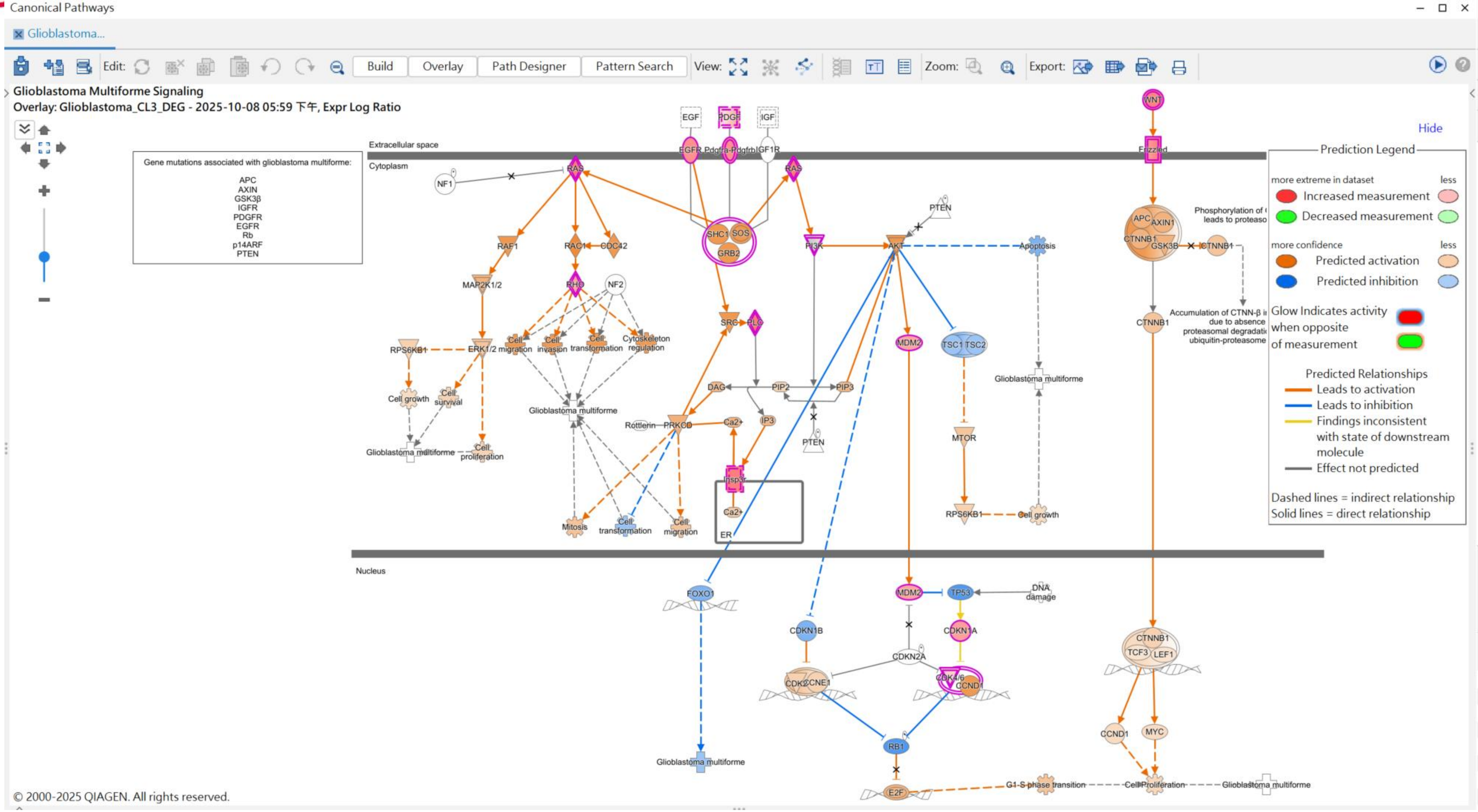
		Category 1		
		Group 1	Group 2	Total
Category 2	Group 1	a	b	a+b
	Group 2	c	d	c+d
	Total	a+c	b+d	a+b+c+d = n

$$\text{p-value} = \frac{(a+b)!(c+d)!(a+c)!(b+d)!}{n!a!b!c!d!}$$

P-value = 2.08×10^{-12}

We can reject the null hypothesis

Glioblastoma pathway



Canonical Pathways

Glioblastoma...

Glioblastoma Multiforme Signaling

Overlay: Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午, Expr Log Ratio

Gene mutations associated with glioblastoma multiforme:

APC
AXIN
GSK3β
IGFR
PDGFR
EGFR
Rb
p14ARF
PTEN

Prediction Legend

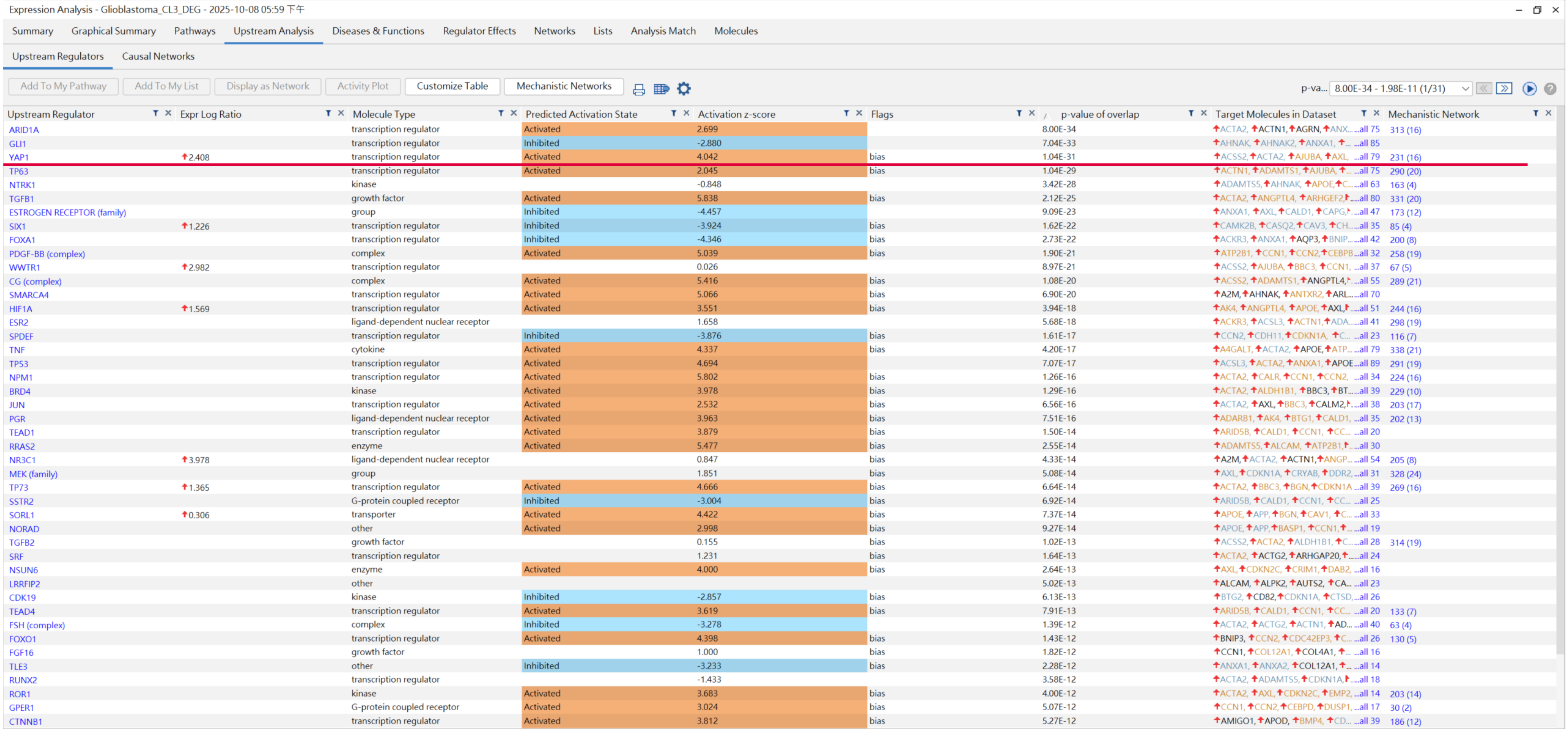
more extreme in dataset		less
🟥	Increased measurement	🟥
🟩	Decreased measurement	🟩
more confidence		less
●	Predicted activation	●
●	Predicted inhibition	●

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

Upstream regulator

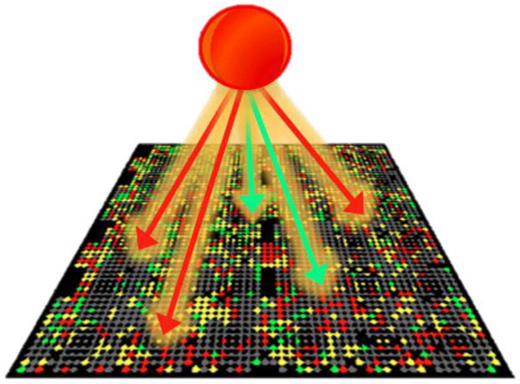


Expression Analysis - Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午

p-va... 8.00E-34 - 1.98E-11 (1/31)

Upstream Regulator	Expr Log Ratio	Molecule Type	Predicted Activation State	Activation z-score	Flags	p-value of overlap	Target Molecules in Dataset	Mechanistic Network
ARID1A		transcription regulator	Activated	2.699		8.00E-34	↑ACTA2, ↑ACTN1, ↑AGRN, ↑ANX... ...all 75	313 (16)
GLI1		transcription regulator	Inhibited	-2.880		7.04E-33	↑AHNAK, ↑AHNAK2, ↑ANXA1, ↑... ...all 85	
YAP1	↑2.408	transcription regulator	Activated	4.042	bias	1.04E-31	↑ACSS2, ↑ACTA2, ↑AJUBA, ↑AXL, ...all 79	231 (16)
TP63		transcription regulator	Activated	2.045	bias	1.04E-29	↑ACTN1, ↑ADAMTS1, ↑AJUBA, ↑... ...all 75	290 (20)
NTRK1		kinase		-0.848		3.42E-28	↑ADAMTS5, ↑AHNAK, ↑APOE, ↑C... ...all 63	163 (4)
TGFB1		growth factor	Activated	5.838	bias	2.12E-25	↑ACTA2, ↑ANGPTL4, ↑ARHGEF2, ↑... ...all 80	331 (20)
ESTROGEN RECEPTOR (family)		group	Inhibited	-4.457		9.09E-23	↑ANXA1, ↑AXL, ↑CALD1, ↑CAPG, ↑... ...all 47	173 (12)
SIX1	↑1.226	transcription regulator	Inhibited	-3.924	bias	1.62E-22	↑CAMK2B, ↑CASQ2, ↑CAV3, ↑CH... ...all 35	85 (4)
FOXA1		transcription regulator	Inhibited	-4.346	bias	2.73E-22	↑ACKR3, ↑ANXA1, ↑AQP3, ↑BNIP... ...all 42	200 (8)
PDGF-BB (complex)		complex	Activated	5.039	bias	1.90E-21	↑ATP2B1, ↑CCN1, ↑CCN2, ↑CEBPB ...all 32	258 (19)
WWTR1	↑2.982	transcription regulator		0.026		8.97E-21	↑ACSS2, ↑AJUBA, ↑BBC3, ↑CCN1, ...all 37	67 (5)
CG (complex)		complex	Activated	5.416	bias	1.08E-20	↑ACSS2, ↑ADAMTS1, ↑ANGPTL4, ↑... ...all 55	289 (21)
SMARCA4		transcription regulator	Activated	5.066	bias	6.90E-20	↑A2M, ↑AHNAK, ↑ANTXR2, ↑ARL... ...all 70	
HIF1A	↑1.569	transcription regulator	Activated	3.551	bias	3.94E-18	↑AK4, ↑ANGPTL4, ↑APOE, ↑AXL, ↑... ...all 51	244 (16)
ESR2		ligand-dependent nuclear receptor		1.658		5.68E-18	↑ACKR3, ↑ACSL3, ↑ACTN1, ↑ADA... ...all 41	298 (19)
SPDEF		transcription regulator	Inhibited	-3.876	bias	1.61E-17	↑CCN2, ↑CDH11, ↑CDKN1A, ↑C... ...all 23	116 (7)
TNF		cytokine	Activated	4.337	bias	4.20E-17	↑A4GALT, ↑ACTA2, ↑APOE, ↑ATP... ...all 79	338 (21)
TP53		transcription regulator	Activated	4.694		7.07E-17	↑ACSL3, ↑ACTA2, ↑ANXA1, ↑APOE ...all 89	291 (19)
NPM1		transcription regulator	Activated	5.802	bias	1.26E-16	↑ACTA2, ↑CALR, ↑CCN1, ↑CCN2, ...all 34	224 (16)
BRD4		kinase	Activated	3.978	bias	1.29E-16	↑ACTA2, ↑ALDH1B1, ↑BBC3, ↑BT... ...all 39	229 (10)
JUN		transcription regulator	Activated	2.532	bias	6.56E-16	↑ACTA2, ↑AXL, ↑BBC3, ↑CALM2, ↑... ...all 38	203 (17)
PGR		ligand-dependent nuclear receptor	Activated	3.963	bias	7.51E-16	↑ADARB1, ↑AK4, ↑BTG1, ↑CALD1, ...all 35	202 (13)
TEAD1		transcription regulator	Activated	3.879	bias	1.50E-14	↑ARID5B, ↑CALD1, ↑CCN1, ↑CC... ...all 20	
RRAS2		enzyme	Activated	5.477	bias	2.55E-14	↑ADAMTS5, ↑ALCAM, ↑ATP2B1, ↑... ...all 30	
NR3C1	↑3.978	ligand-dependent nuclear receptor		0.847	bias	4.33E-14	↑A2M, ↑ACTA2, ↑ACTN1, ↑ANGP... ...all 54	205 (8)
MEK (family)		group		1.851	bias	5.08E-14	↑AXL, ↑CDKN1A, ↑CRYAB, ↑DDR2, ...all 31	328 (24)
TP73	↑1.365	transcription regulator	Activated	4.666	bias	6.64E-14	↑ACTA2, ↑BBC3, ↑BGN, ↑CDKN1A ...all 39	269 (16)
SSTR2		G-protein coupled receptor	Inhibited	-3.004	bias	6.92E-14	↑ARID5B, ↑CALD1, ↑CCN1, ↑CC... ...all 25	
SORL1	↑0.306	transporter	Activated	4.422	bias	7.37E-14	↑APOE, ↑APP, ↑BGN, ↑CAV1, ↑C... ...all 33	
NORAD		other	Activated	2.998	bias	9.27E-14	↑APOE, ↑APP, ↑BASP1, ↑CCN1, ↑... ...all 19	
TGFB2		growth factor		0.155	bias	1.02E-13	↑ACSS2, ↑ACTA2, ↑ALDH1B1, ↑C... ...all 28	314 (19)
SRF		transcription regulator		1.231	bias	1.64E-13	↑ACTA2, ↑ACTG2, ↑ARHGAP20, ↑... ...all 24	
NSUN6		enzyme	Activated	4.000	bias	2.64E-13	↑AXL, ↑CDKN2C, ↑CRIM1, ↑DAB2, ...all 16	
LRRFIP2		other				5.02E-13	↑ALCAM, ↑ALPK2, ↑AUTS2, ↑CA... ...all 23	
CDK19		kinase	Inhibited	-2.857	bias	6.13E-13	↑BTG2, ↑CD82, ↑CDKN1A, ↑CTSD, ...all 26	
TEAD4		transcription regulator	Activated	3.619	bias	7.91E-13	↑ARID5B, ↑CALD1, ↑CCN1, ↑CC... ...all 20	133 (7)
FSH (complex)		complex	Inhibited	-3.278		1.39E-12	↑ACTA2, ↑ACTG2, ↑ACTN1, ↑AD... ...all 40	63 (4)
FOXO1		transcription regulator	Activated	4.398	bias	1.43E-12	↑BNIP3, ↑CCN2, ↑CDC42EP3, ↑C... ...all 26	130 (5)
FGF16		growth factor		1.000	bias	1.82E-12	↑CCN1, ↑COL12A1, ↑COL4A1, ↑... ...all 16	
TLE3		other	Inhibited	-3.233	bias	2.28E-12	↑ANXA1, ↑ANXA2, ↑COL12A1, ↑... ...all 14	
RUNX2		transcription regulator		-1.433		3.58E-12	↑ACTA2, ↑ADAMTS5, ↑CDKN1A, ↑... ...all 18	
ROR1		kinase	Activated	3.683	bias	4.00E-12	↑ACTA2, ↑AXL, ↑CDKN2C, ↑EMP2, ...all 14	203 (14)
GPER1		G-protein coupled receptor	Activated	3.024	bias	5.07E-12	↑CCN1, ↑CCN2, ↑CEBPD, ↑DUSP1, ...all 17	30 (2)
CTNNB1		transcription regulator	Activated	3.812	bias	5.27E-12	↑AMIGO1, ↑APOD, ↑BMP4, ↑CD... ...all 39	186 (12)

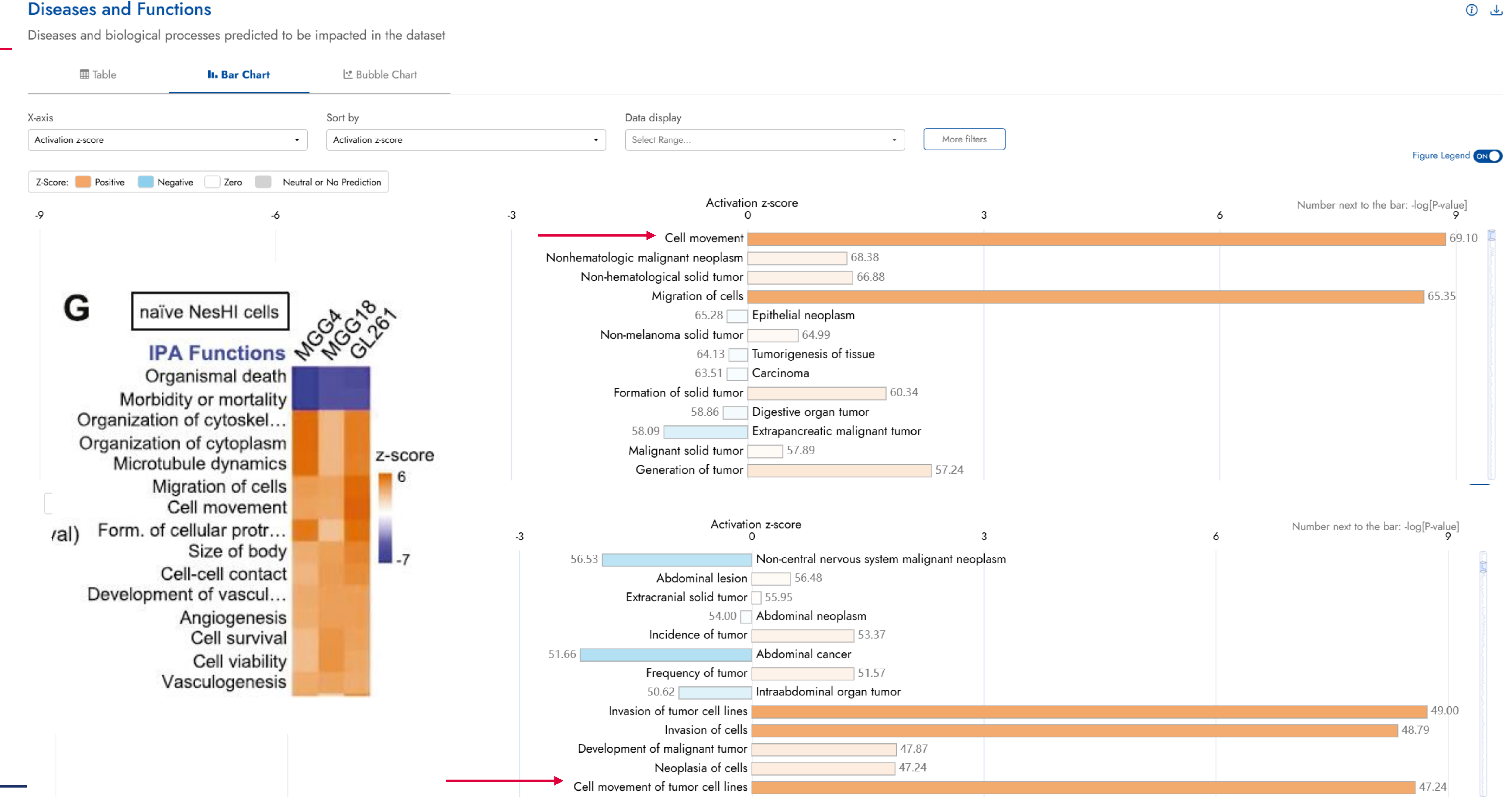
Upstream Regulator Analysis: *How does it work?*



- 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

11/11/2025



Diseases and Functions

Diseases and biological processes predicted to be impacted in the dataset

X-axis
Activation z-score

Sort by
Activation z-score

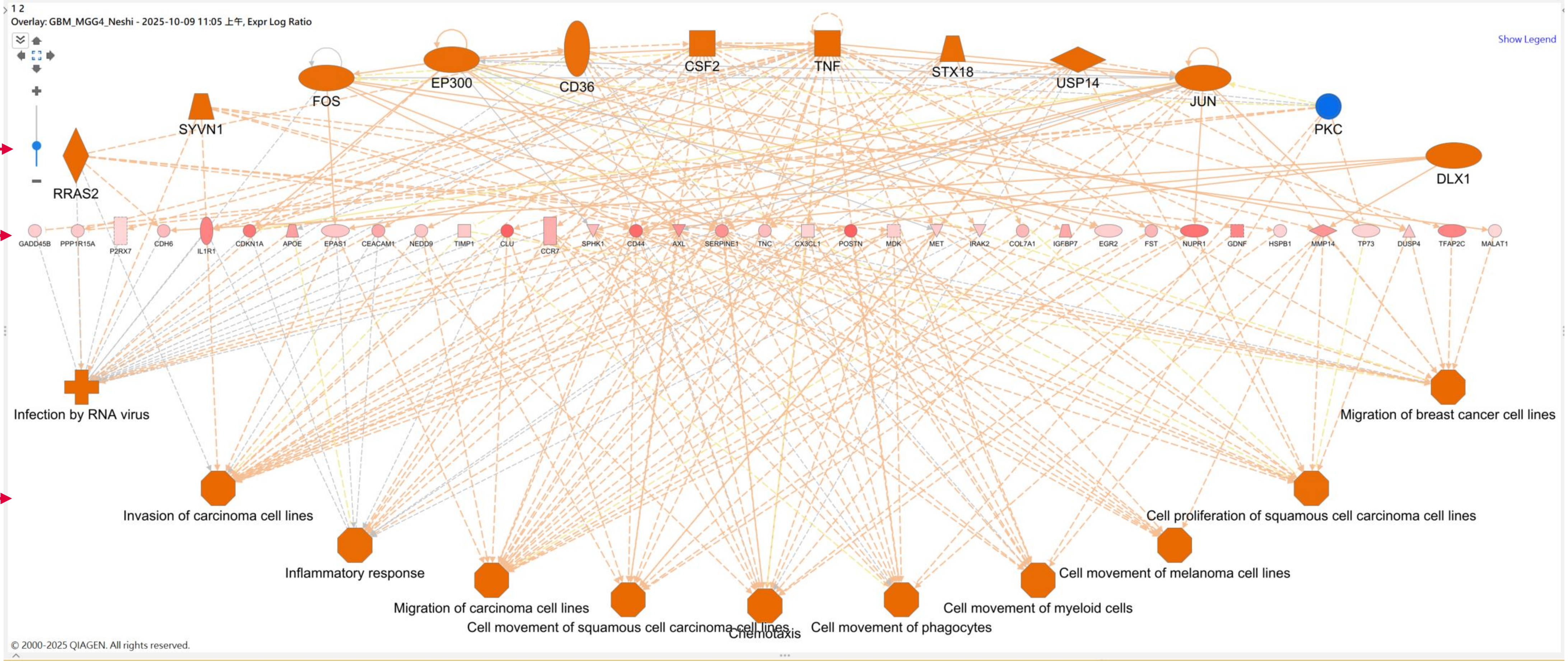
Data display
Select Range...

Regulate effect

Predict upstream regulator

DEG in our dataset

Downstream effected



1 2

Overlay: GBM_MGG4_Neshi - 2025-10-09 11:05 上午, Expr Log Ratio

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Analysis Match

How signatures are created and compared

- Data source from Omicsoft datalands

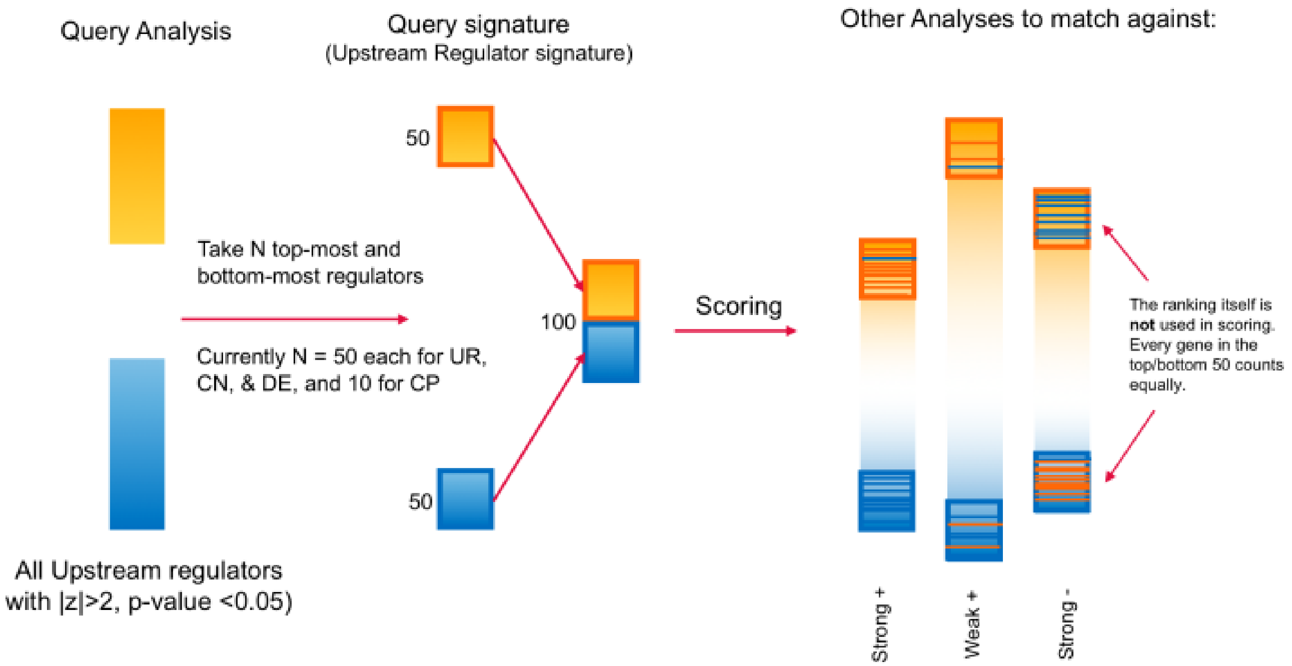
Canonical Pathways (up to 20 pathways)

Upstream Regulators (up to 100 regulators)

Causal Networks (up to 100 master regulators)

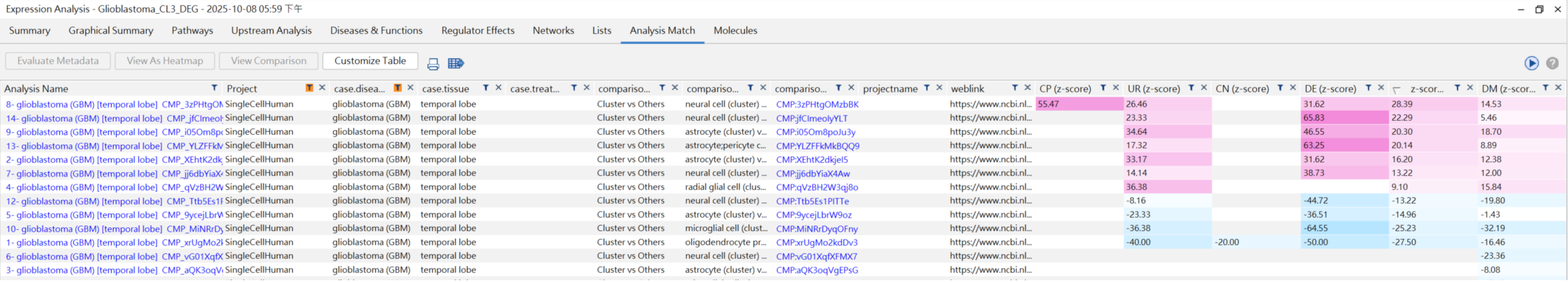
Diseases & Functions (up to 100 diseases or functions)

Example



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

Analysis Match



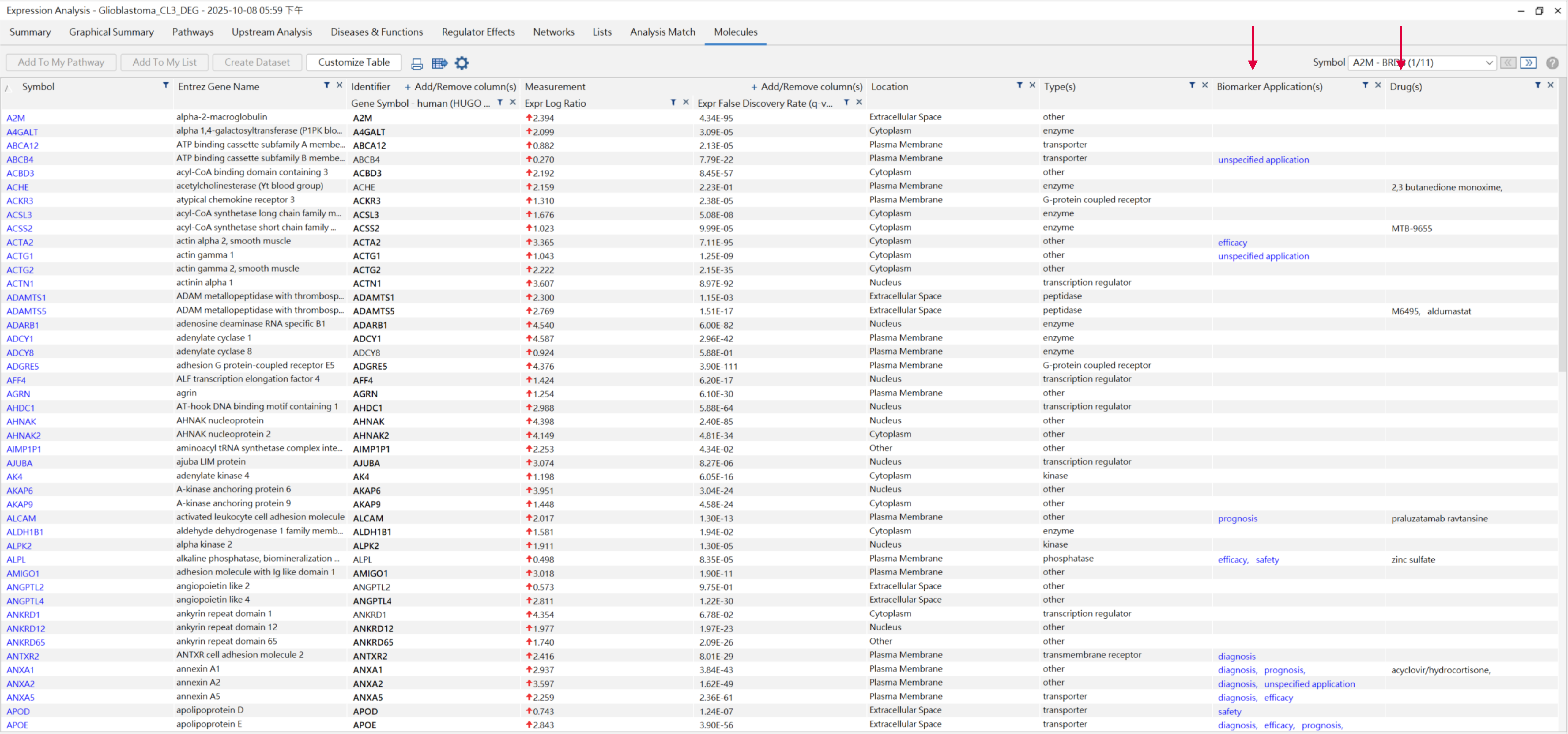
Expression Analysis - Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午

Analysis Name	Project	case.disea...	case.tissue	case.treat...	compariso...	compariso...	compariso...	projectname	weblink	CP (z-score)	UR (z-score)	CN (z-score)	DE (z-score)	z-scor...	DM (z-scor...
8- glioblastoma (GBM) [temporal lobe] CMP_3zPHtgOM	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	neural cell (cluster) ...	CMP:3zPHtgOMzbBK		https://www.ncbi.nl...	55.47	26.46		31.62	28.39	14.53
14- glioblastoma (GBM) [temporal lobe] CMP_jfClmeol	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	neural cell (cluster) ...	CMP:jfClmeolyYLT		https://www.ncbi.nl...		23.33		65.83	22.29	5.46
9- glioblastoma (GBM) [temporal lobe] CMP_i05Om8pc	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	astrocyte (cluster) v...	CMP:i05Om8poJu3y		https://www.ncbi.nl...		34.64		46.55	20.30	18.70
13- glioblastoma (GBM) [temporal lobe] CMP_YLZFFkM	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	astrocyte;pericyte c...	CMP:YLZFFkMkBQQ9		https://www.ncbi.nl...		17.32		63.25	20.14	8.89
2- glioblastoma (GBM) [temporal lobe] CMP_XEhtK2dk	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	astrocyte (cluster) v...	CMP:XEhtK2dkjel5		https://www.ncbi.nl...		33.17		31.62	16.20	12.38
7- glioblastoma (GBM) [temporal lobe] CMP_jj6dbYiaX	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	neural cell (cluster) ...	CMP:jj6dbYiaX4Aw		https://www.ncbi.nl...		14.14		38.73	13.22	12.00
4- glioblastoma (GBM) [temporal lobe] CMP_qVzBH2W	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	radial glial cell (clus...	CMP:qVzBH2W3qj8o		https://www.ncbi.nl...		36.38			9.10	15.84
12- glioblastoma (GBM) [temporal lobe] CMP_Ttb5Es1F	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	neural cell (cluster) ...	CMP:Ttb5Es1PITTe		https://www.ncbi.nl...		-8.16		-44.72	-13.22	-19.80
5- glioblastoma (GBM) [temporal lobe] CMP_9ycejLbrW	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	astrocyte (cluster) v...	CMP:9ycejLbrW9oz		https://www.ncbi.nl...		-23.33		-36.51	-14.96	-1.43
10- glioblastoma (GBM) [temporal lobe] CMP_MiNRrDy	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	microglial cell (clust...	CMP:MiNRrDyqOFny		https://www.ncbi.nl...		-36.38		-64.55	-25.23	-32.19
1- glioblastoma (GBM) [temporal lobe] CMP_xrUgMo2k	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	oligodendrocyte pr...	CMP:xrUgMo2kdDv3		https://www.ncbi.nl...		-40.00	-20.00	-50.00	-27.50	-16.46
6- glioblastoma (GBM) [temporal lobe] CMP_vG01XqfX	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	neural cell (cluster) ...	CMP:vG01XqfXFMX7		https://www.ncbi.nl...						-23.36
3- glioblastoma (GBM) [temporal lobe] CMP_aQK3oqV	SingleCellHuman	glioblastoma (GBM)	temporal lobe		Cluster vs Others	astrocyte (cluster) v...	CMP:aQK3oqVgEPsG		https://www.ncbi.nl...						-8.08

Project

Case

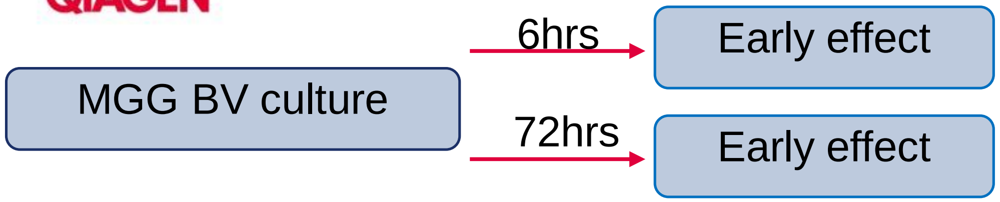
Molecules



Expression Analysis - Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午

Symbol	Entrez Gene Name	Identifier	Measurement		Location	Type(s)	Biomarker Application(s)	Drug(s)
		Gene Symbol - human (HUGO ...	Expr Log Ratio	Expr False Discovery Rate (q-v...				
A2M	alpha-2-macroglobulin	A2M	↑2.394	4.34E-95	Extracellular Space	other		
A4GALT	alpha 1,4-galactosyltransferase (P1PK blo...	A4GALT	↑2.099	3.09E-05	Cytoplasm	enzyme		
ABCA12	ATP binding cassette subfamily A membe...	ABCA12	↑0.882	2.13E-05	Plasma Membrane	transporter		
ABCB4	ATP binding cassette subfamily B membe...	ABCB4	↑0.270	7.79E-22	Plasma Membrane	transporter	unspecified application	
ACBD3	acyl-CoA binding domain containing 3	ACBD3	↑2.192	8.45E-57	Cytoplasm	other		
ACHE	acetylcholinesterase (Yt blood group)	ACHE	↑2.159	2.23E-01	Plasma Membrane	enzyme		2,3 butanedione monoxime,
ACKR3	atypical chemokine receptor 3	ACKR3	↑1.310	2.38E-05	Plasma Membrane	G-protein coupled receptor		
ACSL3	acyl-CoA synthetase long chain family m...	ACSL3	↑1.676	5.08E-08	Cytoplasm	enzyme		
ACSS2	acyl-CoA synthetase short chain family ...	ACSS2	↑1.023	9.99E-05	Cytoplasm	enzyme		MTB-9655
ACTA2	actin alpha 2, smooth muscle	ACTA2	↑3.365	7.11E-95	Cytoplasm	other	efficacy	
ACTG1	actin gamma 1	ACTG1	↑1.043	1.25E-09	Cytoplasm	other	unspecified application	
ACTG2	actin gamma 2, smooth muscle	ACTG2	↑2.222	2.15E-35	Cytoplasm	other		
ACTN1	actinin alpha 1	ACTN1	↑3.607	8.97E-92	Nucleus	transcription regulator		
ADAMTS1	ADAM metallopeptidase with thrombosp...	ADAMTS1	↑2.300	1.15E-03	Extracellular Space	peptidase		
ADAMTS5	ADAM metallopeptidase with thrombosp...	ADAMTS5	↑2.769	1.51E-17	Extracellular Space	peptidase		M6495, aldumastat
ADARB1	adenosine deaminase RNA specific B1	ADARB1	↑4.540	6.00E-82	Nucleus	enzyme		
ADCY1	adenylate cyclase 1	ADCY1	↑4.587	2.96E-42	Plasma Membrane	enzyme		
ADCY8	adenylate cyclase 8	ADCY8	↑0.924	5.88E-01	Plasma Membrane	enzyme		
ADGRE5	adhesion G protein-coupled receptor E5	ADGRE5	↑4.376	3.90E-111	Plasma Membrane	G-protein coupled receptor		
AFF4	ALF transcription elongation factor 4	AFF4	↑1.424	6.20E-17	Nucleus	transcription regulator		
AGRN	agrin	AGRN	↑1.254	6.10E-30	Plasma Membrane	other		
AHDC1	AT-hook DNA binding motif containing 1	AHDC1	↑2.988	5.88E-64	Nucleus	transcription regulator		
AHNAK	AHNAK nucleoprotein	AHNAK	↑4.398	2.40E-85	Nucleus	other		
AHNAK2	AHNAK nucleoprotein 2	AHNAK2	↑4.149	4.81E-34	Cytoplasm	other		
AIMP1P1	aminoacyl tRNA synthetase complex inte...	AIMP1P1	↑2.253	4.34E-02	Other	other		
AJUBA	ajuba LIM protein	AJUBA	↑3.074	8.27E-06	Nucleus	transcription regulator		
AK4	adenylate kinase 4	AK4	↑1.198	6.05E-16	Cytoplasm	kinase		
AKAP6	A-kinase anchoring protein 6	AKAP6	↑3.951	3.04E-24	Nucleus	other		
AKAP9	A-kinase anchoring protein 9	AKAP9	↑1.448	4.58E-24	Cytoplasm	other		
ALCAM	activated leukocyte cell adhesion molecule	ALCAM	↑2.017	1.30E-13	Plasma Membrane	other	prognosis	praluzatamab ravtansine
ALDH1B1	aldehyde dehydrogenase 1 family memb...	ALDH1B1	↑1.581	1.94E-02	Cytoplasm	enzyme		
ALPK2	alpha kinase 2	ALPK2	↑1.911	1.30E-05	Nucleus	kinase		
ALPL	alkaline phosphatase, biomineralization ...	ALPL	↑0.498	8.35E-05	Plasma Membrane	phosphatase	efficacy, safety	zinc sulfate
AMIGO1	adhesion molecule with Ig like domain 1	AMIGO1	↑3.018	1.90E-11	Plasma Membrane	other		
ANGPTL2	angiopoietin like 2	ANGPTL2	↑0.573	9.75E-01	Extracellular Space	other		
ANGPTL4	angiopoietin like 4	ANGPTL4	↑2.811	1.22E-30	Extracellular Space	other		
ANKRD1	ankyrin repeat domain 1	ANKRD1	↑4.354	6.78E-02	Cytoplasm	transcription regulator		
ANKRD12	ankyrin repeat domain 12	ANKRD12	↑1.977	1.97E-23	Nucleus	other		
ANKRD65	ankyrin repeat domain 65	ANKRD65	↑1.740	2.09E-26	Other	other		
ANTXR2	ANTXR cell adhesion molecule 2	ANTXR2	↑2.416	8.01E-29	Plasma Membrane	transmembrane receptor	diagnosis	
ANXA1	annexin A1	ANXA1	↑2.937	3.84E-43	Plasma Membrane	other	diagnosis, prognosis,	acyclovir/hydrocortisone,
ANXA2	annexin A2	ANXA2	↑3.597	1.62E-49	Plasma Membrane	other	diagnosis, unspecified application	
ANXA5	annexin A5	ANXA5	↑2.259	2.36E-61	Plasma Membrane	transporter	diagnosis, efficacy	
APOD	apolipoprotein D	APOD	↑0.743	1.24E-07	Extracellular Space	transporter	safety	
APOE	apolipoprotein E	APOE	↑2.843	3.90E-56	Extracellular Space	transporter	diagnosis, efficacy, prognosis,	

Protein omics upload data



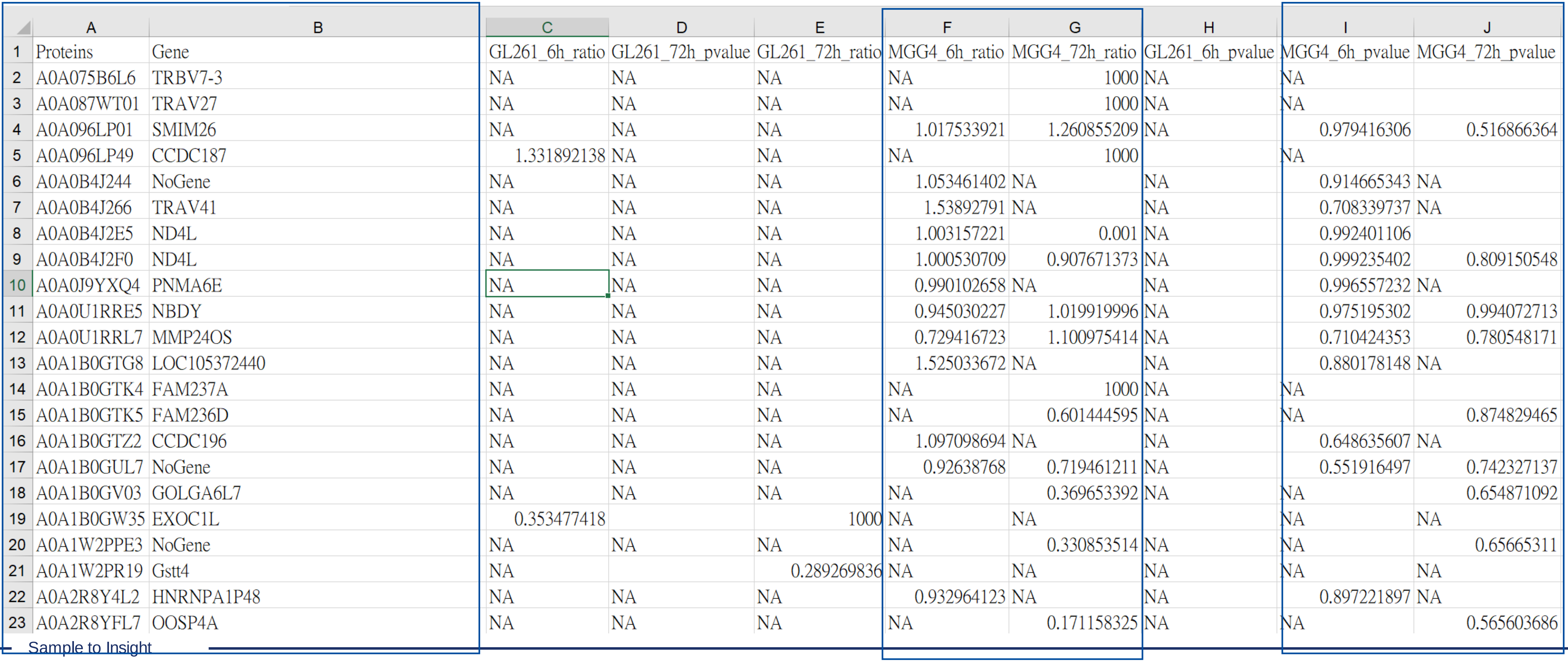
MGG BV culture

6hrs

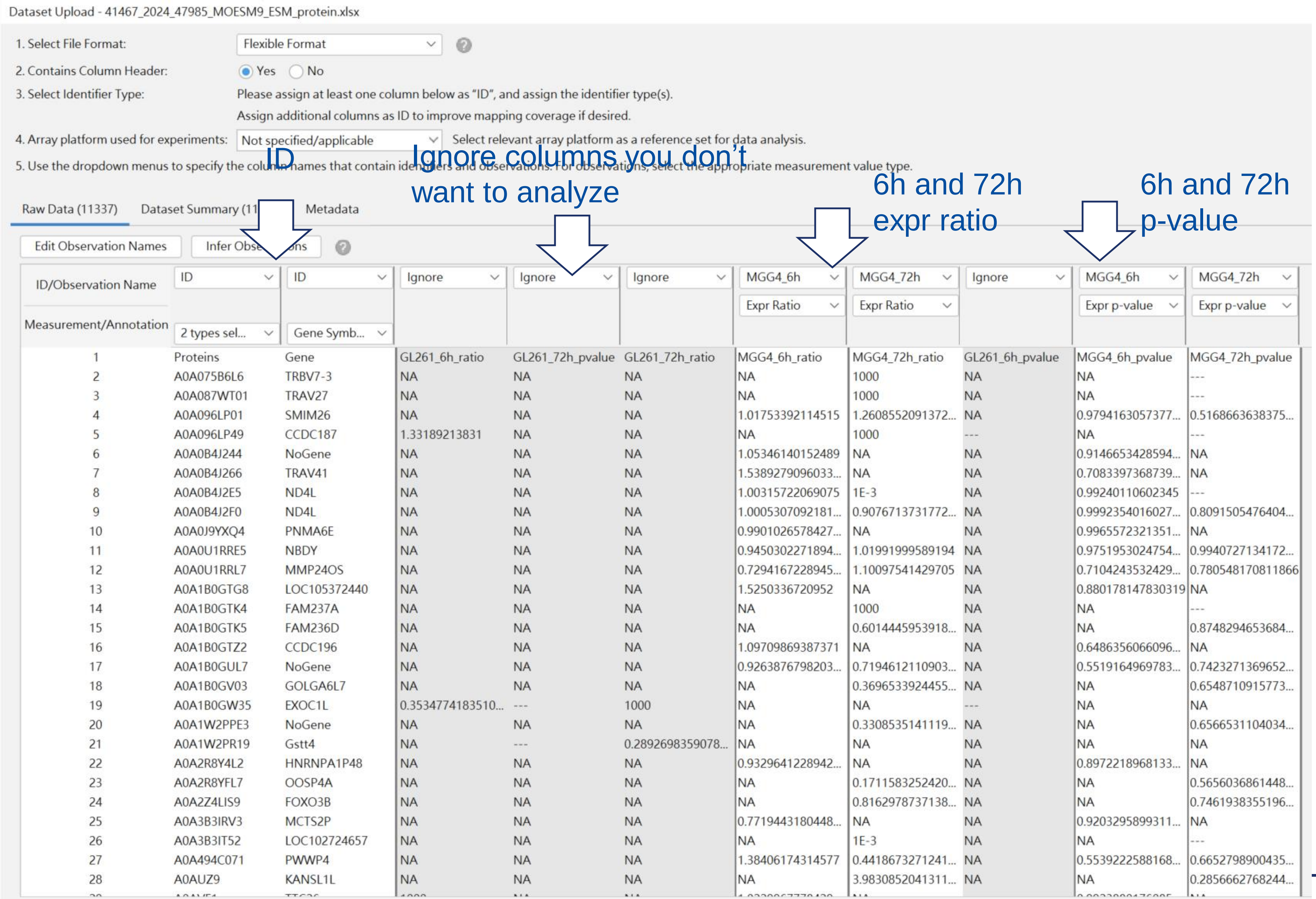
Early effect

72hrs

Early effect



	A	B	C	D	E	F	G	H	I	J
1	Proteins	Gene	GL261_6h_ratio	GL261_72h_pvalue	GL261_72h_ratio	MGG4_6h_ratio	MGG4_72h_ratio	GL261_6h_pvalue	MGG4_6h_pvalue	MGG4_72h_pvalue
2	A0A075B6L6	TRBV7-3	NA	NA	NA	NA	1000	NA	NA	
3	A0A087WT01	TRAV27	NA	NA	NA	NA	1000	NA	NA	
4	A0A096LP01	SMIM26	NA	NA	NA	1.017533921	1.260855209	NA	0.979416306	0.516866364
5	A0A096LP49	CCDC187	1.331892138	NA	NA	NA	1000		NA	
6	A0A0B4J244	NoGene	NA	NA	NA	1.053461402	NA	NA	0.914665343	NA
7	A0A0B4J266	TRAV41	NA	NA	NA	1.53892791	NA	NA	0.708339737	NA
8	A0A0B4J2E5	ND4L	NA	NA	NA	1.003157221	0.001	NA	0.992401106	
9	A0A0B4J2F0	ND4L	NA	NA	NA	1.000530709	0.907671373	NA	0.999235402	0.809150548
10	A0A0J9YXQ4	PNMA6E	NA	NA	NA	0.990102658	NA	NA	0.996557232	NA
11	A0A0U1RRE5	NBDY	NA	NA	NA	0.945030227	1.019919996	NA	0.975195302	0.994072713
12	A0A0U1RRL7	MMP24OS	NA	NA	NA	0.729416723	1.100975414	NA	0.710424353	0.780548171
13	A0A1B0GTG8	LOC105372440	NA	NA	NA	1.525033672	NA	NA	0.880178148	NA
14	A0A1B0GTK4	FAM237A	NA	NA	NA	NA	1000	NA	NA	
15	A0A1B0GTK5	FAM236D	NA	NA	NA	NA	0.601444595	NA	NA	0.874829465
16	A0A1B0GTZ2	CCDC196	NA	NA	NA	1.097098694	NA	NA	0.648635607	NA
17	A0A1B0GUL7	NoGene	NA	NA	NA	0.92638768	0.719461211	NA	0.551916497	0.742327137
18	A0A1B0GV03	GOLGA6L7	NA	NA	NA	NA	0.369653392	NA	NA	0.654871092
19	A0A1B0GW35	EXOC1L	0.353477418		1000	NA	NA		NA	NA
20	A0A1W2PPE3	NoGene	NA	NA	NA	NA	0.330853514	NA	NA	0.65665311
21	A0A1W2PR19	Gstt4	NA		0.289269836	NA	NA	NA	NA	NA
22	A0A2R8Y4L2	HNRNPA1P48	NA	NA	NA	0.932964123	NA	NA	0.897221897	NA
23	A0A2R8YFL7	OOSP4A	NA	NA	NA	NA	0.171158325	NA	NA	0.565603686



Dataset Upload - 41467_2024_47985_MOESM9_ESM_protein.xlsx

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 names that contain identifiers and observations. For observations, select the appropriate measurement value type.

ID/Observation Name	ID	ID	Ignore	Ignore	Ignore	MGG4_6h	MGG4_72h	Ignore	MGG4_6h	MGG4_72h
Measurement/Annotation	2 types sel...	Gene Symb...				Expr Ratio	Expr Ratio		Expr p-value	Expr p-value
1	Proteins	Gene	GL261_6h_ratio	GL261_72h_pvalue	GL261_72h_ratio	MGG4_6h_ratio	MGG4_72h_ratio	GL261_6h_pvalue	MGG4_6h_pvalue	MGG4_72h_pvalue
2	A0A075B6L6	TRBV7-3	NA	NA	NA	NA	1000	NA	NA	---
3	A0A087WT01	TRAV27	NA	NA	NA	NA	1000	NA	NA	---
4	A0A096LP01	SMIM26	NA	NA	NA	1.01753392114515	1.2608552091372...	NA	0.9794163057377...	0.5168663638375...
5	A0A096LP49	CCDC187	1.33189213831	NA	NA	NA	1000	---	NA	---
6	A0A0B4J244	NoGene	NA	NA	NA	1.05346140152489	NA	NA	0.9146653428594...	NA
7	A0A0B4J266	TRAV41	NA	NA	NA	1.5389279096033...	NA	NA	0.7083397368739...	NA
8	A0A0B4J2E5	ND4L	NA	NA	NA	1.00315722069075	1E-3	NA	0.99240110602345	---
9	A0A0B4J2F0	ND4L	NA	NA	NA	1.0005307092181...	0.9076713731772...	NA	0.9992354016027...	0.8091505476404...
10	A0A0J9YXQ4	PNMA6E	NA	NA	NA	0.9901026578427...	NA	NA	0.9965572321351...	NA
11	A0A0U1RRE5	NBDY	NA	NA	NA	0.9450302271894...	1.01991999589194	NA	0.9751953024754...	0.9940727134172...
12	A0A0U1RRL7	MMP24OS	NA	NA	NA	0.7294167228945...	1.10097541429705	NA	0.7104243532429...	0.780548170811866
13	A0A1B0GTG8	LOC105372440	NA	NA	NA	1.5250336720952	NA	NA	0.880178147830319	NA
14	A0A1B0GTK4	FAM237A	NA	NA	NA	NA	1000	NA	NA	---
15	A0A1B0GTK5	FAM236D	NA	NA	NA	NA	0.6014445953918...	NA	NA	0.8748294653684...
16	A0A1B0GTZ2	CCDC196	NA	NA	NA	1.09709869387371	NA	NA	0.6486356066096...	NA
17	A0A1B0GUL7	NoGene	NA	NA	NA	0.9263876798203...	0.7194612110903...	NA	0.5519164969783...	0.7423271369652...
18	A0A1B0GV03	GOLGA6L7	NA	NA	NA	NA	0.3696533924455...	NA	NA	0.6548710915773...
19	A0A1B0GW35	EXOC1L	0.3534774183510...	---	1000	NA	NA	---	NA	NA
20	A0A1W2PPE3	NoGene	NA	NA	NA	NA	0.3308535141119...	NA	NA	0.6566531104034...
21	A0A1W2PR19	Gstt4	NA	---	0.2892698359078...	NA	NA	NA	NA	NA
22	A0A2R8Y4L2	HNRNPA1P48	NA	NA	NA	0.9329641228942...	NA	NA	0.8972218968133...	NA
23	A0A2R8YFL7	OOSP4A	NA	NA	NA	NA	0.1711583252420...	NA	NA	0.5656036861448...
24	A0A2Z4LIS9	FOXO3B	NA	NA	NA	NA	0.8162978737138...	NA	NA	0.7461938355196...
25	A0A3B3IRV3	MCTS2P	NA	NA	NA	0.7719443180448...	NA	NA	0.9203295899311...	NA
26	A0A3B3IT52	LOC102724657	NA	NA	NA	NA	1E-3	NA	NA	---
27	A0A494C071	PWWP4	NA	NA	NA	1.38406174314577	0.4418673271241...	NA	0.5539222588168...	0.6652798900435...
28	A0AUZ9	KANSL1L	NA	NA	NA	NA	3.9830852041311...	NA	NA	0.2856662768244...

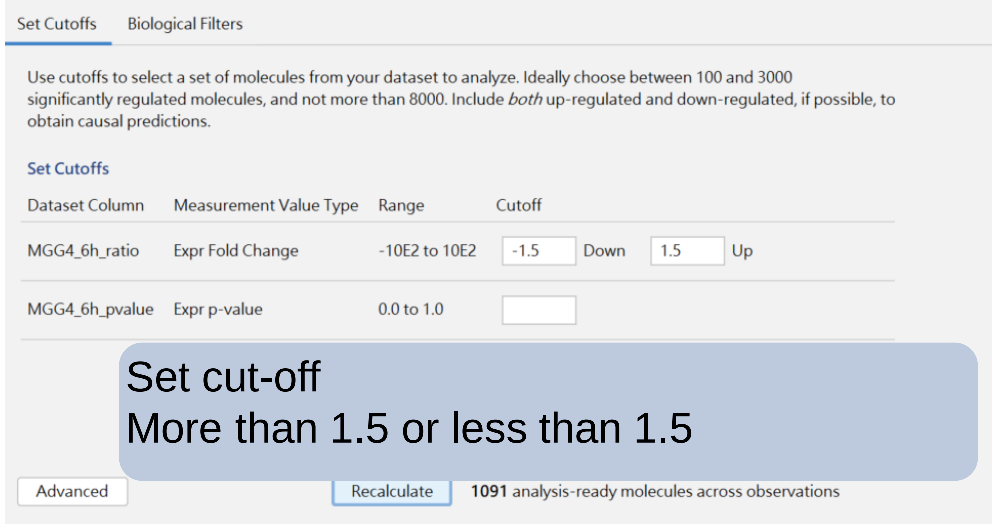
ID

Ignore columns you don't want to analyze

6h and 72h expr ratio

6h and 72h p-value

Filter setting and biological filter



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.

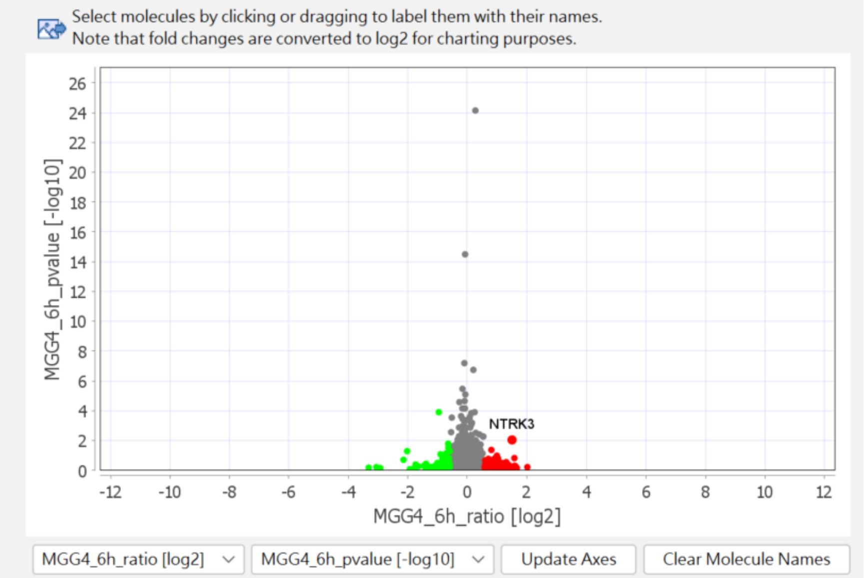
Set Cutoffs

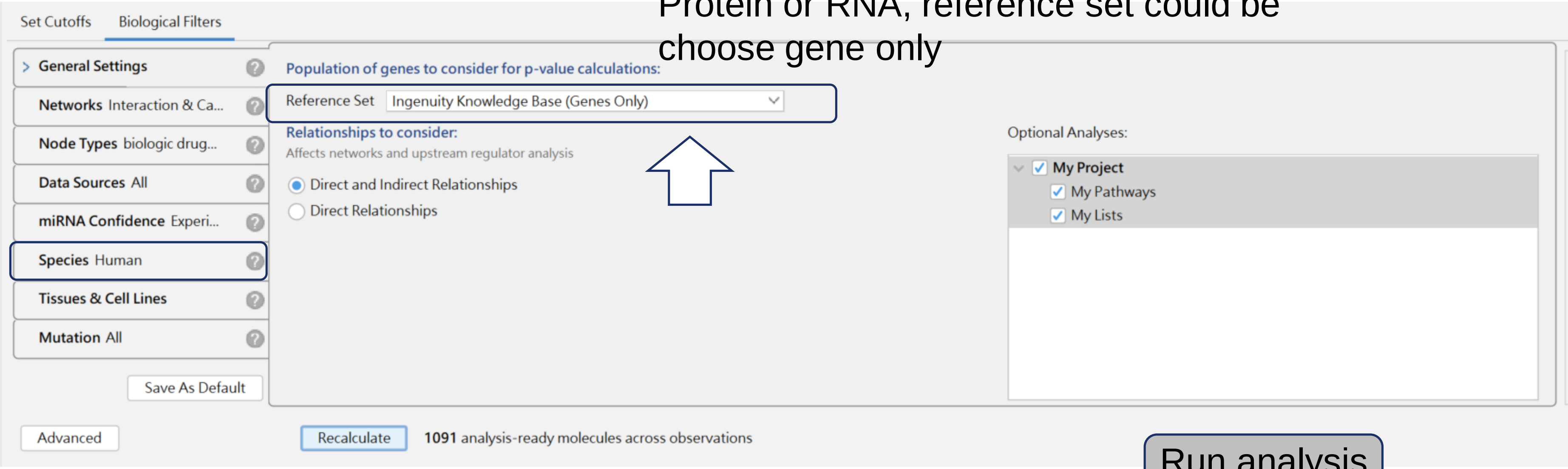
Dataset Column	Measurement Value Type	Range	Cutoff
MGG4_6h_ratio	Expr Fold Change	-10E2 to 10E2	-1.5 Down 1.5 Up
MGG4_6h_pvalue	Expr p-value	0.0 to 1.0	

1091 analysis-ready molecules across observations

Set cut-off
More than 1.5 or less than 1.5

After filter, you can get volcano plot


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



- **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 Only)

Relationships to consider:
Affects networks and upstream regulator analysis
● Direct and Indirect Relationships
○ Direct Relationships

Optional Analyses:
☑ My Project
  ☑ My Pathways
  ☑ My Lists

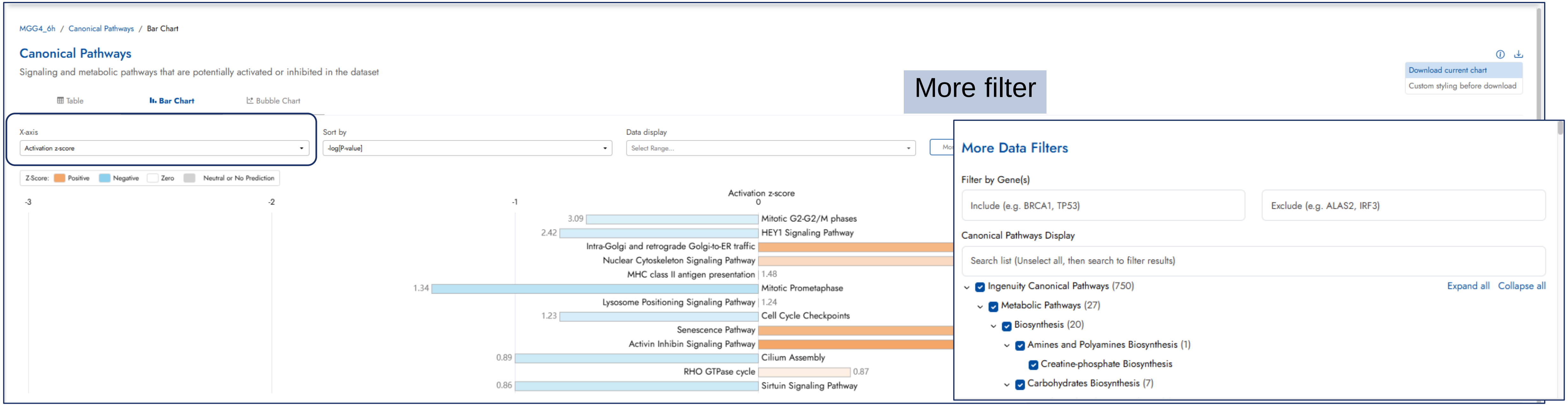
1091 analysis-ready molecules across observations

Protein or RNA, reference set could be choose gene only

According to gene name, It will automatically identified Genes from which species

Run analysis

More filter



MGG4_6h / Canonical Pathways / Bar Chart

Canonical Pathways

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

X-axis: Activation z-score

Sort by: -log[P-value]

Data display: Select Range...

Download current chart
Custom styling before download

More Data Filters

Filter by Gene(s)

Include (e.g. BRCA1, TP53)

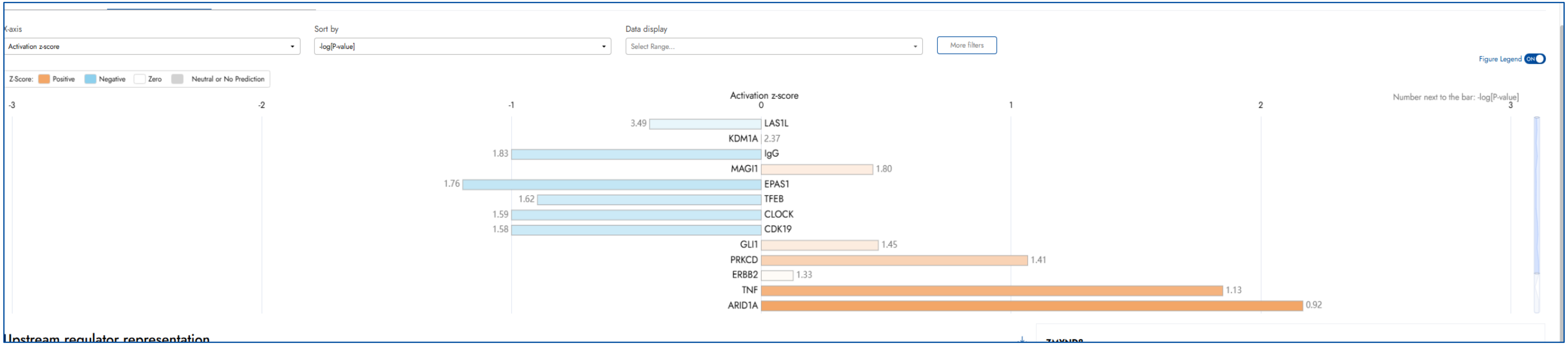
Exclude (e.g. ALAS2, IRF3)

Canonical Pathways Display

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

Expand all   Collapse all

- ☑ Ingenuity Canonical Pathways (750)
  - ☑ Metabolic Pathways (27)
    - ☑ Biosynthesis (20)
      - ☑ Amines and Polyamines Biosynthesis (1)
        - ☑ Creatine-phosphate Biosynthesis
      - ☑ Carbohydrates Biosynthesis (7)



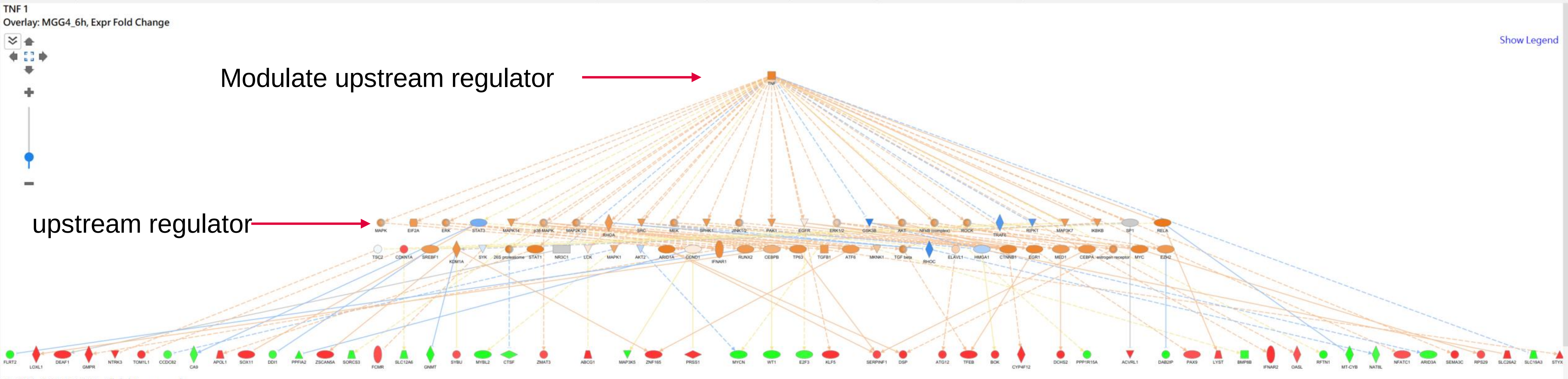
-axis
Activation z-score

Sort by
-log[P-value]

Data display
Select Range...

Upstream regulator representation

Casual network

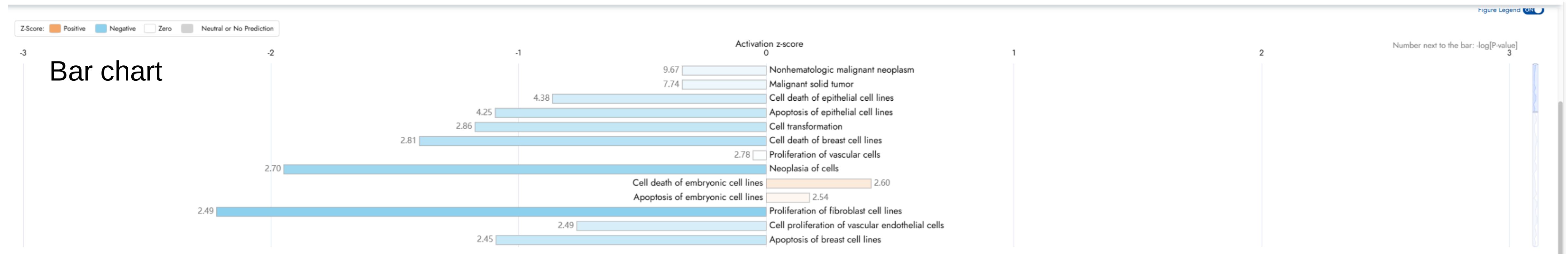


Modulate upstream regulator

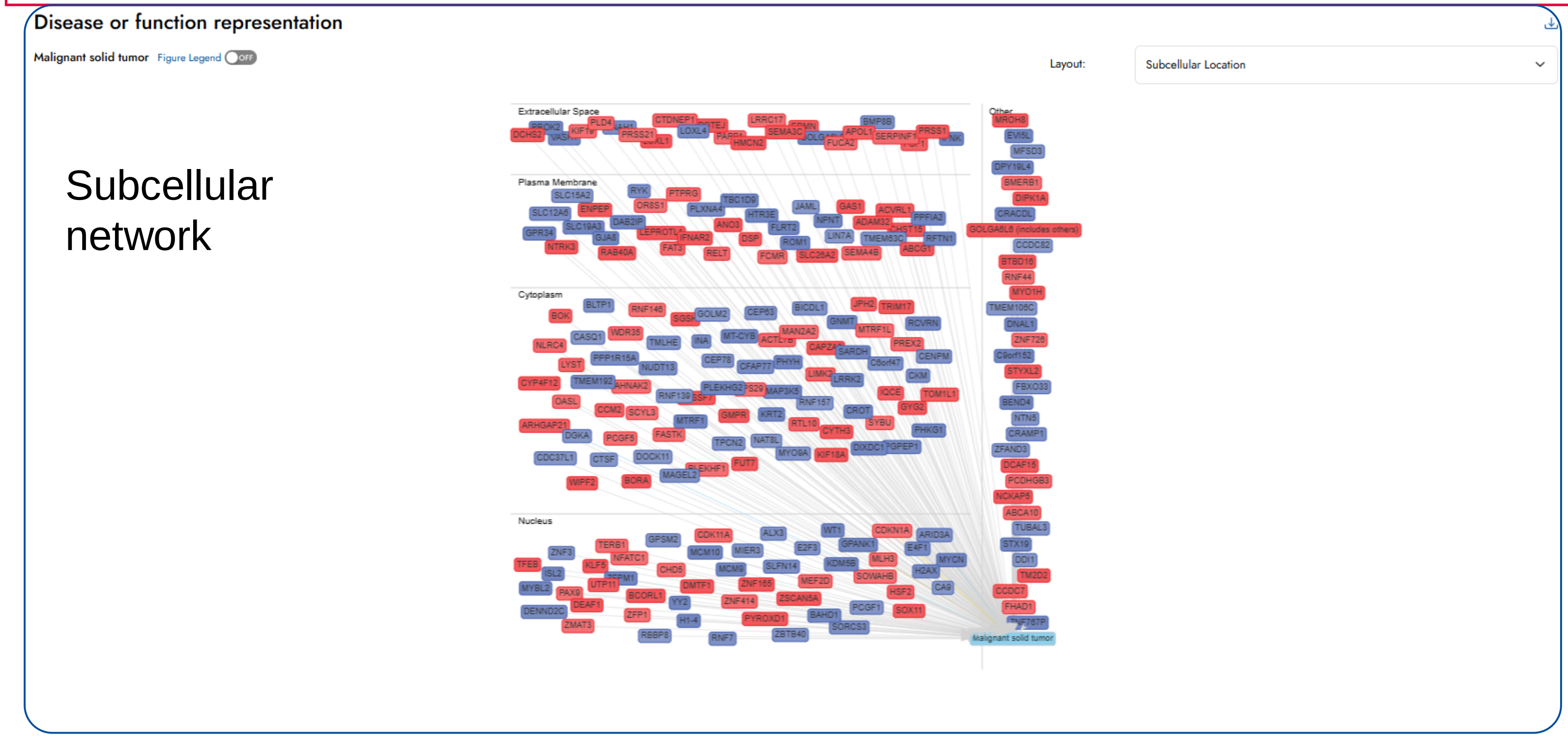
upstream regulator

Differential expression genes

Disease and function



Bar chart

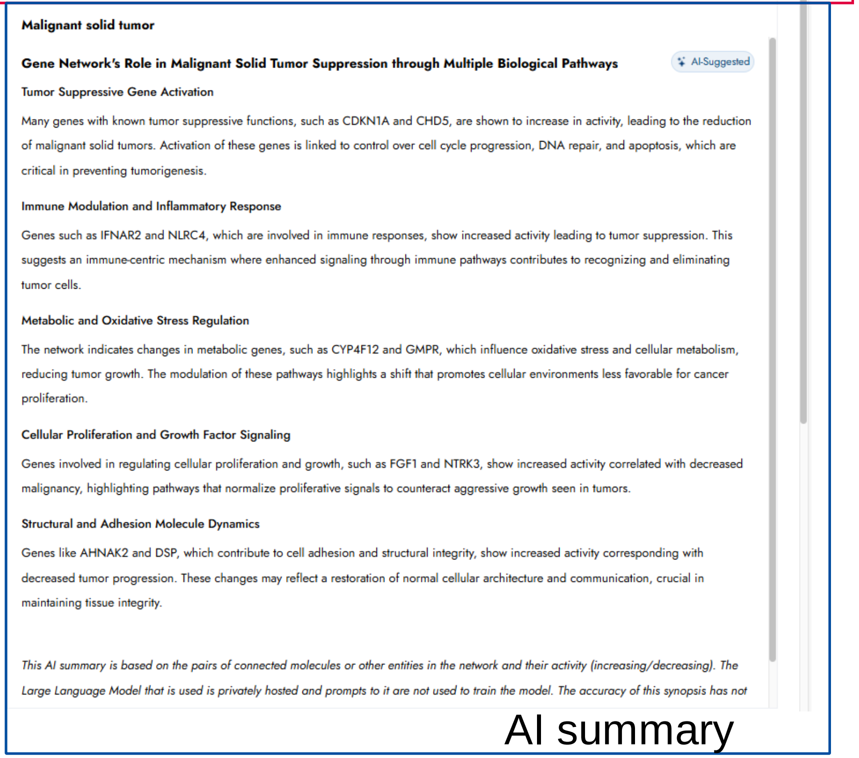


Disease or function representation

Malignant solid tumor Figure Legend OFF

Layout: Subcellular Location

Subcellular network



Malignant solid tumor

Gene Network's Role in Malignant Solid Tumor Suppression through Multiple Biological Pathways

Tumor Suppressive Gene Activation

Many genes with known tumor suppressive functions, such as CDKN1A and CHD5, are shown to increase in activity, leading to the reduction of malignant solid tumors. Activation of these genes is linked to control over cell cycle progression, DNA repair, and apoptosis, which are critical in preventing tumorigenesis.

Immune Modulation and Inflammatory Response

Genes such as IFNAR2 and NLRC4, which are involved in immune responses, show increased activity leading to tumor suppression. This suggests an immune-centric mechanism where enhanced signaling through immune pathways contributes to recognizing and eliminating tumor cells.

Metabolic and Oxidative Stress Regulation

The network indicates changes in metabolic genes, such as CYP4F12 and GMPR, which influence oxidative stress and cellular metabolism, reducing tumor growth. The modulation of these pathways highlights a shift that promotes cellular environments less favorable for cancer proliferation.

Cellular Proliferation and Growth Factor Signaling

Genes involved in regulating cellular proliferation and growth, such as FGF1 and NTRK3, show increased activity correlated with decreased malignancy, highlighting pathways that normalize proliferative signals to counteract aggressive growth seen in tumors.

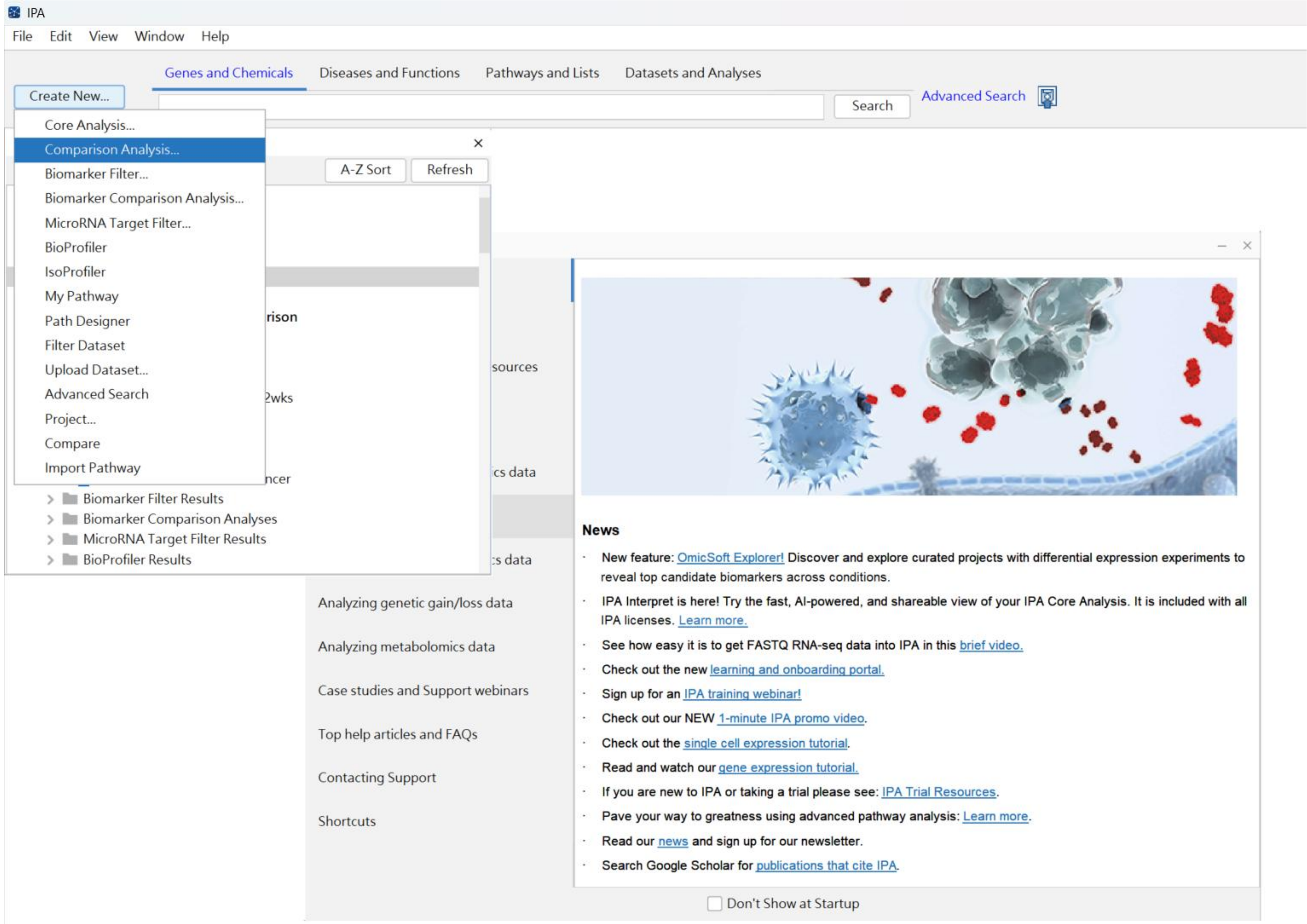
Structural and Adhesion Molecule Dynamics

Genes like AHNAK2 and DSP, which contribute to cell adhesion and structural integrity, show increased activity corresponding with decreased tumor progression. These changes may reflect a restoration of normal cellular architecture and communication, crucial in maintaining tissue integrity.

This AI summary is based on the pairs of connected molecules or other entities in the network and their activity (increasing/decreasing). The Large Language Model that is used is privately hosted and prompts to it are not used to train the model. The accuracy of this synopsis has not

AI summary

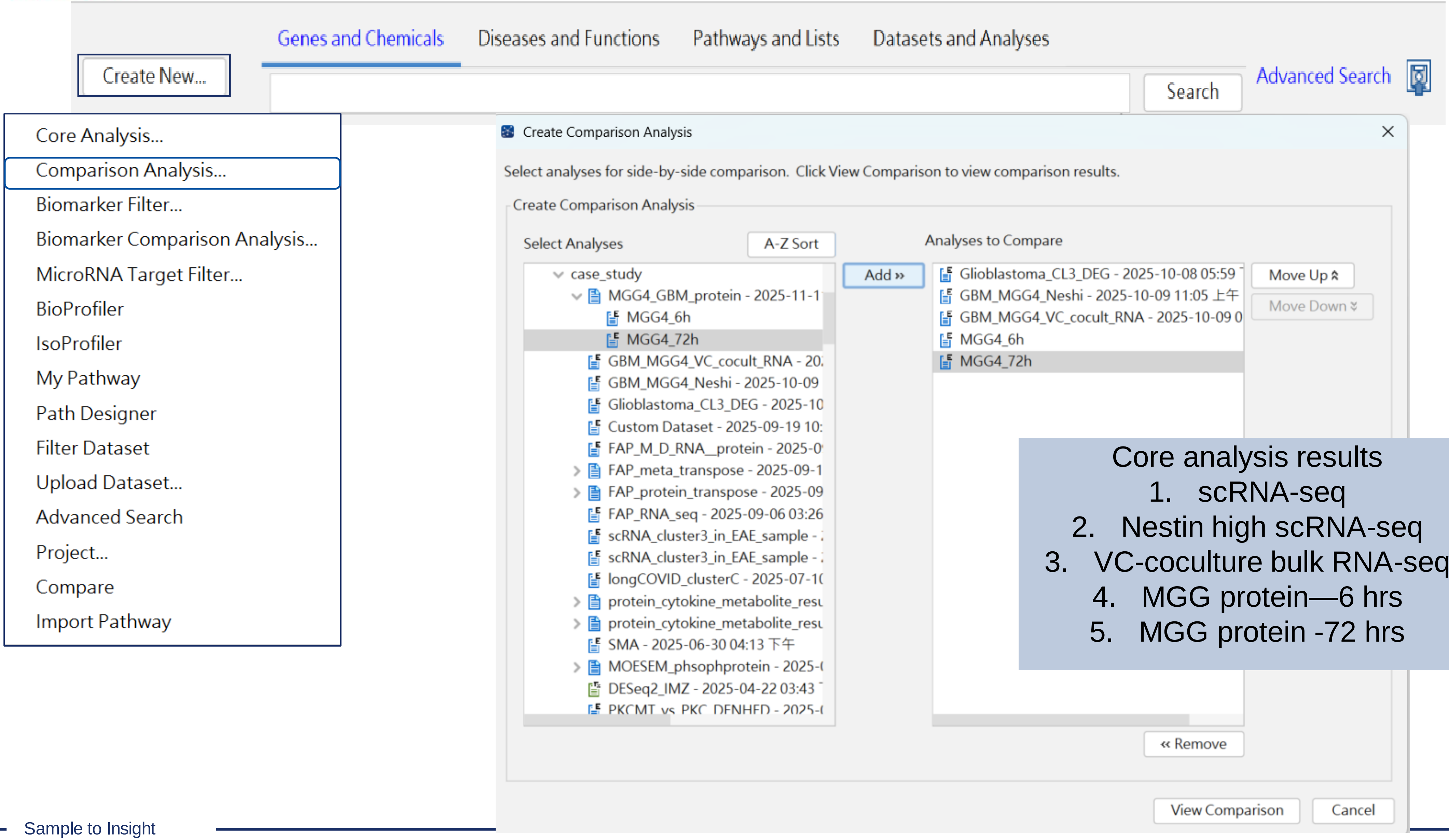
Comparison analysis



News

- New feature: OmicSoft Explorer! Discover and explore curated projects with differential expression experiments to reveal top candidate biomarkers across conditions.
- IPA Interpret is here! Try the fast, AI-powered, and shareable view of your IPA Core Analysis. It is included with all IPA licenses. Learn more.
- See how easy it is to get FASTQ RNA-seq data into IPA in this brief video.
- Check out the new learning and onboarding portal.
- Sign up for an IPA training webinar!
- Check out our NEW 1-minute IPA promo video.
- Check out the single cell expression tutorial.
- Read and watch our gene expression tutorial.
- If you are new to IPA or taking a trial please see: IPA Trial Resources.
- Pave your way to greatness using advanced pathway analysis: Learn more.
- Read our news and sign up for our newsletter.
- Search Google Scholar for publications that cite IPA.

Comparison analysis



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

Select Analyses:

- case_study
  - MGG4_GBM_protein - 2025-11-1
    - MGG4_6h
    - MGG4_72h
  - GBM_MGG4_VC_cocult_RNA - 20
  - GBM_MGG4_Neshi - 2025-10-09
  - Glioblastoma_CL3_DEG - 2025-10
  - Custom Dataset - 2025-09-19 10:
  - FAP_M_D_RNA__protein - 2025-0
  - FAP_meta_transpose - 2025-09-1
  - FAP_protein_transpose - 2025-09
  - FAP_RNA_seq - 2025-09-06 03:26
  - scRNA_cluster3_in_EAE_sample -
  - scRNA_cluster3_in_EAE_sample -
  - longCOVID_clusterC - 2025-07-10
  - protein_cytokine_metabolite_resu
  - protein_cytokine_metabolite_resu
  - SMA - 2025-06-30 04:13 下午
  - MOESEM_phsophprotein - 2025-
  - DESeq2_IMZ - 2025-04-22 03:43
  - PKCMT_vs_PKC_DENHFD - 2025-

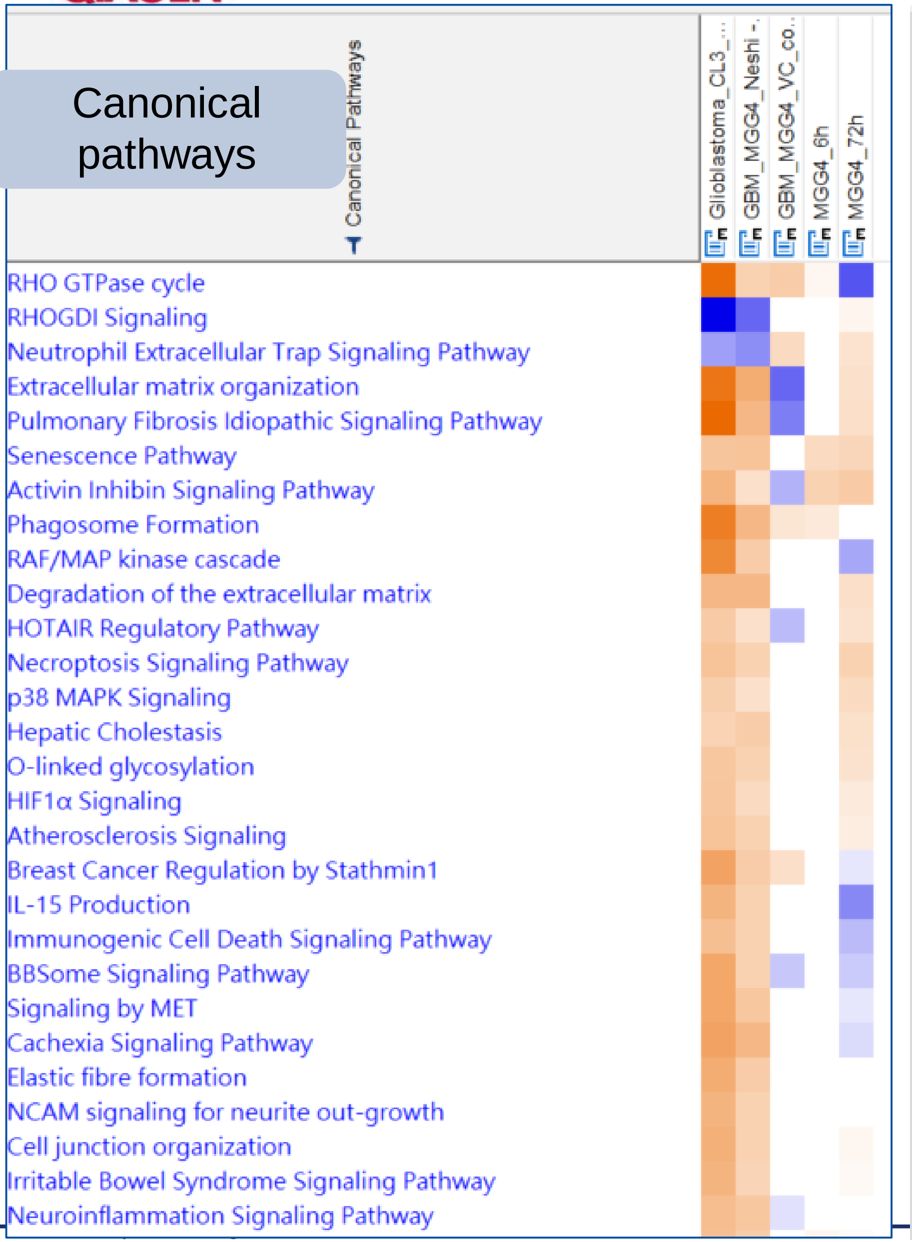
Analyses to Compare:

- Glioblastoma_CL3_DEG - 2025-10-08 05:59
- GBM_MGG4_Neshi - 2025-10-09 11:05 上午
- GBM_MGG4_VC_cocult_RNA - 2025-10-09 0
- MGG4_6h
- MGG4_72h

Core analysis results

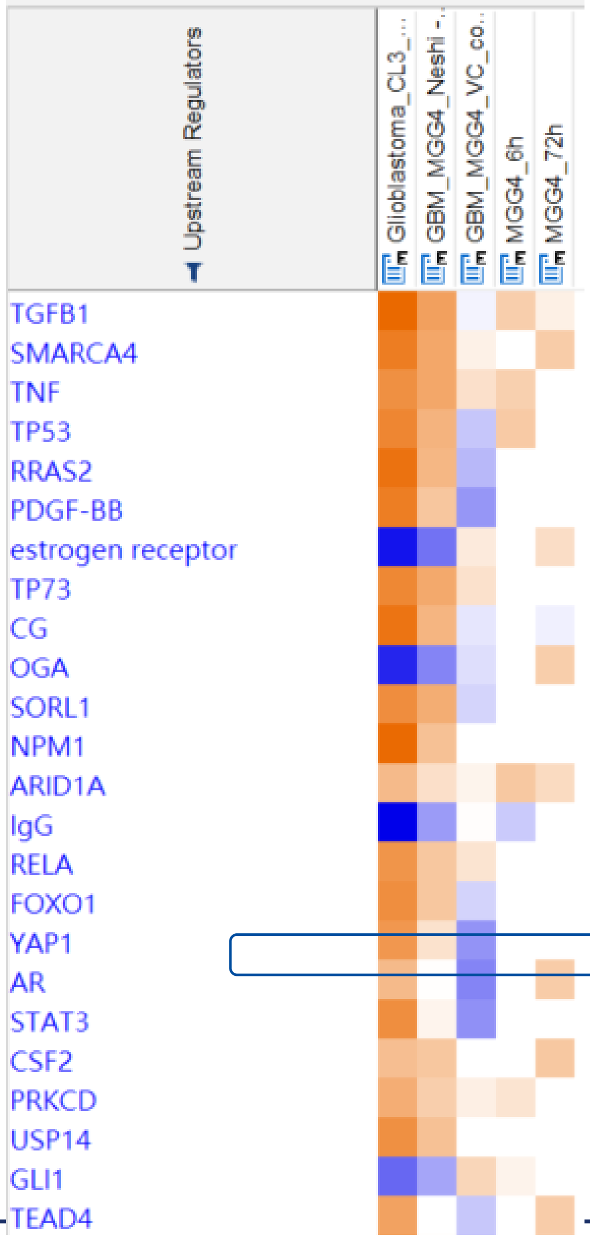
1. scRNA-seq
2. Nestin high scRNA-seq
3. VC-coculture bulk RNA-seq
4. MGG protein—6 hrs
5. MGG protein -72 hrs

Compare analysis

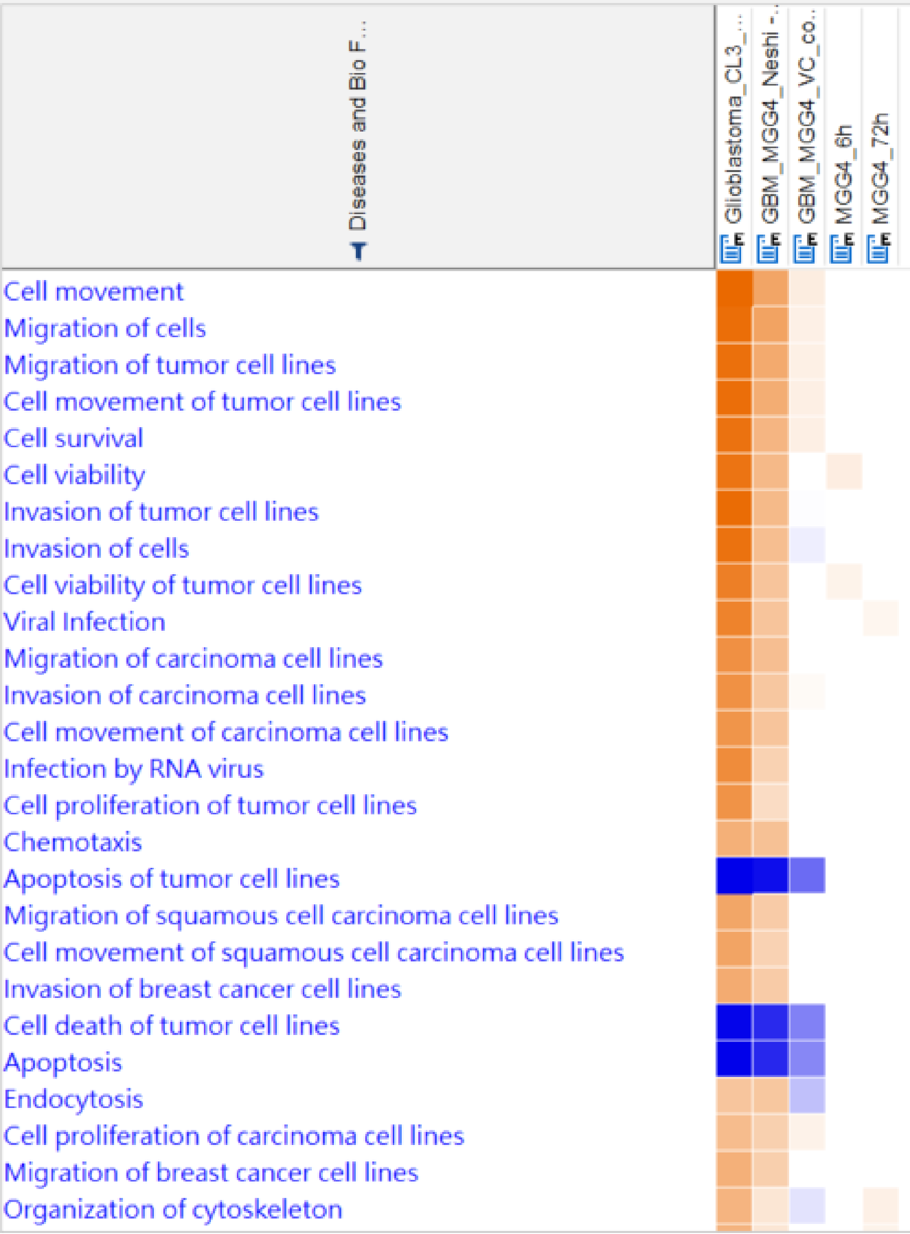


Canonical pathways

RHO GTPase cycle
RHOGDI Signaling
Neutrophil Extracellular Trap Signaling Pathway
Extracellular matrix organization
Pulmonary Fibrosis Idiopathic Signaling Pathway
Senescence Pathway
Activin Inhibin Signaling Pathway
Phagosome Formation
RAF/MAP kinase cascade
Degradation of the extracellular matrix
HOTAIR Regulatory Pathway
Necroptosis Signaling Pathway
p38 MAPK Signaling
Hepatic Cholestasis
O-linked glycosylation
HIF1α Signaling
Atherosclerosis Signaling
Breast Cancer Regulation by Stathmin1
IL-15 Production
Immunogenic Cell Death Signaling Pathway
BBSome Signaling Pathway
Signaling by MET
Cachexia Signaling Pathway
Elastic fibre formation
NCAM signaling for neurite out-growth
Cell junction organization
Irritable Bowel Syndrome Signaling Pathway
Neuroinflammation Signaling Pathway

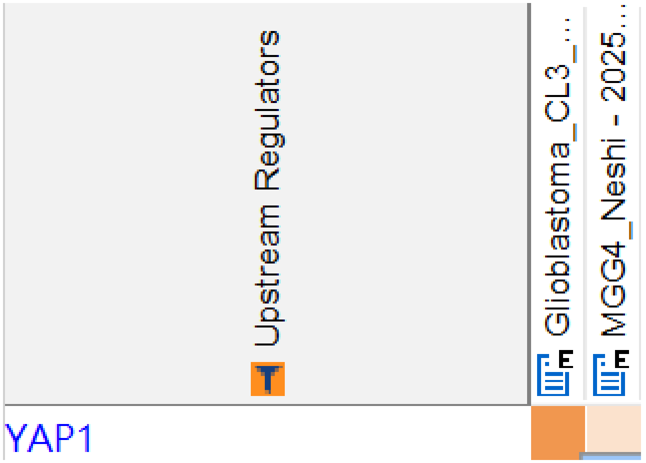


TGFB1
SMARCA4
TNF
TP53
RRAS2
PDGF-BB
estrogen receptor
TP73
CG
OGA
SORL1
NPM1
ARID1A
IgG
RELA
FOXO1
YAP1
AR
STAT3
CSF2
PRKCD
USP14
GLI1
TEAD4



Cell movement
Migration of cells
Migration of tumor cell lines
Cell movement of tumor cell lines
Cell survival
Cell viability
Invasion of tumor cell lines
Invasion of cells
Cell viability of tumor cell lines
Viral Infection
Migration of carcinoma cell lines
Invasion of carcinoma cell lines
Cell movement of carcinoma cell lines
Infection by RNA virus
Cell proliferation of tumor cell lines
Chemotaxis
Apoptosis of tumor cell lines
Migration of squamous cell carcinoma cell lines
Cell movement of squamous cell carcinoma cell lines
Invasion of breast cancer cell lines
Cell death of tumor cell lines
Apoptosis
Endocytosis
Cell proliferation of carcinoma cell lines
Migration of breast cancer cell lines
Organization of cytoskeleton

Upstream analysis

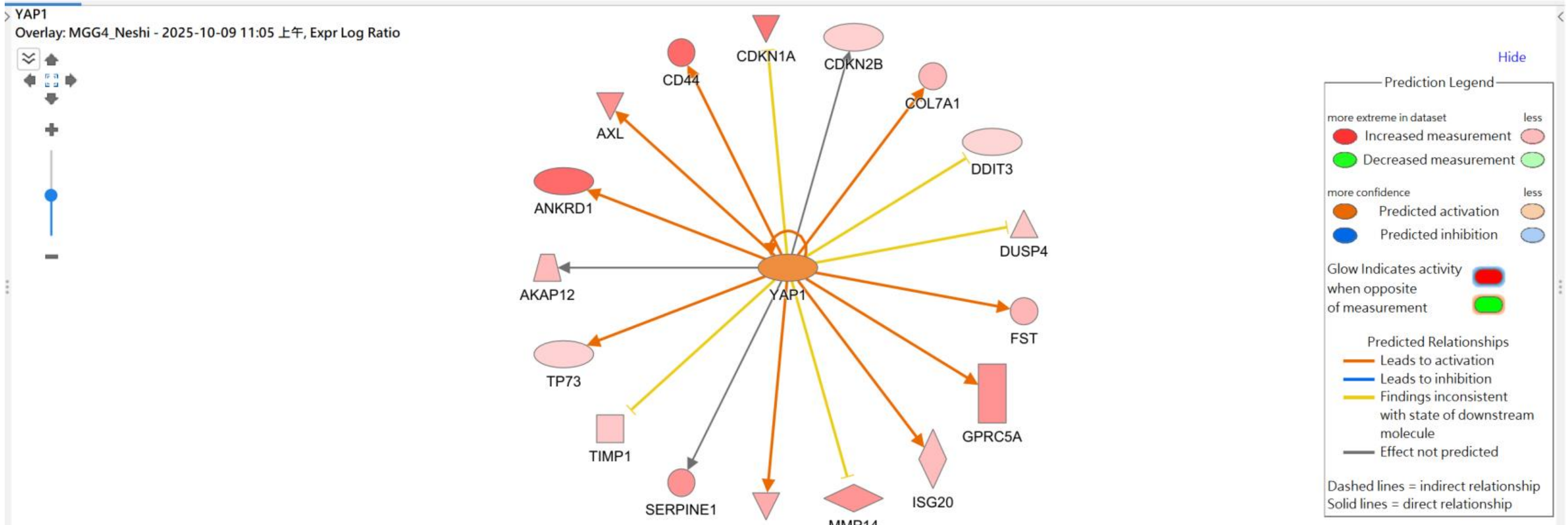


Upstream Regulators

Glioblastoma_CL3_...

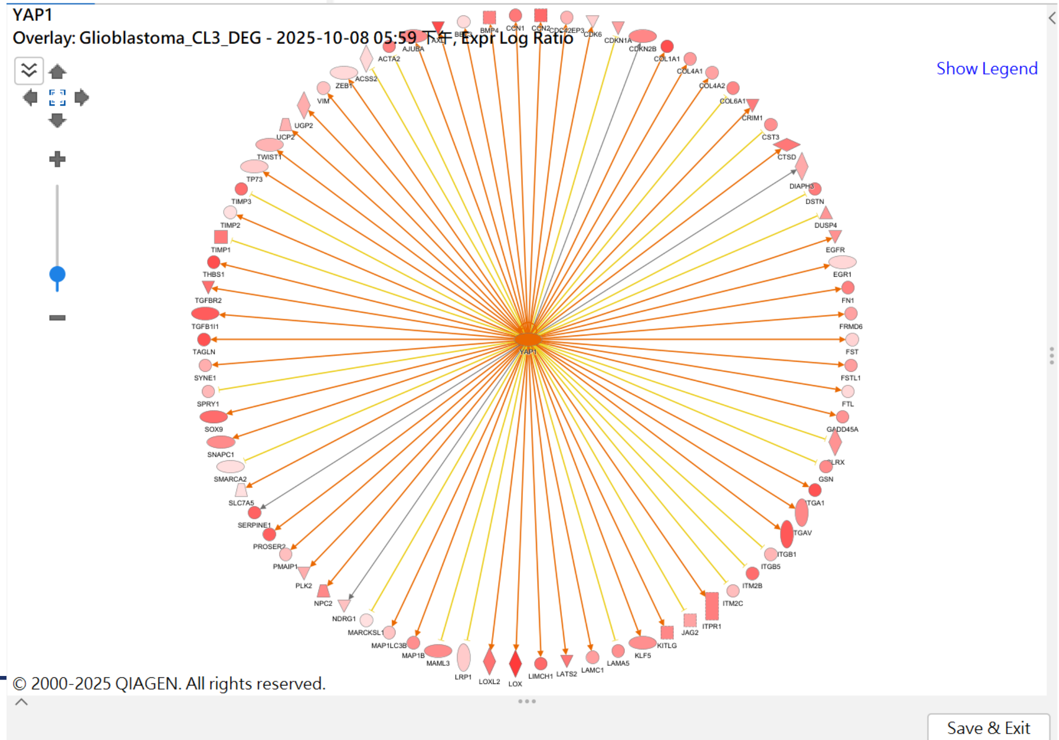
MGG4_Neshi - 2025...

YAP1



YAP1

Overlay: MGG4_Neshi - 2025-10-09 11:05 上午, Expr Log Ratio



YAP1

Overlay: Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午, Expr Log Ratio

Summary

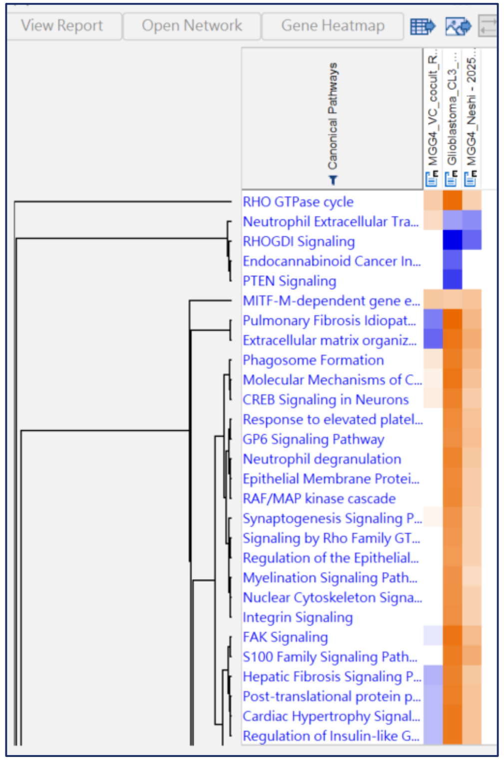
scRNA-seq

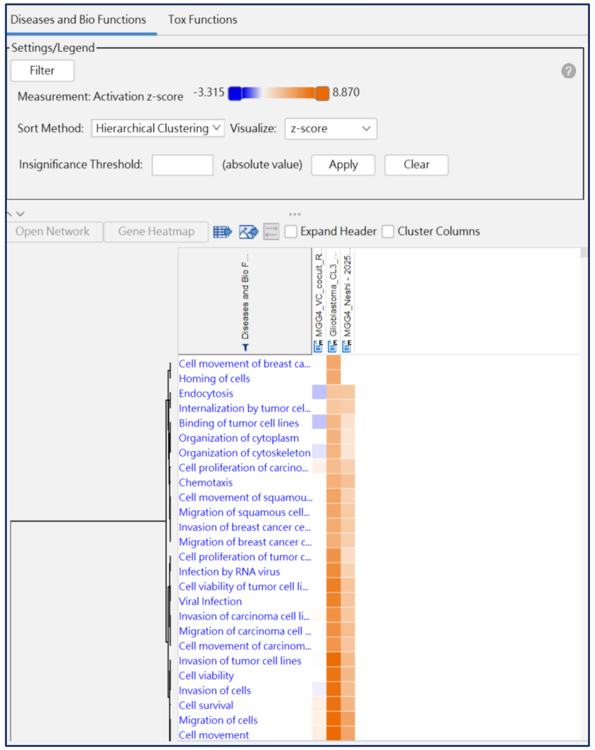
	A	B	C	D	E	F
1	gene ID	avg_log2FC	pct.1	pct.2	padj	AUROC
2	SPARC	3.867	100%	33%	8.18e-152	0.975
3	TPM1	3.56	99%	33%	2.72e-146	0.966
4	MAP3K7CL	5.597	96%	19%	1.23e-142	0.961
5	MEF2A	4.523	99%	37%	1.70e-141	0.959
6	MYL6	3.44	96%	35%	1.35e-133	0.946
7	CALD				7e-133	0.945
8	ITGB				6e-133	0.944
9	IGFBP				9e-132	0.943
10	BCAI				8e-131	0.941
11	CAVIN				3e-130	0.94
12	NR3C				0e-128	0.938
13	TIMP1	3.533	93%	30%	2.68e-123	0.929
14	VIM	1.625	98%	41%	2.08e-122	0.927
15	CRYAB	3.064	93%	19%	6.90e-122	0.926
16	CDH11	4.002	95%	33%	5.26e-121	0.925
17	GSN	3.102	93%	33%	6.48e-120	0.923
18	KANK2	3.742	94%	33%	2.43e-119	0.922
19	TM4SF1	3.854	94%	37%	4.00e-117	0.918
20	ZFP36L1	2.982	96%	36%	1.87e-116	0.917
21	FN1	3.354	92%	30%	2.58e-115	0.915
22	SPTBN1	3.739	94%	39%	1.75e-114	0.913
23	EMP3	2.638	93%	31%	1.16e-114	0.913
24	ITM2B	3.849	95%	41%	3.20e-113	0.911
25	STK38L	4.457	92%	35%	1.28e-111	0.908
26	PDE4DIP	3.516	93%	38%	2.40e-111	0.908
27	ADGRE5	4.376	91%	36%	3.90e-111	0.907
28	NUAK1	4.15	91%	22%	7.51e-111	0.907
29	ZNF106	3.997	90%	36%	1.27e-107	0.901
30	MYLK	3.724	90%	31%	2.29e-107	0.9
31	LTBP1	3.505	90%	23%	8.39e-107	0.899
32	MAP1B	2.958	92%	37%	1.58e-106	0.899
33	SOD3	2.683	91%	22%	1.39e-105	0.897
34	COL6A2	4.302	88%	23%	1.00e-104	0.895
35	IQGAP1	3.676	91%	39%	1.88e-104	0.895
36	PPIC	3.216	91%	36%	3.25e-104	0.894
37	COL11A1	2.976	91%	40%	9.62e-104	0.894
38	CD164	4.074	92%	39%	7.25e-103	0.892
39	CRIP2	2.772	93%	37%	4.32e-103	0.892
40	LMNA	2.4	91%	34%	1.04e-102	0.892
41	NCK2	3.456	92%	36%	1.07e-101	0.89

Proteiomics

	A	B	C	D	E	F
1	Proteins	Gene	MGG4_6h_ratio	MGG4_72h_ratio	MGG4_6h_pvalue	MGG4_72h_pvalue
2	A0A075B6L6	TRBV7-3	NA	1000	NA	
3	A0A087WT01	TRAV27	NA	1000	NA	
4	A0A096LP01	SMIM26	1.017533921	1.260855209	0.979416306	0.516866364
5	A0A096LP49	CCDC187	N			
6	A0A0B4J244	NoGene			3	NA
7	A0A0B4J266	TRAV41			7	NA
8	A0A0B4J2E5	ND4L			6	
9	A0A0B4J2F0	ND4L			2	0.809150548
10	A0A0J9YXQ4	PNMA6E	0.990102658	NA	0.996557232	NA
11	A0A0U1RRE5	NBDY	0.945030227	1.019919996	0.975195302	0.994072713
12	A0A0U1RRL7	MMP24OS	0.729416723	1.100975414	0.710424353	0.780548171
13	A0A1B0GTG8	LOC105372440	1.525033672	NA	0.880178148	NA
14	A0A1B0GTK4	FAM237A	NA	1000	NA	
15	A0A1B0GTK5	FAM236D	NA	0.601444595	NA	0.874829465
16	A0A1B0GTZ2	CCDC196	1.097098694	NA	0.648635607	NA
17	A0A1B0GUL7	NoGene	0.92638768	0.719461211	0.551916497	0.742327137
18	A0A1B0GV03	GOLGA6L7	NA	0.369653392	NA	0.654871092
19	A0A1B0GW35	EXOC1L	NA	NA	NA	NA
20	A0A1W2PPE3	NoGene	NA	0.330853514	NA	0.65665311
21	A0A1W2PR19	Gstt4	NA	NA	NA	NA
22	A0A2R8Y4L2	HNRNPA1P48	0.932964123	NA	0.897221897	NA
23	A0A2R8YFL7	OOSP4A	NA	0.171158325	NA	0.565603686
24	A0A2Z4LIS9	FOXO3B	NA	0.816297874	NA	0.746193836
25	A0A3B3IRV3	MCTS2P	0.771944318	NA	0.92032959	NA
26	A0A3B3IT52	LOC102724657	NA	0.001	NA	
27	A0A494C071	PWWP4	1.384061743	0.441867327	0.553922259	0.66527989
28	A0AUZ9	KANSL1L	NA	0.039830852	NA	0.285666277
29	A0AVF1	TTC26	1.022996778	NA	0.992388018	NA
30	A0AVI2	FER1L5	NA	0.779299583	NA	0.423141069
31	A0AVI4	TMEM129	1000	NA		NA
32	A0AVK6	E2F8	NA	0.415308593	NA	
33	A0AVT1	UBA6	0.981580462	0.940285808	0.451750265	0.213078782

Comparison analysis





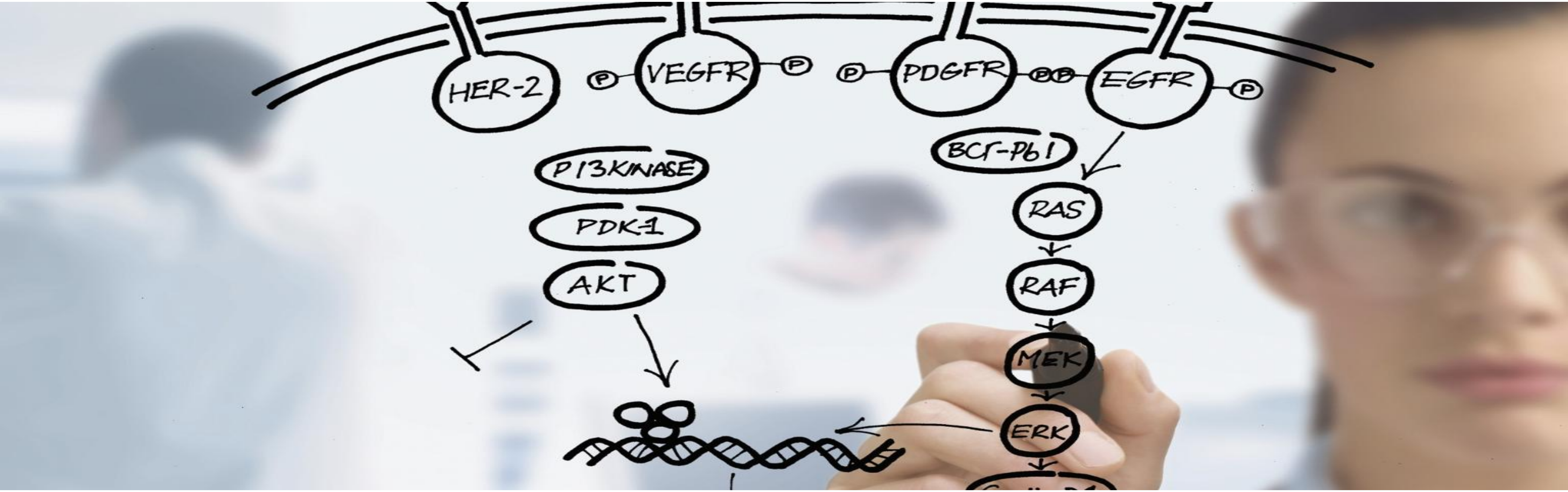
Measurement: Activation z-score -3.315 8.870

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value)

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



歡迎與我們聯絡

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:

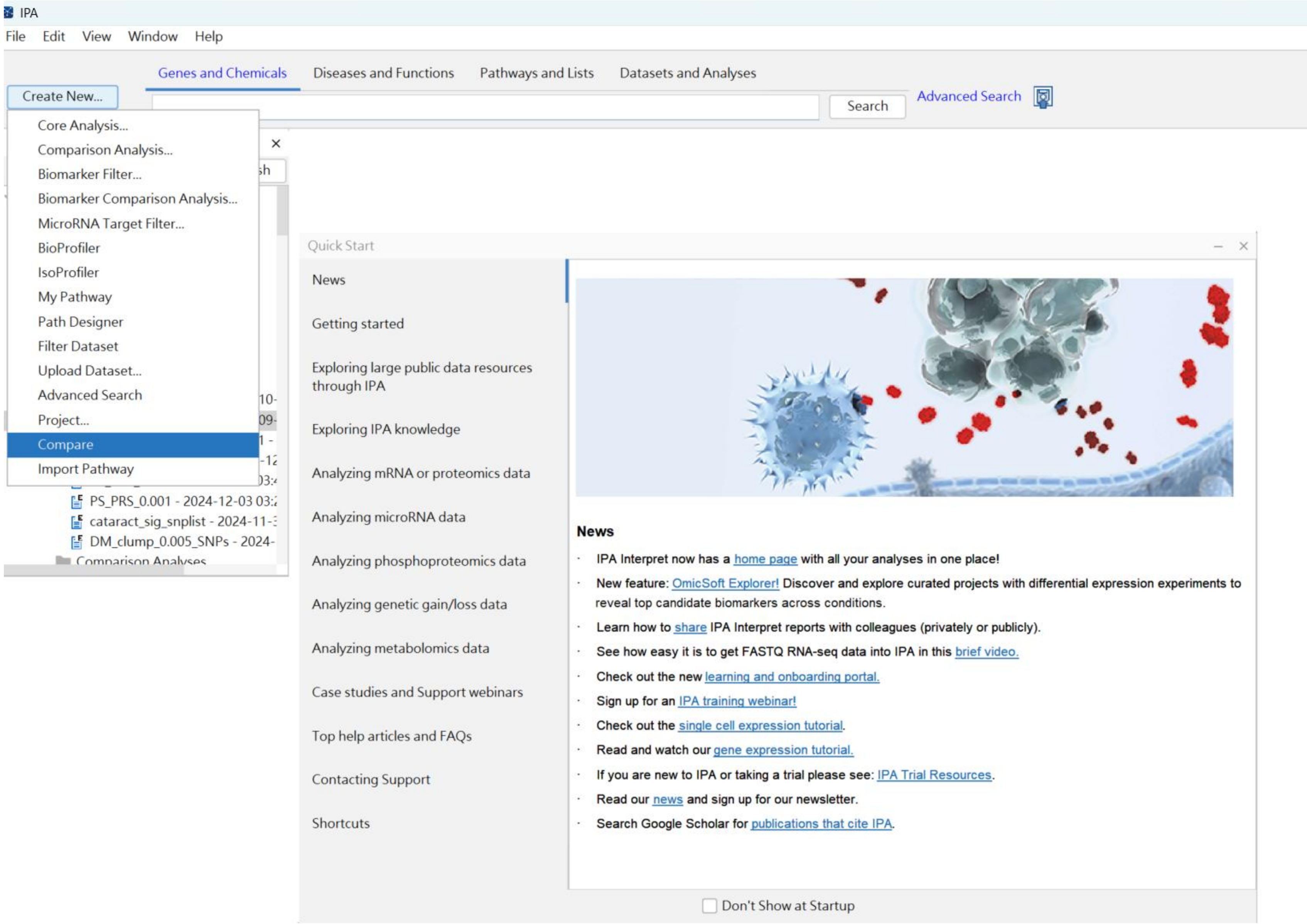
黃馨誼 專案副理	Hsinyihuang@gga.asia	02-2795 1777 #2509
熊嘉妮 專案副理	ChristineHsiung@gga.asia	02-2795 1777 #2505

Compare

Create new

↓

Compare



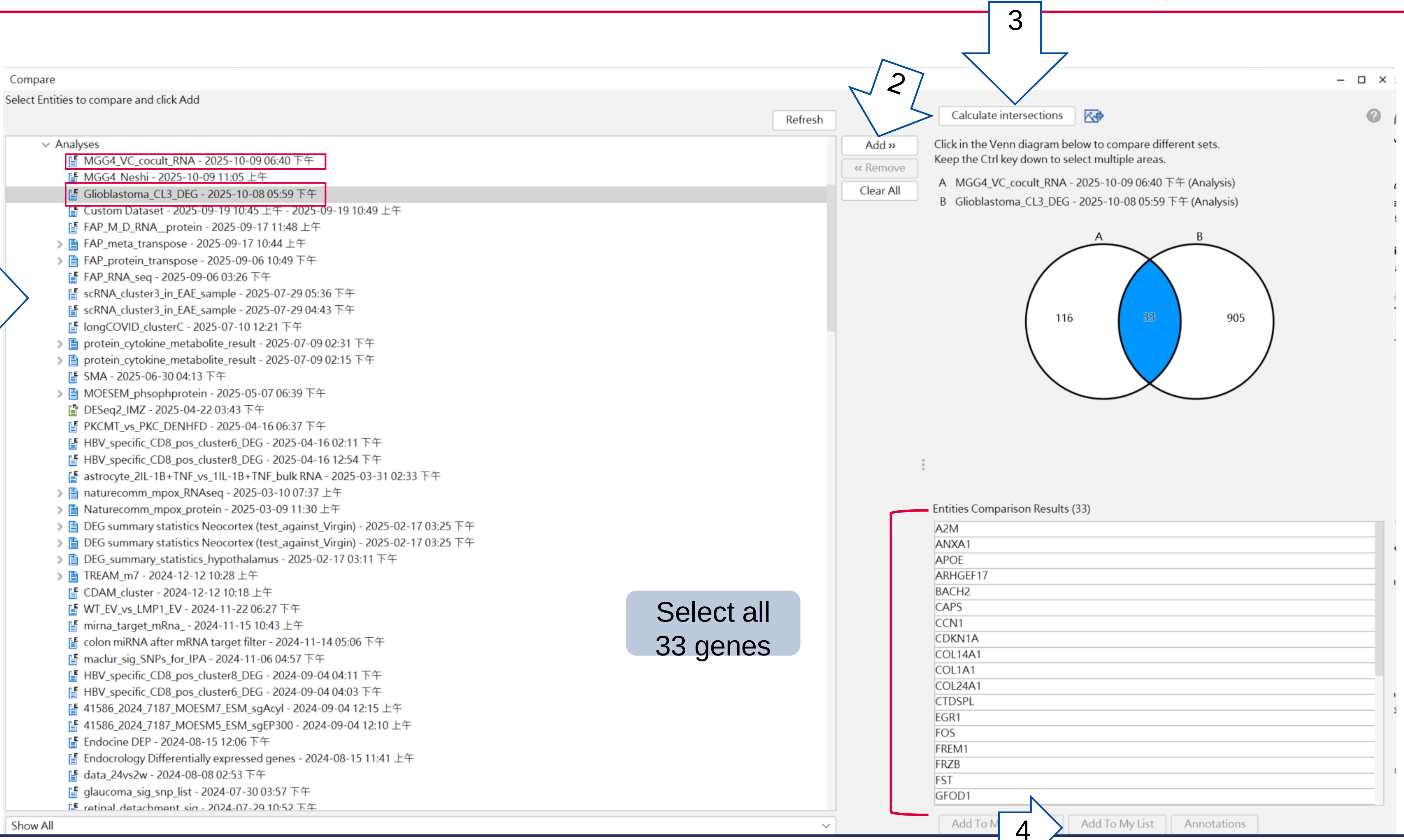
News

- IPA Interpret now has a home page with all your analyses in one place!
- New feature: OmicSoft Explorer! Discover and explore curated projects with differential expression experiments to reveal top candidate biomarkers across conditions.
- Learn how to share IPA Interpret reports with colleagues (privately or publicly).
- See how easy it is to get FASTQ RNA-seq data into IPA in this brief video.
- Check out the new learning and onboarding portal.
- Sign up for an IPA training webinar!
- Check out the single cell expression tutorial.
- Read and watch our gene expression tutorial.
- If you are new to IPA or taking a trial please see: IPA Trial Resources.
- Read our news and sign up for our newsletter.
- Search Google Scholar for publications that cite IPA.

Add scRNA and bulk RNA data

Calculate intersection

Add to my list



Compare

Select Entities to compare and click Add

Analyses
- MGG4_VC_cocult_RNA - 2025-10-09 06:40 下午
- MGG4_Neshi - 2025-10-09 11:05 上午
- Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午
- Custom Dataset - 2025-09-19 10:45 上午 - 2025-09-19 10:49 上午
- FAP_M_D_RNA__protein - 2025-09-17 11:48 上午
- FAP_meta_transpose - 2025-09-17 10:44 上午
- FAP_protein_transpose - 2025-09-06 10:49 下午
- FAP_RNA_seq - 2025-09-06 03:26 下午
- scRNA_cluster3_in_EAE_sample - 2025-07-29 05:36 下午
- scRNA_cluster3_in_EAE_sample - 2025-07-29 04:43 下午
- longCOVID_clusterC - 2025-07-10 12:21 下午
- protein_cytokine_metabolite_result - 2025-07-09 02:31 下午
- protein_cytokine_metabolite_result - 2025-07-09 02:15 下午
- SMA - 2025-06-30 04:13 下午
- MOESEM_phsophprotein - 2025-05-07 06:39 下午
- DESeq2_IMZ - 2025-04-22 03:43 下午
- PKCMT_vs_PKC_DENHFD - 2025-04-16 06:37 下午
- HBV_specific_CD8_pos_cluster6_DEG - 2025-04-16 02:11 下午
- HBV_specific_CD8_pos_cluster8_DEG - 2025-04-16 12:54 下午
- astrocyte_2IL-1B+TNF_vs_1IL-1B+TNF_bulk RNA - 2025-03-31 02:33 下午
- naturecomm_mpox_RNAseq - 2025-03-10 07:37 上午
- Naturecomm_mpox_protein - 2025-03-09 11:30 上午
- DEG summary statistics Neocortex (test_against_Virgin) - 2025-02-17 03:25 下午
- DEG summary statistics Neocortex (test_against_Virgin) - 2025-02-17 03:25 下午
- DEG_summary_statistics_hypothalamus - 2025-02-17 03:11 下午
- TREAM_m7 - 2024-12-12 10:28 上午
- CDAM_cluster - 2024-12-12 10:18 上午
- WT_EV_vs_LMP1_EV - 2024-11-22 06:27 下午
- mirna_target_mRna_ - 2024-11-15 10:43 上午
- colon miRNA after mRNA target filter - 2024-11-14 05:06 下午
- maclur_sig_SNPs_for_IPA - 2024-11-06 04:57 下午
- HBV_specific_CD8_pos_cluster8_DEG - 2024-09-04 04:11 下午
- HBV_specific_CD8_pos_cluster6_DEG - 2024-09-04 04:03 下午
- 41586_2024_7187_MOESM7_ESM_sgAcyl - 2024-09-04 12:15 上午
- 41586_2024_7187_MOESM5_ESM_sgEP300 - 2024-09-04 12:10 上午
- Endocine DEP - 2024-08-15 12:06 下午
- Endocrology Differentially expressed genes - 2024-08-15 11:41 上午
- data_24vs2w - 2024-08-08 02:53 下午
- glaucoma_sig_snp_list - 2024-07-30 03:57 下午
- retinal_detachment_sig - 2024-07-29 10:52 下午

Show All

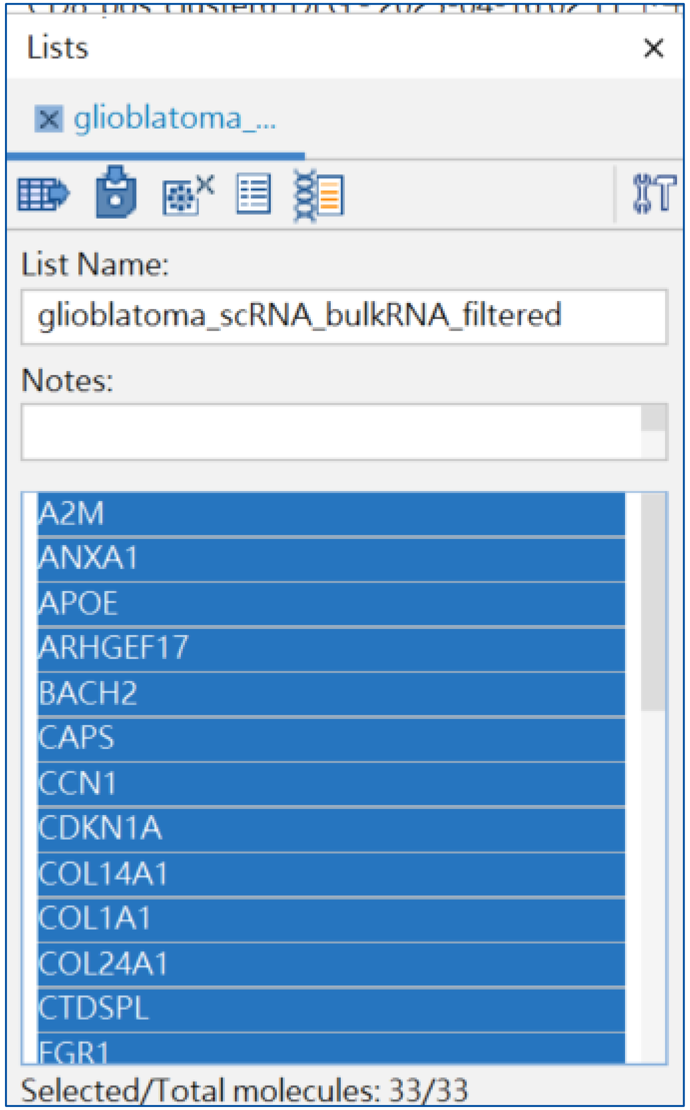
Click in the Venn diagram below to compare different sets.
Keep the Ctrl key down to select multiple areas.

A MGG4_VC_cocult_RNA - 2025-10-09 06:40 下午 (Analysis)
B Glioblastoma_CL3_DEG - 2025-10-08 05:59 下午 (Analysis)

Entities Comparison Results (33)

A2M
ANXA1
APOE
ARHGEF17
BACH2
CAPS
CCN1
CDKN1A
COL14A1
COL1A1
COL24A1
CTDSPL
EGR1
FOS
FREM1
FRZB
FST
GFOD1

Select all 33 genes



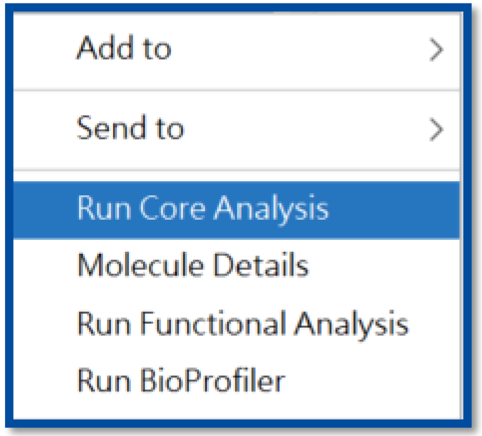
List Name: glioblatoma_scRNA_bulkRNA_filtered

Notes:

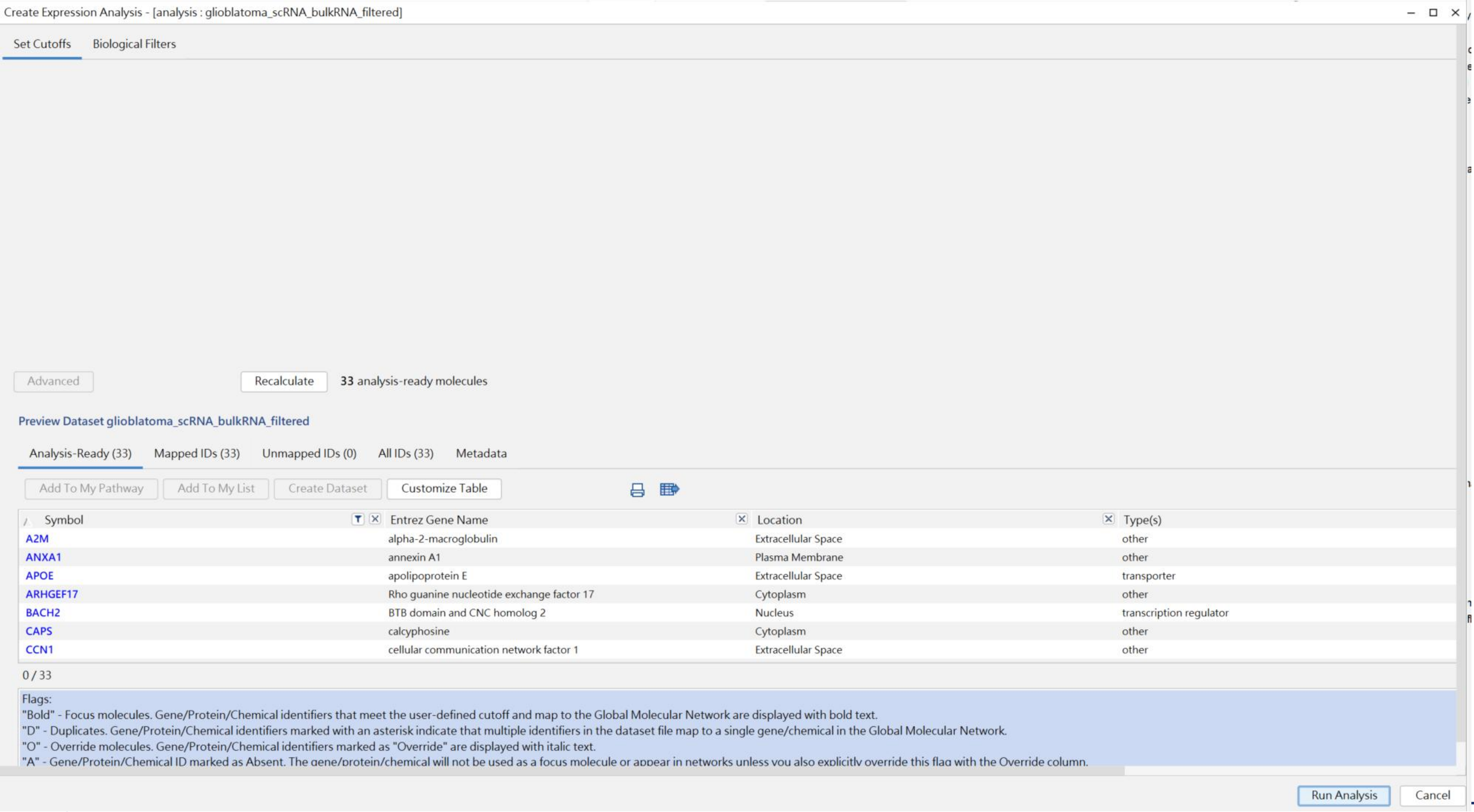
A2M
ANXA1
APOE
ARHGEF17
BACH2
CAPS
CCN1
CDKN1A
COL14A1
COL1A1
COL24A1
CTDSPL
EGR1

Selected/Total molecules: 33/33

Press the right button



Core analysis



33 analysis-ready molecules

Preview Dataset glioblatoma_scRNA_bulkRNA_filtered

Symbol	Entrez Gene Name	Location	Type(s)
A2M	alpha-2-macroglobulin	Extracellular Space	other
ANXA1	annexin A1	Plasma Membrane	other
APOE	apolipoprotein E	Extracellular Space	transporter
ARHGEF17	Rho guanine nucleotide exchange factor 17	Cytoplasm	other
BACH2	BTB domain and CNC homolog 2	Nucleus	transcription regulator
CAPS	calcyphosine	Cytoplasm	other
CCN1	cellular communication network factor 1	Extracellular Space	other

0 / 33

Flags:
"Bold" - Focus molecules. Gene/Protein/Chemical identifiers that meet the user-defined cutoff and map to the Global Molecular Network are displayed with bold text.
"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.