Mechanistic Interpretation of the Ovarian Cancer Tumor Microenvironment Using Single-Cell and Spatial Transcriptomics with IPA

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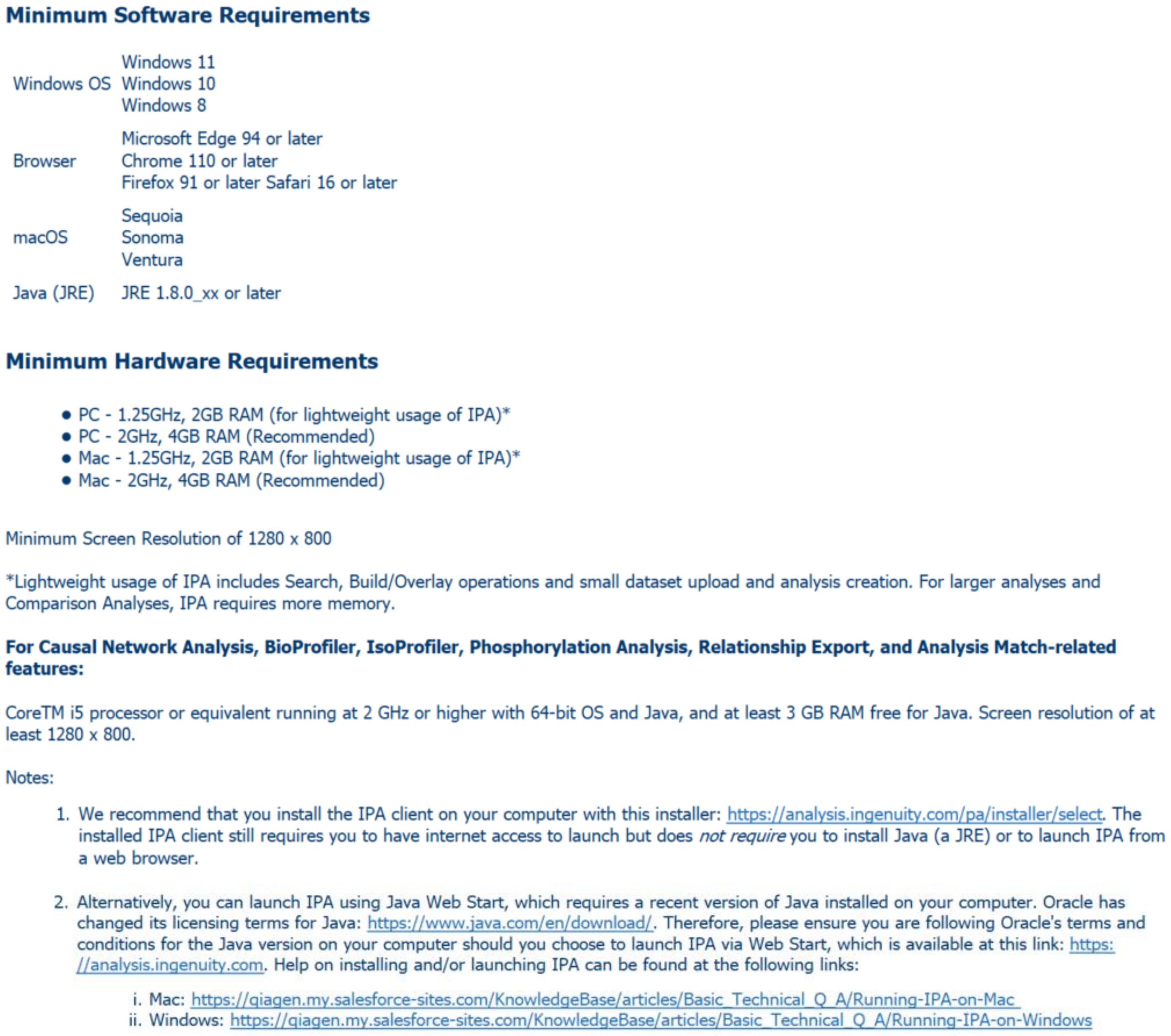
System Requirements



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

Machine Learning pathway

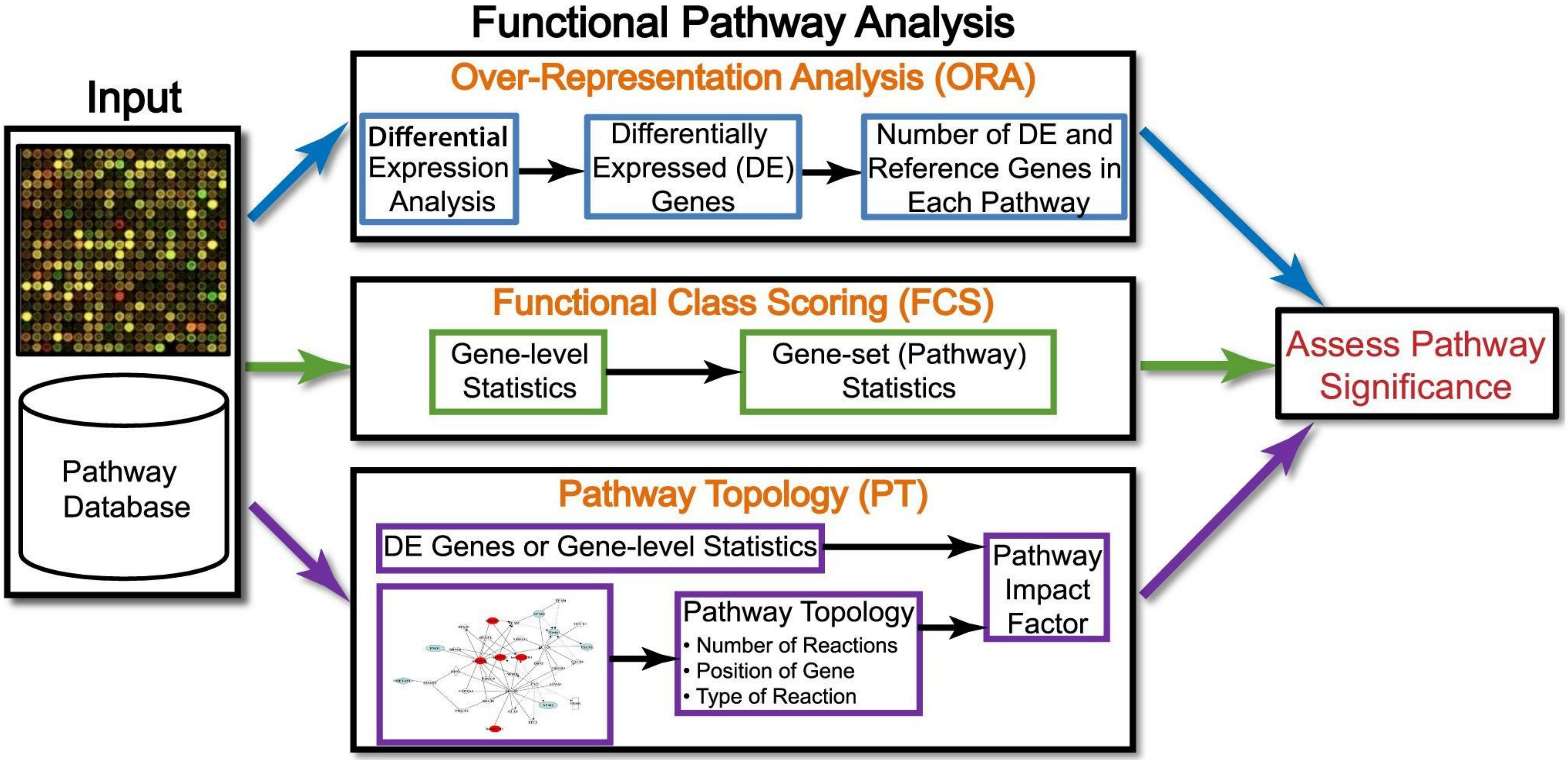
Interpreting your ′omics data using IPA

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

Comparison 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

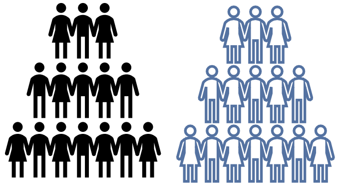
- Number of Reactions
- Position of Gene
- Type of Reaction

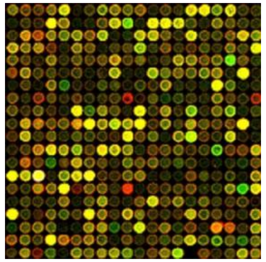
Assess Pathway Significance

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

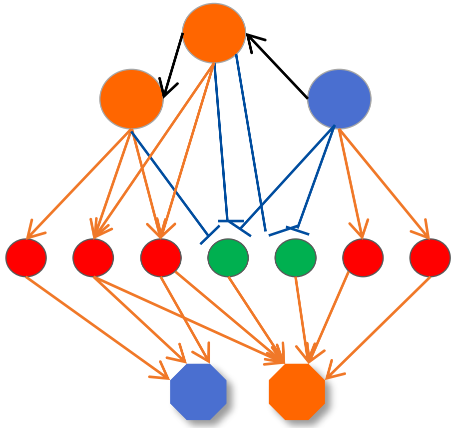
Network

ORA/FCS/Topology Pathway Analysis

Machine learning

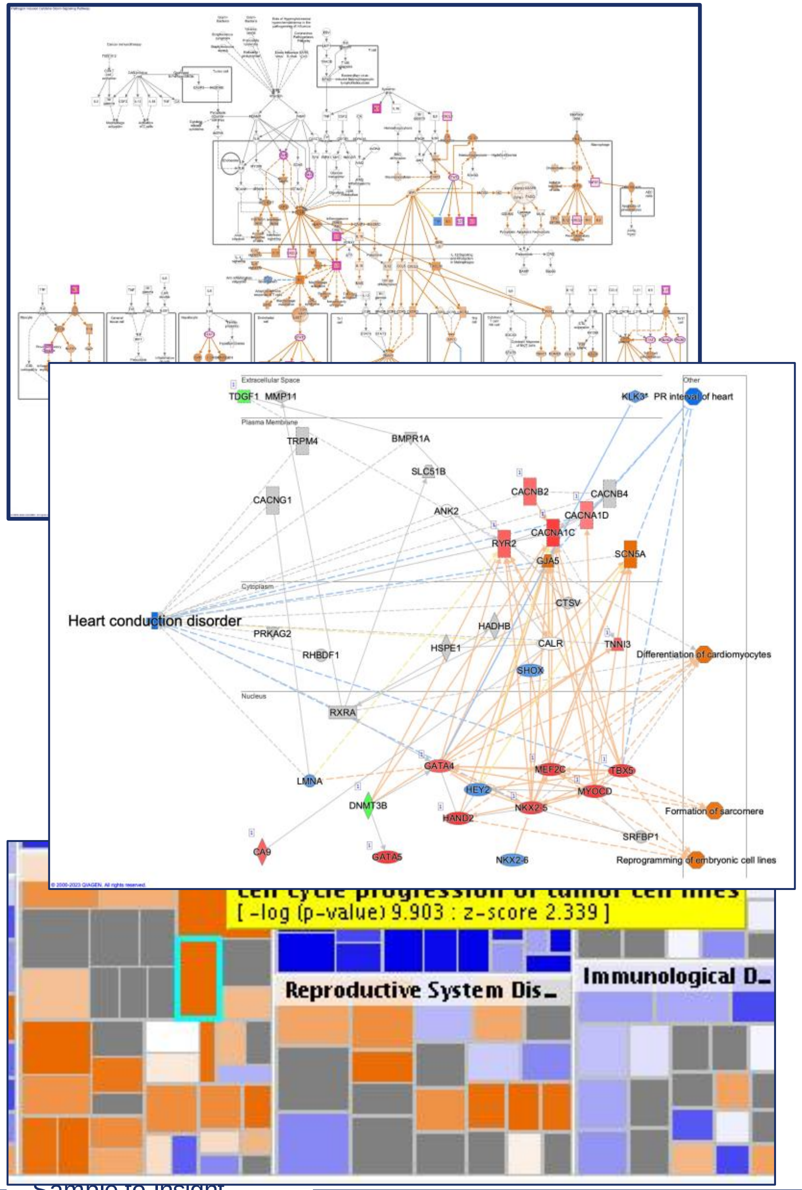
→

What do they relate to each other?

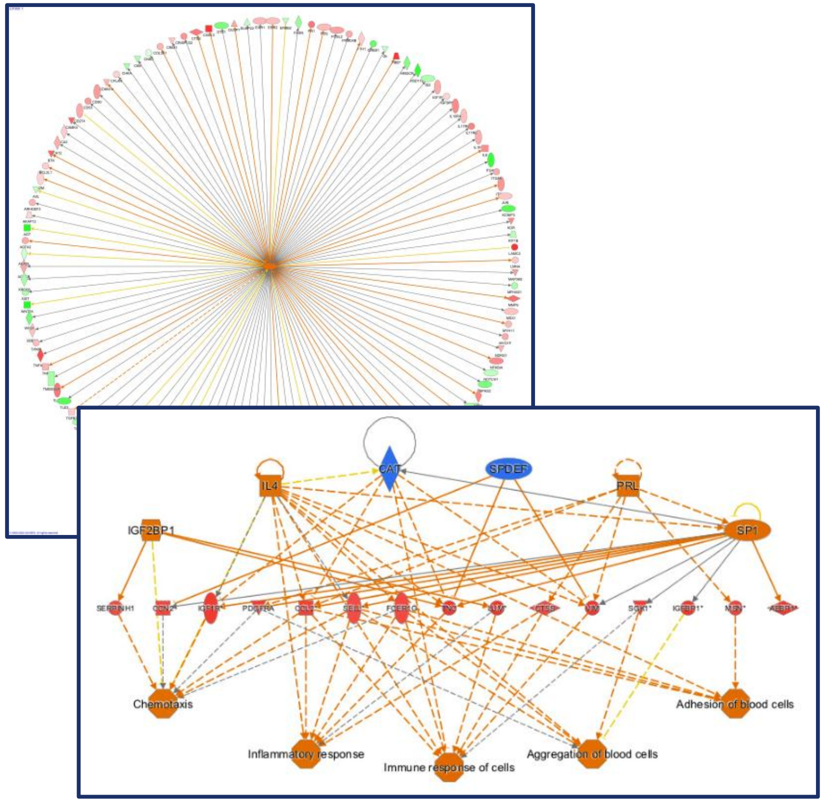


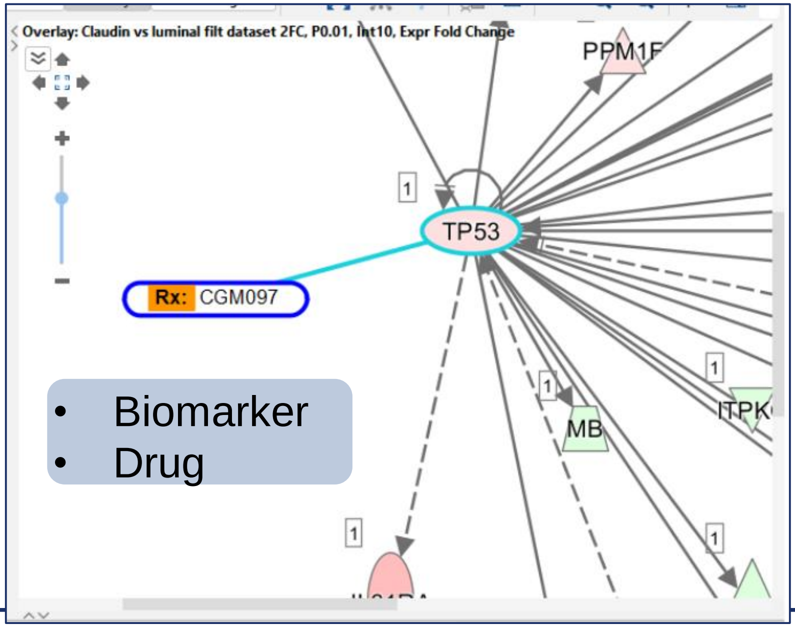
What are the relationship between each molecules?

What Can We Achieve with IPA?

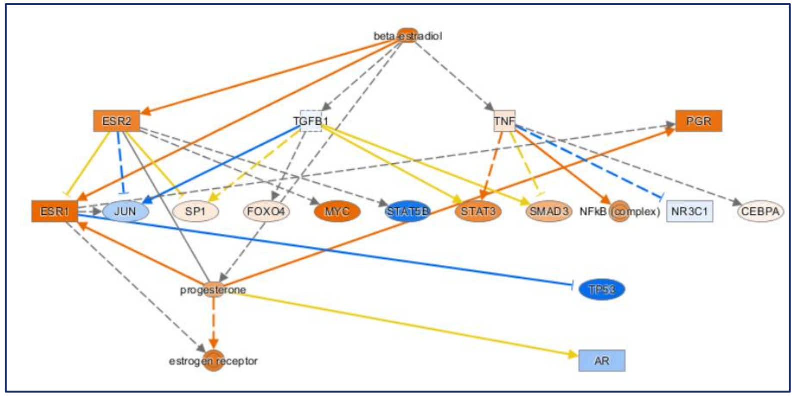


1. Canonical pathway
2. Machine Learning disease pathway
3. Disease and function
4. Upstream regulator
5. Regulate effect
6. Network



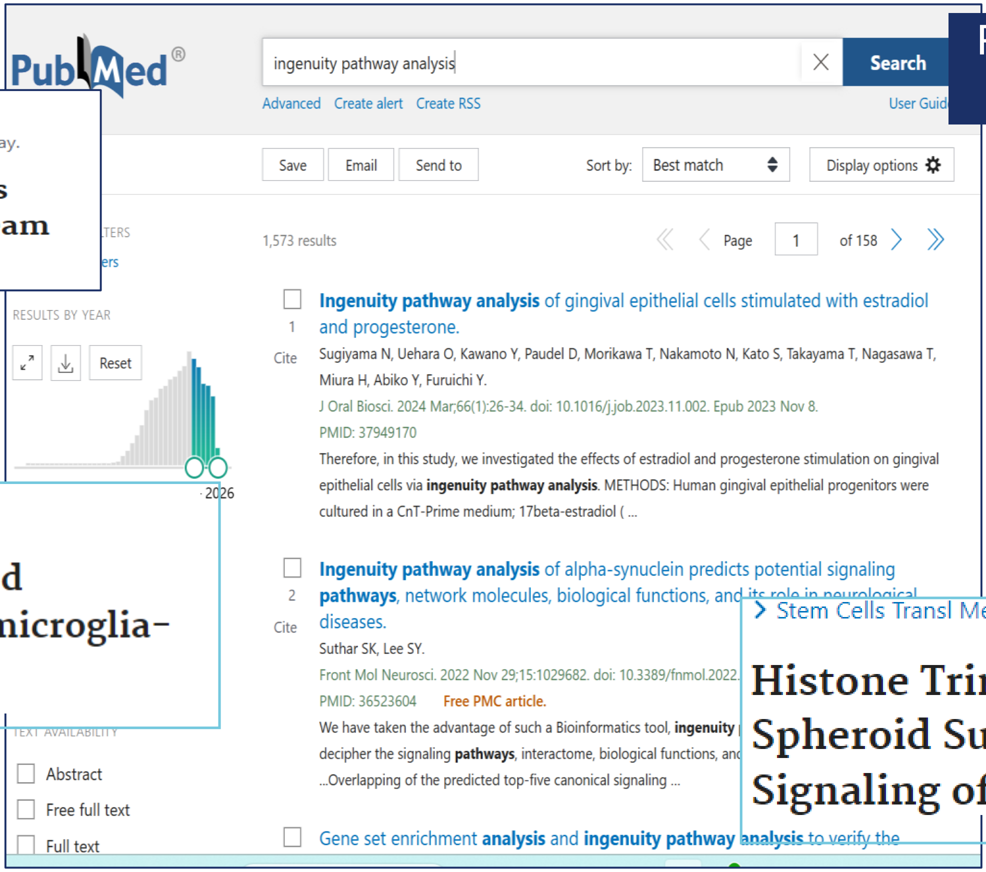

Overlay: Claudin vs luminal filt dataset 2FC, P0.01, Int10, Expr Fold Change

- Biomarker
- Drug



Publication using Qiagen Ingenuity Pathway Analysis

From 2020-2026
1,537literatures



PubMed®

ingenuity pathway analysis

Search

Advanced Create alert Create RSS User Guid

Save Email Send to Sort by: Best match Display options

1,573 results Page 1 of 158

RESULTS BY YEAR

Reset

2026

☐ 1 Cite **Ingenuity pathway analysis** of gingival epithelial cells stimulated with estradiol and progesterone.
Sugiyama N, Uehara O, Kawano Y, Paudel D, Morikawa T, Nakamoto N, Kato S, Takayama T, Nagasawa T, Miura H, Abiko Y, Furuichi Y.
J Oral Biosci. 2024 Mar;66(1):26-34. doi: 10.1016/j.job.2023.11.002. Epub 2023 Nov 8.
PMID: 37949170
Therefore, in this study, we investigated the effects of estradiol and progesterone stimulation on gingival epithelial cells via **ingenuity pathway analysis**. METHODS: Human gingival epithelial progenitors were cultured in a CnT-Prime medium; 17beta-estradiol (...

☐ 2 Cite **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.
PMID: 36523604 Free PMC article.
We have taken the advantage of such a Bioinformatics tool, **ingenuity**
decipher the signaling **pathways**, interactome, biological functions, and
...Overlapping of the predicted top-five canonical signaling ...

TEXT AVAILABILITY
☐ Abstract
☐ Free full text
☐ Full text

☐ Gene set enrichment **analysis** and **ingenuity pathway analysis** to verify the

> 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

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

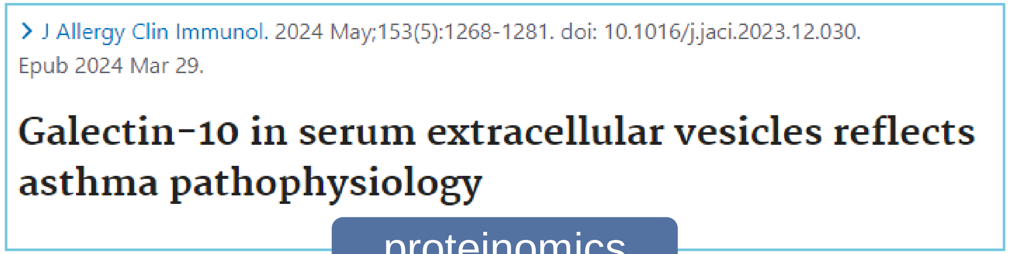
Deletion of Slc9a1 in Cx3cr1⁺ cells stimulated microglial subcluster CREB1 signaling and microglia-oligodendrocyte crosstalk

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

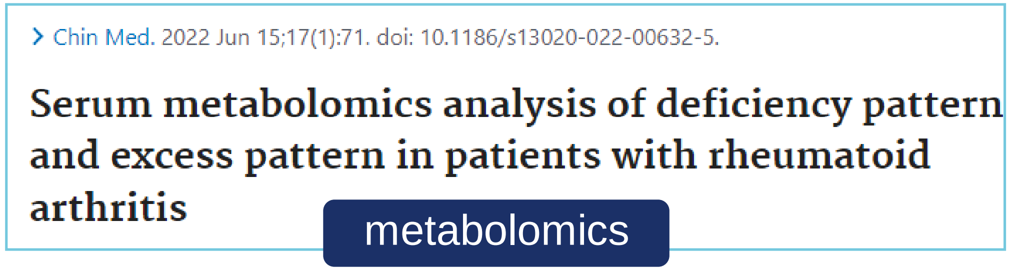
Single-cell RNA-seq



> 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

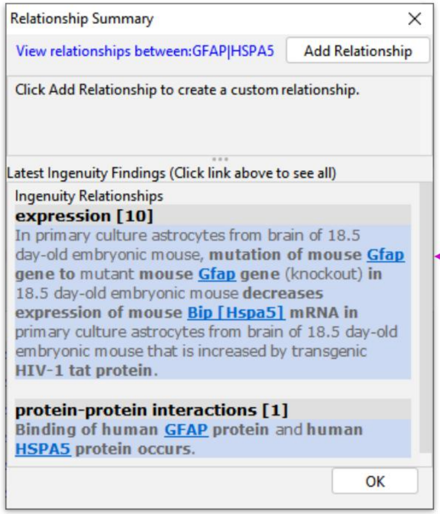


> Chin Med. 2022 Jun 15;17(1):71. doi: 10.1186/s13020-022-00632-5.

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

metabolomics

Every connection in IPA is backed by literature findings



Relationship Summary

View relationships between:GFAP|HSPA5

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

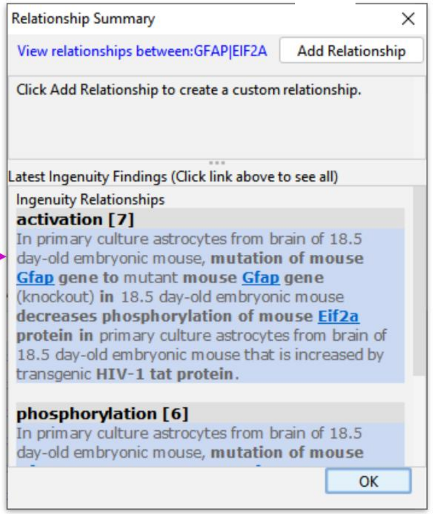
Ingenuity Relationships

expression [10]

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

protein-protein interactions [1]

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



Relationship Summary

View relationships between:GFAP|EIF2A

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

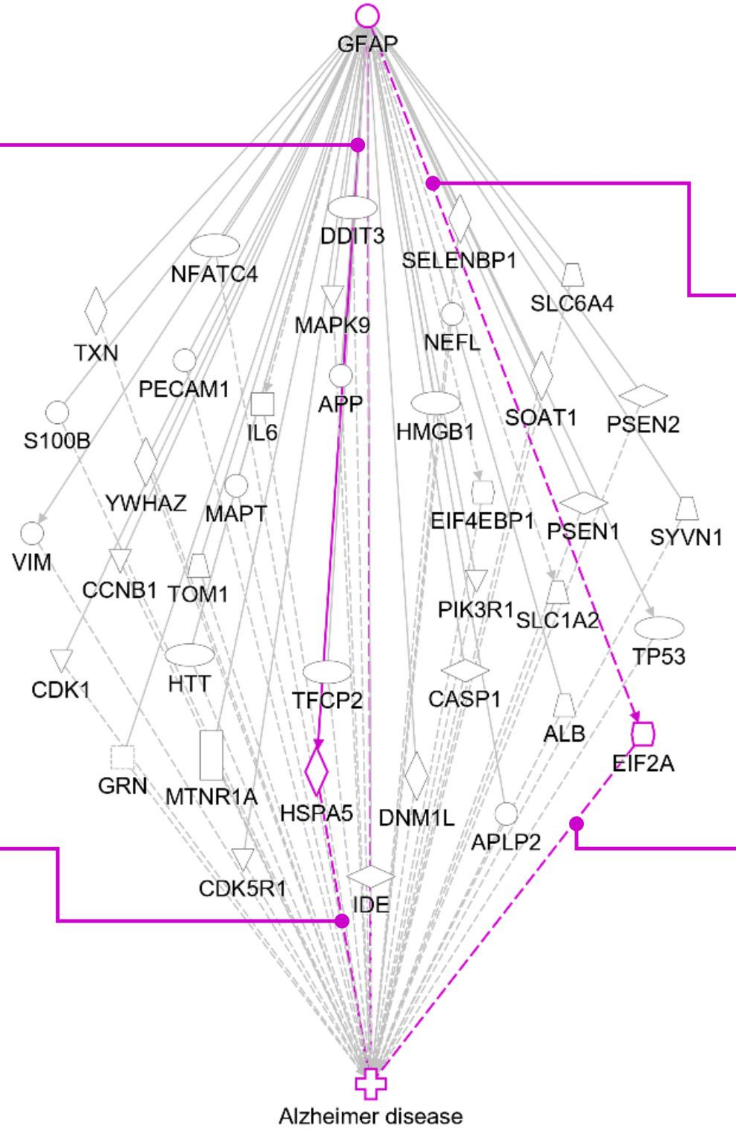
Ingenuity Relationships

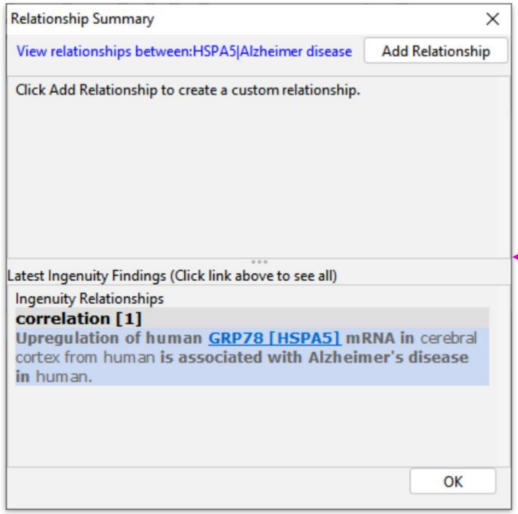
activation [7]

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

phosphorylation [6]

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





Relationship Summary

View relationships between:HSPA5|Alzheimer disease

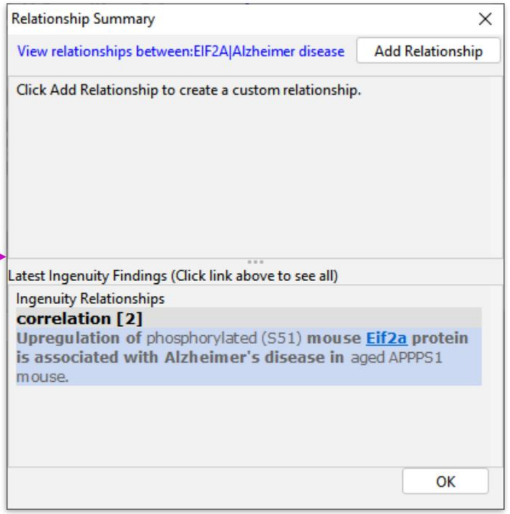
Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [1]

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



Relationship Summary

View relationships between:EIF2A|Alzheimer disease

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [2]

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

Species Support within IPA

Fully supported:

Human

Mouse

Rat

What species identifiers are accepted for analysis by IPA?

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

Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

Supported Identifiers for Data Upload

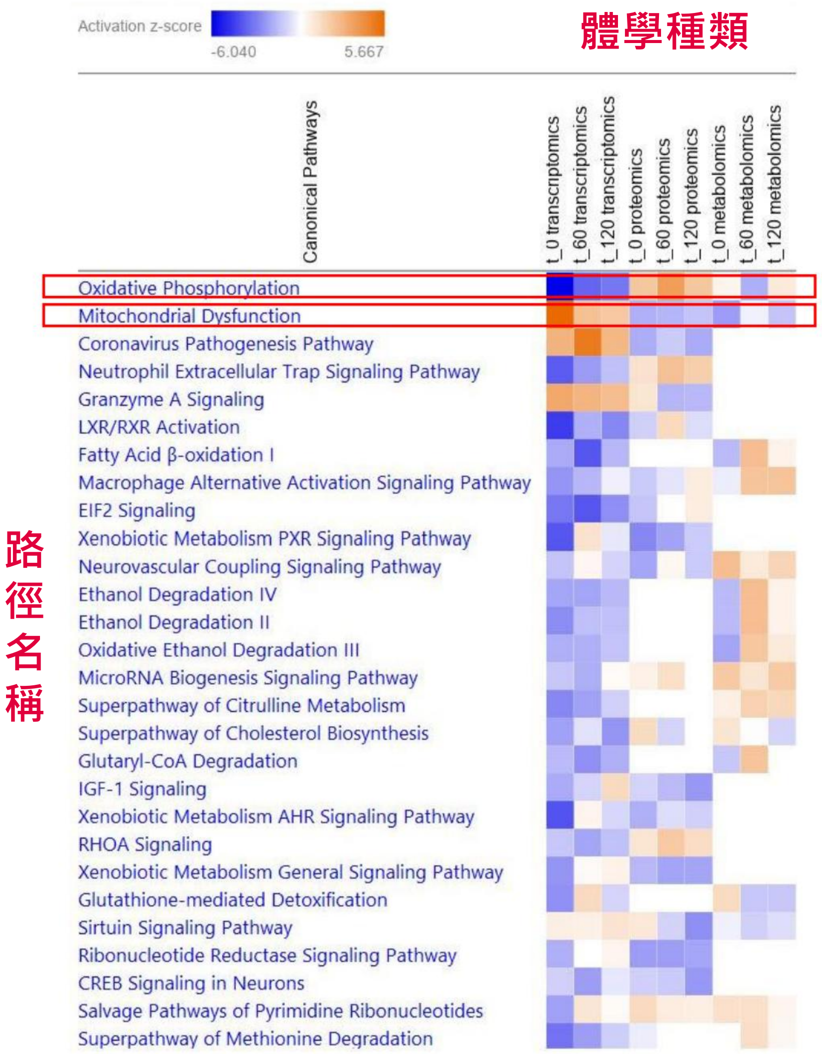
Get more complete mapping during dataset upload!

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

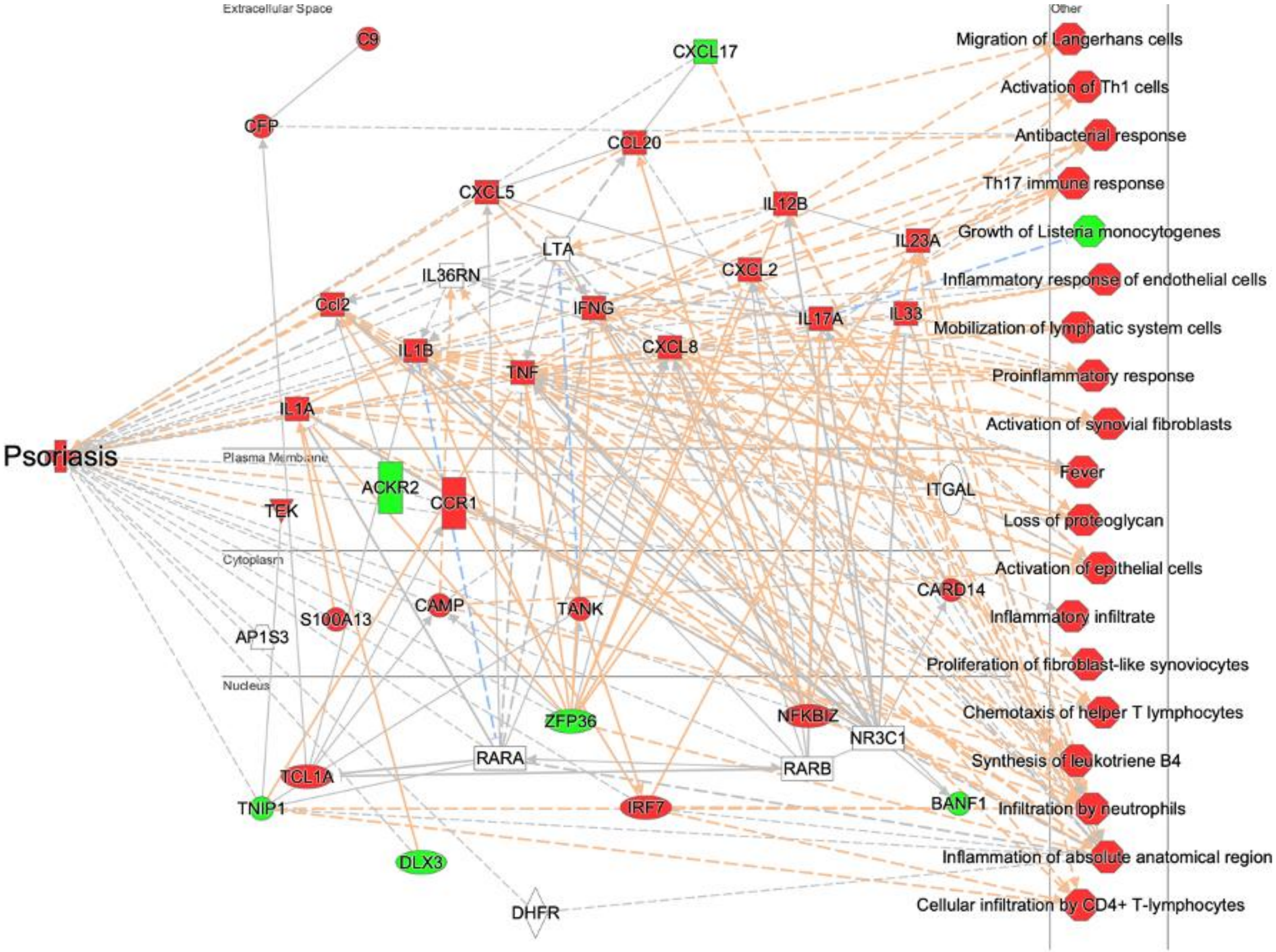
- RNA-seq
- scRNA-seq
- Microarray
- Nanostring
- qPCR
- ChIP-seq
- Proteomics
- Metabolomics
- RNAi
- CRISPR
- WGS/WES etc.



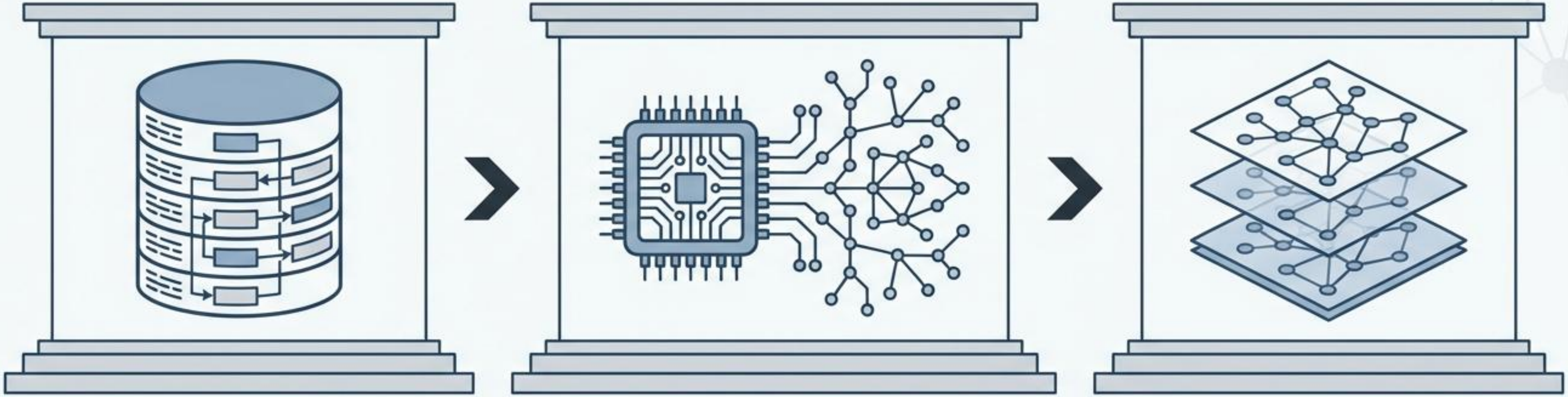
體學種類

路徑名稱

Real-World Application: The Psoriasis Network



Birding Global Literature with Empirical Data



The Source: QIAGEN Knowledge Base

Mining decades of **causal findings.**

The Engine: Machine Learning Generation

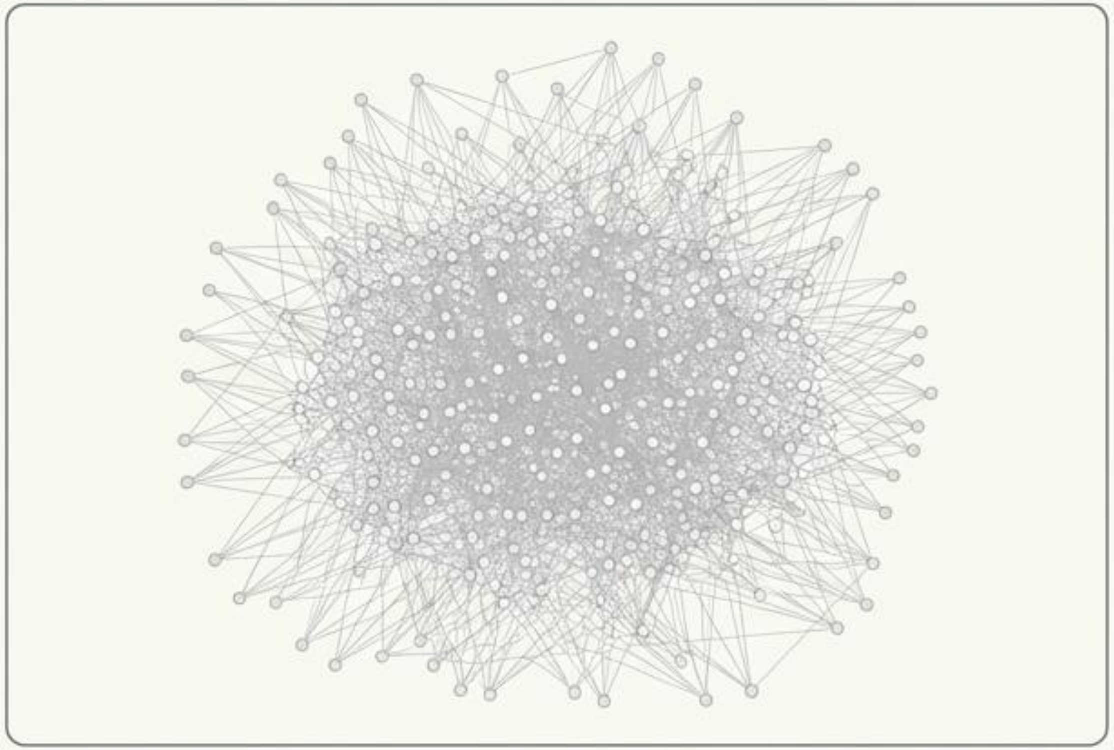
Automated creation of **~1500 disease, phenotype,** and **function pathways** to prioritize **key causal genes.**

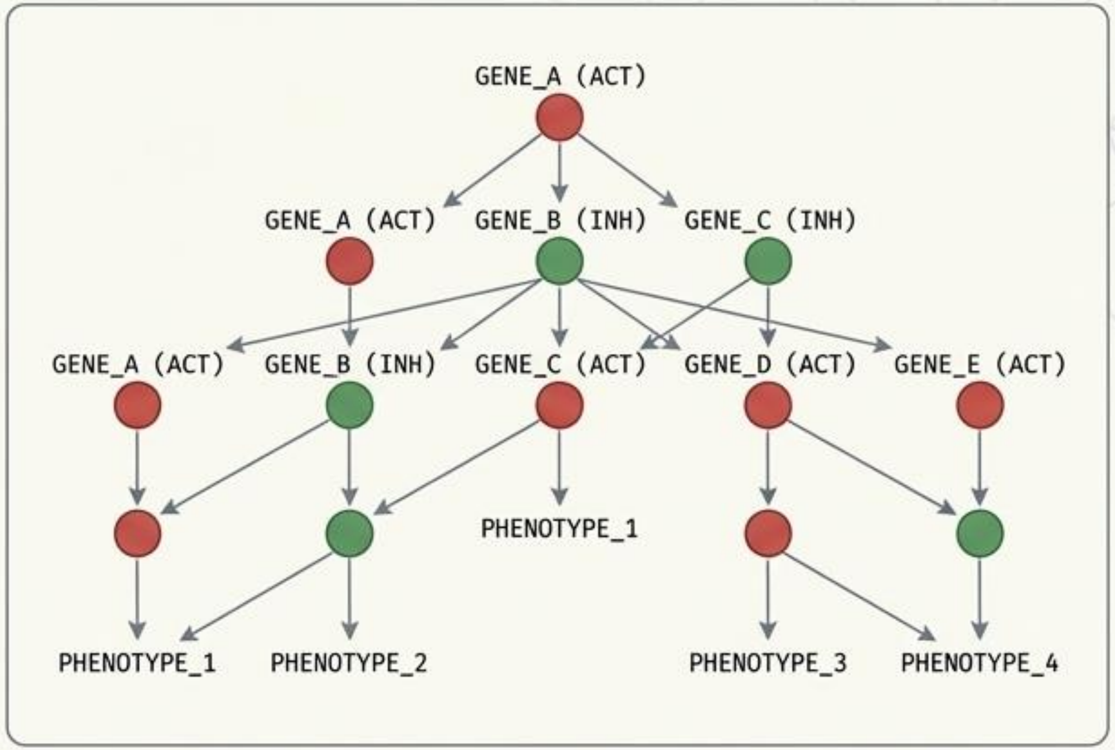
The Application: Data Overlay

Mapping **custom expression datasets** onto **predictive networks** to uncover **novel etiology.**

ML Disease Pathways visualize a **human-readable set** of the most important **causally connected genes**—revealing **known players** and inferring **novel participants.**

Prioritizing Causal Importance Over Exhaustive Cataloging





What it is NOT

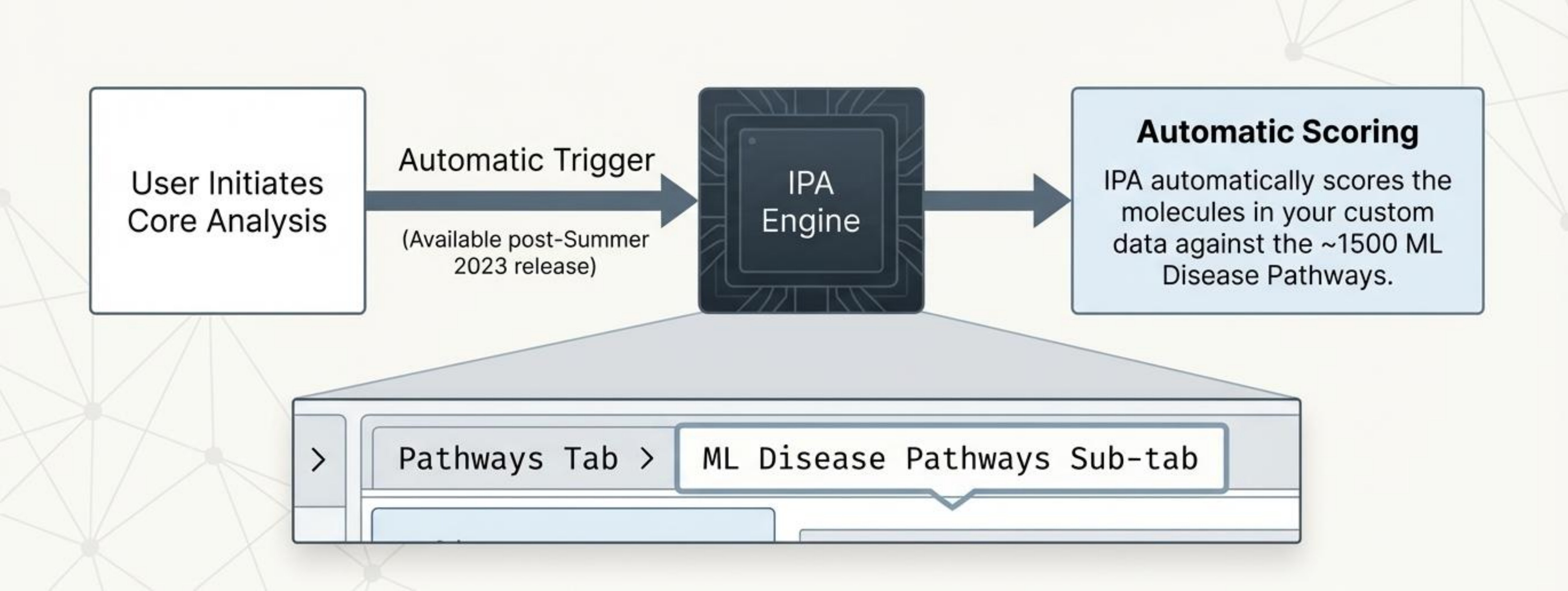
Comprehensive Catalogs: Overwhelming, unprioritized mapping of every single associated gene.

What it IS

ML Disease Pathways: A human-readable prioritization of the most critical causally connected genes and phenotypes.

`Objective: Suggest genes with similar regulatory patterns to implicate them as potentially important in the disease, utilizing inferred implicit associations.`

Directly through Core analysis



User Initiates Core Analysis

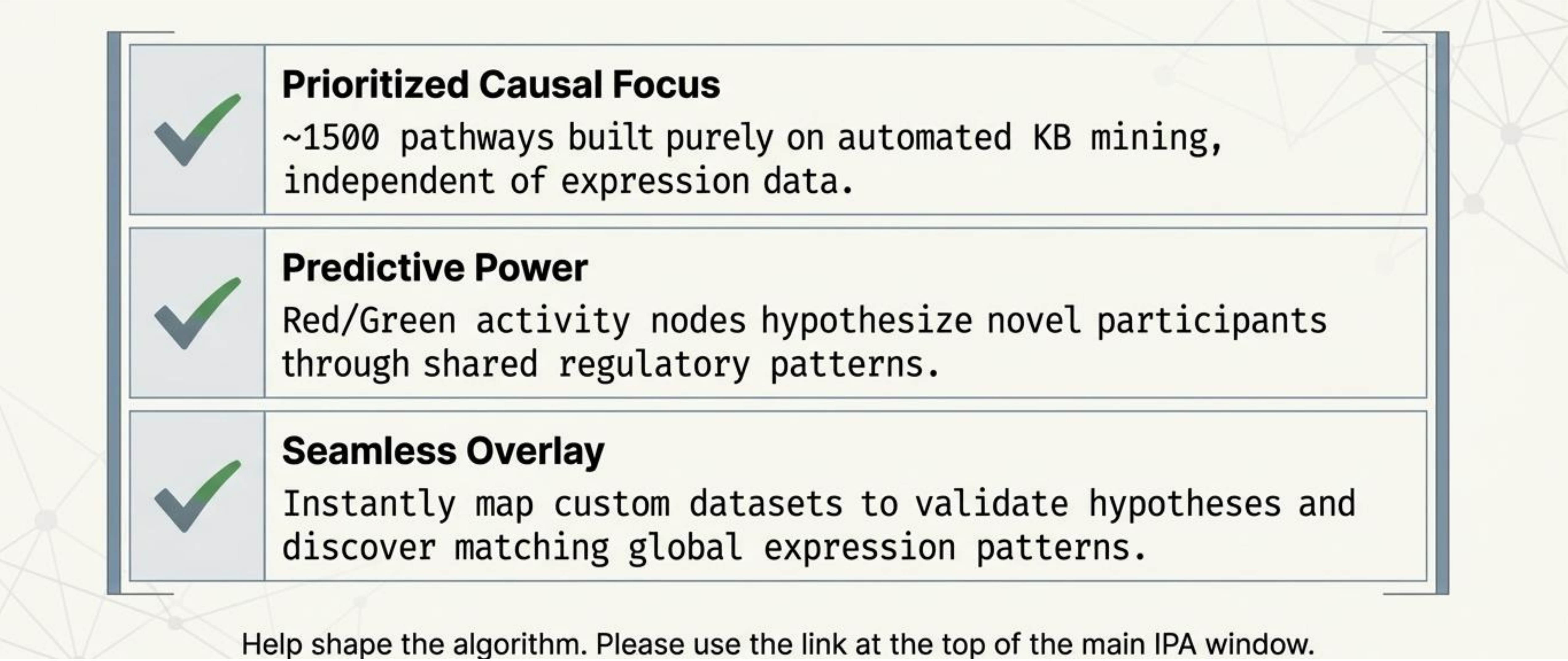
Automatic Trigger

(Available post-Summer 2023 release)

IPA Engine

Automatic Scoring

IPA automatically scores the molecules in your custom data against the ~1500 ML Disease Pathways.



- ✓ **Prioritized Causal Focus**
  ~1500 pathways built purely on automated KB mining, independent of expression data.
- ✓ **Predictive Power**
  Red/Green activity nodes hypothesize novel participants through shared regulatory patterns.
- ✓ **Seamless Overlay**
  Instantly map custom datasets to validate hypotheses and discover matching global expression patterns.

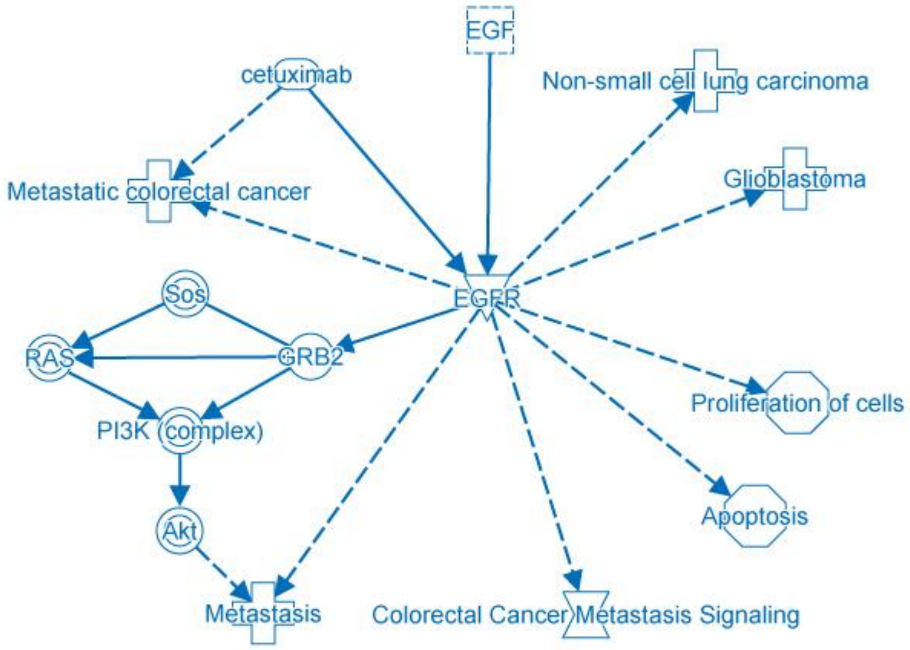
Help shape the algorithm. Please use the link at the top of the main IPA window.

QIAGEN IPA – a dual approach to data analysis

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

Example of Biomedical Knowledge Base findings

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



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

EGF – EGFR

[one of many]

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

cetuximab – EGFR

[one of many]

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

EGFR – Proliferation of cells

[one of many]

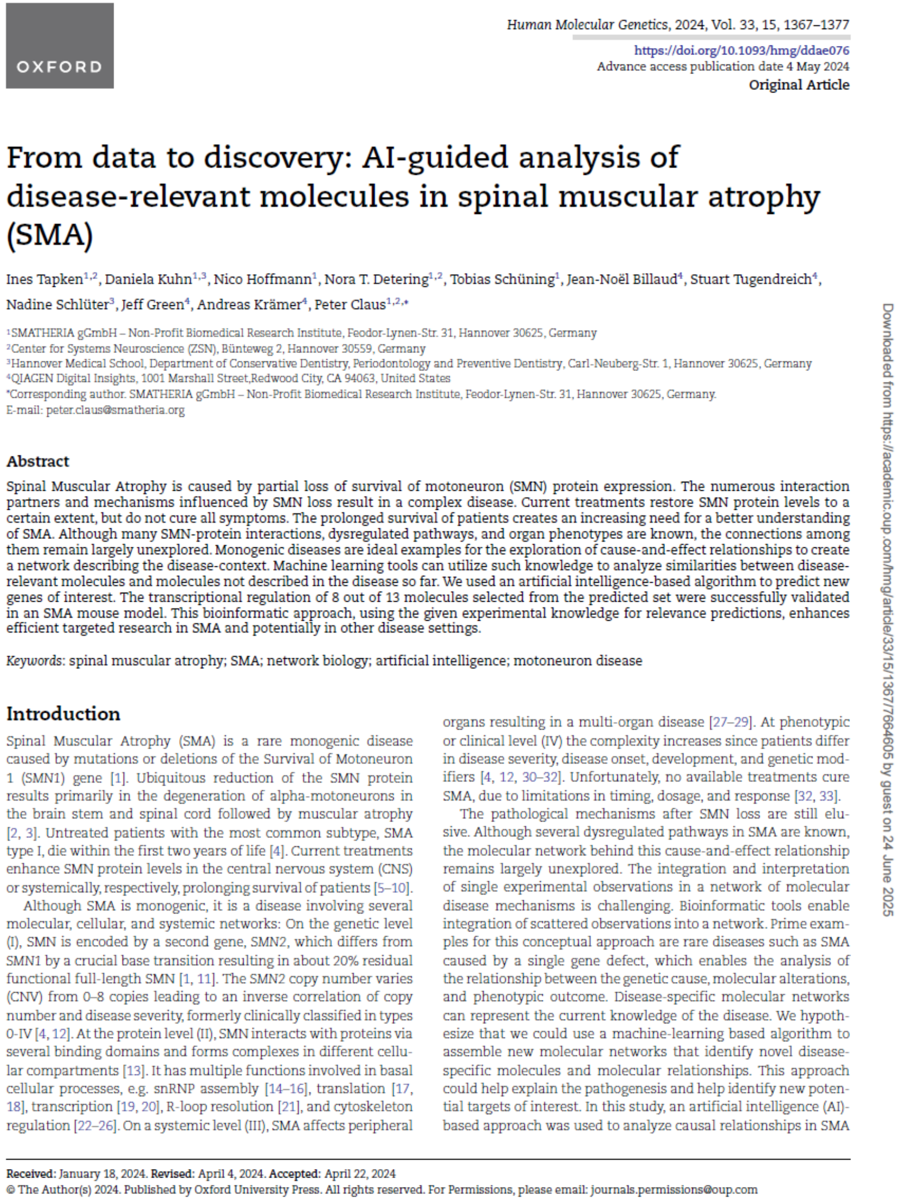
Type: causation
Direction: directional
Effect: increases
Tissue or primary cell: epithelial cells
Subcellular location: plasma membrane
Source: PubMed PMID: 22674072

EGFR – Glioblastoma

[one of many]

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

Dig into biology and test hypotheses in silico



OXFORD

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

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

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

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[4]QIAGEN Digital Insights, 1001 Marshall Street,Redwood City, CA 94063, United States
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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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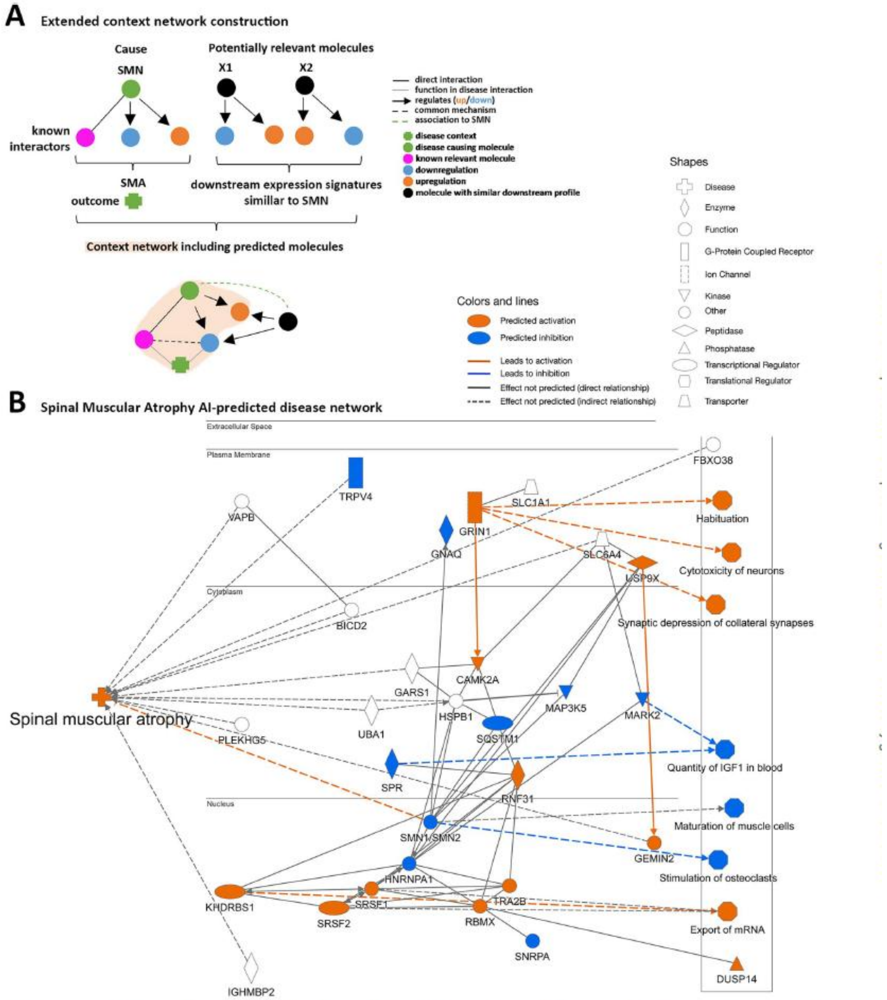


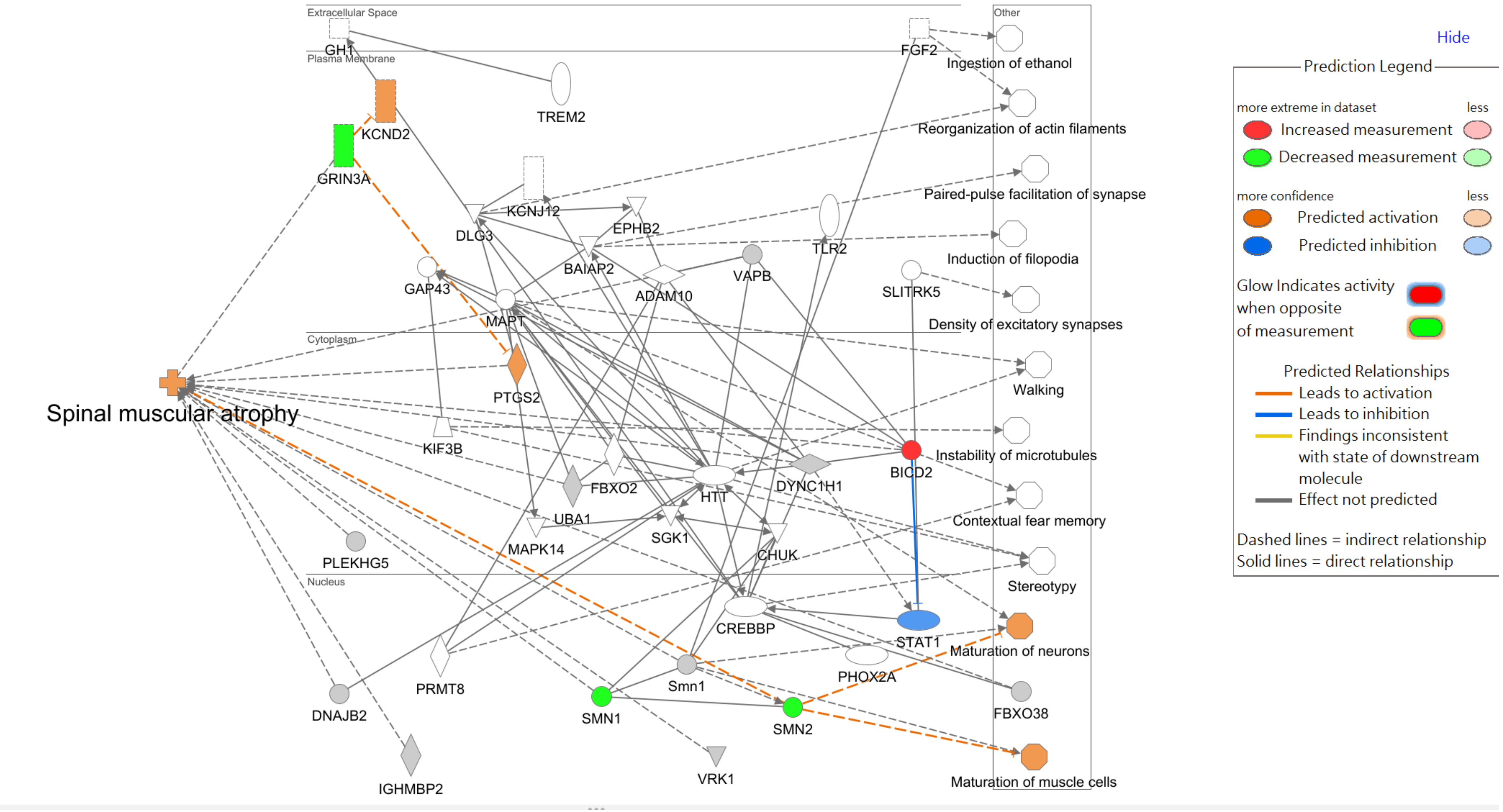
Figure 1. Artificial intelligence-predicted context network for spinal muscular atrophy. (A) Schematic representation of the AI-prediction algorithm and network construction. SMN (green circle) is the genetic cause and SMA (green cross) the disease outcome. In the QIAGEN Knowledge Base (QKB), interactors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

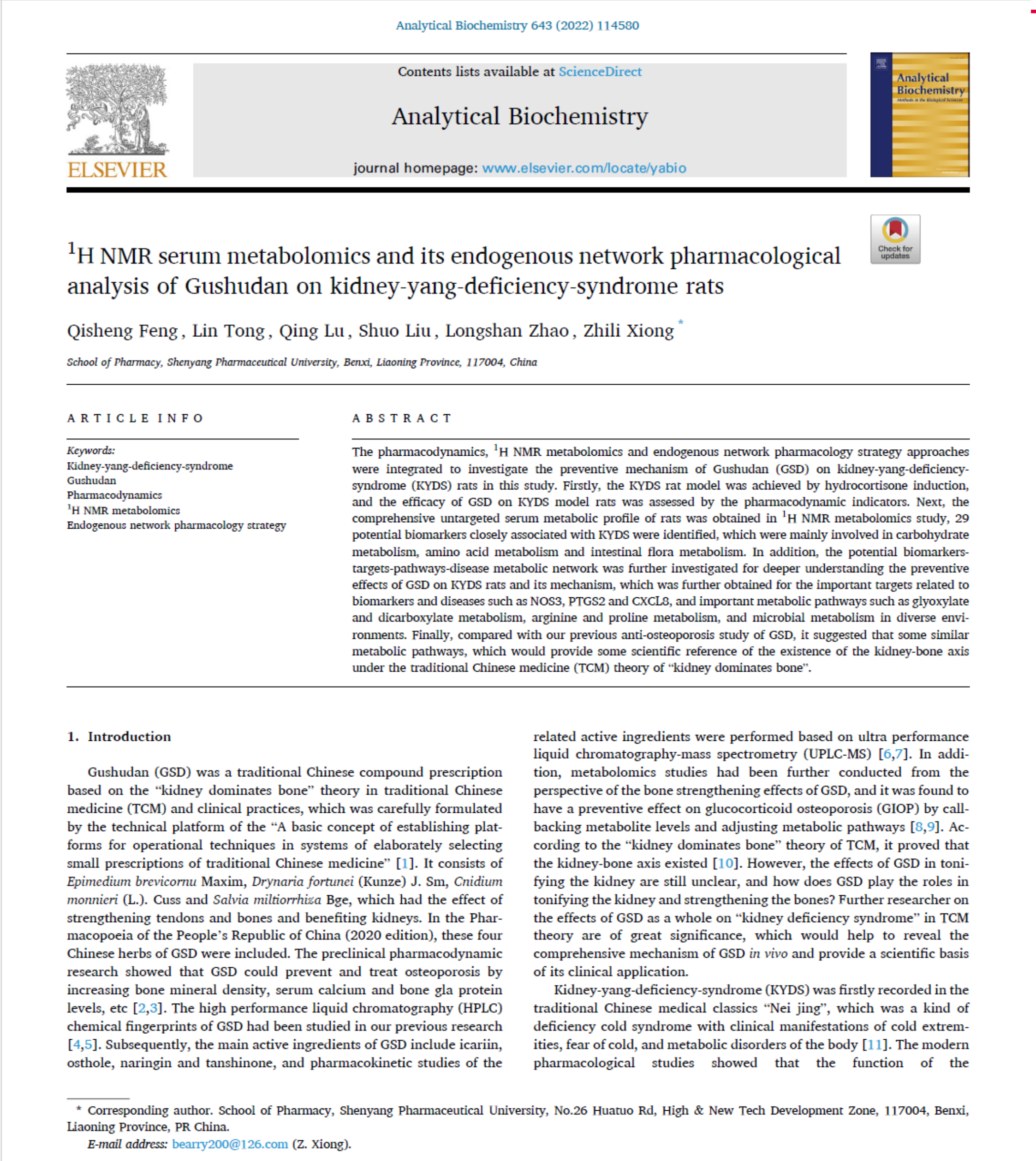
Machine learning pathway

Download the related Genes of disease

Upload dataset and Core analysis

Machine learning Pathway





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^{1}H NMR serum metabolomics and its endogenous network pharmacological analysis of Gushudan on kidney-yang-deficiency-syndrome rats

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Gushudan
Pharmacodynamics
^{1}H NMR metabolomics
Endogenous network pharmacology strategy

ABSTRACT

The pharmacodynamics, ^{1}H NMR metabolomics and endogenous network pharmacology strategy approaches were integrated to investigate the preventive mechanism of Gushudan (GSD) on kidney-yang-deficiency-syndrome (KYDS) rats in this study. Firstly, the KYDS rat model was achieved by hydrocortisone induction, and the efficacy of GSD on KYDS model rats was assessed by the pharmacodynamic indicators. Next, the comprehensive untargeted serum metabolic profile of rats was obtained in ^{1}H NMR metabolomics study, 29 potential biomarkers closely associated with KYDS were identified, which were mainly involved in carbohydrate metabolism, amino acid metabolism and intestinal flora metabolism. In addition, the potential biomarkers-targets-pathways-disease metabolic network was further investigated for deeper understanding the preventive effects of GSD on KYDS rats and its mechanism, which was further obtained for the important targets related to biomarkers and diseases such as NOS3, PTGS2 and CXCL8, and important metabolic pathways such as glyoxylate and dicarboxylate metabolism, arginine and proline metabolism, and microbial metabolism in diverse environments. Finally, compared with our previous anti-osteoporosis study of GSD, it suggested that some similar metabolic pathways, which would provide some scientific reference of the existence of the kidney-bone axis under the traditional Chinese medicine (TCM) theory of "kidney dominates bone".

1. Introduction

Gushudan (GSD) was a traditional Chinese compound prescription based on the "kidney dominates bone" theory in traditional Chinese medicine (TCM) and clinical practices, which was carefully formulated by the technical platform of the "A basic concept of establishing platforms for operational techniques in systems of elaborately selecting small prescriptions of traditional Chinese medicine" [1]. It consists of *Epimedium brevicornu* Maxim, *Drynaria fortunei* (Kunze) J. Sm, *Cnidium monnieri* (L.). Cuss and *Salvia miltiorrhiza* Bge, which had the effect of strengthening tendons and bones and benefiting kidneys. In the Pharmacopoeia of the People's Republic of China (2020 edition), these four Chinese herbs of GSD were included. The preclinical pharmacodynamic research showed that GSD could prevent and treat osteoporosis by increasing bone mineral density, serum calcium and bone gla protein levels, etc [2,3]. The high performance liquid chromatography (HPLC) chemical fingerprints of GSD had been studied in our previous research [4,5]. Subsequently, the main active ingredients of GSD include icariin, osthole, naringin and tanshinone, and pharmacokinetic studies of the related active ingredients were performed based on ultra performance liquid chromatography-mass spectrometry (UPLC-MS) [6,7]. In addition, metabolomics studies had been further conducted from the perspective of the bone strengthening effects of GSD, and it was found to have a preventive effect on glucocorticoid osteoporosis (GIOP) by call-backing metabolite levels and adjusting metabolic pathways [8,9]. According to the "kidney dominates bone" theory of TCM, it proved that the kidney-bone axis existed [10]. However, the effects of GSD in tonifying the kidney are still unclear, and how does GSD play the roles in tonifying the kidney and strengthening the bones? Further researcher on the effects of GSD as a whole on "kidney deficiency syndrome" in TCM theory are of great significance, which would help to reveal the comprehensive mechanism of GSD *in vivo* and provide a scientific basis of its clinical application.

Kidney-yang-deficiency-syndrome (KYDS) was firstly recorded in the traditional Chinese medical classics "Nei jing", which was a kind of deficiency cold syndrome with clinical manifestations of cold extremities, fear of cold, and metabolic disorders of the body [11]. The modern pharmacological studies showed that the function of the

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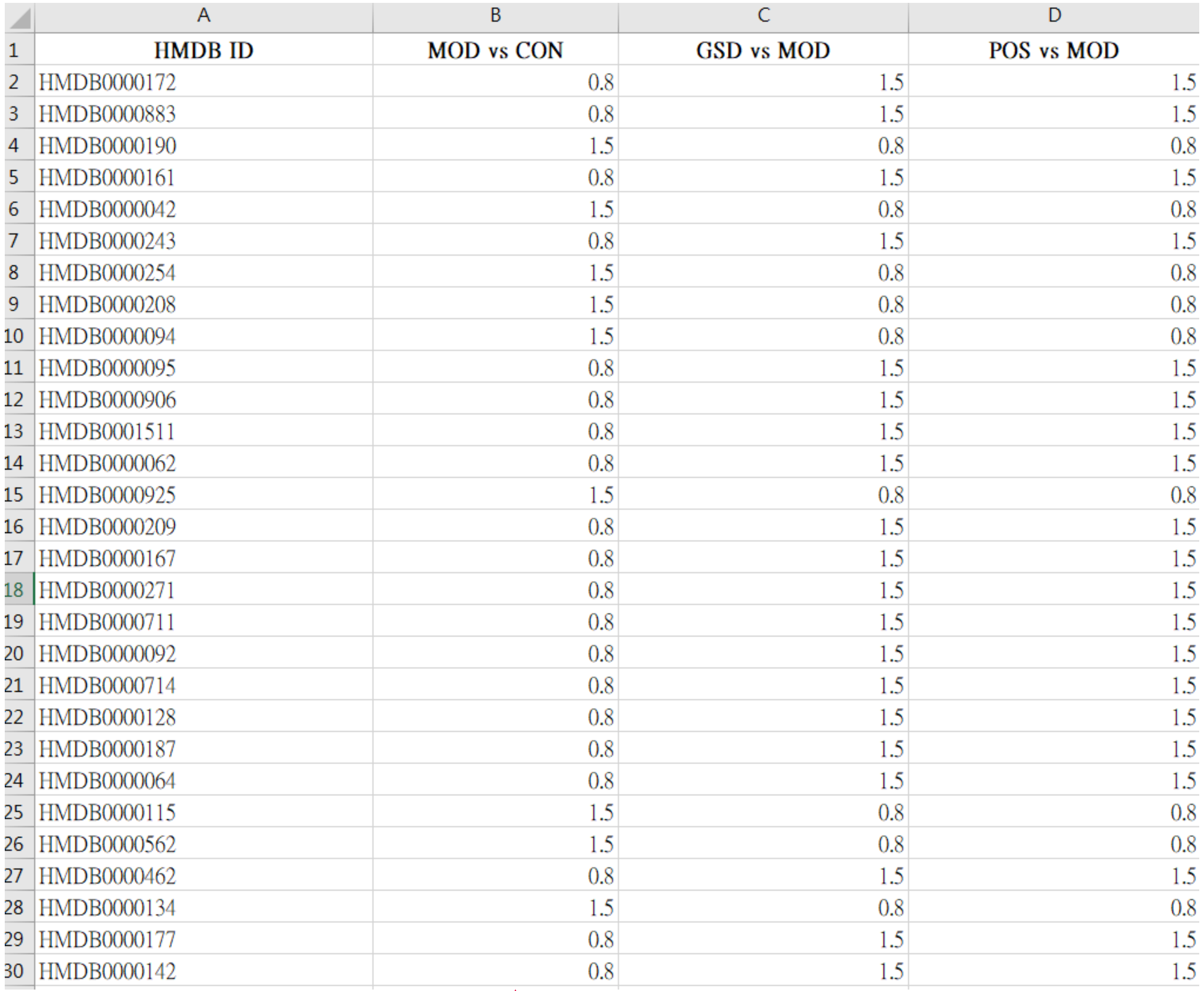
E-mail address: bearry200@126.com (Z. Xiong).



	A	B	C	D
1	HMDB ID	MOD vs CON	GSD vs MOD	POS vs MOD
2	HMDB0000172	0.8	1.5	1.5
3	HMDB0000883	0.8	1.5	1.5
4	HMDB0000190	1.5	0.8	0.8
5	HMDB0000161	0.8	1.5	1.5
6	HMDB0000042	1.5	0.8	0.8
7	HMDB0000243	0.8	1.5	1.5
8	HMDB0000254	1.5	0.8	0.8
9	HMDB0000208	1.5	0.8	0.8
10	HMDB0000094	1.5	0.8	0.8
11	HMDB0000095	0.8	1.5	1.5
12	HMDB0000906	0.8	1.5	1.5
13	HMDB0001511	0.8	1.5	1.5
14	HMDB0000062	0.8	1.5	1.5
15	HMDB0000925	1.5	0.8	0.8
16	HMDB0000209	0.8	1.5	1.5
17	HMDB0000167	0.8	1.5	1.5
18	HMDB0000271	0.8	1.5	1.5
19	HMDB0000711	0.8	1.5	1.5
20	HMDB0000092	0.8	1.5	1.5
21	HMDB0000714	0.8	1.5	1.5
22	HMDB0000128	0.8	1.5	1.5
23	HMDB0000187	0.8	1.5	1.5
24	HMDB0000064	0.8	1.5	1.5
25	HMDB0000115	1.5	0.8	0.8
26	HMDB0000562	1.5	0.8	0.8
27	HMDB0000462	0.8	1.5	1.5
28	HMDB0000134	1.5	0.8	0.8
29	HMDB0000177	0.8	1.5	1.5
30	HMDB0000142	0.8	1.5	1.5

Disease model

GSD treatment

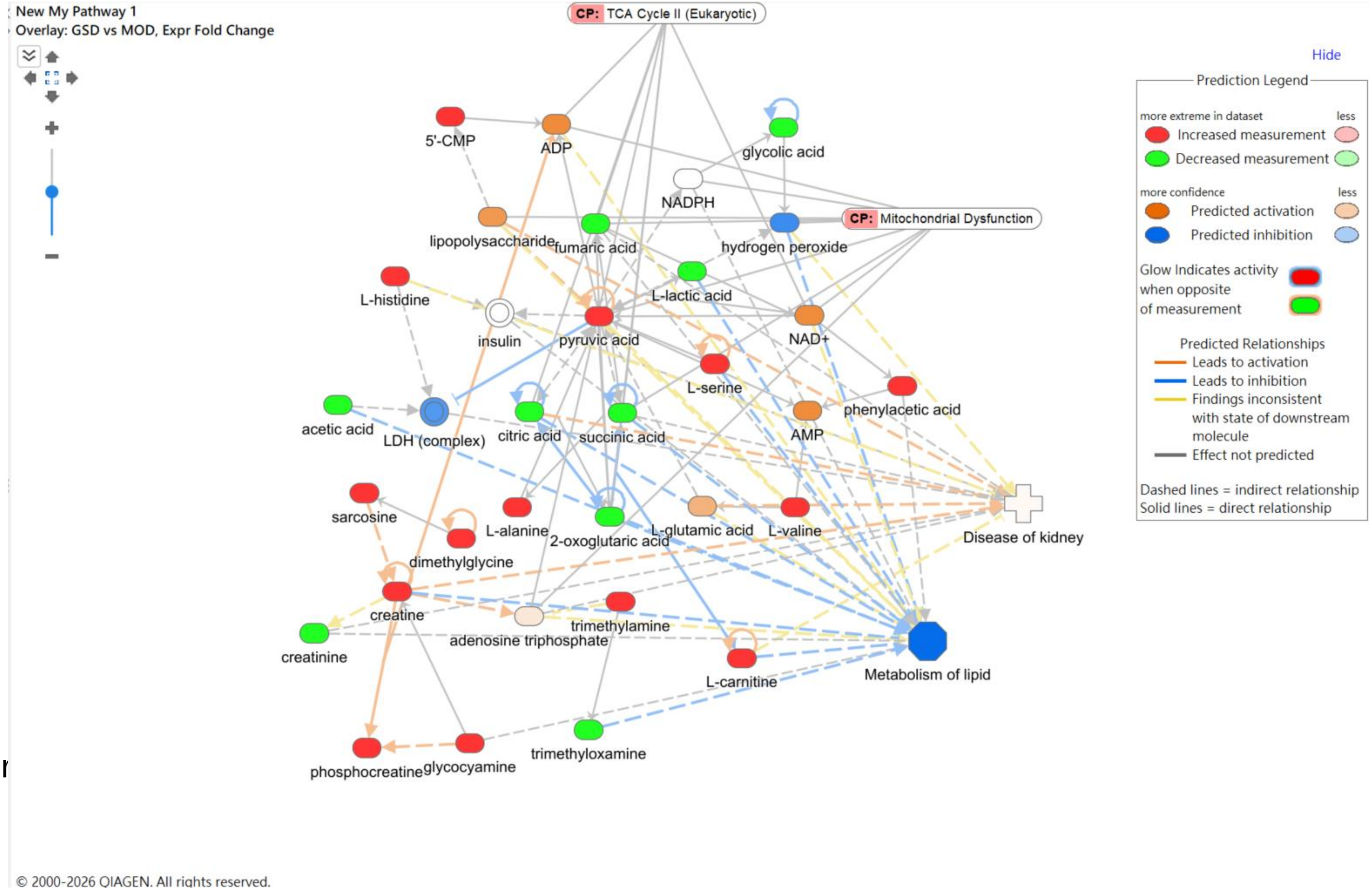
Drug treatment

Create networks from scratch and test activity in silico

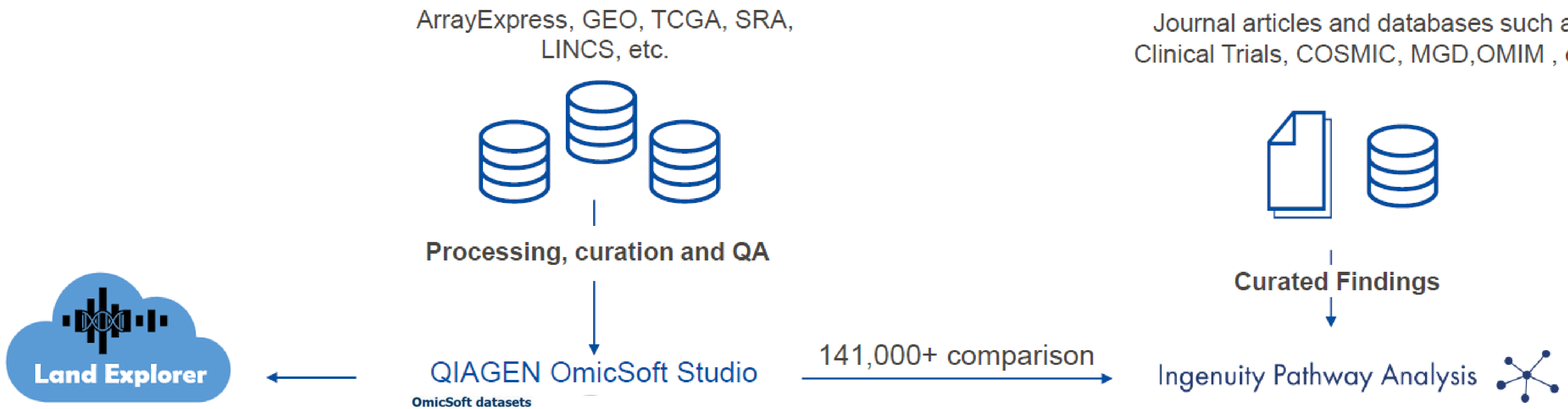
New feature:
Cells and Tissues overlay

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

- Upload list
- Build: grow/network/ path-explore (molecular or disease a function)
- Search for disease
- Path explore
- Overlay: Molecule activity predictor datasets, Drug, Cells & Tissues
- Drug: IPA Chem View


New My Pathway 1
Overlay: GSD vs MOD, Expr Fold Change

QIAGEN IPA Analysis Match and Land Explorer



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

Processing, curation and QA

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

Curated Findings

Land Explorer

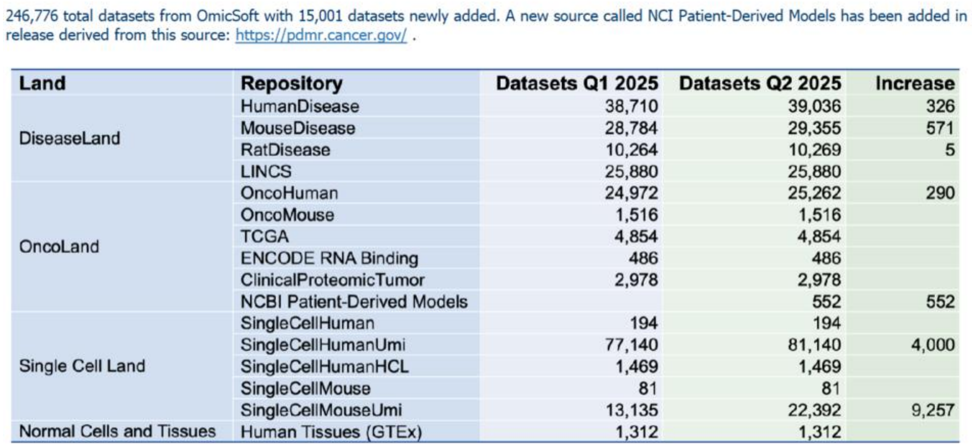
QIAGEN OmicSoft Studio

141,000+ comparison

Ingenuity Pathway Analysis

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

OmicSoft datasets

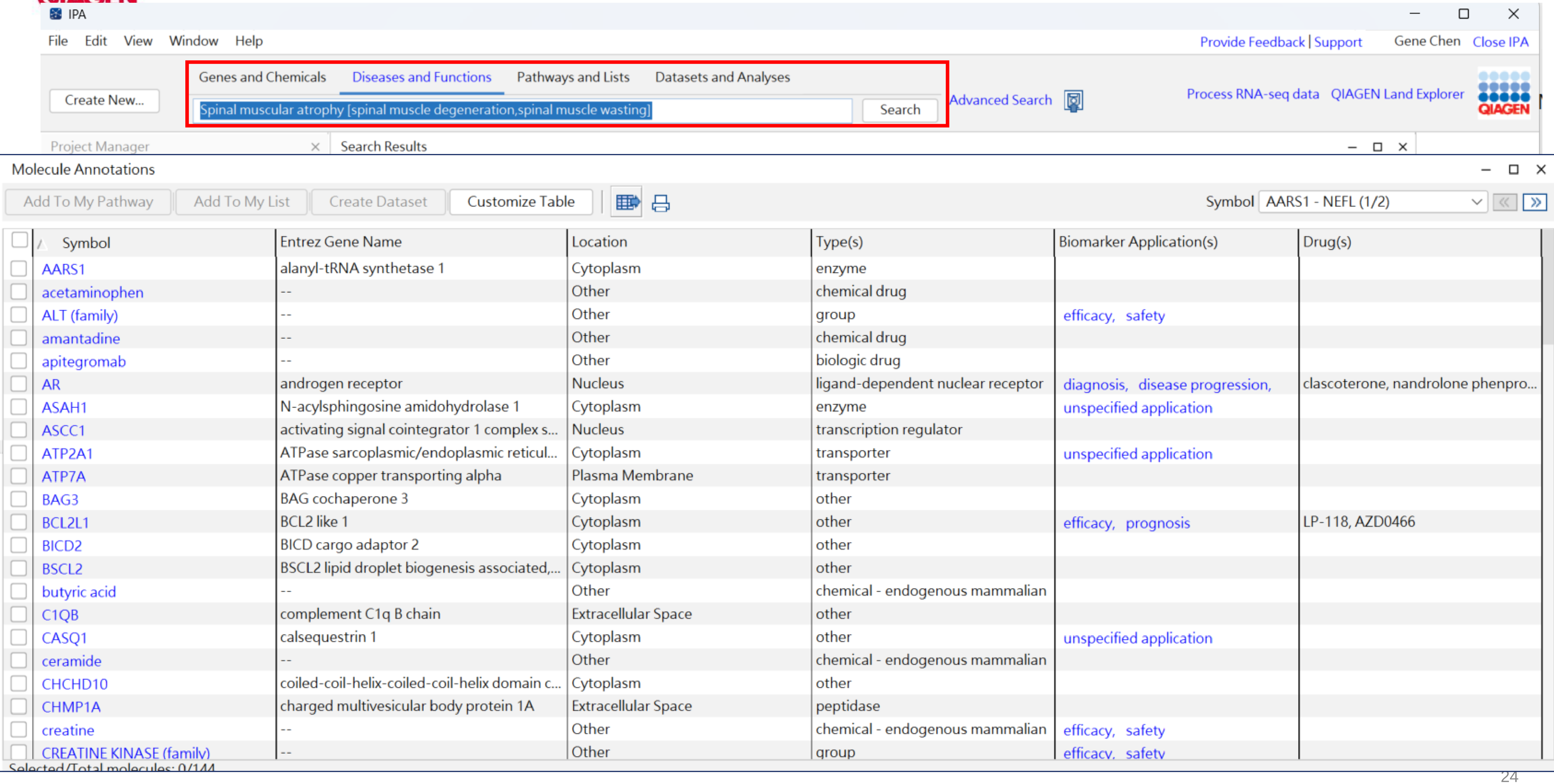


246,776 total datasets from OmicSoft with 15,001 datasets newly added. A new source called NCI Patient-Derived Models has been added in this release derived from this source: https://pdmr.cancer.gov/ .

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

- 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

Diseases and Function



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

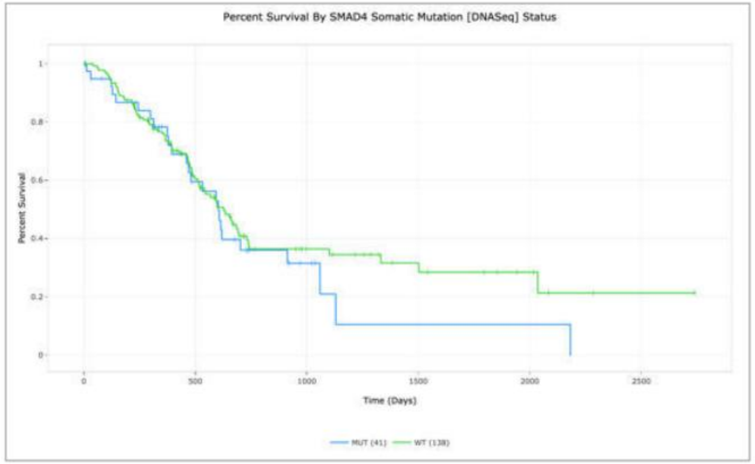
☐	Symbol	Entrez Gene Name	Location	Type(s)	Biomarker Application(s)	Drug(s)
☐	AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme		
☐	acetaminophen	--	Other	chemical drug		
☐	ALT (family)	--	Other	group	efficacy, safety	
☐	amantadine	--	Other	chemical drug		
☐	apitegromab	--	Other	biologic drug		
☐	AR	androgen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

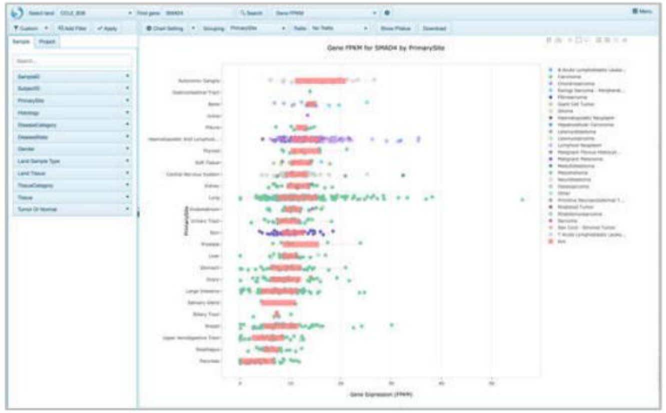
IPA with OmicSoft Land Explorer

Expression in Rat, Mouse, and Human Disease

Mutation frequency

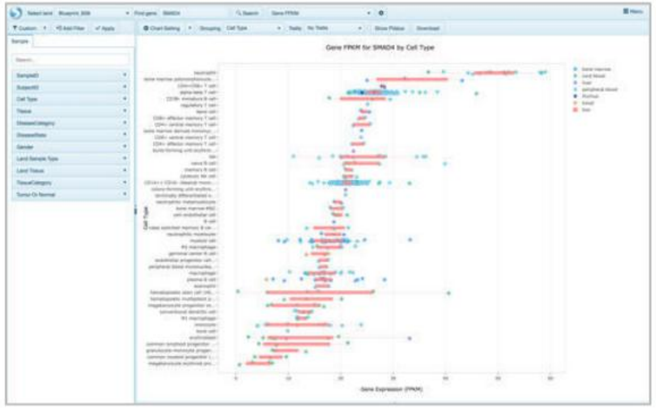


Survival plots



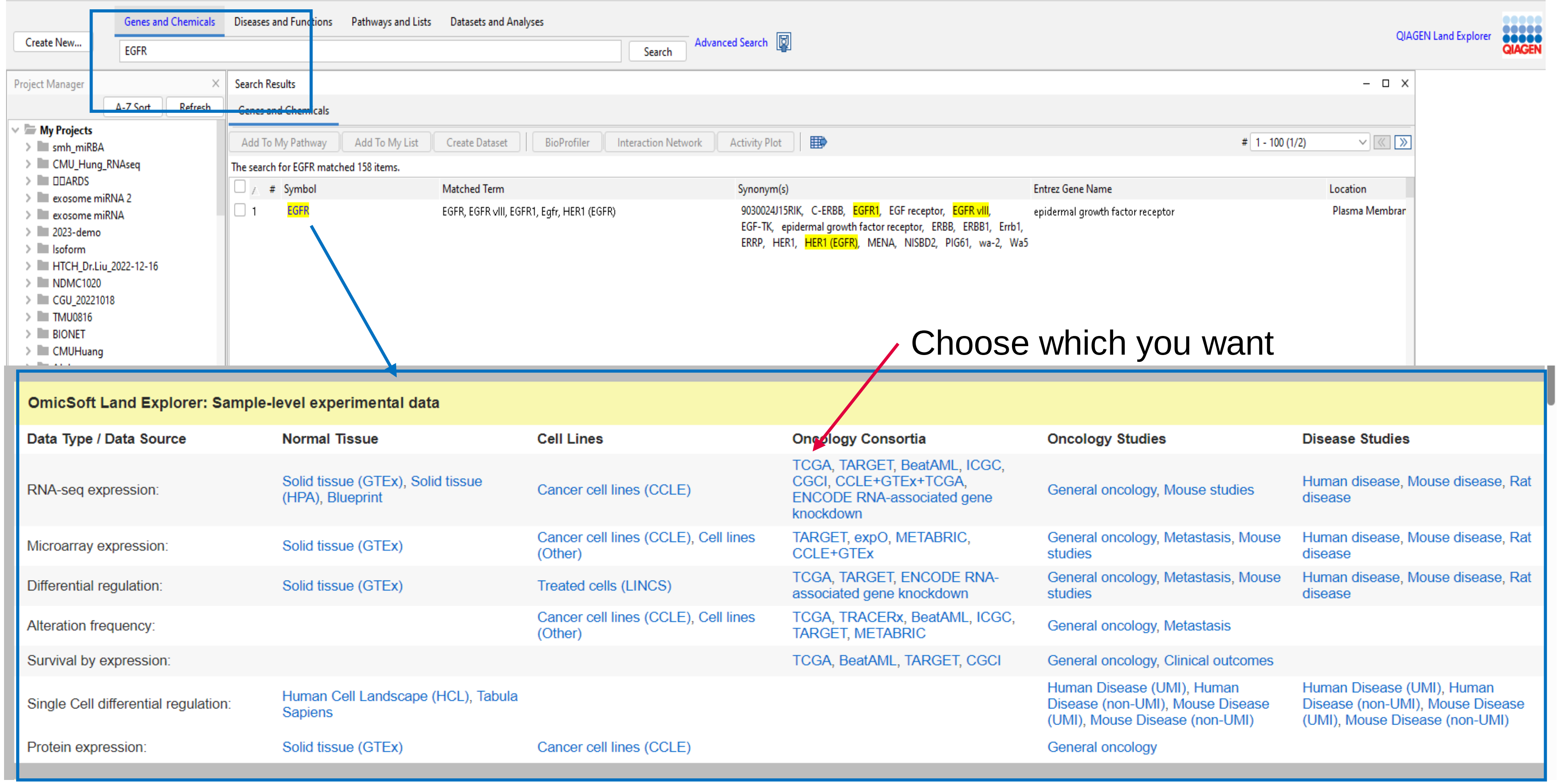
Cell line expression

Tumor expression



Hematopoietic expression (BluePrint)

IPA with OmicSoft Land Explorer



EGFR

The search for EGFR matched 158 items.

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

Choose which you want

OmicSoft Land Explorer: Sample-level experimental data

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

IPA Gene View :OmicSoft Land Explorer

IPA with OmicSoft Land Explorer

- **TCGA-B38-G33**

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

View controller

Download data for current view

Metadata filtering

Select land: TCGA_B38_GC33

Find gene: egfr

Gene FPKM

Grouping: Tumor Type

Trellis: No Trellis

Sample

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

Gender

Check All Check None Invert

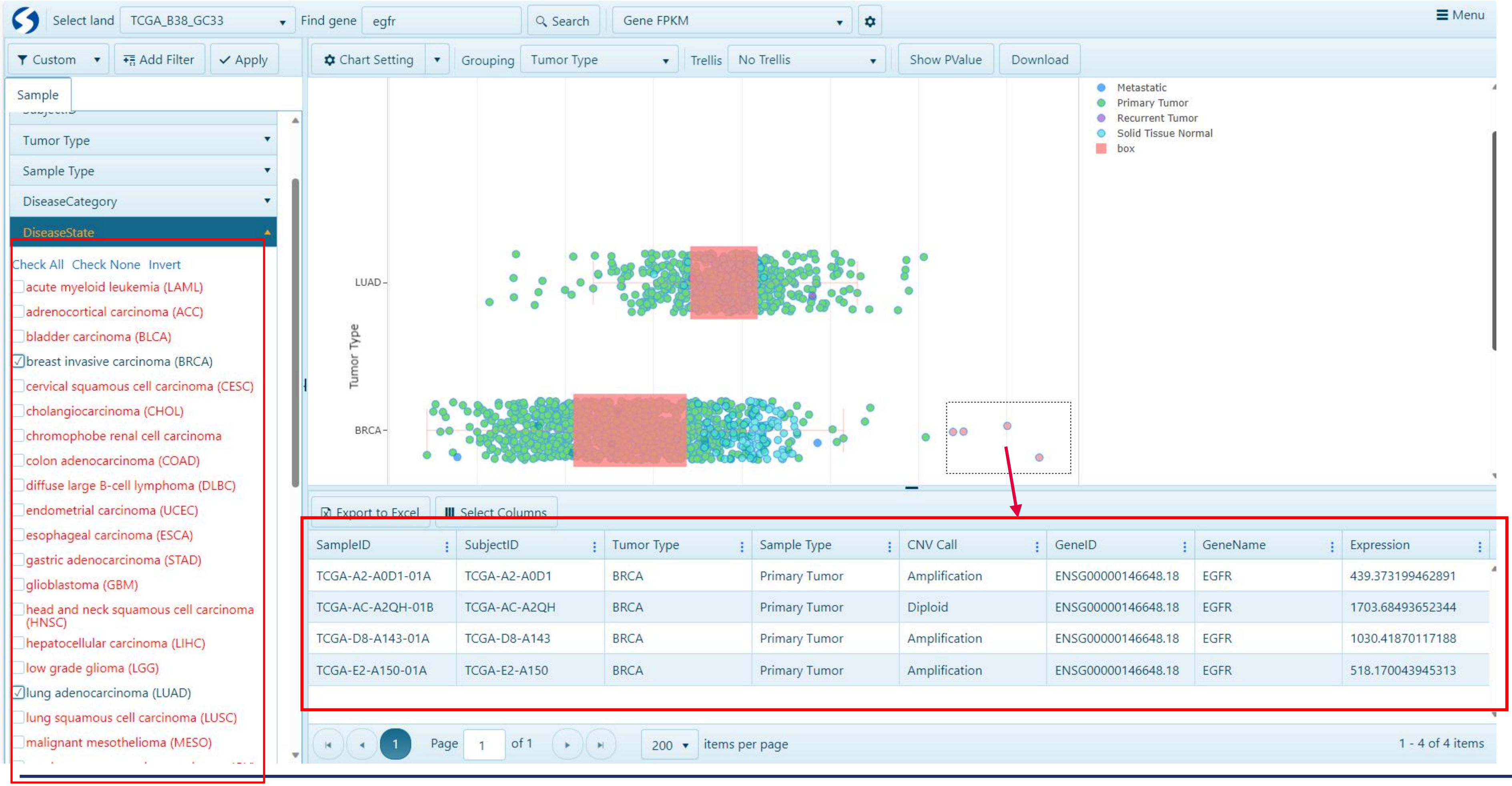
☑ female
☑ male
☐ NA
☐ -missing-

Gene FPKM for EGFR by Tumor Type

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

IPA with OmicSoft Land Explorer

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



Select land: TCGA_B38_GC33
Find gene: egfr
Gene FPKM
Grouping: Tumor Type
Trellis: No Trellis

DiseaseState

Check All Check None Invert

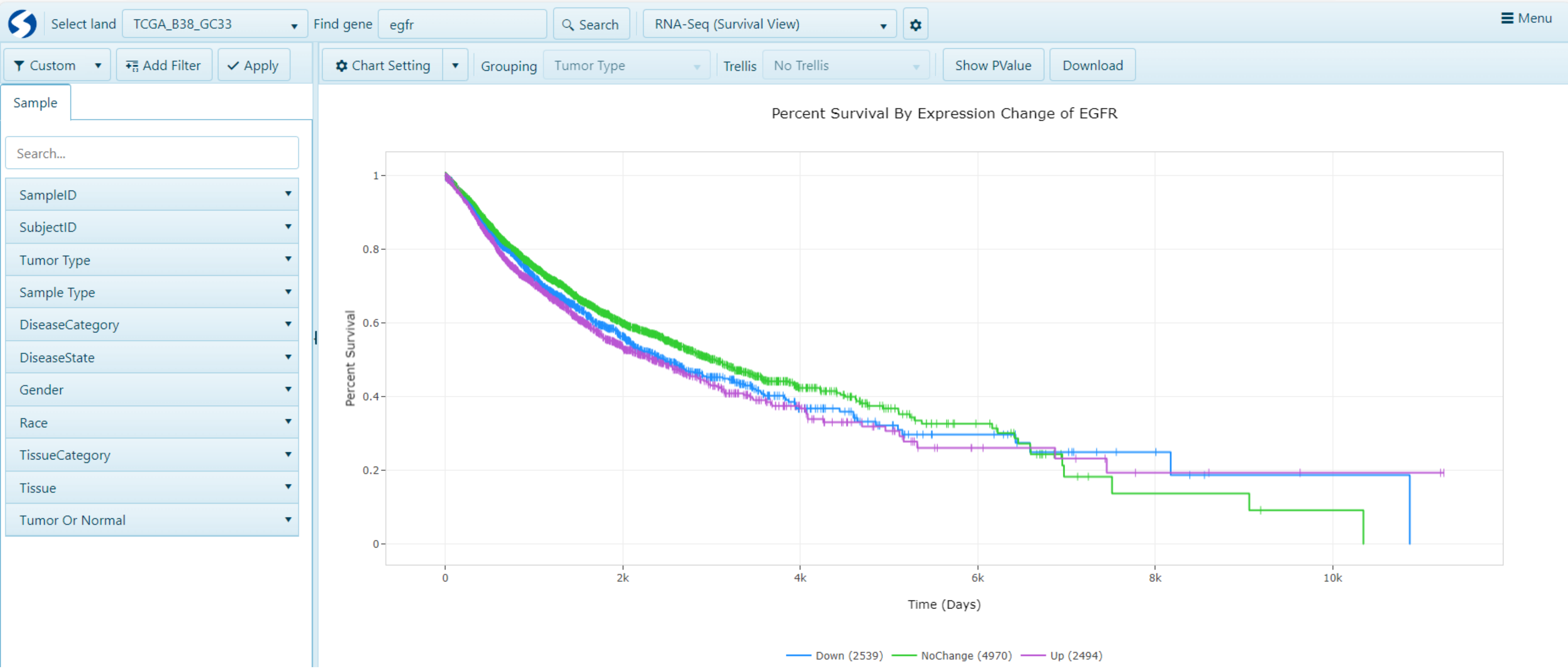
☐ acute myeloid leukemia (LAML)
☐ adrenocortical carcinoma (ACC)
☐ bladder carcinoma (BLCA)
☑ breast invasive carcinoma (BRCA)
☐ cervical squamous cell carcinoma (CESC)
☐ cholangiocarcinoma (CHOL)
☐ chromophobe renal cell carcinoma
☐ colon adenocarcinoma (COAD)
☐ diffuse large B-cell lymphoma (DLBC)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

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

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

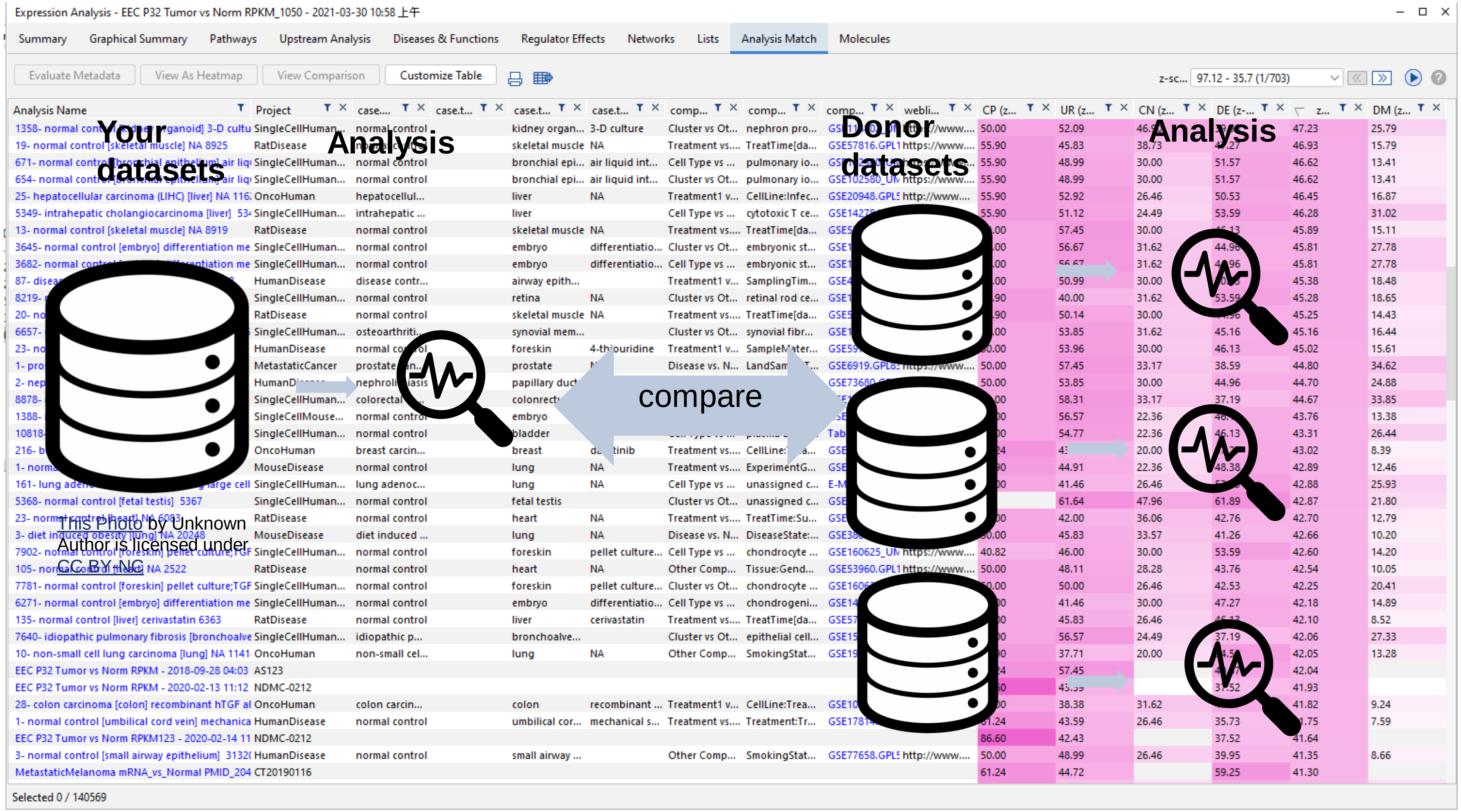
RNA-Seq (Survival View)

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

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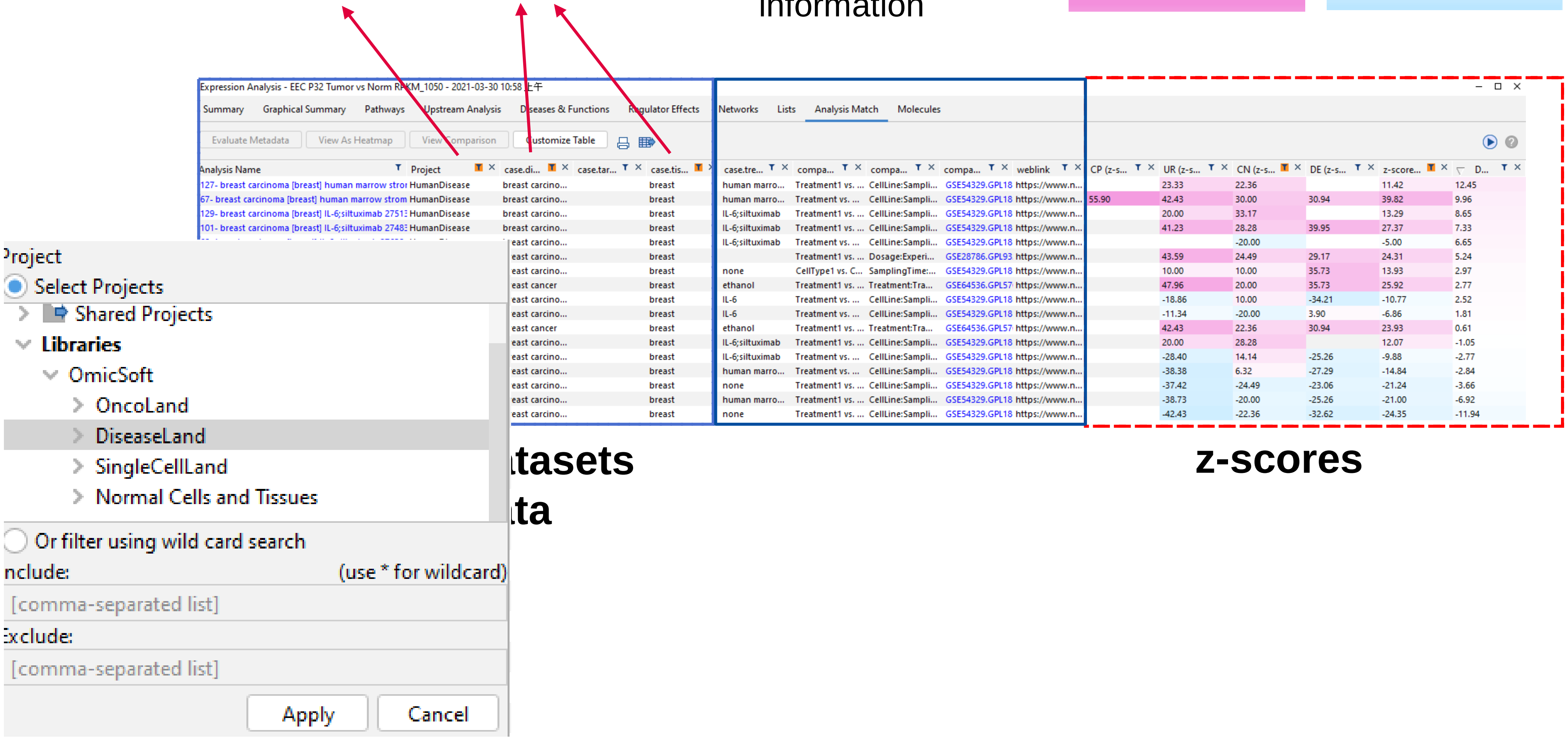
Analysis matching

Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project **Cell & Tissue** Datasets information **similar** **opposite**



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

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

roject

● Select Projects

○ Or filter using wild card search

nclude: (use * for wildcard)

[comma-separated list]

xclude:

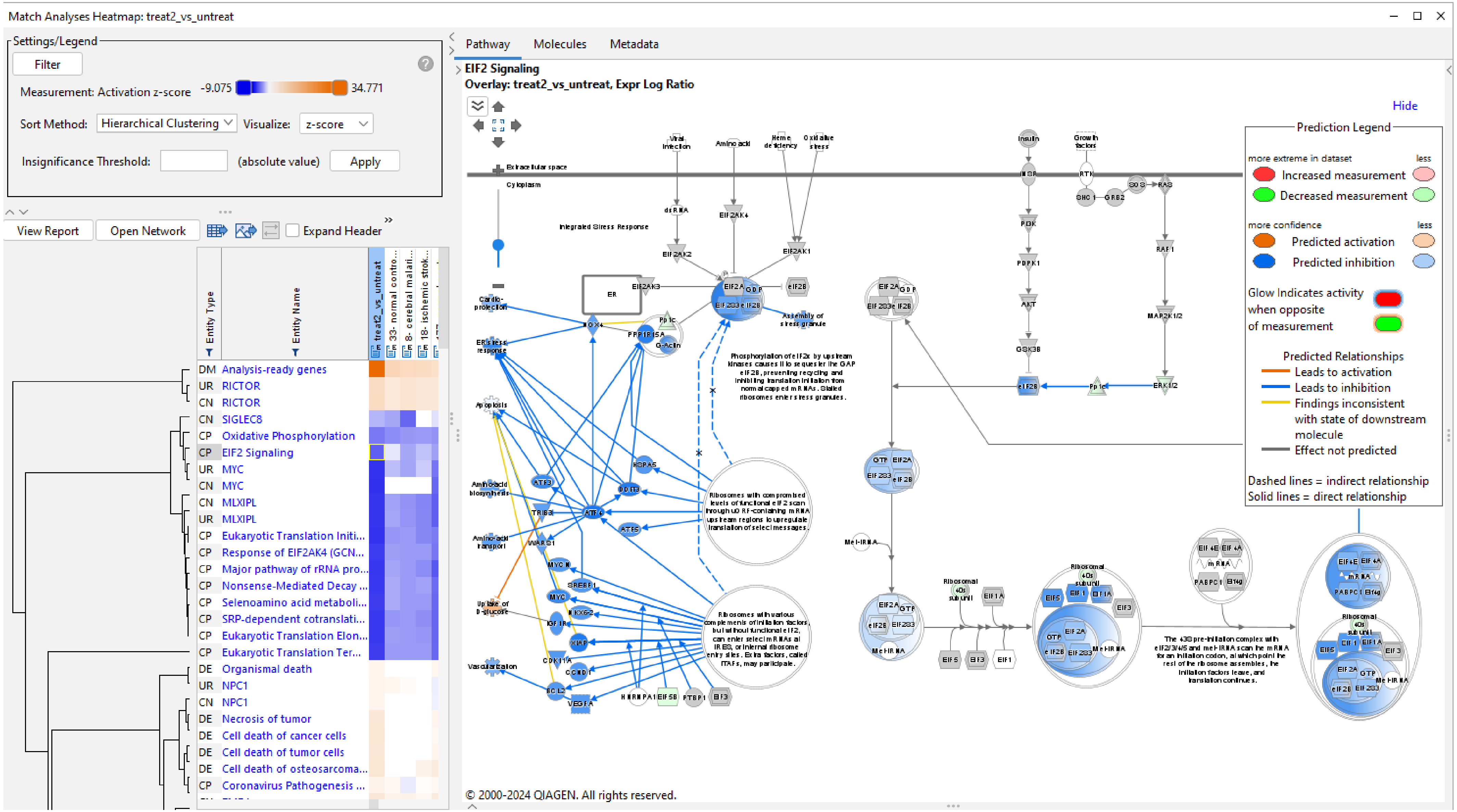
[comma-separated list]

tasets

ta

z-scores

Analysis Match



Match Analyses Heatmap: treat2_vs_untreat

Settings/Legend

Measurement: Activation z-score -9.075 34.771

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value)

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

EIF2 Signaling

Overlay: treat2_vs_untreat, Expr Log Ratio

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.

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

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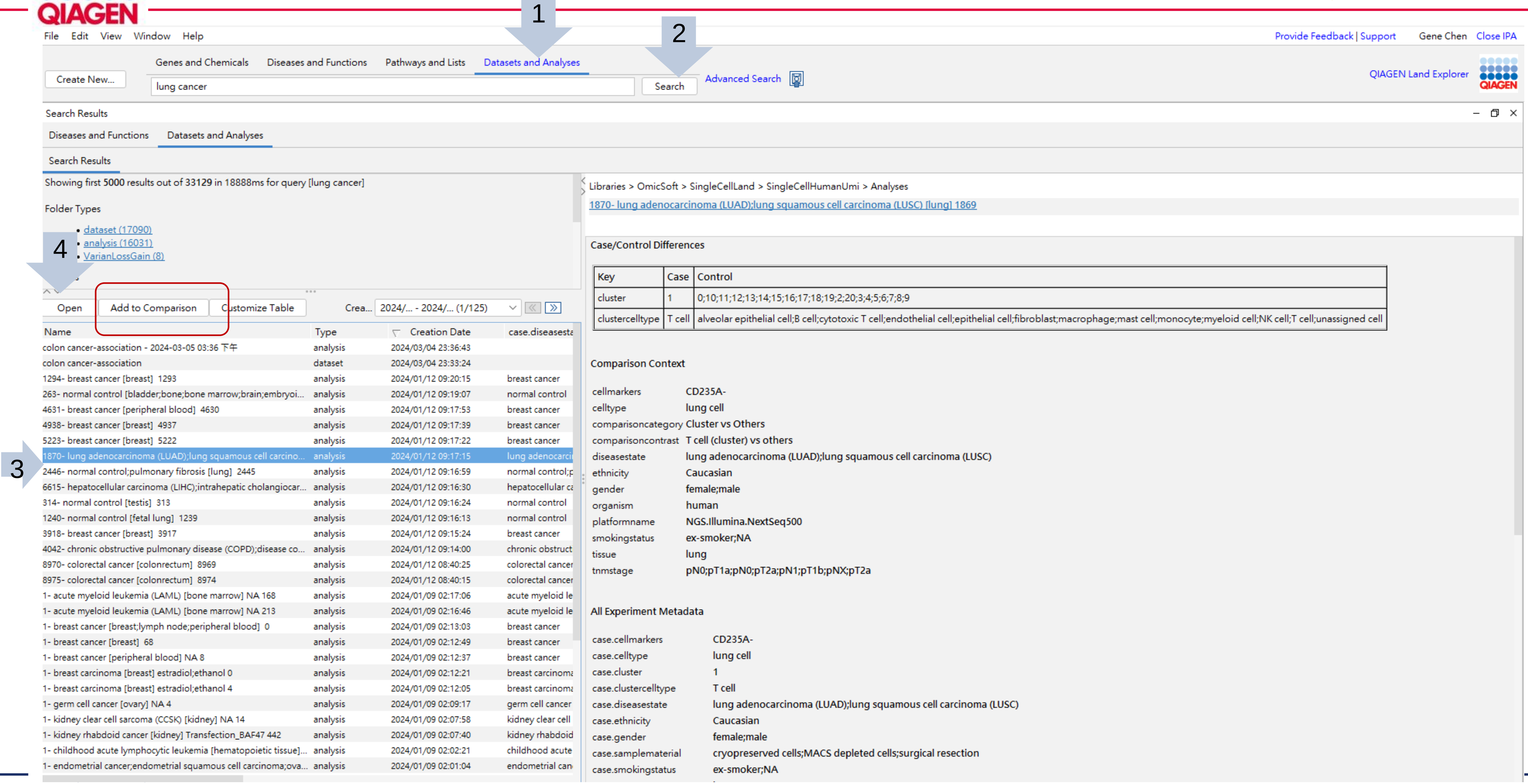
Dataset and analysis search



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

Folder Types

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

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

Libraries > OmicSoft > SingleCellLand > SingleCellHumanUmi > Analyses

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

Case/Control Differences

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

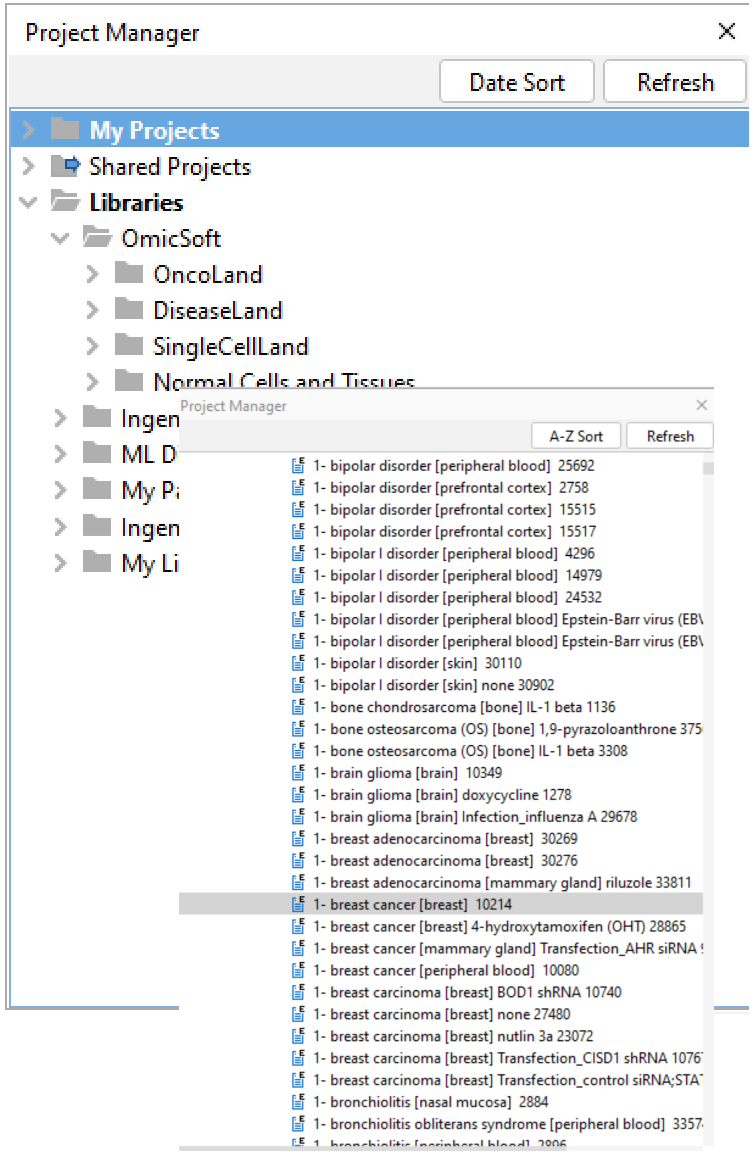
Comparison Context

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

All Experiment Metadata

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

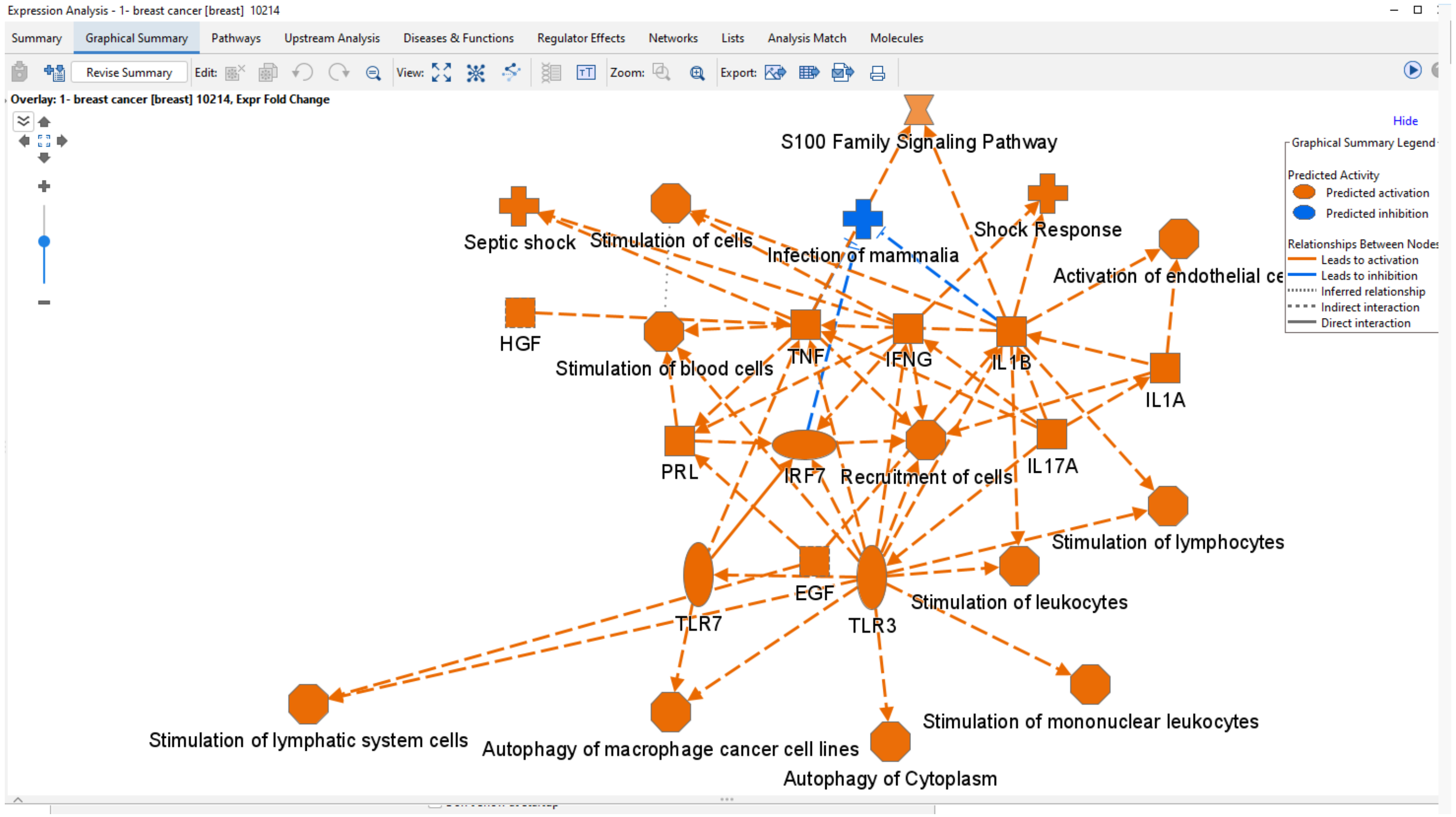
OmicSoft data storage and analysis in IPA



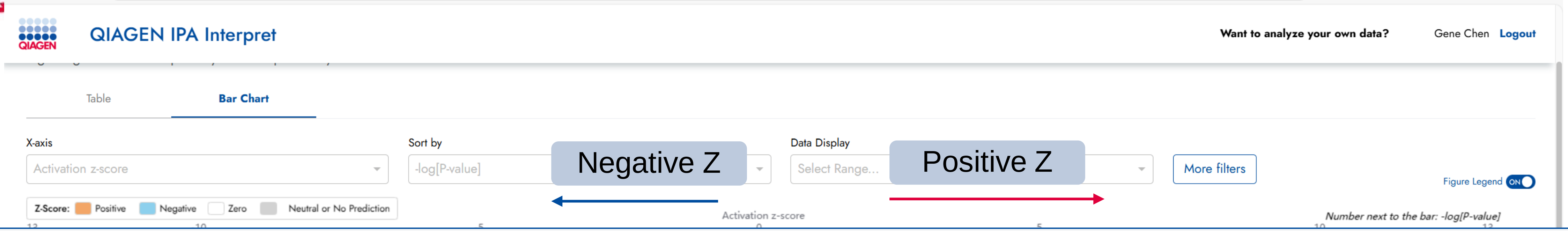
1- bipolar disorder [peripheral blood] 25692
1- bipolar disorder [prefrontal cortex] 2758
1- bipolar disorder [prefrontal cortex] 15515
1- bipolar disorder [prefrontal cortex] 15517
1- bipolar I disorder [peripheral blood] 4296
1- bipolar I disorder [peripheral blood] 14979
1- bipolar I disorder [peripheral 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

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

Graphical summary



IPA interpret canonical pathway bar chart (2025 spring release)



QIAGEN IPA Interpret

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

X-axis
Activation z-score

Sort by: -log[P-value]

Data Display: Select Range...

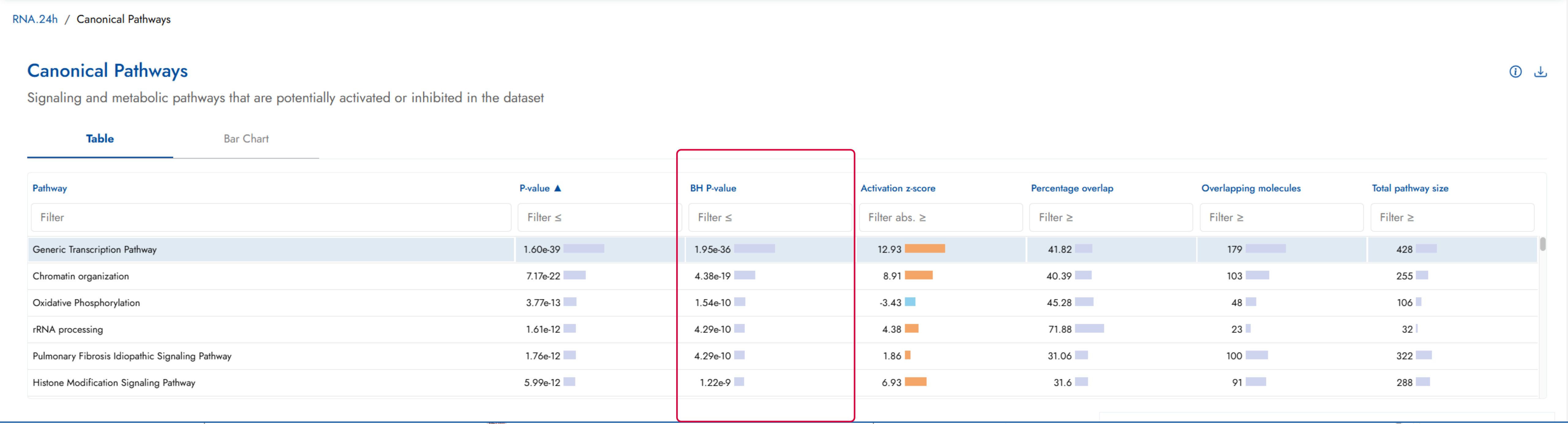
Negative Z ←

Positive Z →

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

Activation z-score

Number next to the bar: -log[P-value]

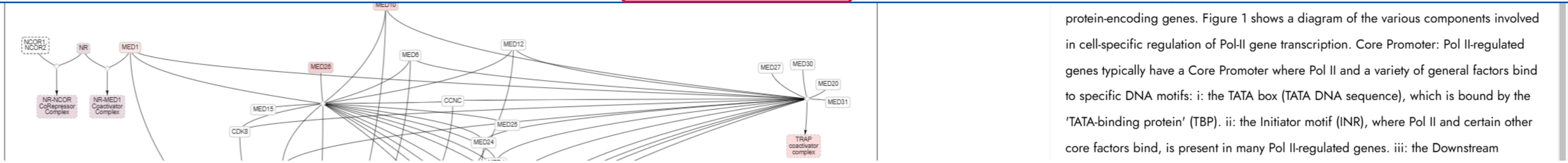


RNA.24h / Canonical Pathways

Canonical Pathways

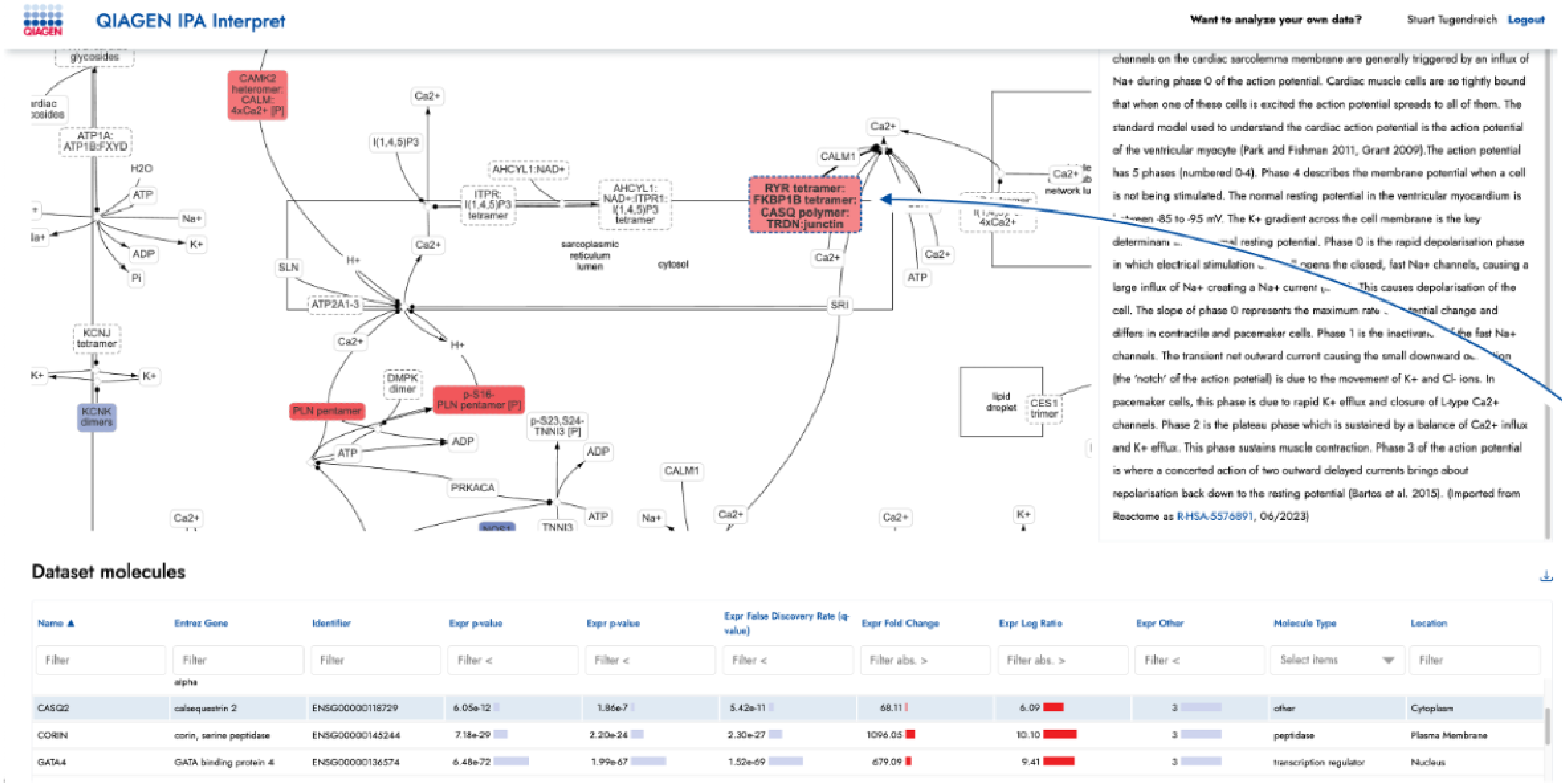
Signaling and metabolic pathways that are potentially activated or inhibited in the dataset

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



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

Highlight nodes of interest in a canonical pathway or network



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

Dataset molecules

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

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

1) Clicking row(s) here

IPA interpret Canonical Pathway Bubble Plot (2025 summer release)

IPA interpret

In canonical pathway, could show volcano bubble plot

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

protein.24 / Canonical Pathways

Canonical Pathways

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

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...

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

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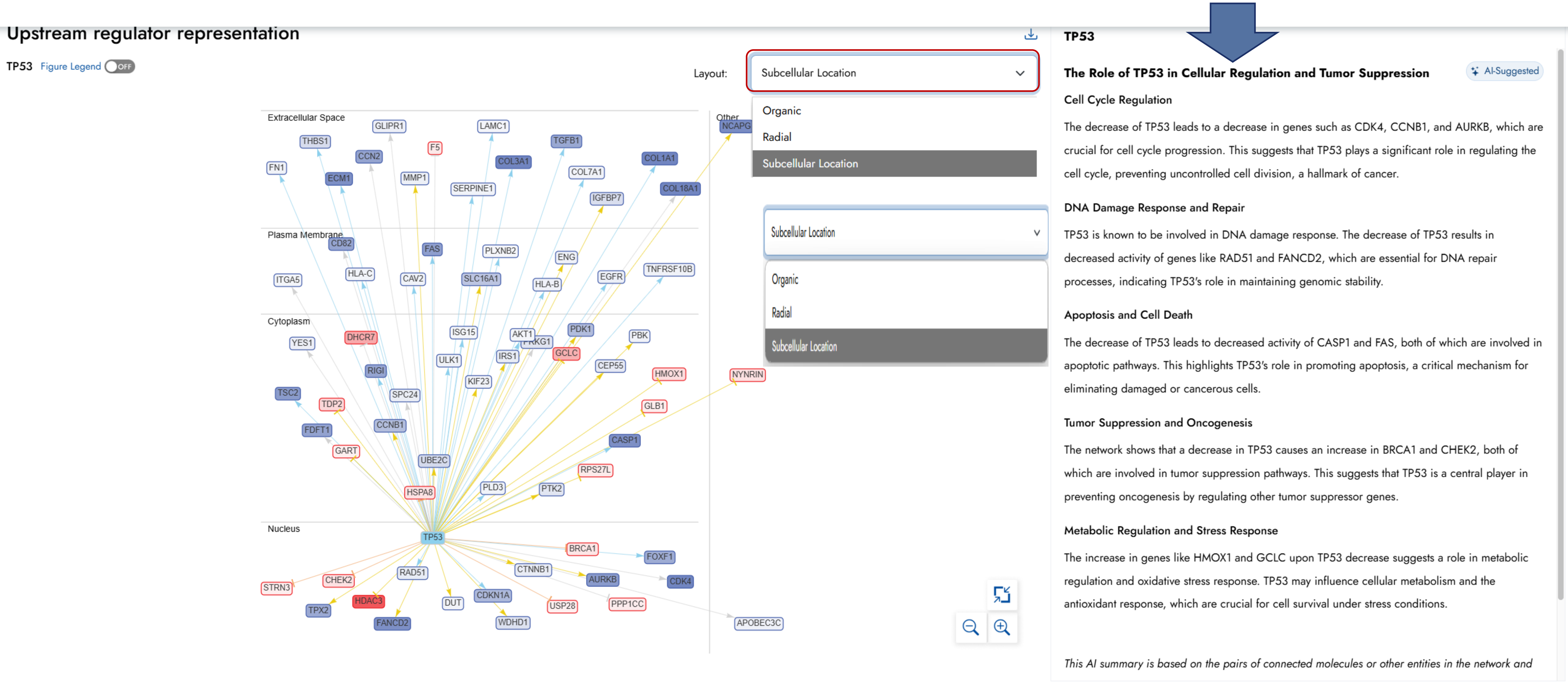
IPA interpret Upstream regulator change layout

AI suggested



Upstream regulator representation

TP53 Figure Legend OFF

Layout: Subcellular Location

TP53

The Role of TP53 in Cellular Regulation and Tumor Suppression

Cell Cycle Regulation

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

DNA Damage Response and Repair

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

Apoptosis and Cell Death

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

Tumor Suppression and Oncogenesis

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

Metabolic Regulation and Stress Response

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

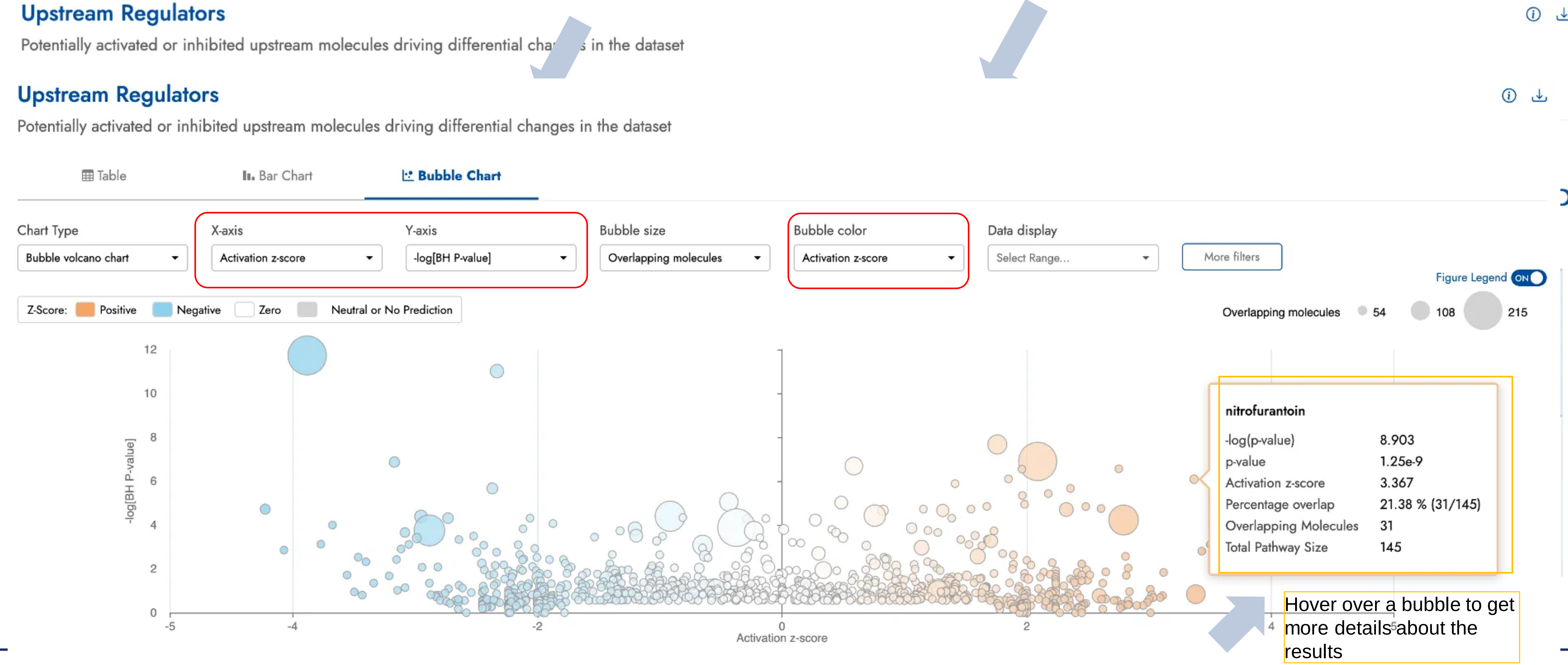
This AI summary is based on the pairs of connected molecules or other entities in the network and

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...

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 in Disease and Function

In disease and functional, It also could show Bubble Chart

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

Diseases and Functions

Diseases and biological processes predicted to be impacted in the dataset

Chart Type: Bubble volcano chart

X-axis: Activation z-score

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

Bubble size: Percentage overlap

Bubble color: Activation z-score

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

More Data Filters

Filter by Gene(s)

Include (e.g. BRCA1, TP5:

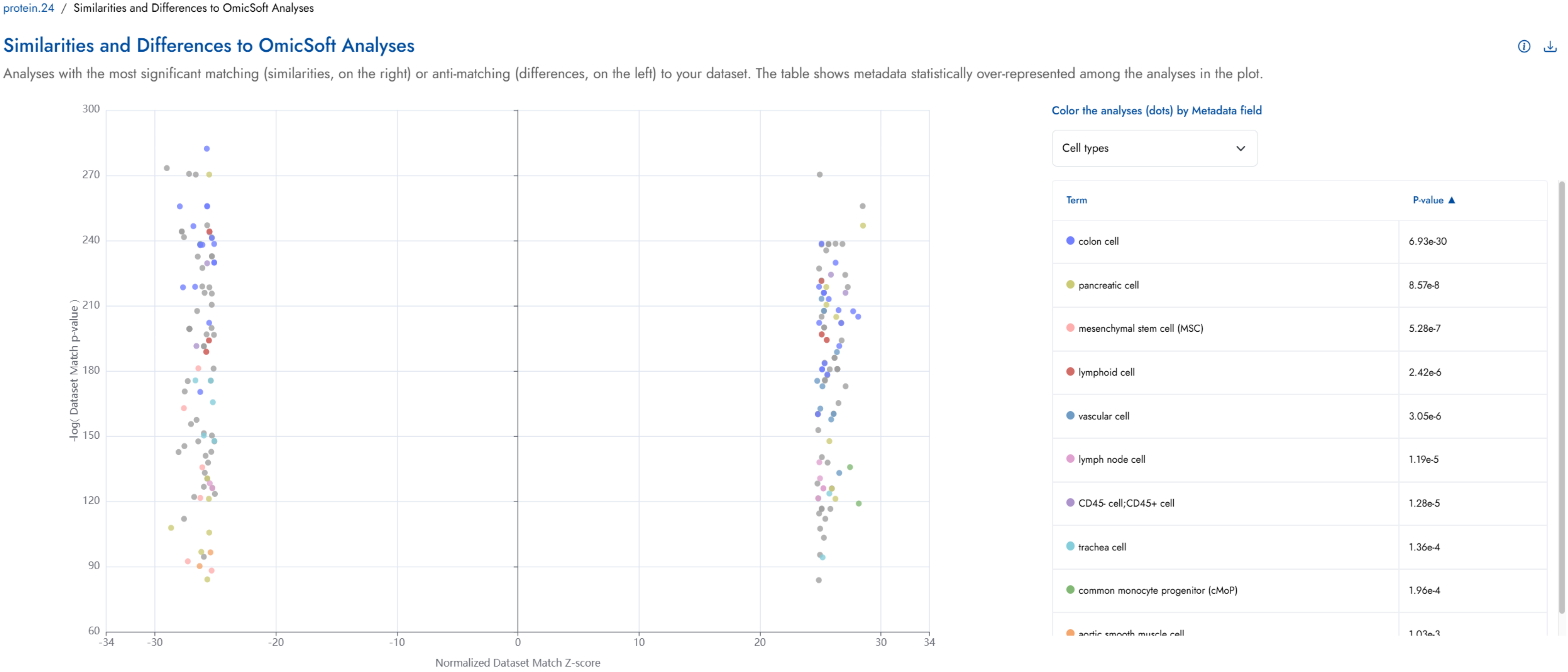
Exclude (e.g. ALAS2, IRF:

Diseases and Functions Display

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

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

Analysis match of Omicsoft analysis



protein.24 / Similarities and Differences to OmicSoft Analyses

Similarities and Differences to OmicSoft Analyses

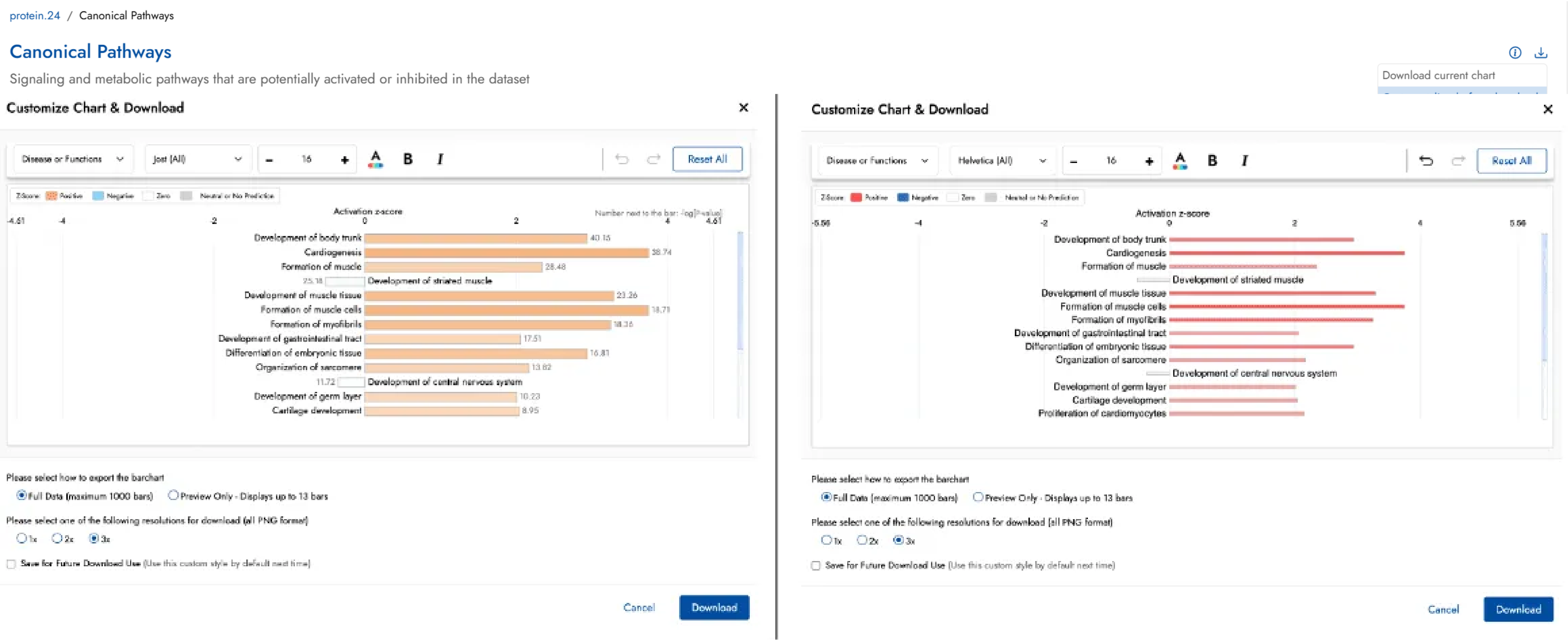
Analyses with the most significant matching (similarities, on the right) or anti-matching (differences, on the left) to your dataset. The table shows metadata statistically over-represented among the analyses in the plot.

Color the analyses (dots) by Metadata field

Cell types

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

Customize bar charts for image export



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

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

Please select how to export the barchart

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

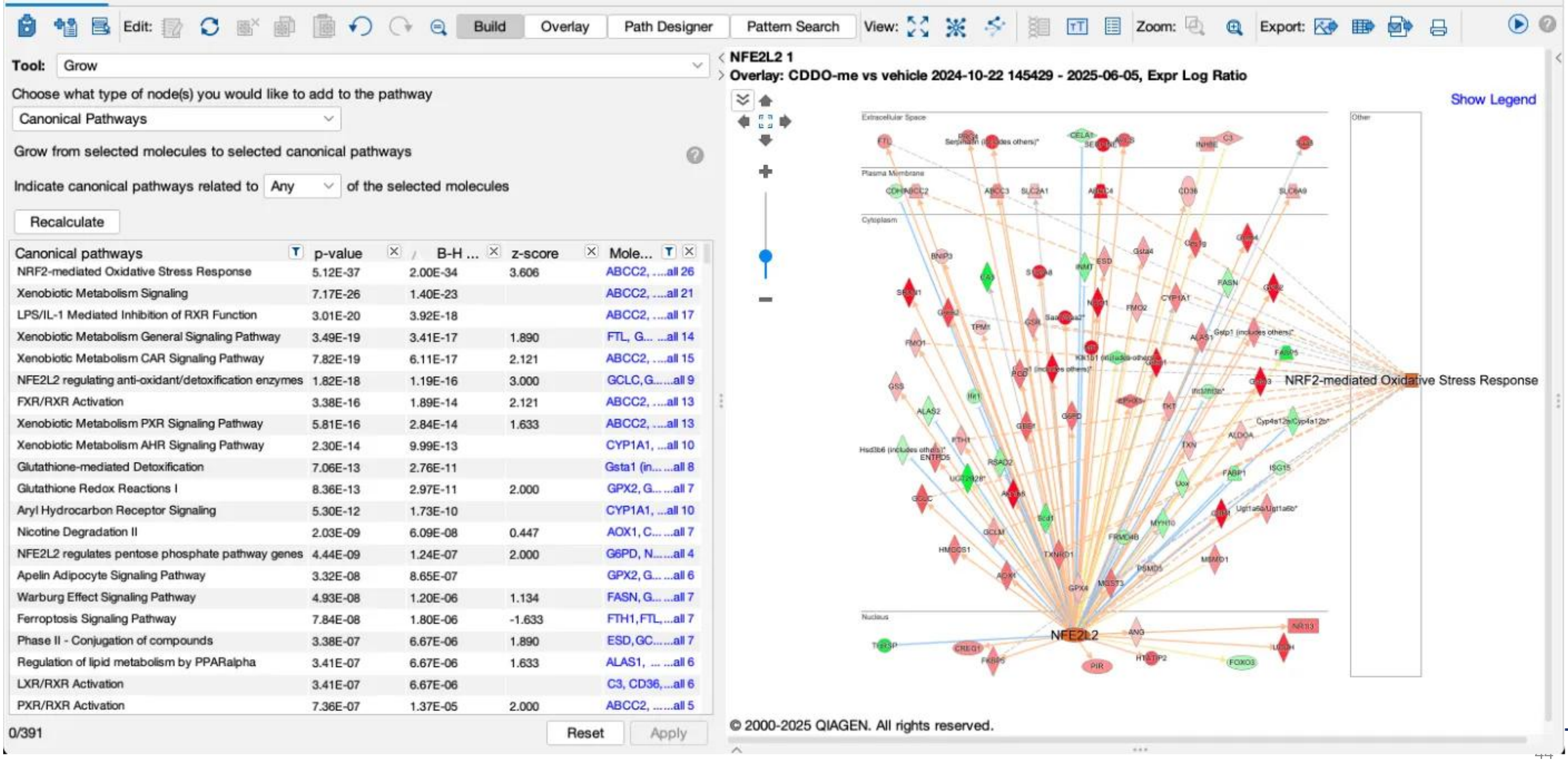
Please select one of the following resolutions for download (all PNG format)

○ 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

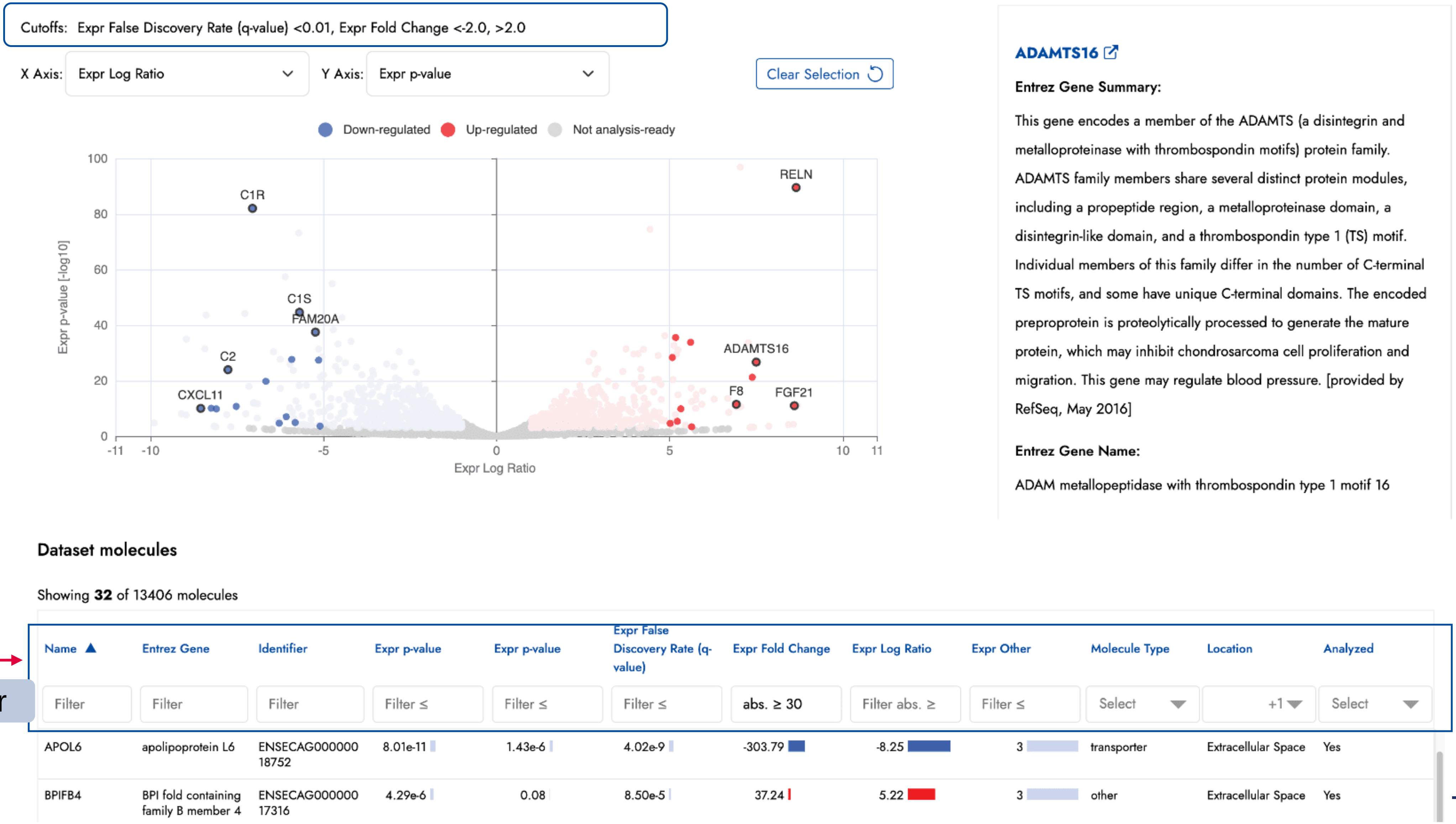
Reset Apply

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 Fall Release (2025)

If we use this cut off and threshold, the plot highlights genes of interest by fading away those that do not meet your criteria.



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

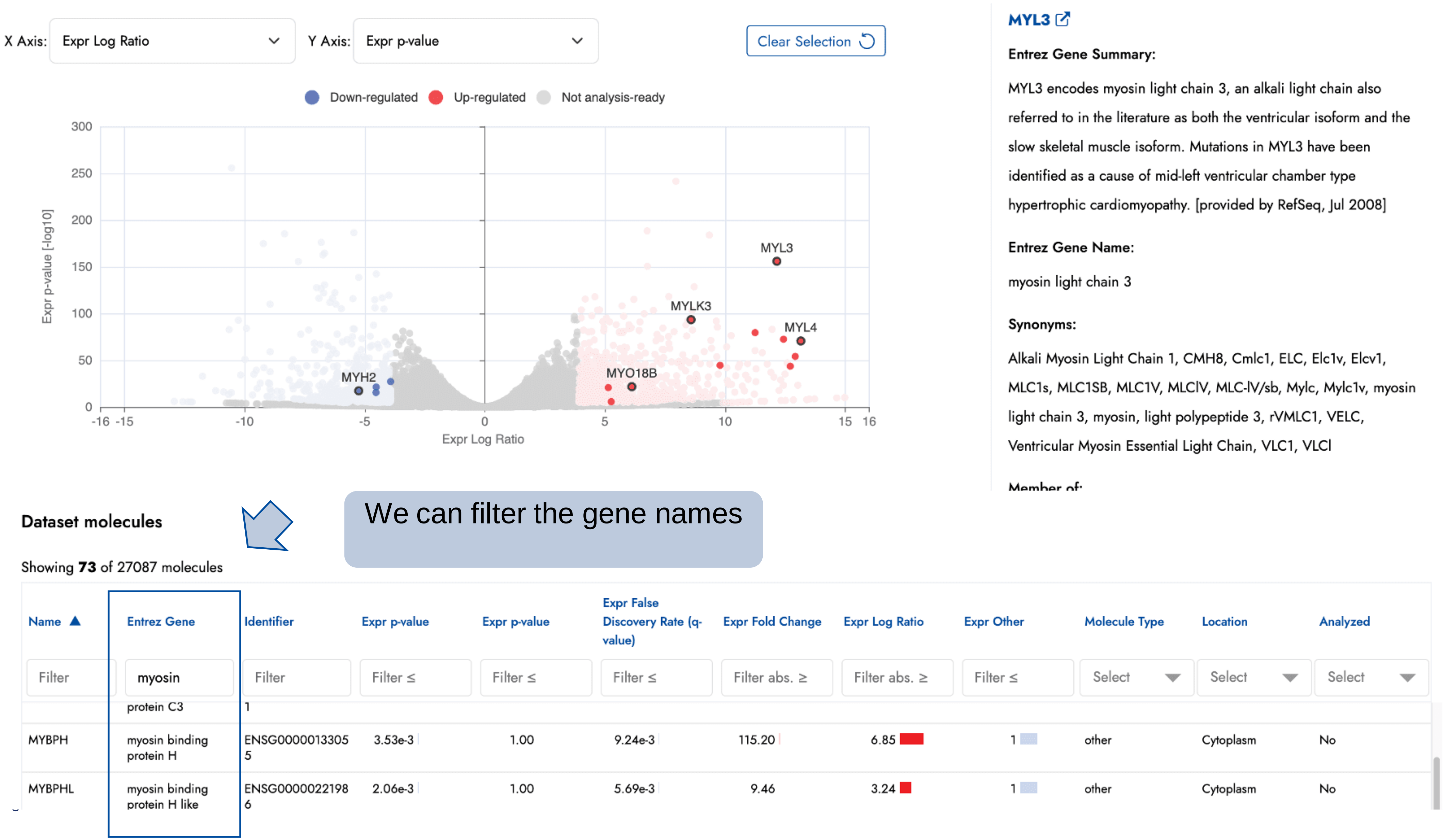
Showing **32** of 13406 molecules

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

Set filter

Sample to

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, MLCIV, MLC-lV/sb, Mylc, Mylc1v, myosin light chain 3, myosin, light polypeptide 3, rVMLC1, VELC, Ventricular Myosin Essential Light Chain, VLC1, VLCl

Member of:

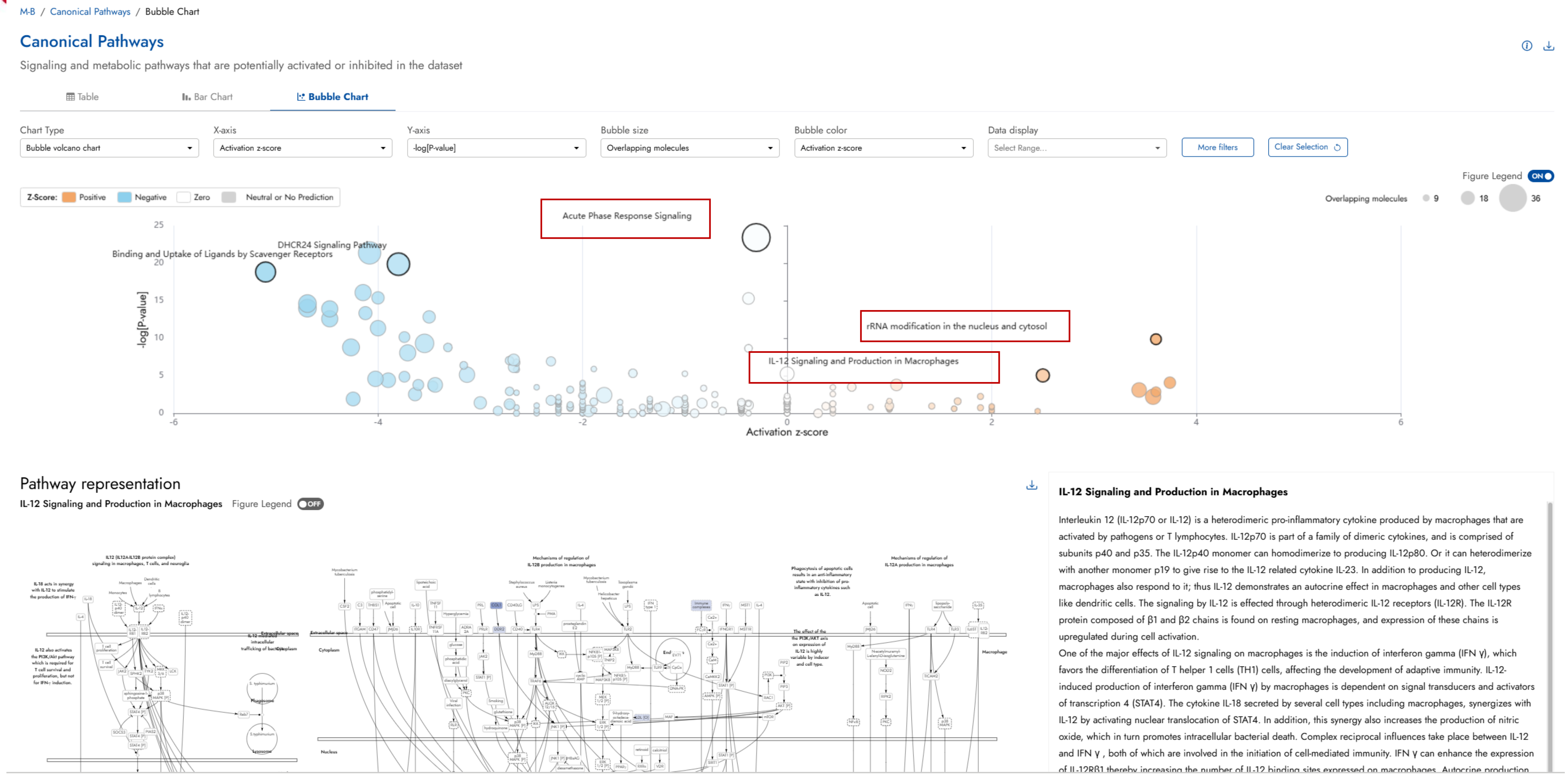
Dataset molecules

We can filter the gene names

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

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



Canonical Pathways

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

Chart Type: Bubble volcano chart
X-axis: Activation z-score
Y-axis: -log[P-value]
Bubble size: Overlapping molecules
Bubble color: Activation z-score
Data display: Select Range...

Pathway representation

IL-12 Signaling and Production in Macrophages

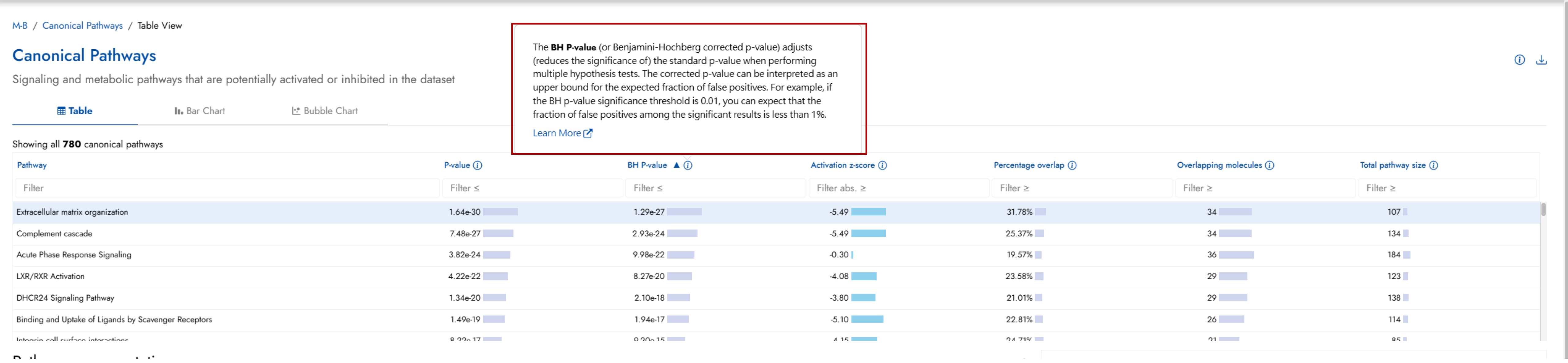
IL-12 Signaling and Production in Macrophages

Interleukin 12 (IL-12p70 or IL-12) is a heterodimeric pro-inflammatory cytokine produced by macrophages that are activated by pathogens or T lymphocytes. IL-12p70 is part of a family of dimeric cytokines, and is comprised of subunits p40 and p35. The IL-12p40 monomer can homodimerize to producing IL-12p80. Or it can heterodimerize with another monomer p19 to give rise to the IL-12 related cytokine IL-23. In addition to producing IL-12, macrophages also respond to it; thus IL-12 demonstrates an autocrine effect in macrophages and other cell types like dendritic cells. The signaling by IL-12 is effected through heterodimeric IL-12 receptors (IL-12R). The IL-12R protein composed of β1 and β2 chains is found on resting macrophages, and expression of these chains is upregulated during cell activation.

One of the major effects of IL-12 signaling on macrophages is the induction of interferon gamma (IFN γ), which favors the differentiation of T helper 1 cells (TH1) cells, affecting the development of adaptive immunity. IL-12-induced production of interferon gamma (IFN γ) by macrophages is dependent on signal transducers and activators of transcription 4 (STAT4). The cytokine IL-18 secreted by several cell types including macrophages, synergizes with IL-12 by activating nuclear translocation of STAT4. In addition, this synergy also increases the production of nitric oxide, which in turn promotes intracellular bacterial death. Complex reciprocal influences take place between IL-12 and IFN γ , both of which are involved in the initiation of cell-mediated immunity. IFN γ can enhance the expression of IL-12Rβ1 thereby increasing the number of IL-12 binding sites expressed on macrophages. Autocrine production

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

Reduced learning curve with accessible definitions for statistics in IPA Interpret



M-B / Canonical Pathways / Table View

Canonical Pathways

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

The **BH P-value** (or Benjamini-Hochberg corrected p-value) adjusts (reduces the significance of) the standard p-value when performing multiple hypothesis tests. The corrected p-value can be interpreted as an upper bound for the expected fraction of false positives. For example, if the BH p-value significance threshold is 0.01, you can expect that the fraction of false positives among the significant results is less than 1%.

Learn More

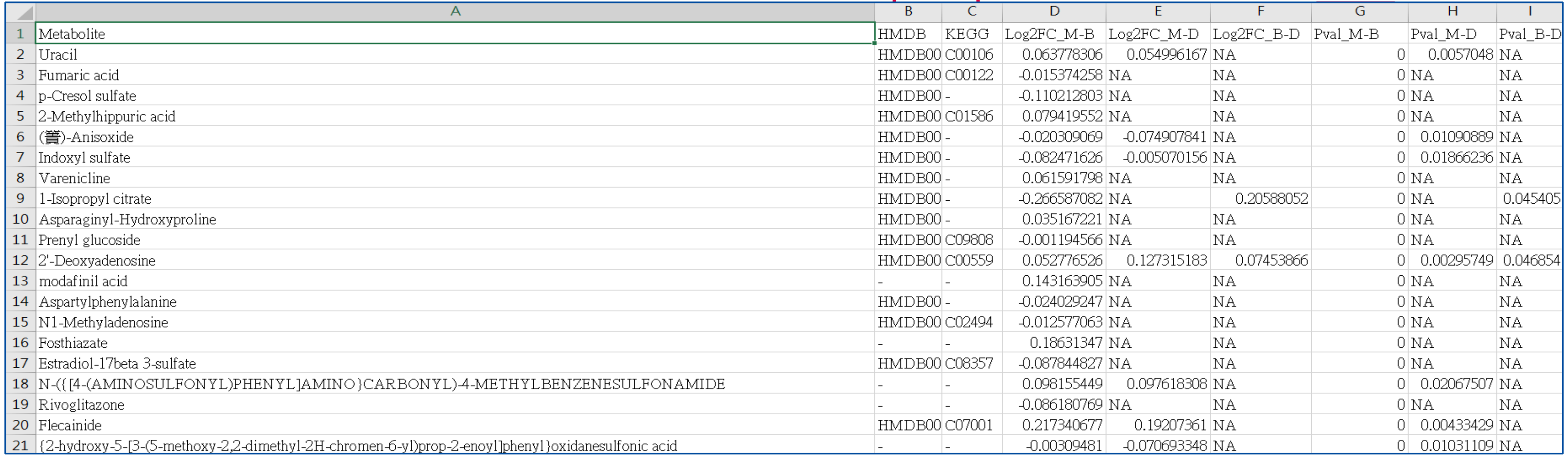
Showing all **780** canonical pathways

Pathway	P-value ⓘ	BH P-value ▲ ⓘ	Activation z-score ⓘ	Percentage overlap ⓘ	Overlapping molecules ⓘ	Total pathway size ⓘ
Filter	Filter ≤	Filter ≤	Filter abs. ≥	Filter ≥	Filter ≥	Filter ≥
Extracellular matrix organization	1.64e-30	1.29e-27	-5.49	31.78%	34	107
Complement cascade	7.48e-27	2.93e-24	-5.49	25.37%	34	134
Acute Phase Response Signaling	3.82e-24	9.98e-22	-0.30	19.57%	36	184
LXR/RXR Activation	4.22e-22	8.27e-20	-4.08	23.58%	29	123
DHCR24 Signaling Pathway	1.34e-20	2.10e-18	-3.80	21.01%	29	138
Binding and Uptake of Ligands by Scavenger Receptors	1.49e-19	1.94e-17	-5.10	22.81%	26	114
Integrin cell surface interactions	8.22e-17	9.20e-15	-4.15	24.71%	21	85

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

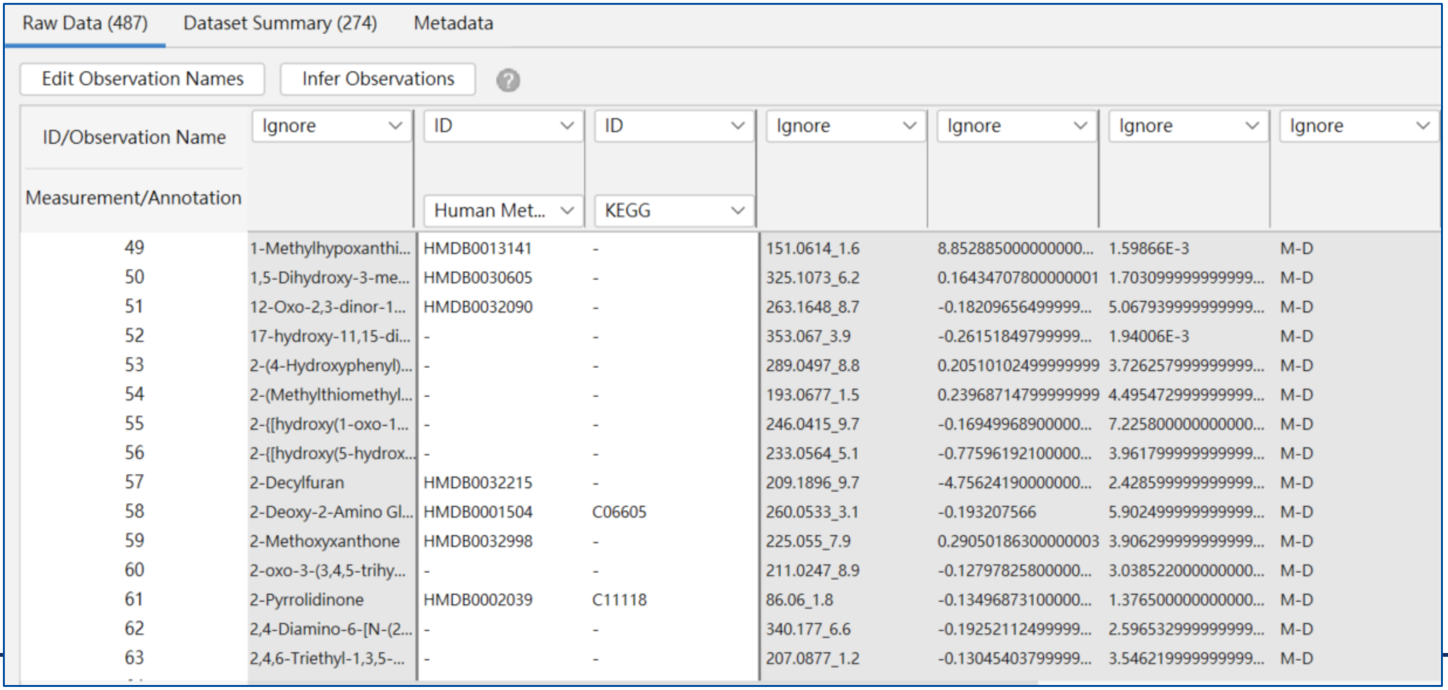
ID not on the left

Multi observation



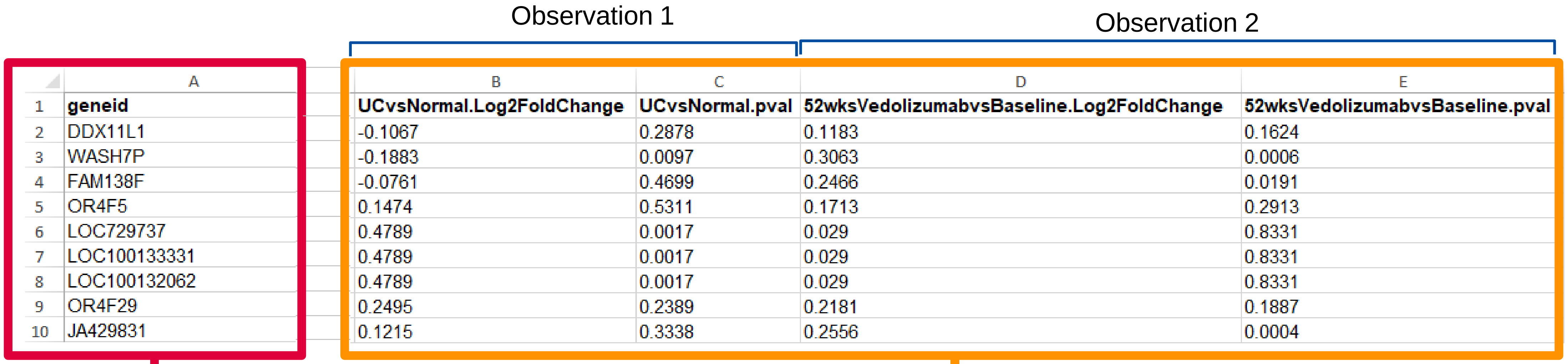
	A	B	C	D	E	F	G	H	I
1	Metabolite	HMDB	KEGG	Log2FC_M-B	Log2FC_M-D	Log2FC_B-D	Pval_M-B	Pval_M-D	Pval_B-D
2	Uracil	HMDB00	C00106	0.063778306	0.054996167	NA	0	0.0057048	NA
3	Fumaric acid	HMDB00	C00122	-0.015374258	NA	NA	0	NA	NA
4	p-Cresol sulfate	HMDB00	-	-0.110212803	NA	NA	0	NA	NA
5	2-Methylhippuric acid	HMDB00	C01586	0.079419552	NA	NA	0	NA	NA
6	(蕢)-Anisoxide	HMDB00	-	-0.020309069	-0.074907841	NA	0	0.01090889	NA
7	Indoxyl sulfate	HMDB00	-	-0.082471626	-0.005070156	NA	0	0.01866236	NA
8	Varenicline	HMDB00	-	0.061591798	NA	NA	0	NA	NA
9	1-Isopropyl citrate	HMDB00	-	-0.266587082	NA	0.20588052	0	NA	0.045405
10	Asparaginyl-Hydroxyproline	HMDB00	-	0.035167221	NA	NA	0	NA	NA
11	Prenyl glucoside	HMDB00	C09808	-0.001194566	NA	NA	0	NA	NA
12	2'-Deoxyadenosine	HMDB00	C00559	0.052776526	0.127315183	0.07453866	0	0.00295749	0.046854
13	modafinil acid	-	-	0.143163905	NA	NA	0	NA	NA
14	Aspartylphenylalanine	HMDB00	-	-0.024029247	NA	NA	0	NA	NA
15	N1-Methyladenosine	HMDB00	C02494	-0.012577063	NA	NA	0	NA	NA
16	Fosthiazate	-	-	0.18631347	NA	NA	0	NA	NA
17	Estradiol-17beta 3-sulfate	HMDB00	C08357	-0.087844827	NA	NA	0	NA	NA
18	N-({[4-(AMINOSULFONYL)PHENYL]AMINO}CARBONYL)-4-METHYLBENZENESULFONAMIDE	-	-	0.098155449	0.097618308	NA	0	0.02067507	NA
19	Rivoglitazone	-	-	-0.086180769	NA	NA	0	NA	NA
20	Flecainide	HMDB00	C07001	0.217340677	0.19207361	NA	0	0.00433429	NA
21	{2-hydroxy-5-[3-(5-methoxy-2,2-dimethyl-2H-chromen-6-yl)prop-2-enoyl]phenyl}oxidanesulfonic acid	-	-	-0.00309481	-0.070693348	NA	0	0.01031109	NA

AI can help pares and map automatically



ID/Observation Name	Ignore	ID	ID	Ignore	Ignore	Ignore	Ignore
Measurement/Annotation		Human Met...	KEGG				
49	1-Methylhypoxanthi...	HMDB0013141	-	151.0614_1.6	8.852885000000000...	1.59866E-3	M-D
50	1,5-Dihydroxy-3-me...	HMDB0030605	-	325.1073_6.2	0.16434707800000001	1.703099999999999...	M-D
51	12-Oxo-2,3-dinor-1...	HMDB0032090	-	263.1648_8.7	-0.18209656499999...	5.067939999999999...	M-D
52	17-hydroxy-11,15-di...	-	-	353.067_3.9	-0.26151849799999...	1.94006E-3	M-D
53	2-(4-Hydroxyphenyl)...	-	-	289.0497_8.8	0.20510102499999999	3.726257999999999...	M-D
54	2-(Methylthiomethyl...	-	-	193.0677_1.5	0.23968714799999999	4.495472999999999...	M-D
55	2-{[hydroxy(1-oxo-1...	-	-	246.0415_9.7	-0.16949968900000...	7.225800000000000...	M-D
56	2-{[hydroxy(5-hydrox...	-	-	233.0564_5.1	-0.77596192100000...	3.961799999999999...	M-D
57	2-Decylfuran	HMDB0032215	-	209.1896_9.7	-4.75624190000000...	2.428599999999999...	M-D
58	2-Deoxy-2-Amino Gl...	HMDB0001504	C06605	260.0533_3.1	-0.193207566	5.902499999999999...	M-D
59	2-Methoxyxanthone	HMDB0032998	-	225.055_7.9	0.29050186300000003	3.906299999999999...	M-D
60	2-oxo-3-(3,4,5-trihy...	-	-	211.0247_8.9	-0.12797825800000...	3.038522000000000...	M-D
61	2-Pyrrolidinone	HMDB0002039	C11118	86.06_1.8	-0.13496873100000...	1.376500000000000...	M-D
62	2,4-Diamino-6-[N-(2...	-	-	340.177_6.6	-0.19252112499999...	2.596532999999999...	M-D
63	2,4,6-Triethyl-1,3,5-...	-	-	207.0877_1.2	-0.13045403799999...	3.546219999999999...	M-D

Formatting ‘omics data before uploading to IPA



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

Analyte identifier REQUIRED to explore enrichment

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

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

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

Change values needed to calculate activity predictions

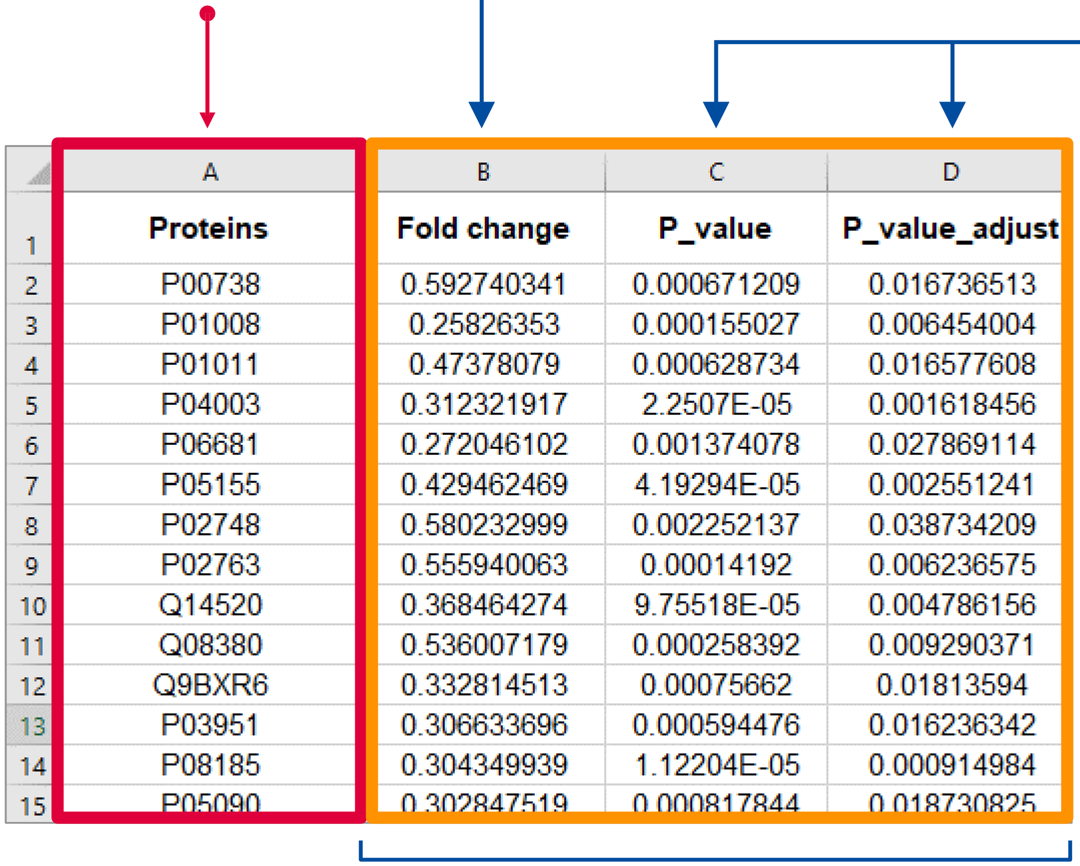
Change value examples: fold changes, ratios, etc.

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

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

Multiple comparisons or observations may be uploaded in one file

Formatting proteomics data before uploading to IPA



IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)

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

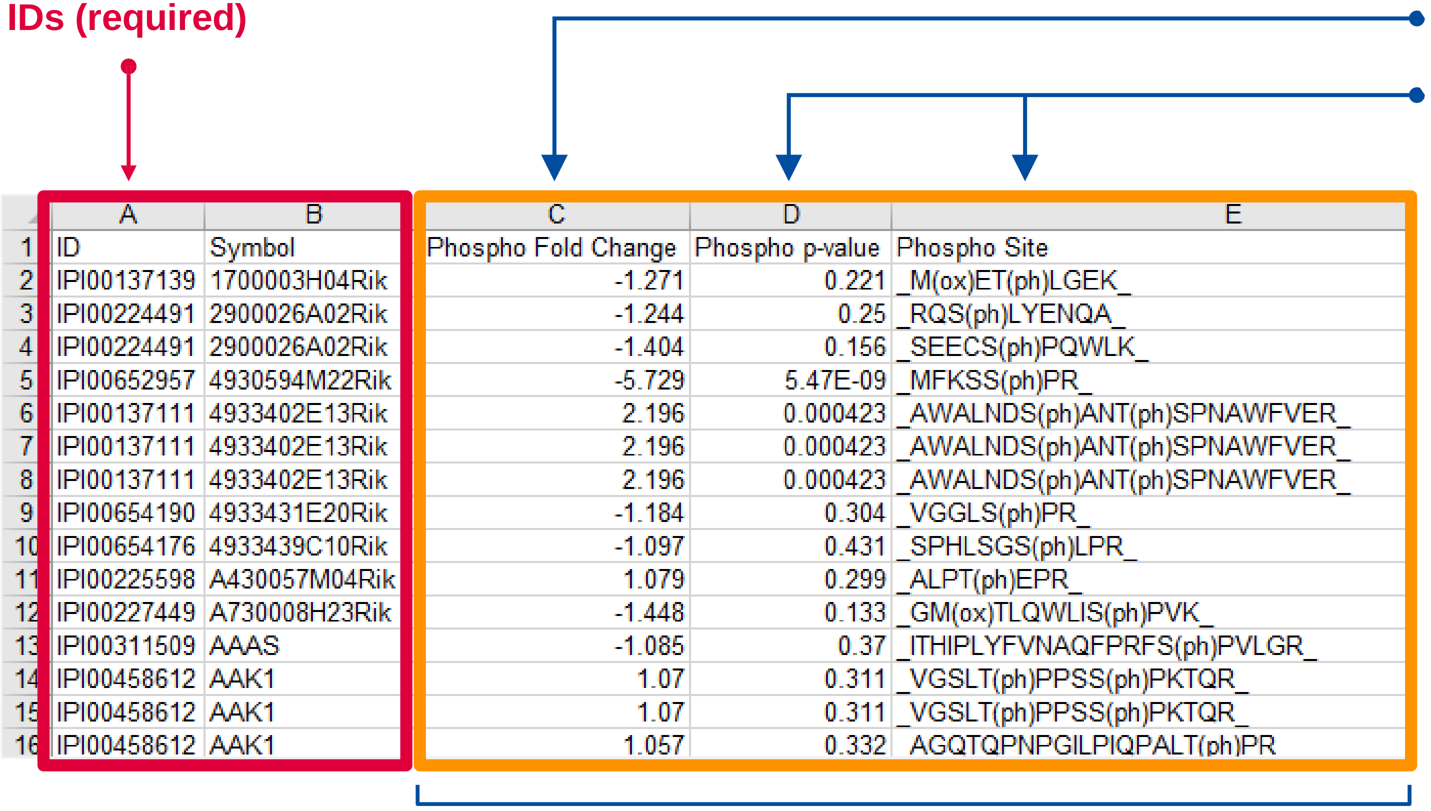
Common protein IDs

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

UniProt ID conversion tool:

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

Formatting proteomics data before uploading to IPA



IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)

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

Observation 1

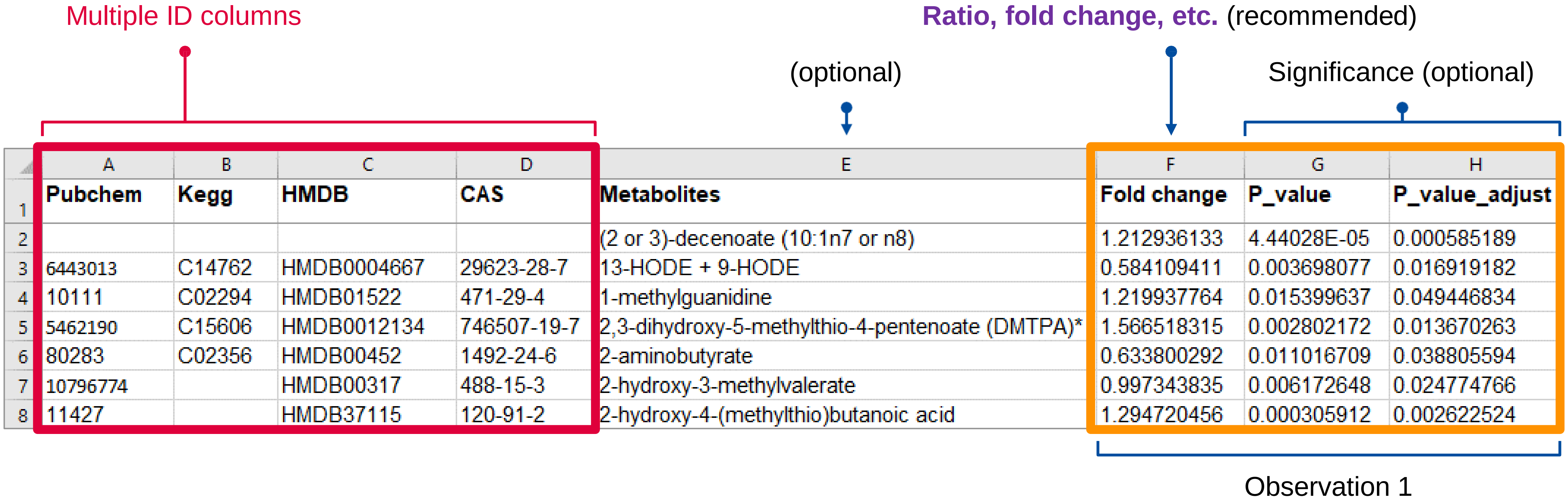
Common protein IDs

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

UniProt ID conversion tool:

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

Formatting metabolomics data before uploading to IPA



Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

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

Observation 1

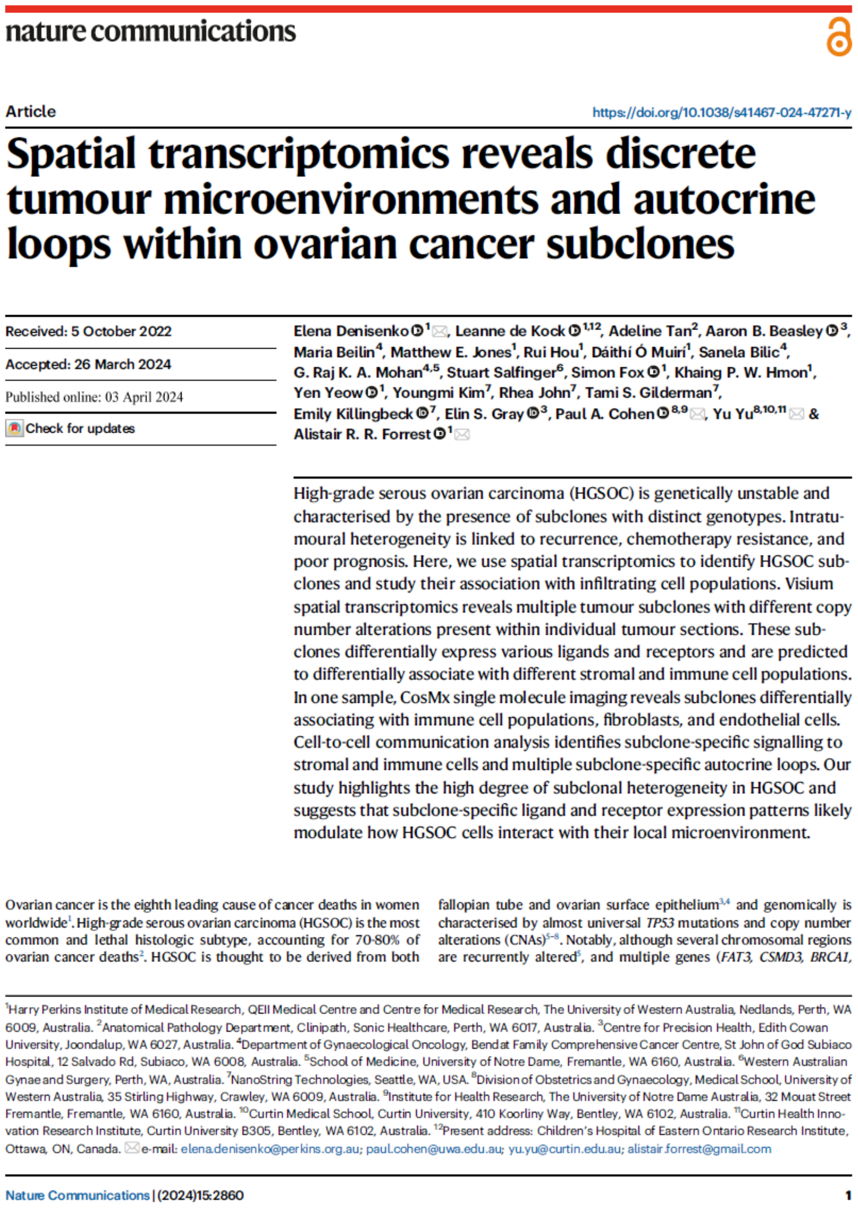
Common metabolite IDs

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

Metabolite ID conversion tools:

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

Case Study Single Cell RNA-seq



nature communications

Article

https://doi.org/10.1038/s41467-024-47271-y

Spatial transcriptomics reveals discrete tumour microenvironments and autocrine loops within ovarian cancer subclones

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High-grade serous ovarian carcinoma (HGSOC) is genetically unstable and characterised by the presence of subclones with distinct genotypes. Intratumoural heterogeneity is linked to recurrence, chemotherapy resistance, and poor prognosis. Here, we use spatial transcriptomics to identify HGSOC subclones and study their association with infiltrating cell populations. Visium spatial transcriptomics reveals multiple tumour subclones with different copy number alterations present within individual tumour sections. These subclones differentially express various ligands and receptors and are predicted to differentially associate with different stromal and immune cell populations. In one sample, CosMx single molecule imaging reveals subclones differentially associating with immune cell populations, fibroblasts, and endothelial cells. Cell-to-cell communication analysis identifies subclone-specific signalling to stromal and immune cells and multiple subclone-specific autocrine loops. Our study highlights the high degree of subclonal heterogeneity in HGSOC and suggests that subclone-specific ligand and receptor expression patterns likely modulate how HGSOC cells interact with their local microenvironment.

Ovarian cancer is the eighth leading cause of cancer deaths in women worldwide[1]. High-grade serous ovarian carcinoma (HGSOC) is the most common and lethal histologic subtype, accounting for 70-80% of ovarian cancer deaths[2]. HGSOC is thought to be derived from both fallopian tube and ovarian surface epithelium[3,4] and genomically is characterised by almost universal *TP53* mutations and copy number alterations (CNAs)[5–8]. Notably, although several chromosomal regions are recurrently altered[5], and multiple genes (*FAT3, CSMD3, BRCA1,*

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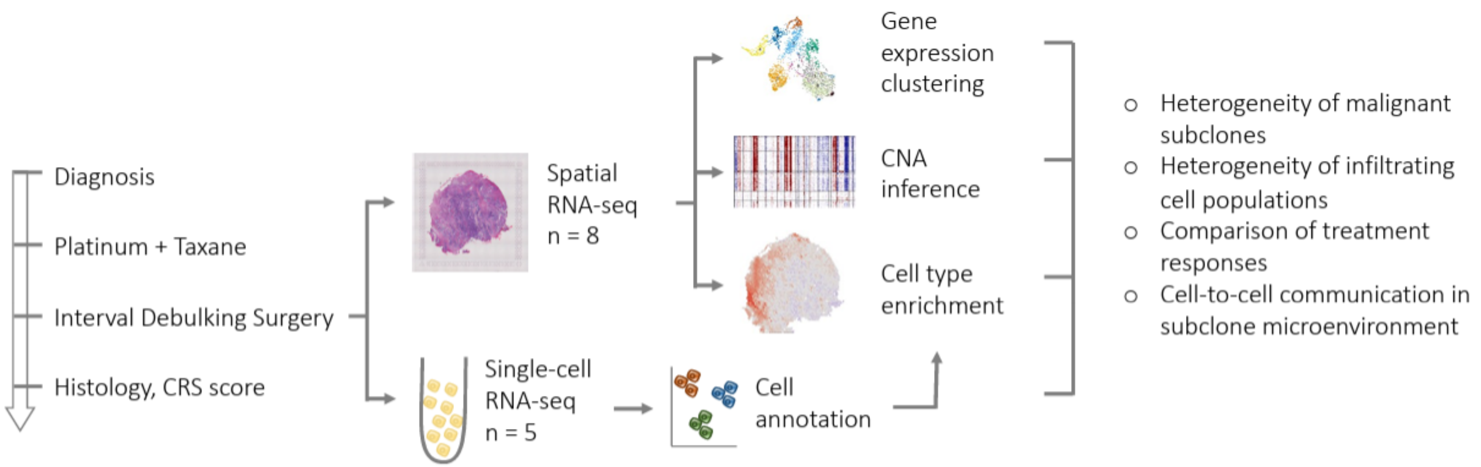
Nature Communications | (2024)15:2860 1



Diagnosis

Platinum + Taxane

Interval Debulking Surgery

Histology, CRS score

Spatial RNA-seq n = 8

Single-cell RNA-seq n = 5

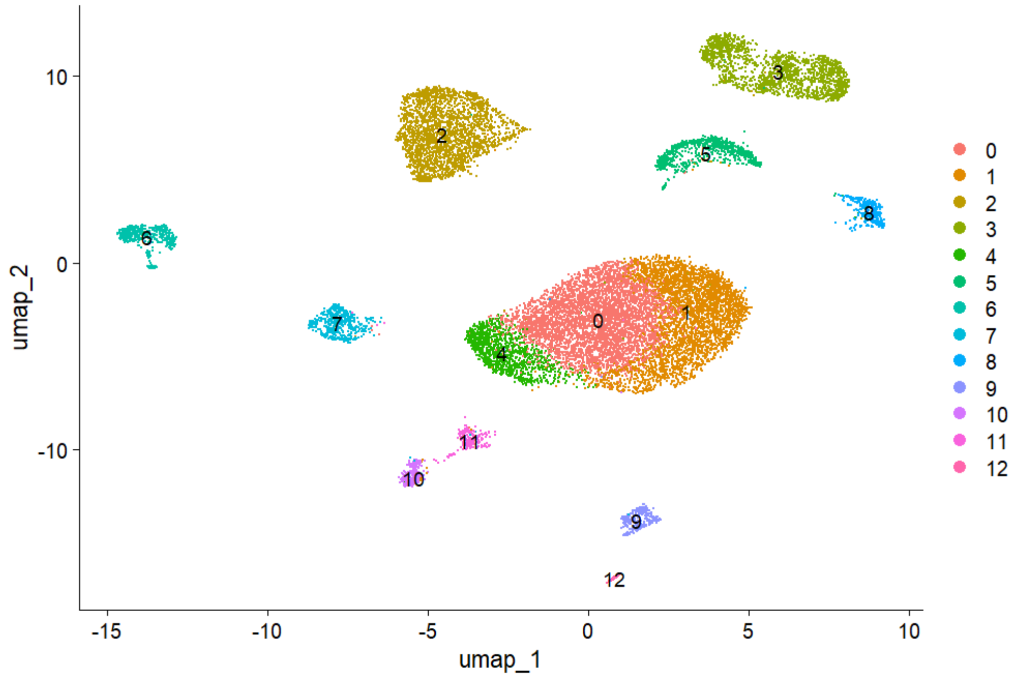
Gene expression clustering

CNA inference

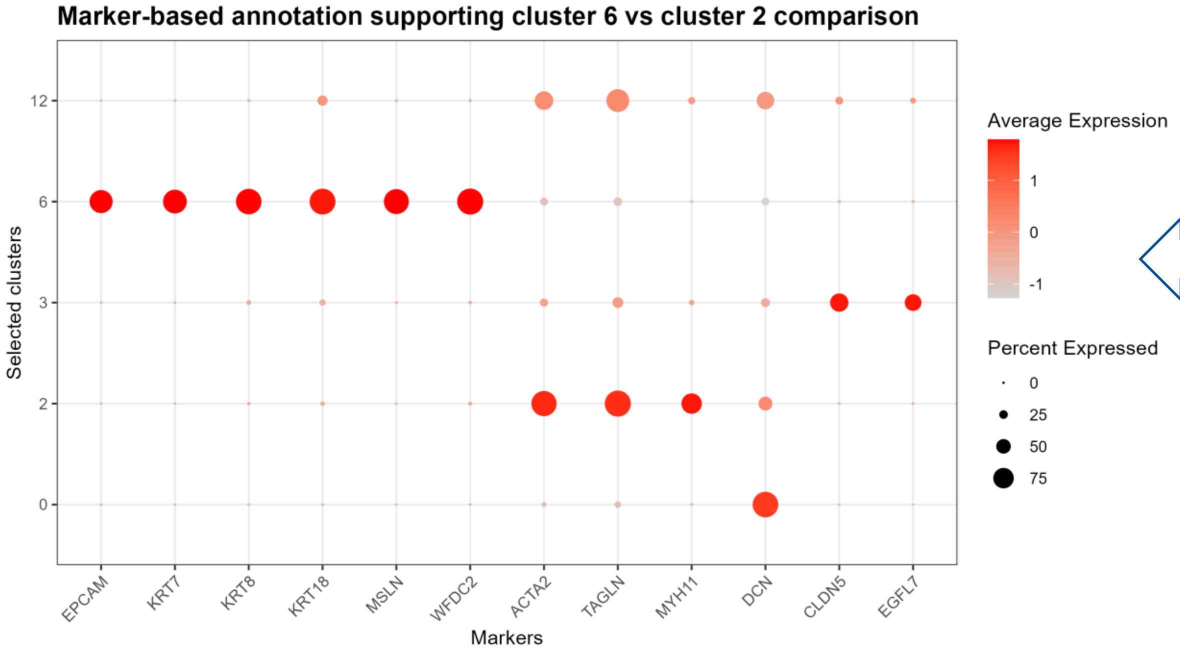
Cell type enrichment

Cell annotation

- Heterogeneity of malignant subclones
- Heterogeneity of infiltrating cell populations
- Comparison of treatment responses
- Cell-to-cell communication in subclone microenvironment

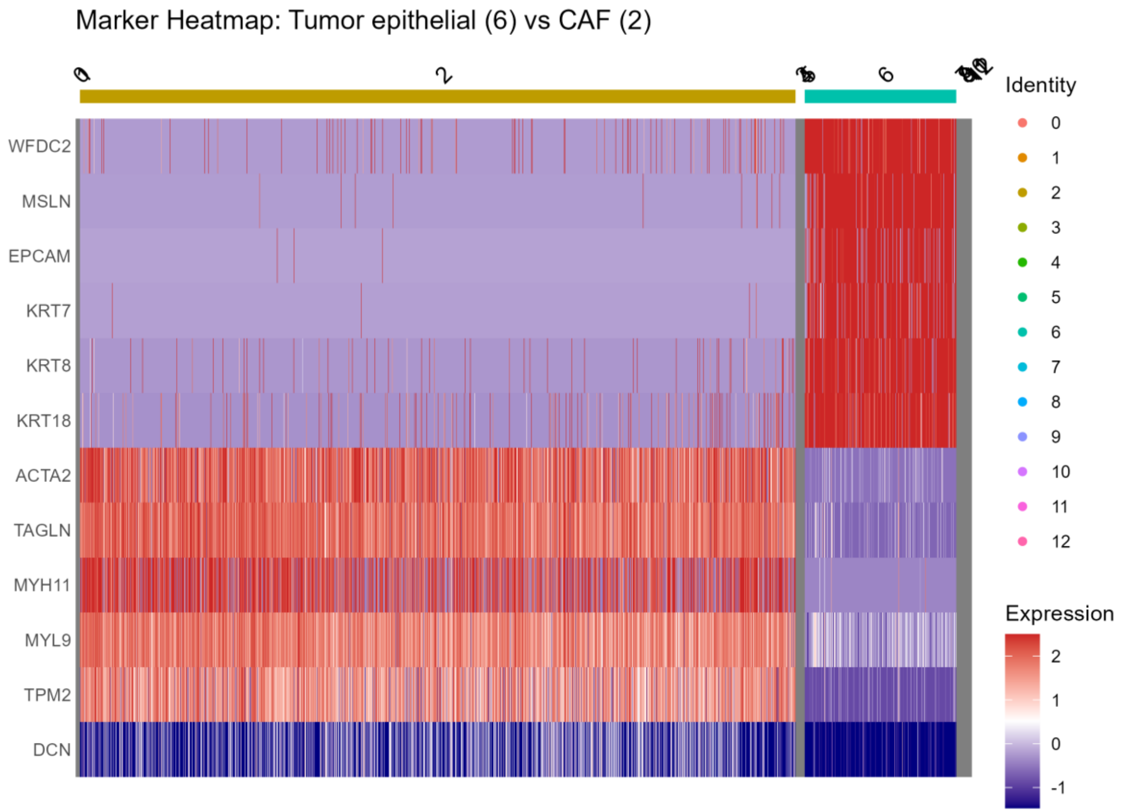


Result of scRNA-seq



Dot plot
Cluster 6 shows epithelial/tumor markers, whereas cluster 2 shows CAF/myofibroblast markers, supporting their annotation as tumor epithelial cells and CAFs.

Heatmap
The heatmap highlights distinct transcriptional programs between cluster 6 and cluster 2, supporting their use for downstream DEG analysis.



scRNA upload dataset

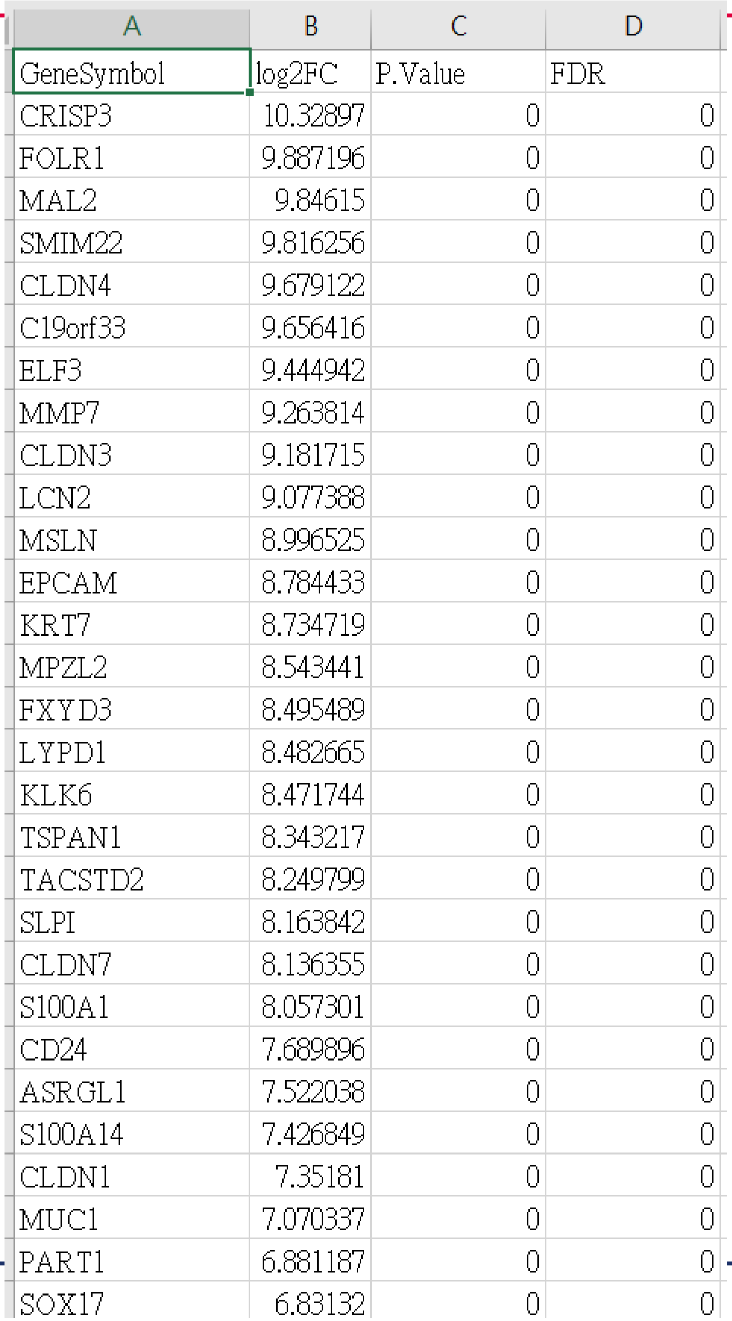
Cluster 6

tumor epithelial program

VS

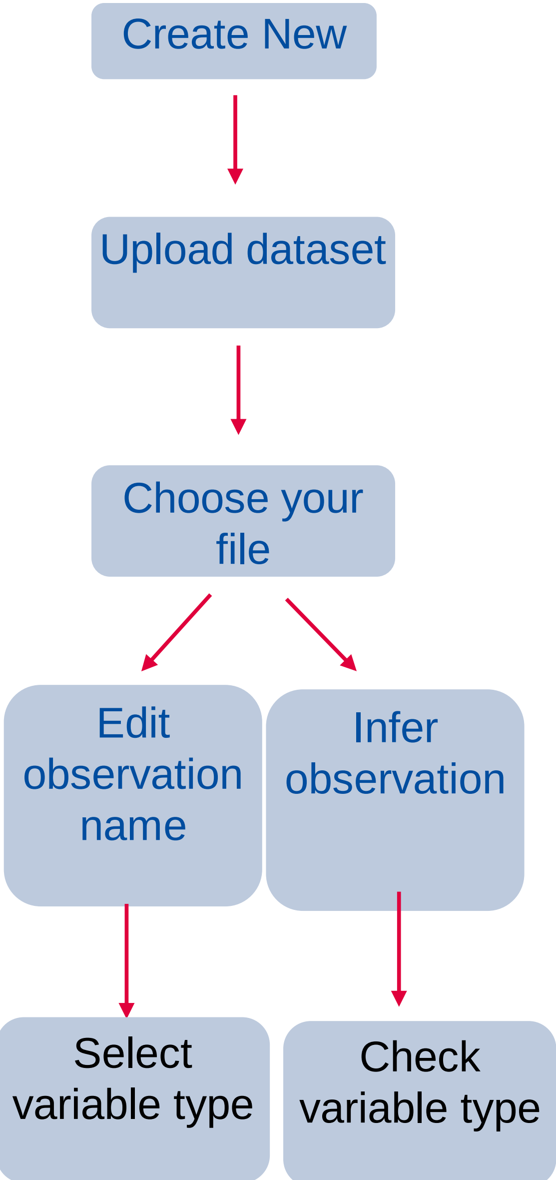
Cluster 2

stromal / CAF program



A	B	C	D
GeneSymbol	log2FC	P.Value	FDR
CRISP3	10.32897	0	0
FOLR1	9.887196	0	0
MAL2	9.84615	0	0
SMIM22	9.816256	0	0
CLDN4	9.679122	0	0
C19orf33	9.656416	0	0
ELF3	9.444942	0	0
MMP7	9.263814	0	0
CLDN3	9.181715	0	0
LCN2	9.077388	0	0
MSLN	8.996525	0	0
EPCAM	8.784433	0	0
KRT7	8.734719	0	0
MPZL2	8.543441	0	0
FXYD3	8.495489	0	0
LYPD1	8.482665	0	0
KLK6	8.471744	0	0
TSPAN1	8.343217	0	0
TACSTD2	8.249799	0	0
SLPI	8.163842	0	0
CLDN7	8.136355	0	0
S100A1	8.057301	0	0
CD24	7.689896	0	0
ASRGL1	7.522038	0	0
S100A14	7.426849	0	0
CLDN1	7.35181	0	0
MUC1	7.070337	0	0
PART1	6.881187	0	0
SOX17	6.83132	0	0

Upload dataset



Create New

Upload dataset

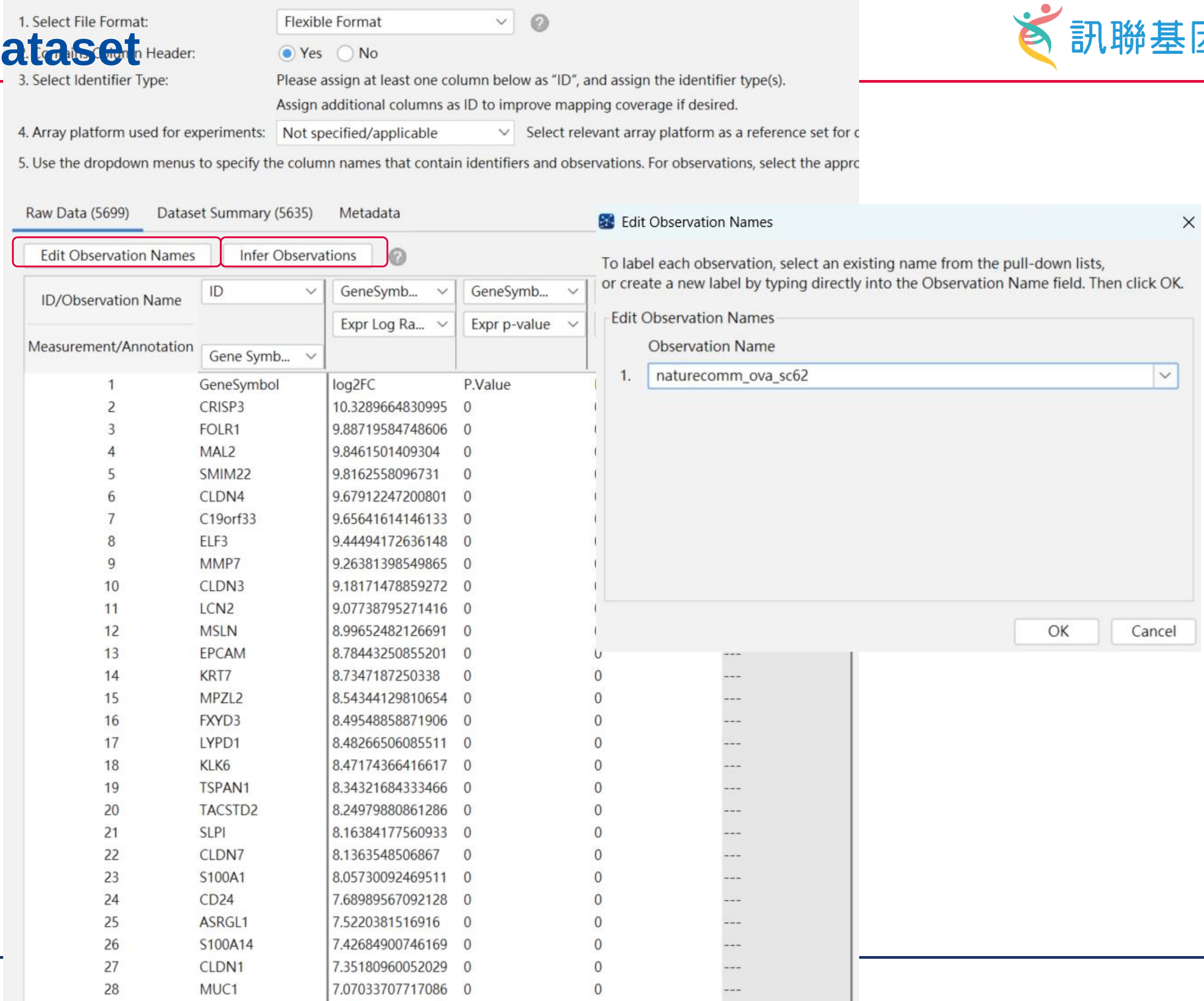
Choose your file

Edit observation name

Infer observation

Select variable type

Check variable type



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 c

5. Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appro

ID/Observation Name	ID	GeneSymb...	GeneSymb...		
Measurement/Annotation	Gene Symb...	Expr Log Ra...	Expr p-value		
1	GeneSymbol	log2FC	P.Value		
2	CRISP3	10.3289664830995	0		
3	FOLR1	9.88719584748606	0		
4	MAL2	9.8461501409304	0		
5	SMIM22	9.8162558096731	0		
6	CLDN4	9.67912247200801	0		
7	C19orf33	9.65641614146133	0		
8	ELF3	9.44494172636148	0		
9	MMP7	9.26381398549865	0		
10	CLDN3	9.18171478859272	0		
11	LCN2	9.07738795271416	0		
12	MSLN	8.99652482126691	0		
13	EPCAM	8.78443250855201	0	0	---
14	KRT7	8.7347187250338	0	0	---
15	MPZL2	8.54344129810654	0	0	---
16	FXYD3	8.49548858871906	0	0	---
17	LYPD1	8.48266506085511	0	0	---
18	KLK6	8.47174366416617	0	0	---
19	TSPAN1	8.34321684333466	0	0	---
20	TACSTD2	8.24979880861286	0	0	---
21	SLPI	8.16384177560933	0	0	---
22	CLDN7	8.1363548506867	0	0	---
23	S100A1	8.05730092469511	0	0	---
24	CD24	7.68989567092128	0	0	---
25	ASRGL1	7.5220381516916	0	0	---
26	S100A14	7.42684900746169	0	0	---
27	CLDN1	7.35180960052029	0	0	---
28	MUC1	7.07033707717086	0	0	---

Edit Observation Names

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

Edit Observation Names

Observation Name

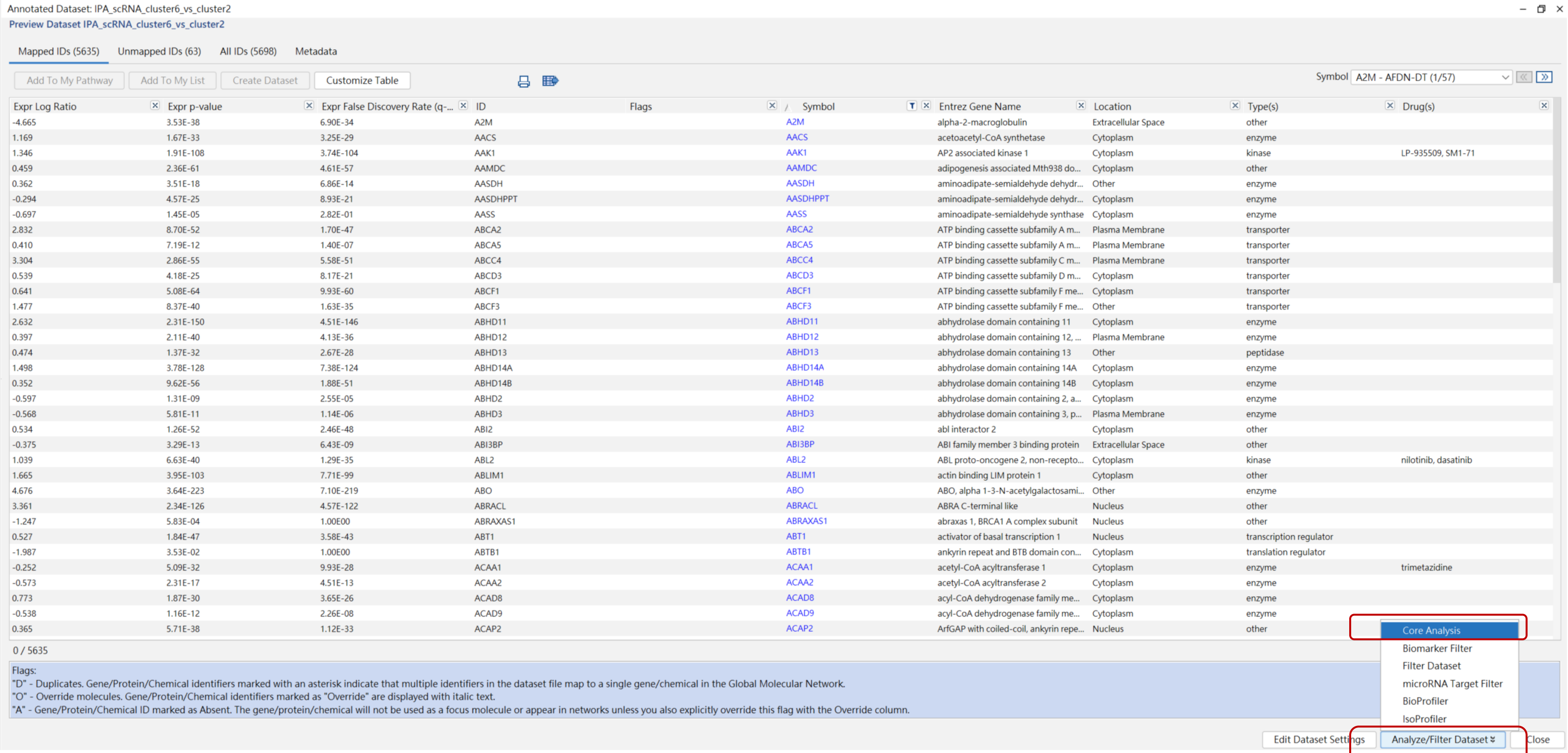
1. naturecomm_ova_sc62

Core analysis

Analyze filter dataset

Core analysis

Set cut off



Annotated Dataset: IPA_scRNA_cluster6_vs_cluster2

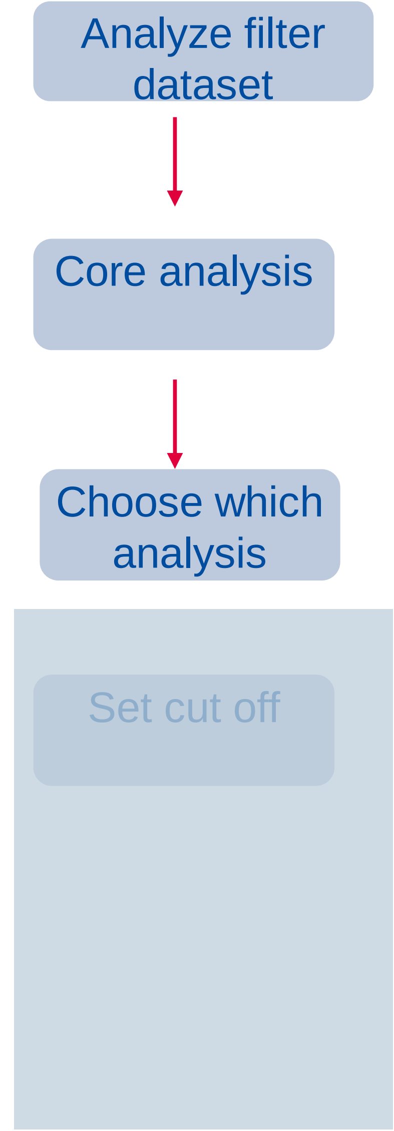
Preview Dataset IPA_scRNA_cluster6_vs_cluster2

Expr Log Ratio	Expr p-value	Expr False Discovery Rate (q-...	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-4.665	3.53E-38	6.90E-34	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	other	
1.169	1.67E-33	3.25E-29	AACS		AACS	acetoacetyl-CoA synthetase	Cytoplasm	enzyme	
1.346	1.91E-108	3.74E-104	AAK1		AAK1	AP2 associated kinase 1	Cytoplasm	kinase	LP-935509, SM1-71
0.459	2.36E-61	4.61E-57	AAMDC		AAMDC	adipogenesis associated Mth938 do...	Cytoplasm	other	
0.362	3.51E-18	6.86E-14	AASDH		AASDH	aminoadipate-semialdehyde dehydr...	Other	enzyme	
-0.294	4.57E-25	8.93E-21	AASDHPPT		AASDHPPT	aminoadipate-semialdehyde dehydr...	Cytoplasm	enzyme	
-0.697	1.45E-05	2.82E-01	AASS		AASS	aminoadipate-semialdehyde synthase	Cytoplasm	enzyme	
2.832	8.70E-52	1.70E-47	ABCA2		ABCA2	ATP binding cassette subfamily A m...	Plasma Membrane	transporter	
0.410	7.19E-12	1.40E-07	ABCA5		ABCA5	ATP binding cassette subfamily A m...	Plasma Membrane	transporter	
3.304	2.86E-55	5.58E-51	ABCC4		ABCC4	ATP binding cassette subfamily C m...	Plasma Membrane	transporter	
0.539	4.18E-25	8.17E-21	ABCD3		ABCD3	ATP binding cassette subfamily D m...	Cytoplasm	transporter	
0.641	5.08E-64	9.93E-60	ABCF1		ABCF1	ATP binding cassette subfamily F me...	Cytoplasm	transporter	
1.477	8.37E-40	1.63E-35	ABCF3		ABCF3	ATP binding cassette subfamily F me...	Other	transporter	
2.632	2.31E-150	4.51E-146	ABHD11		ABHD11	abhydrolase domain containing 11	Cytoplasm	enzyme	
0.397	2.11E-40	4.13E-36	ABHD12		ABHD12	abhydrolase domain containing 12, ...	Plasma Membrane	enzyme	
0.474	1.37E-32	2.67E-28	ABHD13		ABHD13	abhydrolase domain containing 13	Other	peptidase	
1.498	3.78E-128	7.38E-124	ABHD14A		ABHD14A	abhydrolase domain containing 14A	Cytoplasm	enzyme	
0.352	9.62E-56	1.88E-51	ABHD14B		ABHD14B	abhydrolase domain containing 14B	Cytoplasm	enzyme	
-0.597	1.31E-09	2.55E-05	ABHD2		ABHD2	abhydrolase domain containing 2, a...	Cytoplasm	enzyme	
-0.568	5.81E-11	1.14E-06	ABHD3		ABHD3	abhydrolase domain containing 3, p...	Plasma Membrane	enzyme	
0.534	1.26E-52	2.46E-48	ABI2		ABI2	abl interactor 2	Cytoplasm	other	
-0.375	3.29E-13	6.43E-09	ABI3BP		ABI3BP	ABI family member 3 binding protein	Extracellular Space	other	
1.039	6.63E-40	1.29E-35	ABL2		ABL2	ABL proto-oncogene 2, non-recepto...	Cytoplasm	kinase	nilotinib, dasatinib
1.665	3.95E-103	7.71E-99	ABLIM1		ABLIM1	actin binding LIM protein 1	Cytoplasm	other	
4.676	3.64E-223	7.10E-219	ABO		ABO	ABO, alpha 1-3-N-acetylgalactosami...	Other	enzyme	
3.361	2.34E-126	4.57E-122	ABRACL		ABRACL	ABRA C-terminal like	Nucleus	other	
-1.247	5.83E-04	1.00E00	ABRAXAS1		ABRAXAS1	abraxas 1, BRCA1 A complex subunit	Nucleus	other	
0.527	1.84E-47	3.58E-43	ABT1		ABT1	activator of basal transcription 1	Nucleus	transcription regulator	
-1.987	3.53E-02	1.00E00	ABTB1		ABTB1	ankyrin repeat and BTB domain con...	Cytoplasm	translation regulator	
-0.252	5.09E-32	9.93E-28	ACAA1		ACAA1	acetyl-CoA acyltransferase 1	Cytoplasm	enzyme	trimetazidine
-0.573	2.31E-17	4.51E-13	ACAA2		ACAA2	acetyl-CoA acyltransferase 2	Cytoplasm	enzyme	
0.773	1.87E-30	3.65E-26	ACAD8		ACAD8	acyl-CoA dehydrogenase family me...	Cytoplasm	enzyme	
-0.538	1.16E-12	2.26E-08	ACAD9		ACAD9	acyl-CoA dehydrogenase family me...	Cytoplasm	enzyme	
0.365	5.71E-38	1.12E-33	ACAP2		ACAP2	ArfGAP with coiled-coil, ankyrin repe...	Nucleus	other	

0 / 5635

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

Choose which analysis do you want

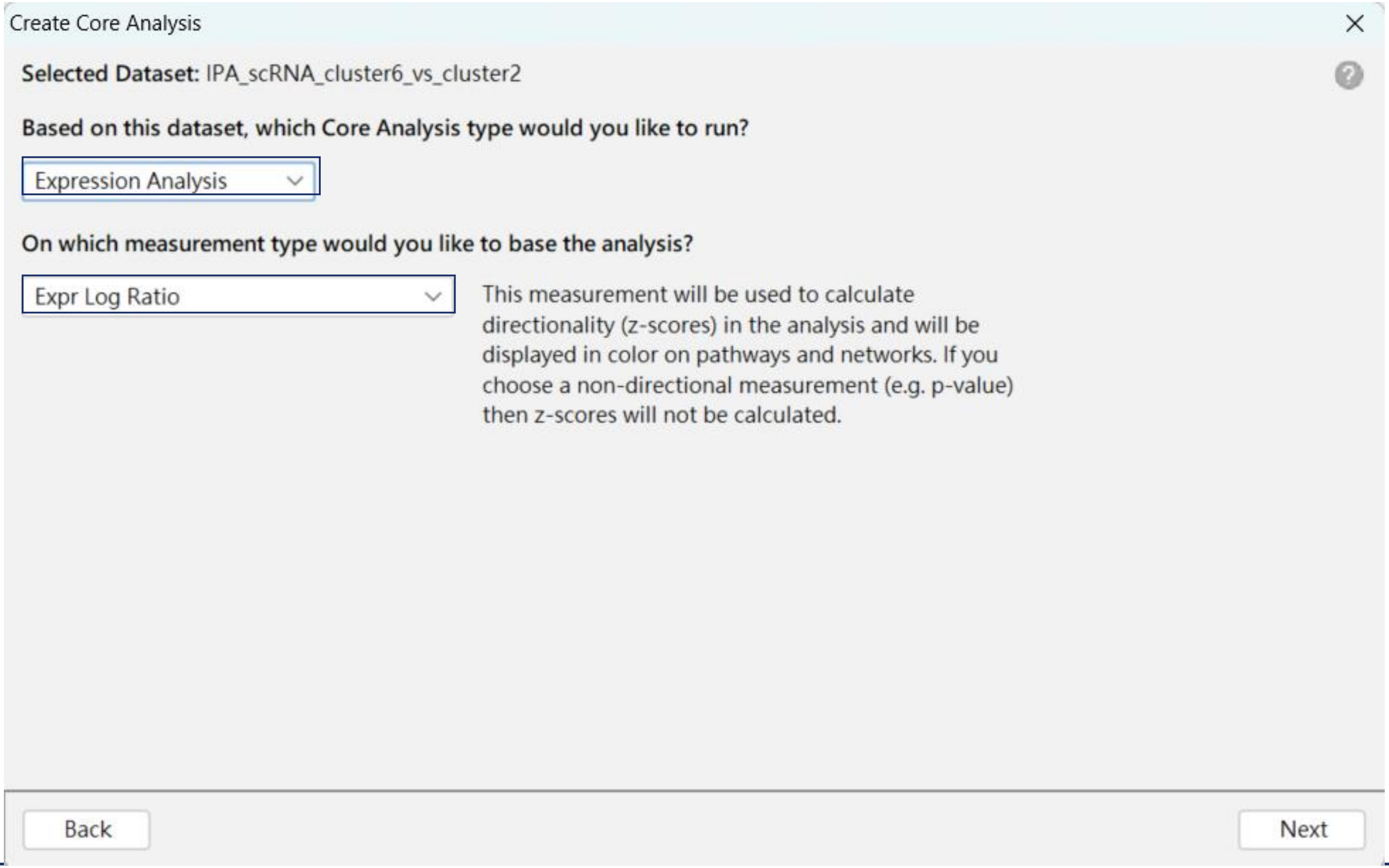


Analyze filter dataset

Core analysis

Choose which analysis

Set cut off



Selected Dataset: IPA_scRNA_cluster6_vs_cluster2

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

Expression Analysis

On which measurement type would you like to base the analysis?

Expr Log Ratio

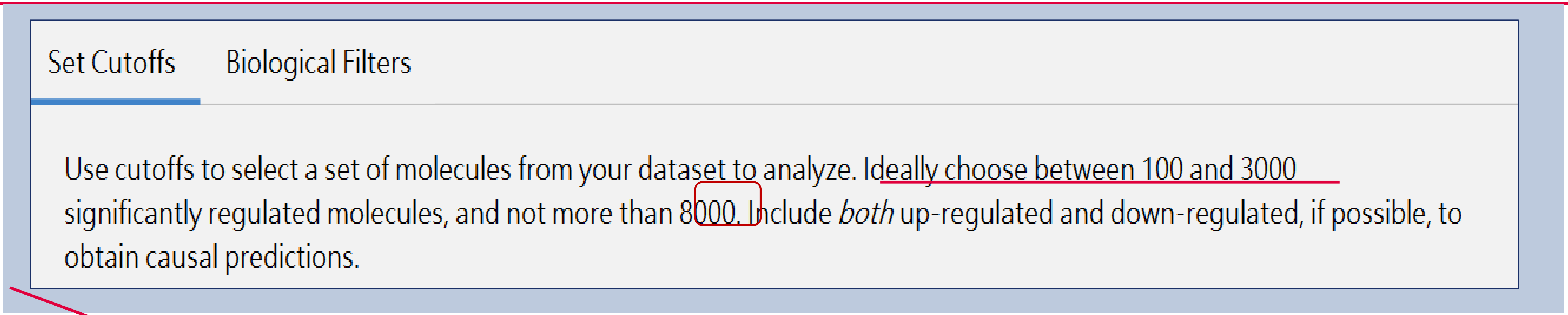
This measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

Set Cutoff

Analyze filter dataset

Core analysis

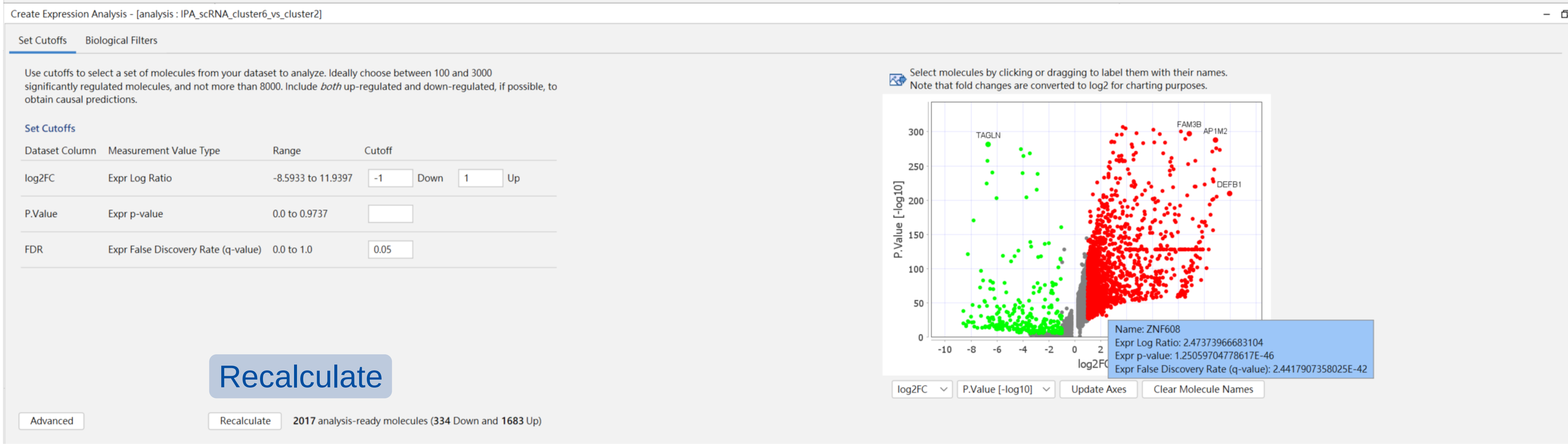
Set cut off



Set Cutoffs Biological Filters

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

Volcano plot



Create Expression Analysis - [analysis : IPA_scRNA_cluster6_vs_cluster2]

Set Cutoffs Biological Filters

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

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff			
log2FC	Expr Log Ratio	-8.5933 to 11.9397	-1	Down	1	Up
P.Value	Expr p-value	0.0 to 0.9737				
FDR	Expr False Discovery Rate (q-value)	0.0 to 1.0	0.05			

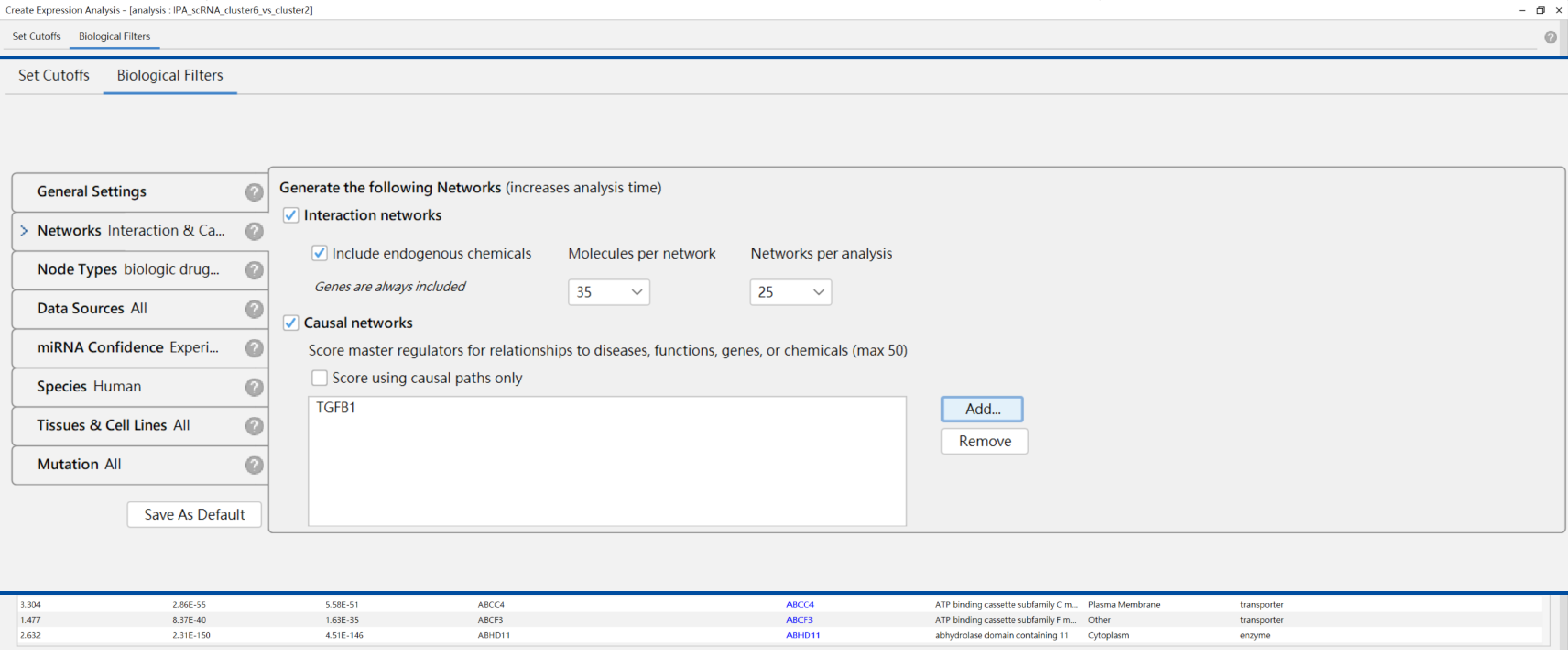
Recalculate

Advanced Recalculate **2017** analysis-ready molecules (**334** Down and **1683** Up)

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

Name: ZNF608
Expr Log Ratio: 2.47373966683104
Expr p-value: 1.25059704778617E-46
Expr False Discovery Rate (q-value): 2.4417907358025E-42

Biological Filter in RNA-seq and Protein -omics



Create Expression Analysis - [analysis : IPA_scRNA_cluster6_vs_cluster2]

General Settings

Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species Human

Tissues & Cell Lines All

Mutation All

Generate the following Networks (increases analysis time)

☑ **Interaction networks**

☑ Include endogenous chemicals

Genes are always included

Molecules per network: 35

Networks per analysis: 25

☑ **Causal networks**

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

☐ Score using causal paths only

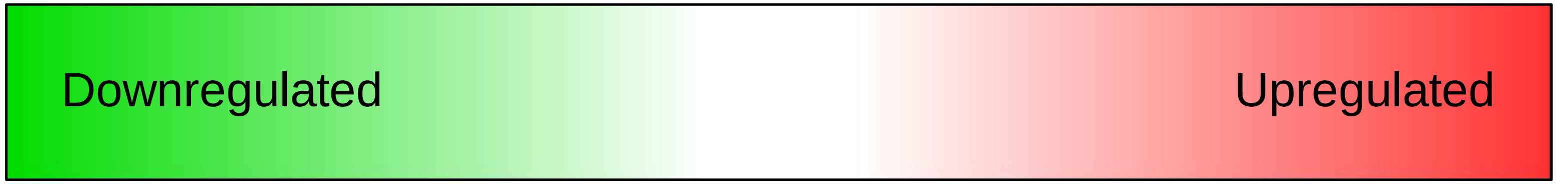
TGFB1

3.304	2.86E-55	5.58E-51	ABCC4	ABCC4	ATP binding cassette subfamily C m...	Plasma Membrane	transporter
1.477	8.37E-40	1.63E-35	ABCF3	ABCF3	ATP binding cassette subfamily F m...	Other	transporter
2.632	2.31E-150	4.51E-146	ABHD11	ABHD11	abhydrolase domain containing 11	Cytoplasm	enzyme

What do colors mean in IPA?

Pathway or gene activity predicted by IPA

Actual measurement of gene expression in your dataset

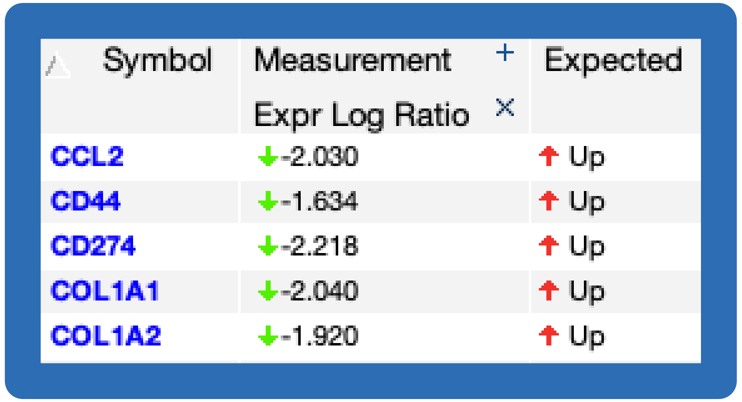


What do z-scores mean in IPA?

Actual dataset measurement

VS.

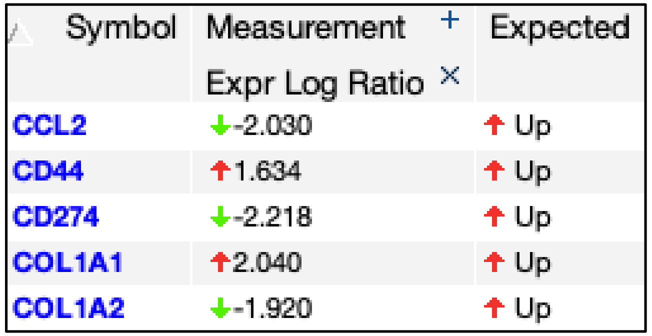
What IPA expects if pathway is activated



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

Pathway inhibited

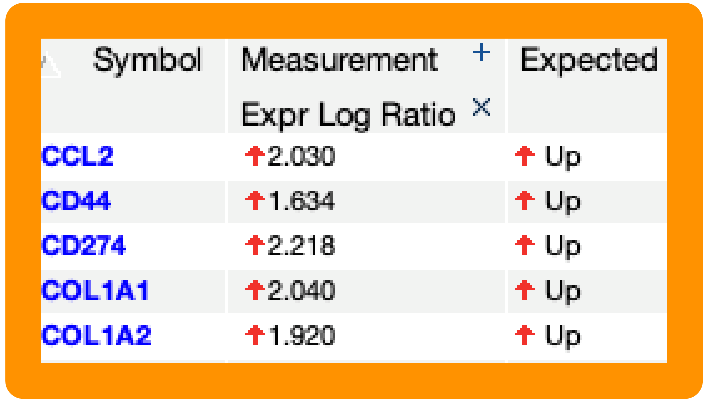
- Z score



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

No clear signal for prediction

Z score = 0



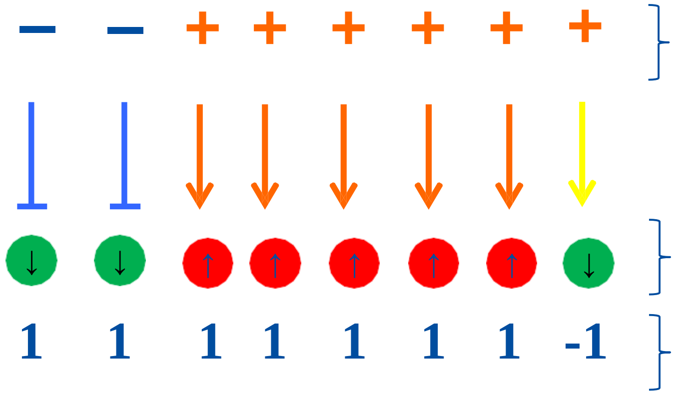
Symbol	Measurement Expr Log Ratio	Expected
CCL2	↑2.030	↑ Up
CD44	↑1.634	↑ Up
CD274	↑2.218	↑ Up
COL1A1	↑2.040	↑ Up
COL1A2	↑1.920	↑ Up

Pathway activated

+ Z score

How well do the actual measurements match the expected measurements?

z-score: Activation prediction



Gene expression from QIAGEN Knowledge Base (literature)

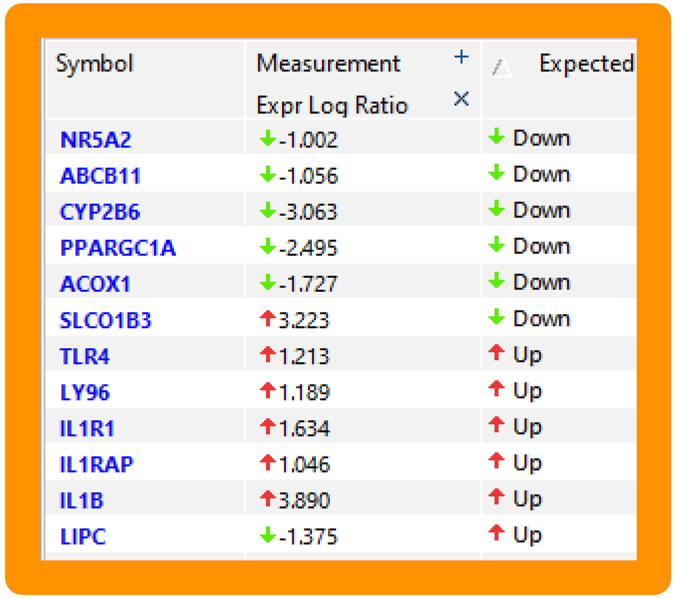
Gene expression in your dataset

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

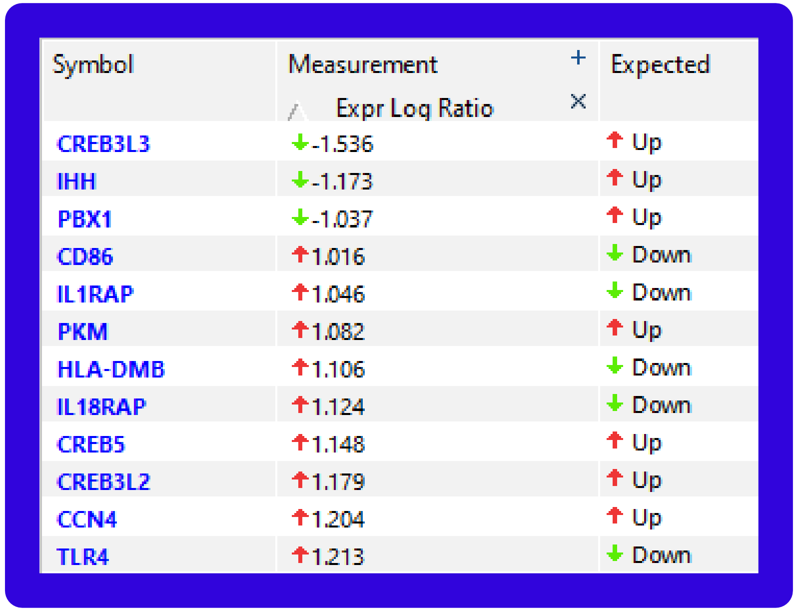
$$z = \frac{x}{\sigma_x} = \frac{\sum_i x_i}{\sqrt{N}} = \frac{N_+ - N_-}{\sqrt{N}} = (7\text{-}1)/\sqrt{8} = 2.12 \text{ (= predicted activation)}$$

- 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

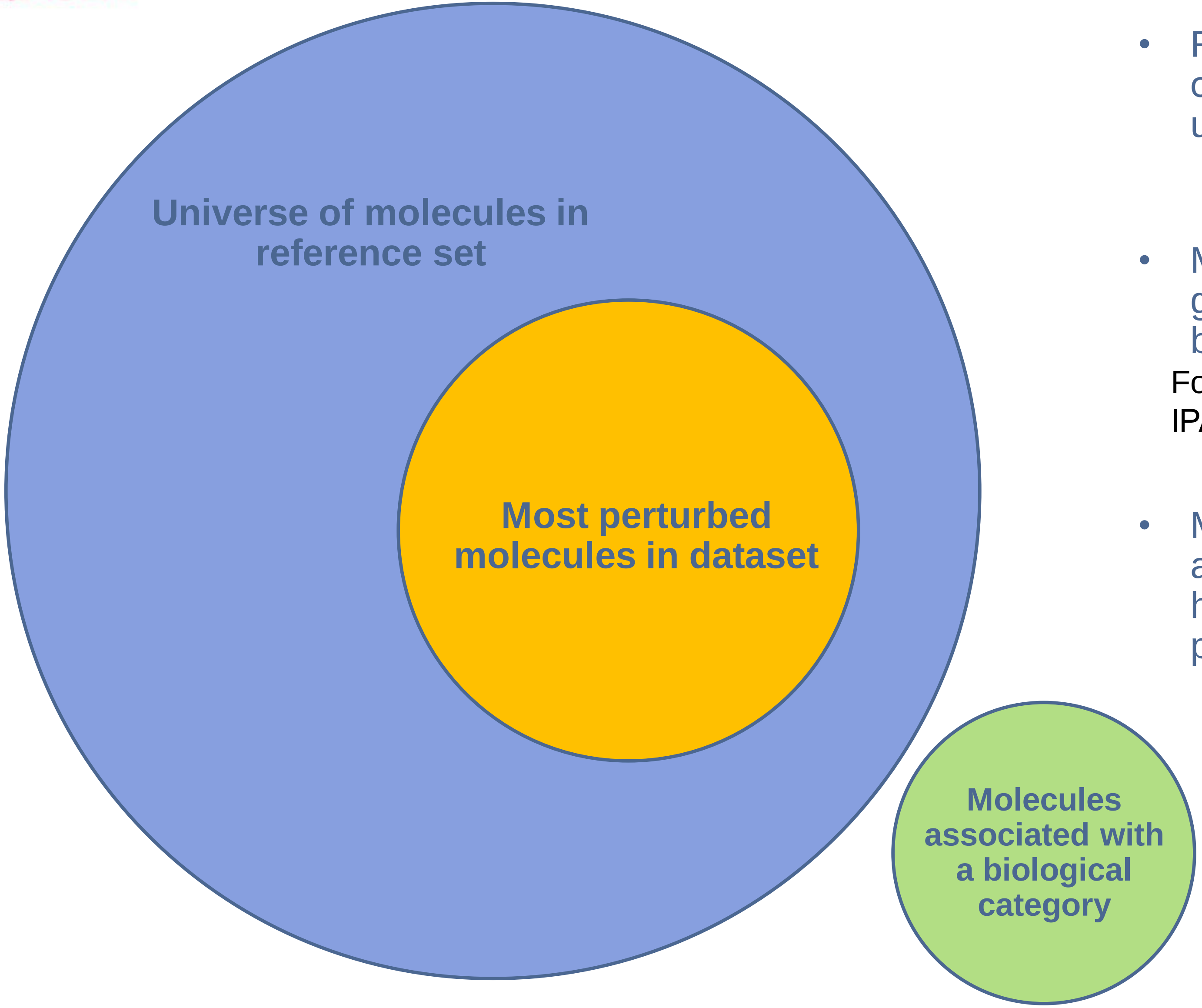
4/12 measurements match expected

Mostly anti-matching

Signal predominantly points to predicted inhibition

IPA Analysis Tabs

Pathway enrichment: P-value of overlap



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

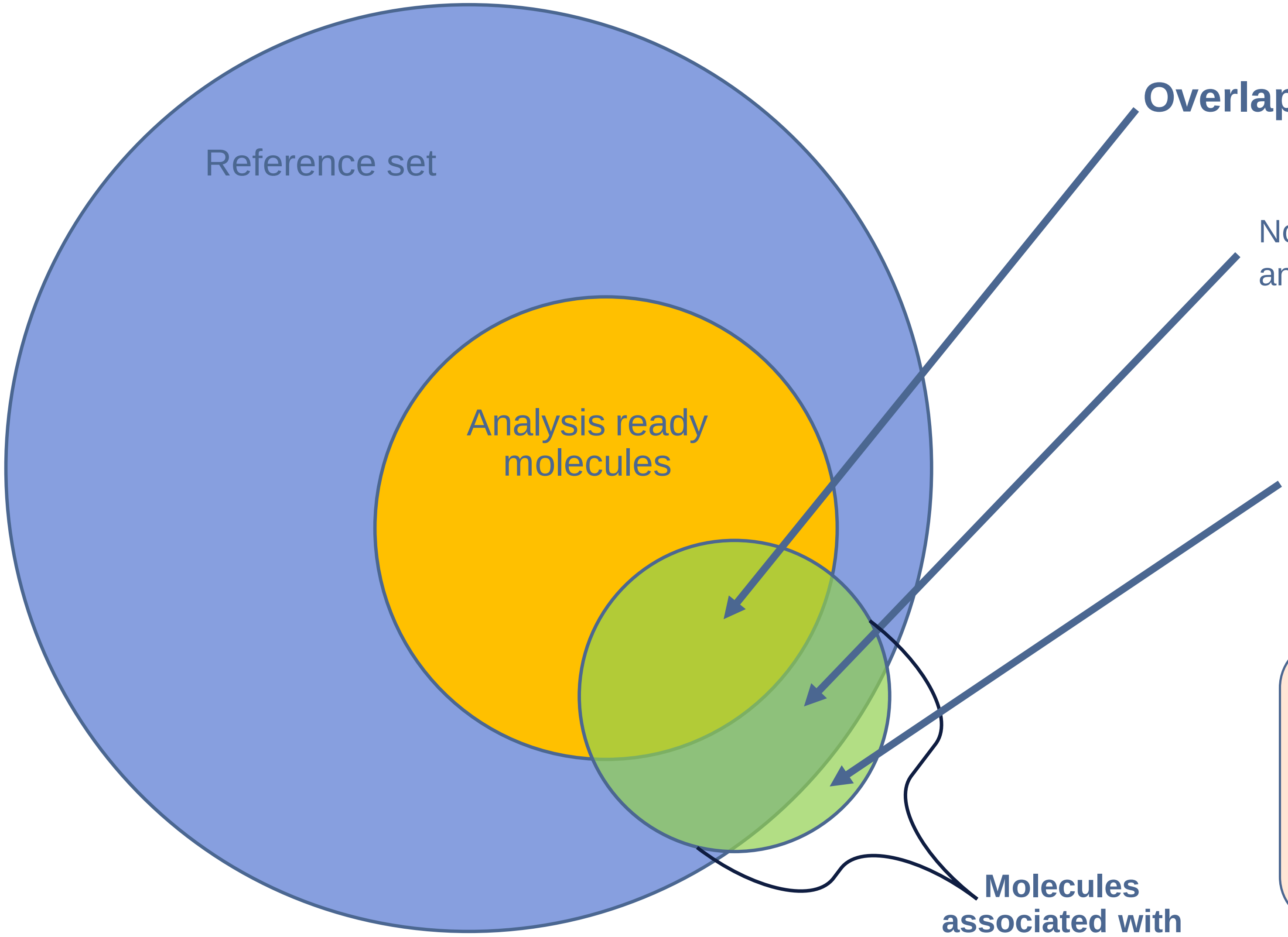
- Most perturbed is a subset of measured genes/proteins that were significantly different between experimental groups

  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

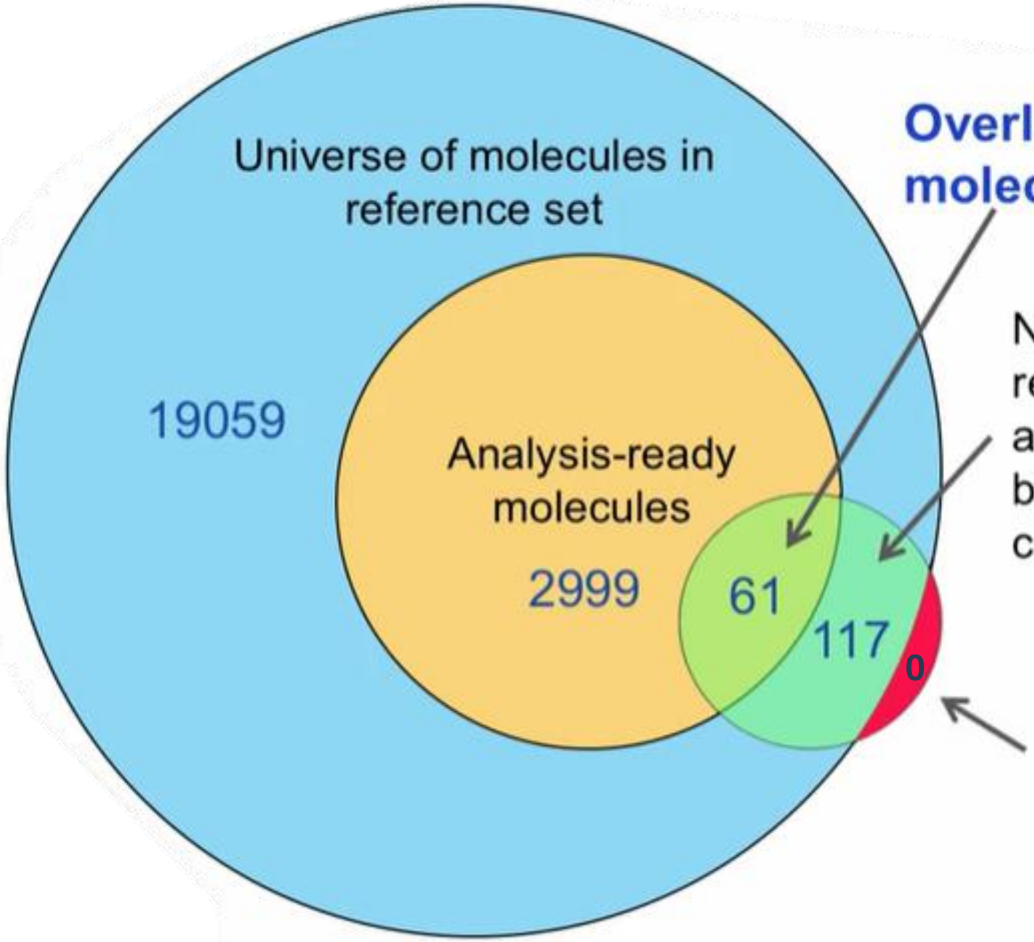
Genes not detected by the technology used and are annotated to a biological category

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

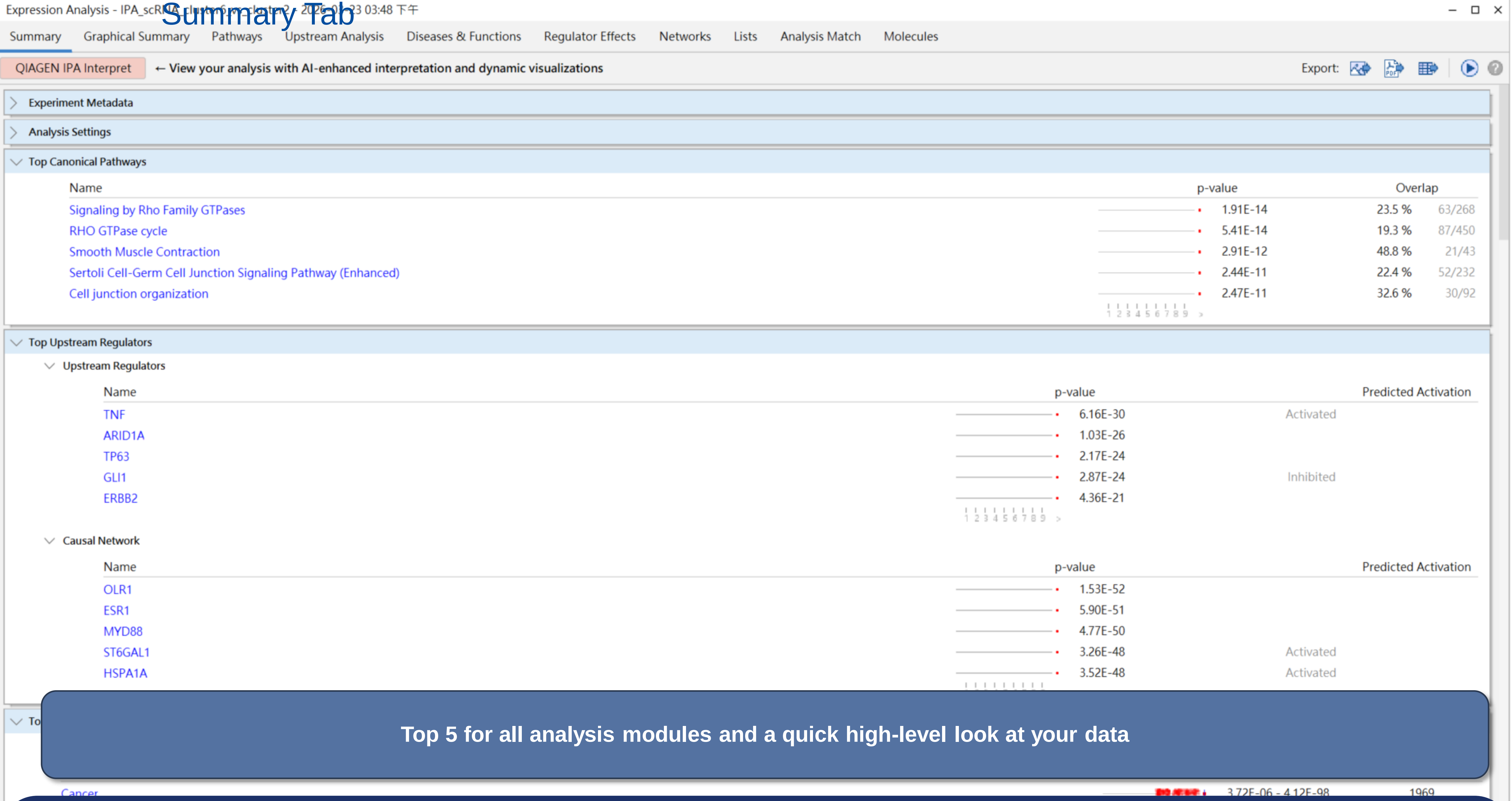
		Category 1		
		Group 1	Group 2	Total
Category 2	Group 1	a	b	a+b
	Group 2	c	d	c+d
	Total	a+c	b+d	a+b+c+d = n

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

P-value = 2.08×10^{-12}

We can reject the null hypothesis

Summary Tab



Expression Analysis - IPA_scRNA_cluster6 vs cluster2 - 2026-0[illegible]-23 03:48 下午

← View your analysis with AI-enhanced interpretation and dynamic visualizations

Top Canonical Pathways

Name	p-value	Overlap	
Signaling by Rho Family GTPases	1.91E-14	23.5 %	63/268
RHO GTPase cycle	5.41E-14	19.3 %	87/450
Smooth Muscle Contraction	2.91E-12	48.8 %	21/43
Sertoli Cell-Germ Cell Junction Signaling Pathway (Enhanced)	2.44E-11	22.4 %	52/232
Cell junction organization	2.47E-11	32.6 %	30/92

Top Upstream Regulators

Upstream Regulators

Name	p-value	Predicted Activation
TNF	6.16E-30	Activated
ARID1A	1.03E-26	
TP63	2.17E-24	
GLI1	2.87E-24	Inhibited
ERBB2	4.36E-21	

Causal Network

Name	p-value	Predicted Activation
OLR1	1.53E-52	
ESR1	5.90E-51	
MYD88	4.77E-50	
ST6GAL1	3.26E-48	Activated
HSPA1A	3.52E-48	Activated

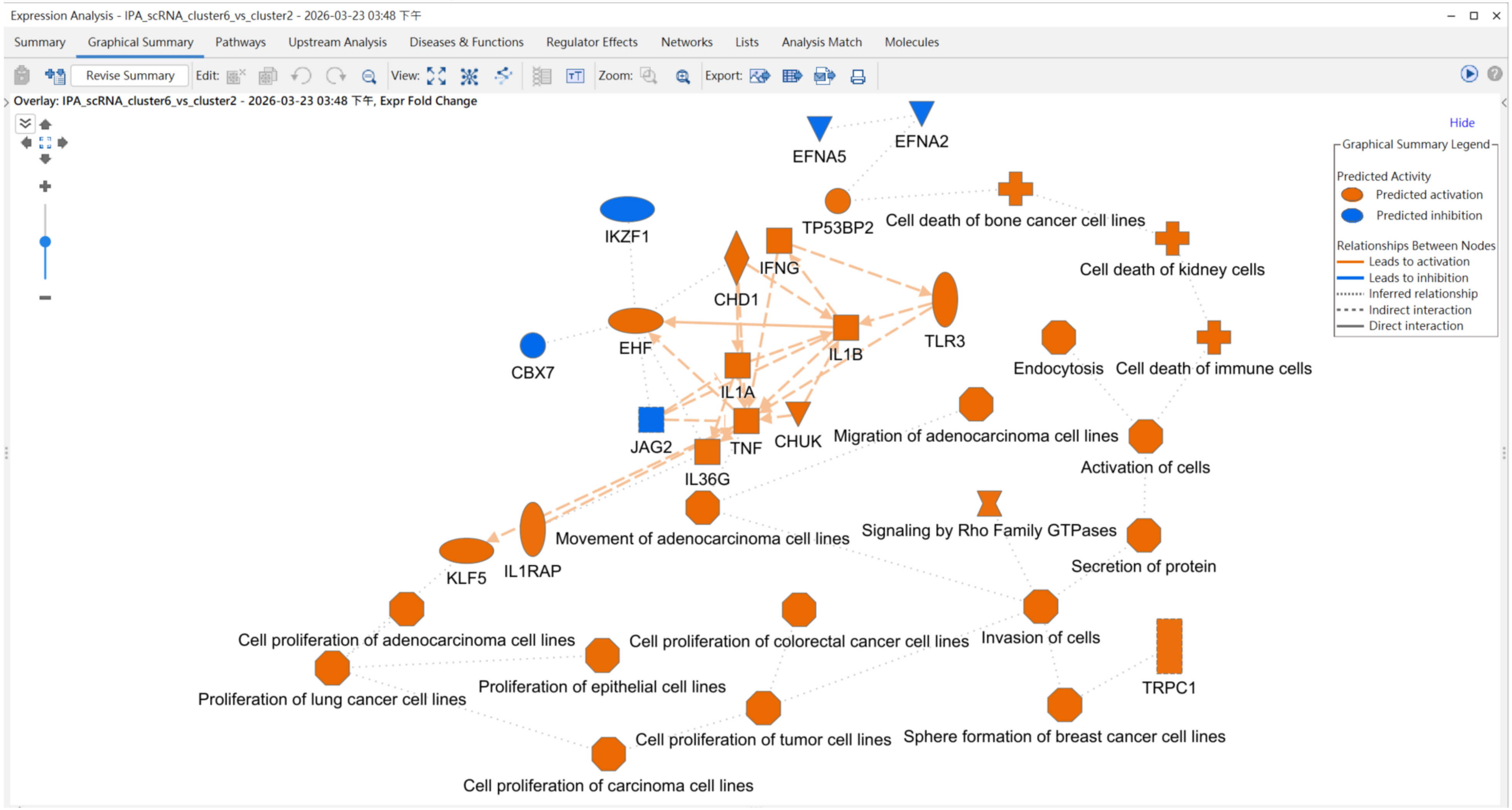
To

Cancer 3.72E-06 - 4.12E-98 1969

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

Graphical Summary Tab

Cluster 6 vs Cluster2

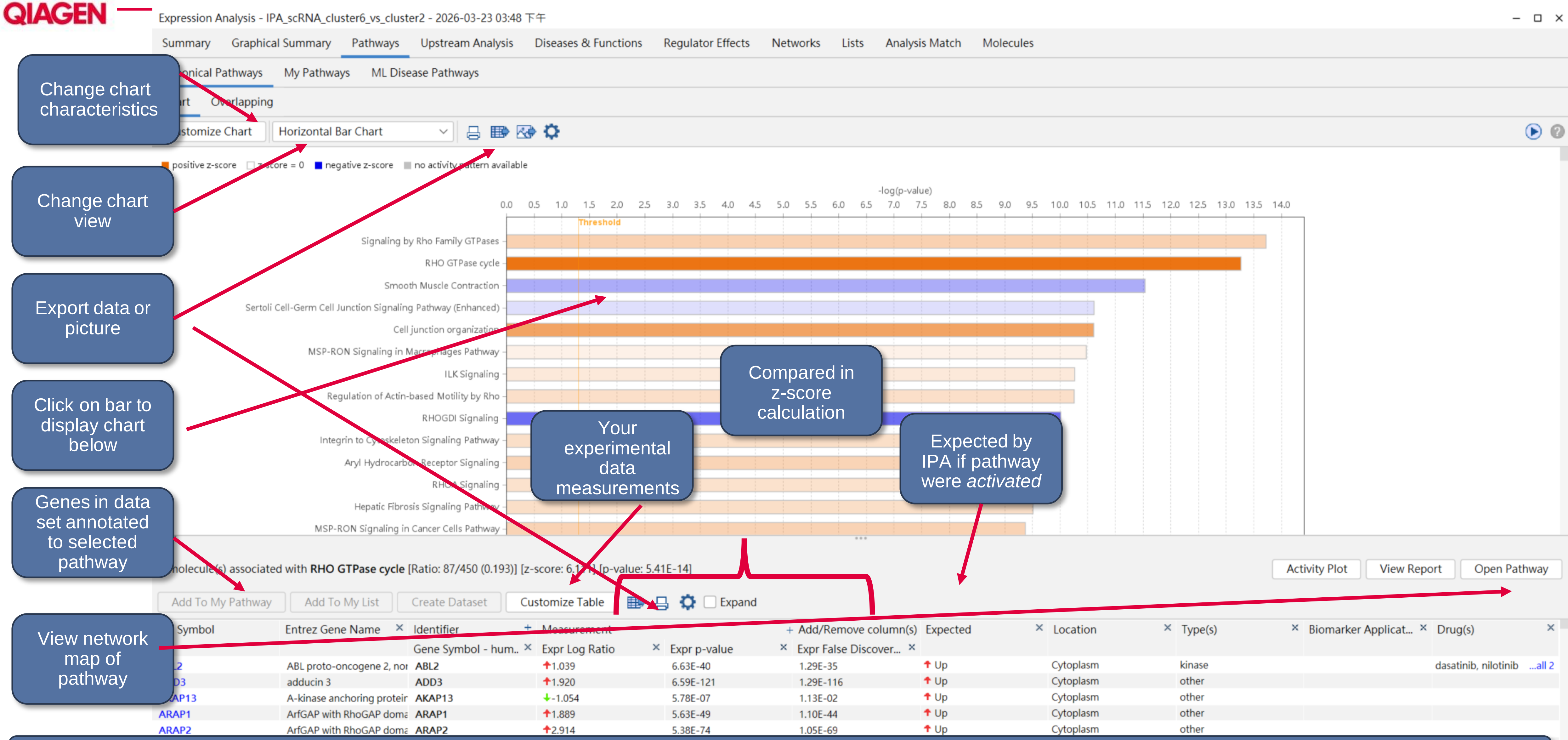


Expression Analysis - IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午

Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Fold Change

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

Pathways Tab



Change chart characteristics

Change chart view

Export data or picture

Click on bar to display chart below

Genes in data set annotated to selected pathway

View network map of pathway

Your experimental data measurements

Compared in z-score calculation

Expected by IPA if pathway were *activated*

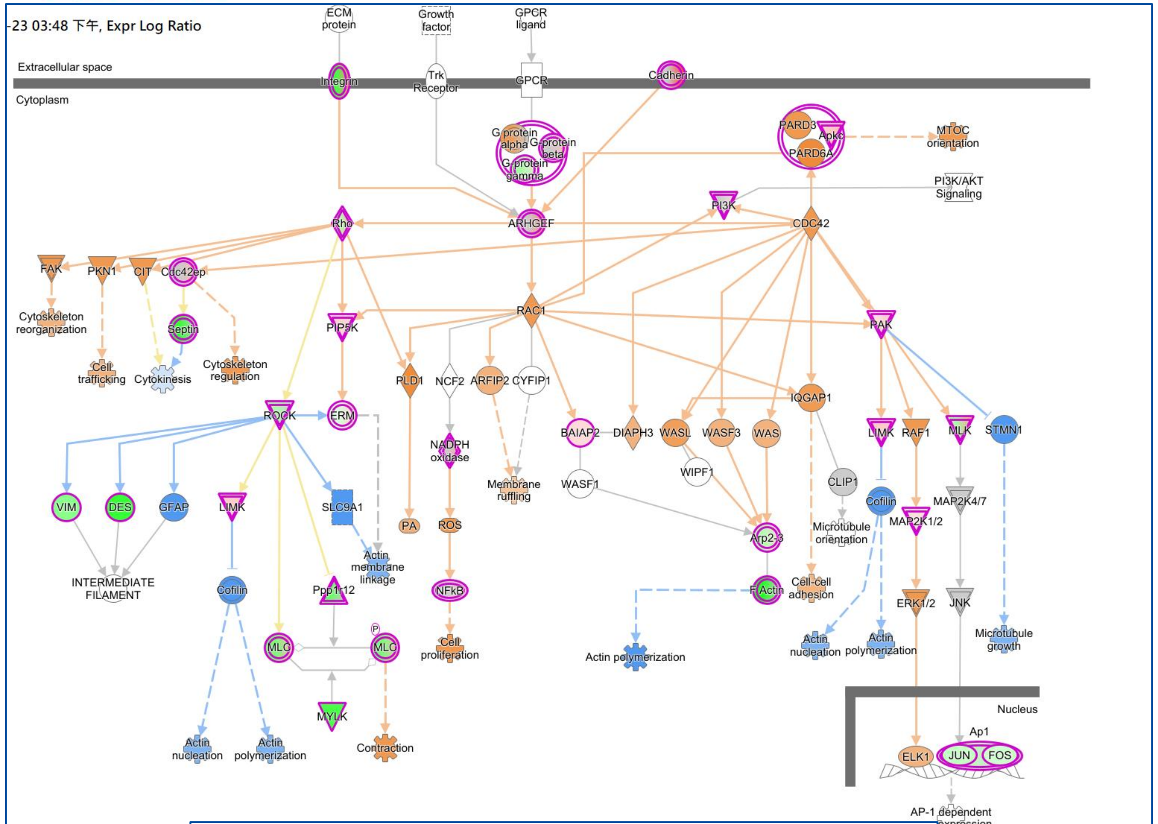
Expression Analysis - IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午

olecule(s) associated with **RHO GTPase cycle** [Ratio: 87/450 (0.193)] [z-score: 6.1[illegible]] [p-value: 5.41E-14]

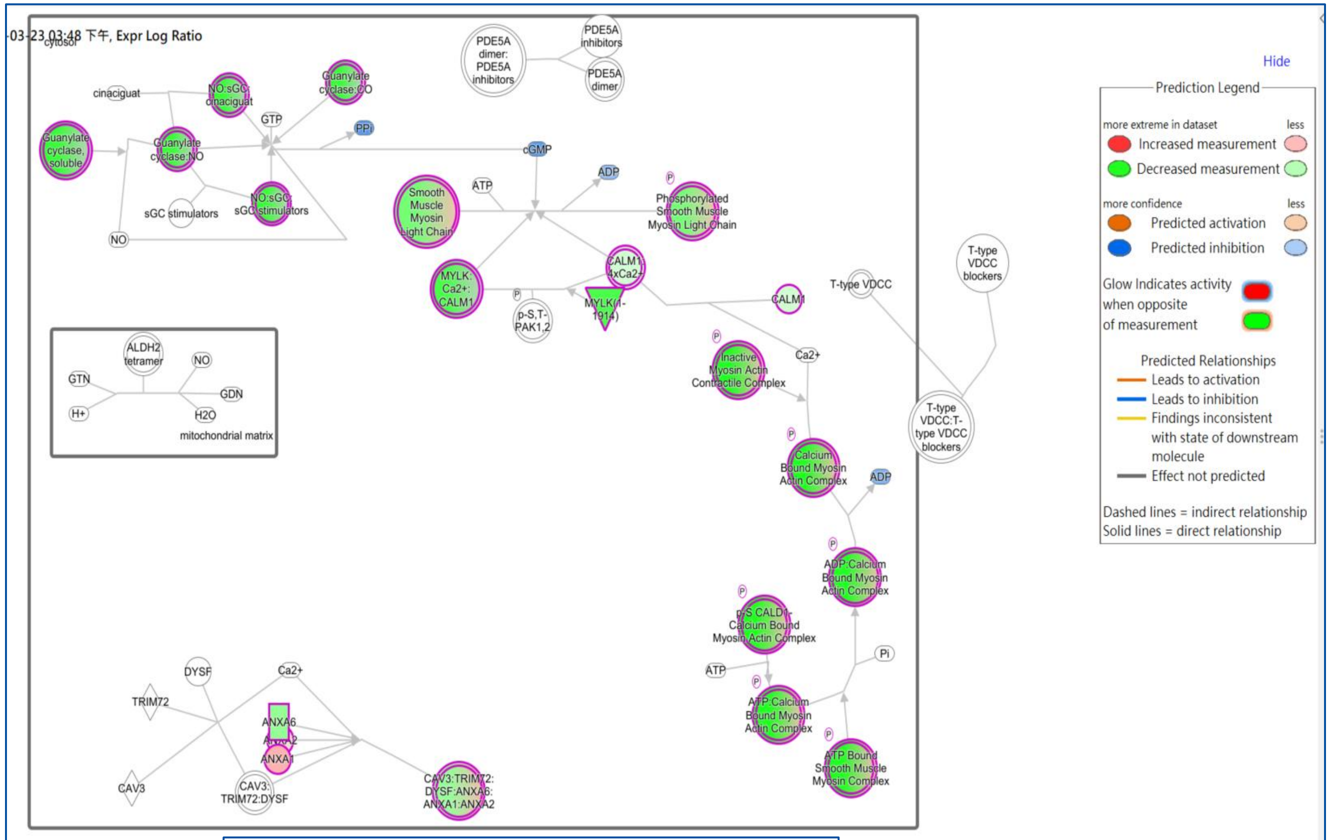
Symbol	Entrez Gene Name	Identifier	Measurement			Expected	Location	Type(s)	Biomarker Applicat...	Drug(s)
		Gene Symbol - hum..	Expr Log Ratio	Expr p-value	Expr False Discover...					
2	ABL proto-oncogene 2, nor	ABL2	↑1.039	6.63E-40	1.29E-35	↑ Up	Cytoplasm	kinase		dasatinib, nilotinib ...all 2
D3	adducin 3	ADD3	↑1.920	6.59E-121	1.29E-116	↑ Up	Cytoplasm	other		
AP13	A-kinase anchoring proteir	AKAP13	↓-1.054	5.78E-07	1.13E-02	↑ Up	Cytoplasm	other		
ARAP1	ArfGAP with RhoGAP doma	ARAP1	↑1.889	5.63E-49	1.10E-44	↑ Up	Cytoplasm	other		
ARAP2	ArfGAP with RhoGAP doma	ARAP2	↑2.914	5.38E-74	1.05E-69	↑ Up	Cytoplasm	other		

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

Canonical Pathway



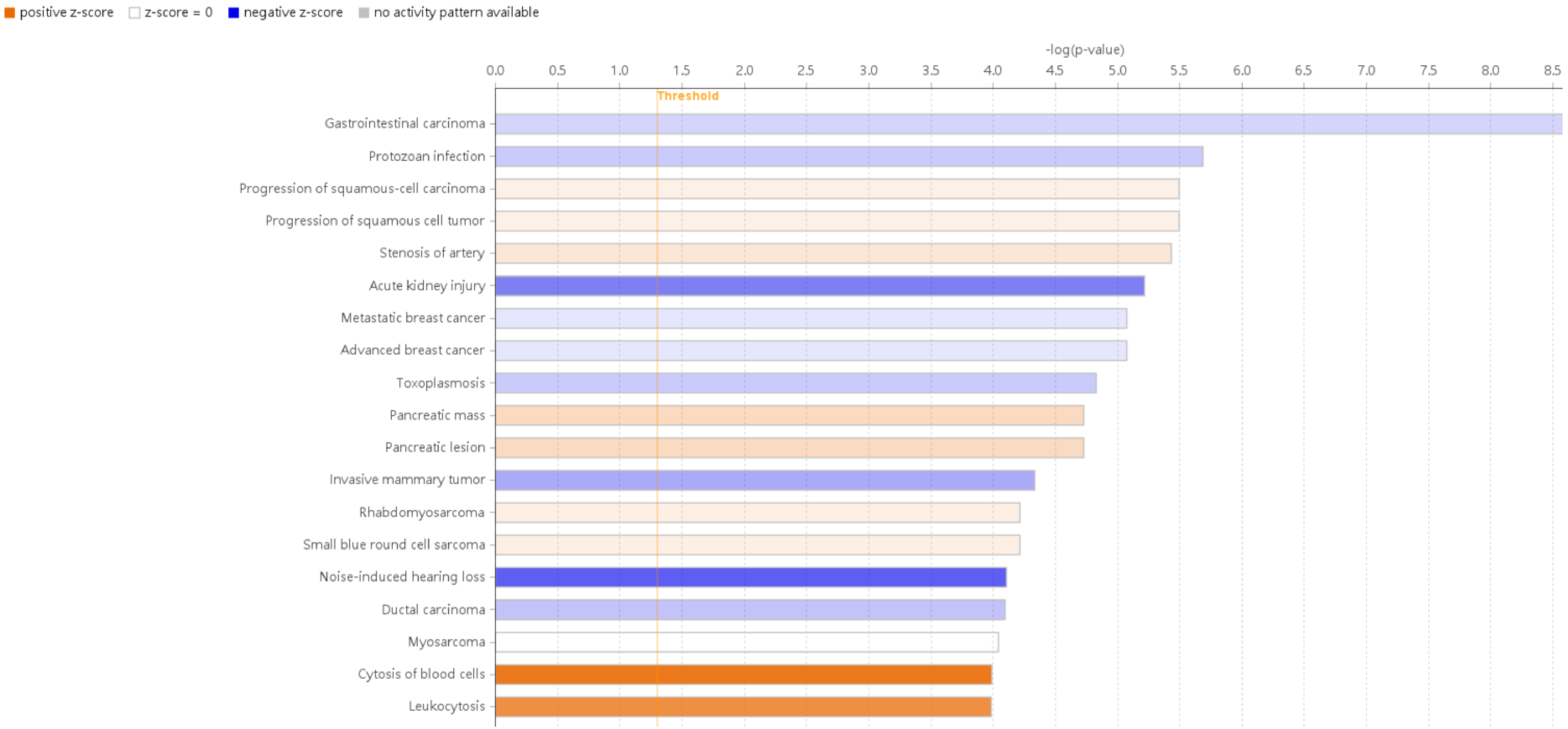
Signaling by Rho family GTPase



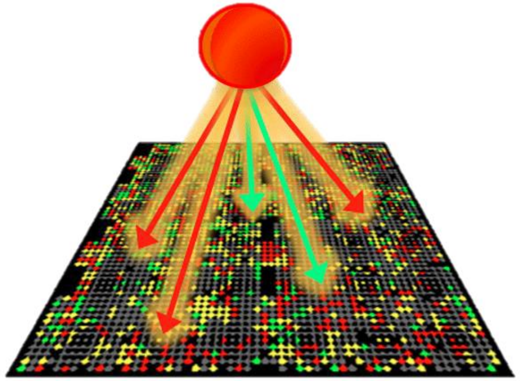
smooth muscle contraction

RHO GTPase Cycle showed a positive z-score, suggesting enhanced cytoskeletal remodeling and motility-related signaling in cluster 6 tumor epithelial cells, whereas Smooth Muscle Contraction showed a negative z-score, consistent with the contractile myofibroblast-like phenotype of cluster 2 CAFs.

ML pathway


positive z-score
z-score = 0
negative z-score
no activity pattern available
-log(p-value)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
8.5
Threshold
Gastrointestinal carcinoma
Protozoan infection
Progression of squamous-cell carcinoma
Progression of squamous cell tumor
Stenosis of artery
Acute kidney injury
Metastatic breast cancer
Advanced breast cancer
Toxoplasmosis
Pancreatic mass
Pancreatic lesion
Invasive mammary tumor
Rhabdomyosarcoma
Small blue round cell sarcoma
Noise-induced hearing loss
Ductal carcinoma
Myosarcoma
Cytosis of blood cells
Leukocytosis

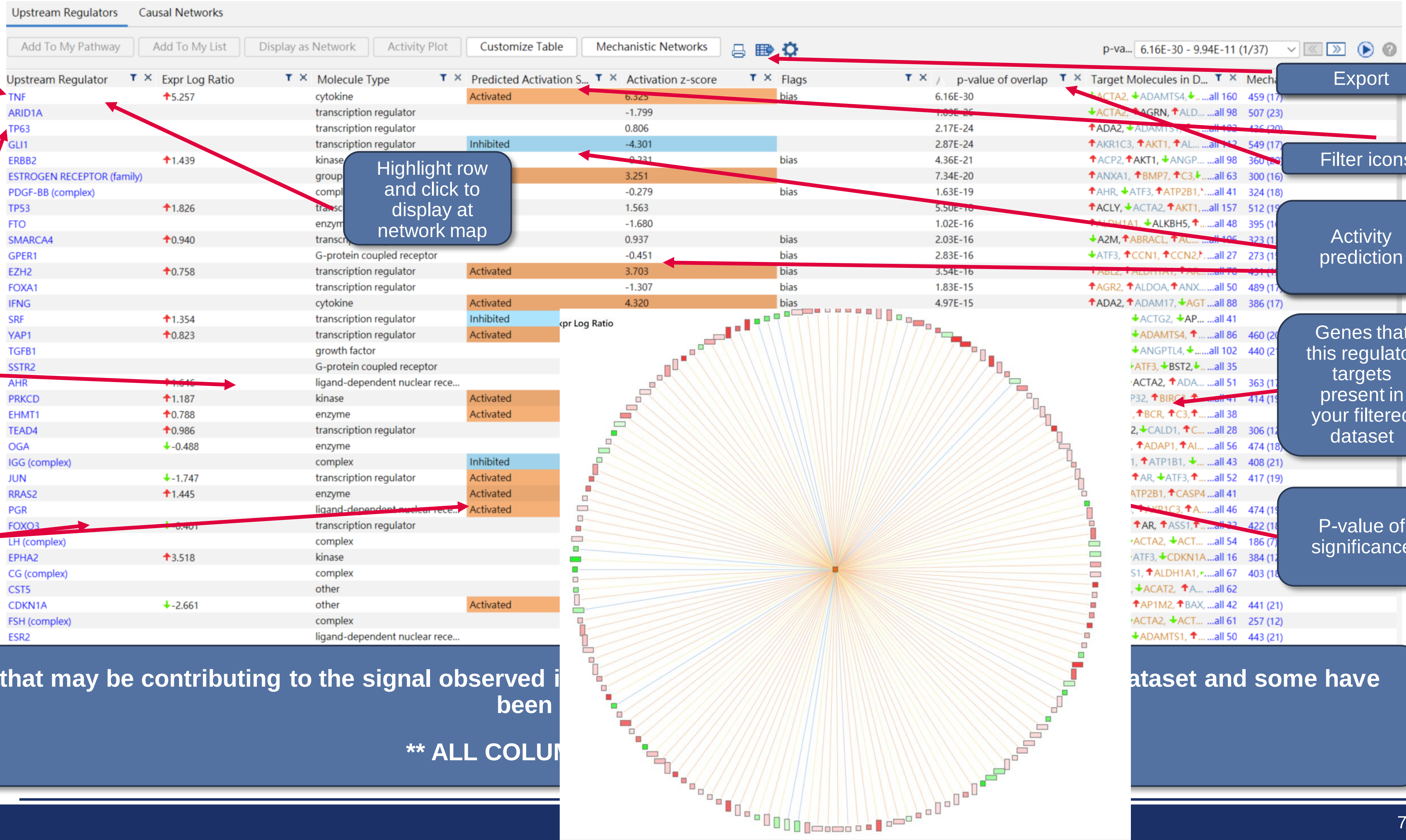
Upstream Regulator Analysis: *How does it work?*



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

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

Upstream Analysis Tab



Upstream Regulator	Expr Log Ratio	Molecule Type	Predicted Activation S...	Activation z-score	Flags	p-value of overlap	Target Molecules in D...	Mecha
TNF	↑5.257	cytokine	Activated	6.325	bias	6.16E-30	↓ACTA2, ↓ADAMTS4, ↓.. ...all 160	459 (17
ARID1A		transcription regulator		-1.799		1.03E-26	↓ACTA2, ↑AGRN, ↑ALD... ...all 98	507 (23)
TP63		transcription regulator		0.806		2.17E-24	↑ADA2, ↓ADAMTS1, ...all 102	436 (20)
GLI1		transcription regulator	Inhibited	-4.301		2.87E-24	↑AKR1C3, ↑AKT1, ↑AL... ...all 112	549 (17)
ERBB2	↑1.439	kinase		-0.231	bias	4.36E-21	↑ACP2, ↑AKT1, ↓ANGP... ...all 98	360 (20)
ESTROGEN RECEPTOR (family)		group		3.251		7.34E-20	↑ANXA1, ↑BMP7, ↑C3, ↓... ...all 63	300 (16)
PDGF-BB (complex)		compl		-0.279	bias	1.63E-19	↑AHR, ↓ATF3, ↑ATP2B1, ...all 41	324 (18)
TP53	↑1.826	transc		1.563		5.50E-18	↑ACLY, ↓ACTA2, ↑AKT1, ...all 157	512 (19
FTO		enzym		-1.680		1.02E-16	↑ALDH1A1, ↓ALKBH5, ↑... ...all 48	395 (1
SMARCA4	↑0.940	transcr		0.937	bias	2.03E-16	↓A2M, ↑ABRACL, ↑AC... ...all 106	323 (1
GPER1		G-protein coupled receptor		-0.451	bias	2.83E-16	↓ATF3, ↑CCN1, ↑CCN2, ...all 27	273 (1
EZH2	↑0.758	transcription regulator	Activated	3.703	bias	3.54E-16	↑ABL2, ↑ALDH1A1, ↑AR... ...all 78	431 (1
FOXA1		transcription regulator		-1.307	bias	1.83E-15	↑AGR2, ↑ALDOA, ↑ANX... ...all 50	489 (17
IFNG		cytokine	Activated	4.320	bias	4.97E-15	↑ADA2, ↑ADAM17, ↓AGT ...all 88	386 (17)
SRF	↑1.354	transcription regulator	Inhibited				↓ACTG2, ↓AP... ...all 41	
YAP1	↑0.823	transcription regulator	Activated				↓ADAMTS4, ↑... ...all 86	460 (2
TGFB1		growth factor					↓ANGPTL4, ↓... ...all 102	440 (2
SSTR2		G-protein coupled receptor					ATF3, ↓BST2, ↓.. ...all 35	
AHR	↑1.646	ligand-dependent nuclear rece...					ACTA2, ↑ADA... ...all 51	363 (1
PRKCD	↑1.187	kinase	Activated				P32, ↑BIRC3, ↑... ...all 41	414 (1
EHMT1	↑0.788	enzyme	Activated				, ↑BCR, ↑C3, ↑... ...all 38	
TEAD4	↑0.986	transcription regulator					2, ↓CALD1, ↑C... ...all 28	306 (1
OGA	↓-0.488	enzyme					, ↑ADAP1, ↑AI... ...all 56	474 (18)
IGG (complex)		complex	Inhibited				1, ↑ATP1B1, ↓... ...all 43	408 (21)
JUN	↓-1.747	transcription regulator	Activated				↑AR, ↓ATF3, ↑... ...all 52	417 (19)
RRAS2	↑1.445	enzyme	Activated				ATP2B1, ↑CASP4 ...all 41	
PGR		ligand-dependent nuclear rece...	Activated				↑AKR1C3, ↑A... ...all 46	474 (1
FOXO3	↓-0.401	transcription regulator					↑AR, ↑ASS1, ↑... ...all 32	422 (1
LH (complex)		complex					ACTA2, ↓ACT... ...all 54	186 (7)
EPHA2	↑3.518	kinase					ATF3, ↓CDKN1A ...all 16	384 (1
CG (complex)		complex					S1, ↑ALDH1A1, ...all 67	403 (1
CST5		other					, ↓ACAT2, ↑A... ...all 62	
CDKN1A	↓-2.661	other	Activated				↑AP1M2, ↑BAX, ...all 42	441 (21)
FSH (complex)		complex					ACTA2, ↓ACT... ...all 61	257 (12)
ESR2		ligand-dependent nuclear rece...					↓ADAMTS1, ↑... ...all 50	443 (21)

Immediately upstream of dataset genes regulators

One additional level upstream of regulatory networks

Measurement from your dataset for this regulator

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

Highlight row and click to display at network map

Export

Filter icons

Activity prediction

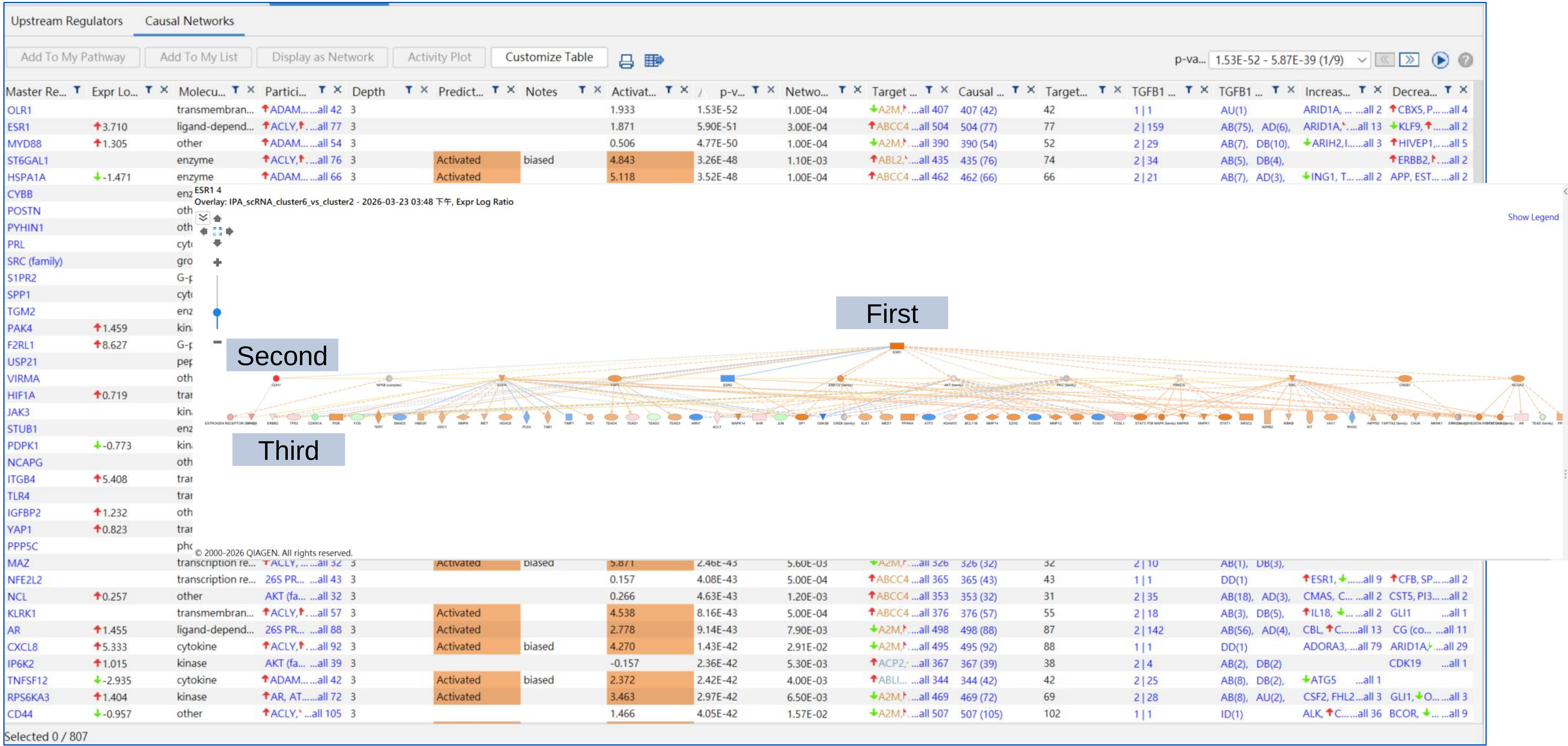
Genes that this regulator targets present in your filtered dataset

P-value of significance

Regulators that may be contributing to the signal observed i ataset and some have been

**** ALL COLU**

Casual network



ESR1 4
Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Log Ratio

First

Second

Third

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Master Re...	Expr Lo...	Molecu...	Partici...	Depth	Predict...	Notes	Activat...	p-v...	Netwo...	Target ...	Causal ...	Target...	TGFB1 ...	TGFB1 ...	Increas...	Decrea...
OLR1		transmembran...	↑ADAM... ...all 42	3			1.933	1.53E-52	1.00E-04	↓A2M,↑...all 407	407 (42)	42	1 | 1	AU(1)	ARID1A, ...all 2	↑CBX5, P... ...all 4
ESR1	↑3.710	ligand-depend...	↑ACLY,↑. ...all 77	3			1.871	5.90E-51	3.00E-04	↑ABCC4 ...all 504	504 (77)	77	2 | 159	AB(75), AD(6),	ARID1A,↑...all 13	↓KLF9, ↑......all 2
MYD88	↑1.305	other	↑ADAM... ...all 54	3			0.506	4.77E-50	1.00E-04	↓A2M,↑...all 390	390 (54)	52	2 | 29	AB(7), DB(10),	↓ARIH2,I......all 3	↑HIVEP1,... ...all 5
ST6GAL1		enzyme	↑ACLY,↑. ...all 76	3	Activated	biased	4.843	3.26E-48	1.10E-03	↑ABL2,↑...all 435	435 (76)	74	2 | 34	AB(5), DB(4),		↑ERBB2,↑. ...all 2
HSPA1A	↓-1.471	enzyme	↑ADAM... ...all 66	3	Activated		5.118	3.52E-48	1.00E-04	↑ABCC4 ...all 462	462 (66)	66	2 | 21	AB(7), AD(3),	↓ING1, T... ...all 2	APP, EST... ...all 2
CYBB		enz														
POSTN		oth														
PYHIN1		oth														
PRL		cyt														
SRC (family)		gro														
S1PR2		G-p														
SPP1		cyt														
TGM2		enz														
PAK4	↑1.459	kin														
F2RL1	↑8.627	G-p														
USP21		pep														
VIRMA		oth														
HIF1A	↑0.719	tra														
JAK3		kin														
STUB1		enz														
PDPK1	↓-0.773	kin														
NCAPG		oth														
ITGB4	↑5.408	tra														
TLR4		tra														
IGFBP2	↑1.232	oth														
YAP1	↑0.823	tra														
PPP5C		pho														
MAZ		transcription re...	↑ACLY, ...all 32	3	Activated	biased	5.871	2.46E-43	5.60E-03	↓A2M,↑...all 326	326 (32)	32	2 | 10	AB(1), DB(3),		
NFE2L2		transcription re...	26S PR... ...all 43	3			0.157	4.08E-43	5.00E-04	↑ABCC4 ...all 365	365 (43)	43	1 | 1	DD(1)	↑ESR1, ↓......all 9	↑CFB, SP... ...all 2
NCL	↑0.257	other	AKT (fa... ...all 32	3			0.266	4.63E-43	1.20E-03	↑ABCC4 ...all 353	353 (32)	31	2 | 35	AB(18), AD(3),	CMAS, C... ...all 2	CST5, PI3... ...all 2
KLRK1		transmembran...	↑ACLY,↑. ...all 57	3	Activated		4.538	8.16E-43	5.00E-04	↑ABCC4 ...all 376	376 (57)	55	2 | 18	AB(3), DB(5),	↑IL18, ↓... ...all 2	GLI1 ...all 1
AR	↑1.455	ligand-depend...	26S PR... ...all 88	3	Activated		2.778	9.14E-43	7.90E-03	↓A2M,↑...all 498	498 (88)	87	2 | 142	AB(56), AD(4),	CBL, ↑C... ...all 13	CG (co... ...all 11
CXCL8	↑5.333	cytokine	↑ACLY,↑. ...all 92	3	Activated	biased	4.270	1.43E-42	2.91E-02	↓A2M,↑...all 495	495 (92)	88	1 | 1	DD(1)	ADORA3,...all 79	ARID1A,↑...all 29
IP6K2	↑1.015	kinase	AKT (fa... ...all 39	3			-0.157	2.36E-42	5.30E-03	↑ACP2,↑ ...all 367	367 (39)	38	2 | 4	AB(2), DB(2)		CDK19 ...all 1
TNFSF12	↓-2.935	cytokine	↑ADAM... ...all 42	3	Activated	biased	2.372	2.42E-42	4.00E-03	↑ABLI... ...all 344	344 (42)	42	2 | 25	AB(8), DB(2),	↓ATG5 ...all 1	
RPS6KA3	↑1.404	kinase	↑AR, AT......all 72	3	Activated		3.463	2.97E-42	6.50E-03	↓A2M,↑...all 469	469 (72)	69	2 | 28	AB(8), AU(2),	CSF2, FHL2...all 3	GLI1, ↓O... ...all 3
CD44	↓-0.957	other	↑ACLY,↑ ...all 105	3			1.466	4.05E-42	1.57E-02	↓A2M,↑...all 507	507 (105)	102	1 | 1	ID(1)	ALK, ↑C... ...all 36	BCOR, ↓... ...all 9

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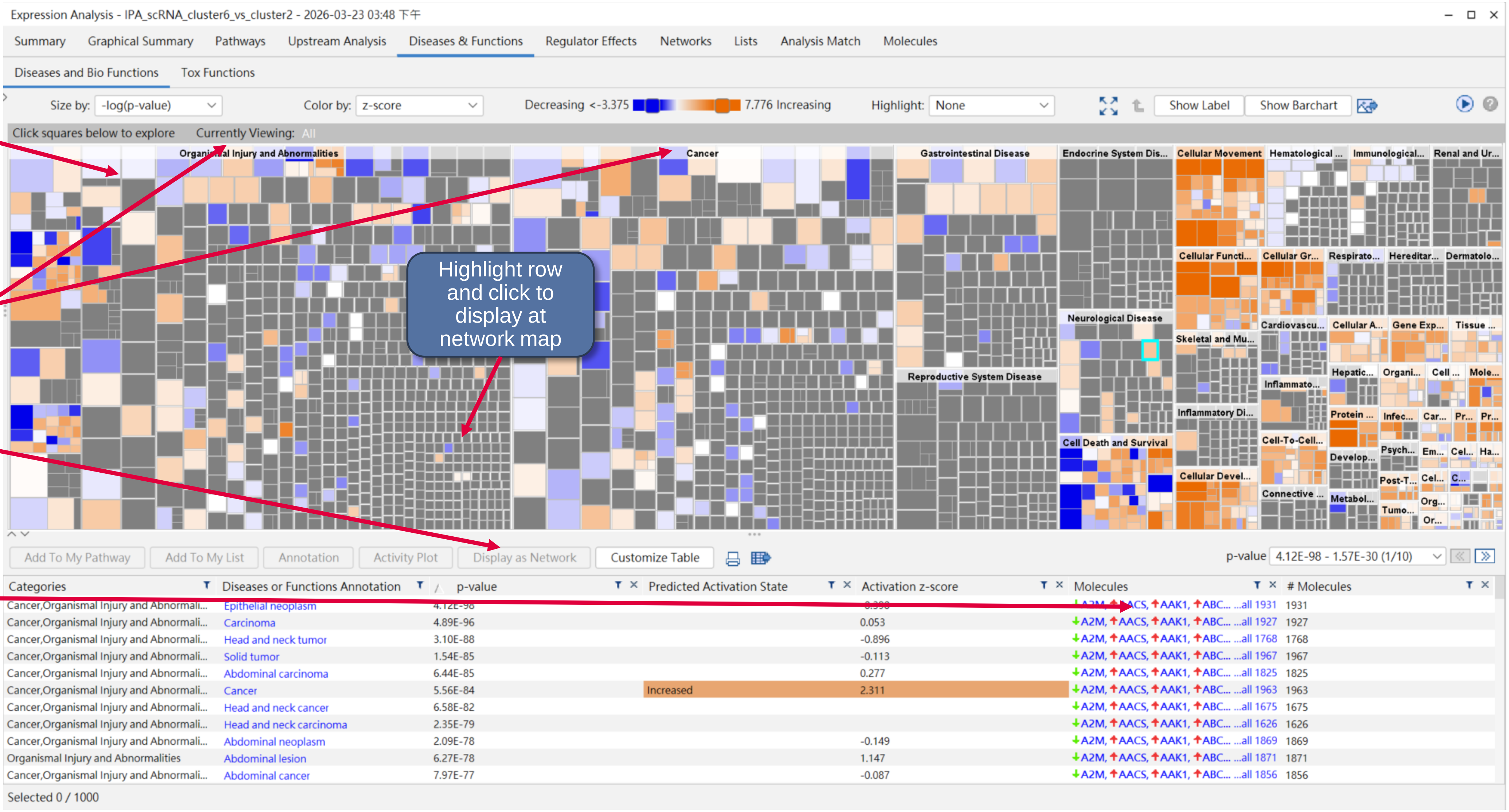
Diseases & Functions Tab

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

Organized by biological themes

Significance of enrichment

Genes from dataset involved in disease or function



Expression Analysis - IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午

Size by: -log(p-value)

Color by: z-score

Decreasing <-3.375 7.776 Increasing

Highlight: None

p-value 4.12E-98 - 1.57E-30 (1/10)

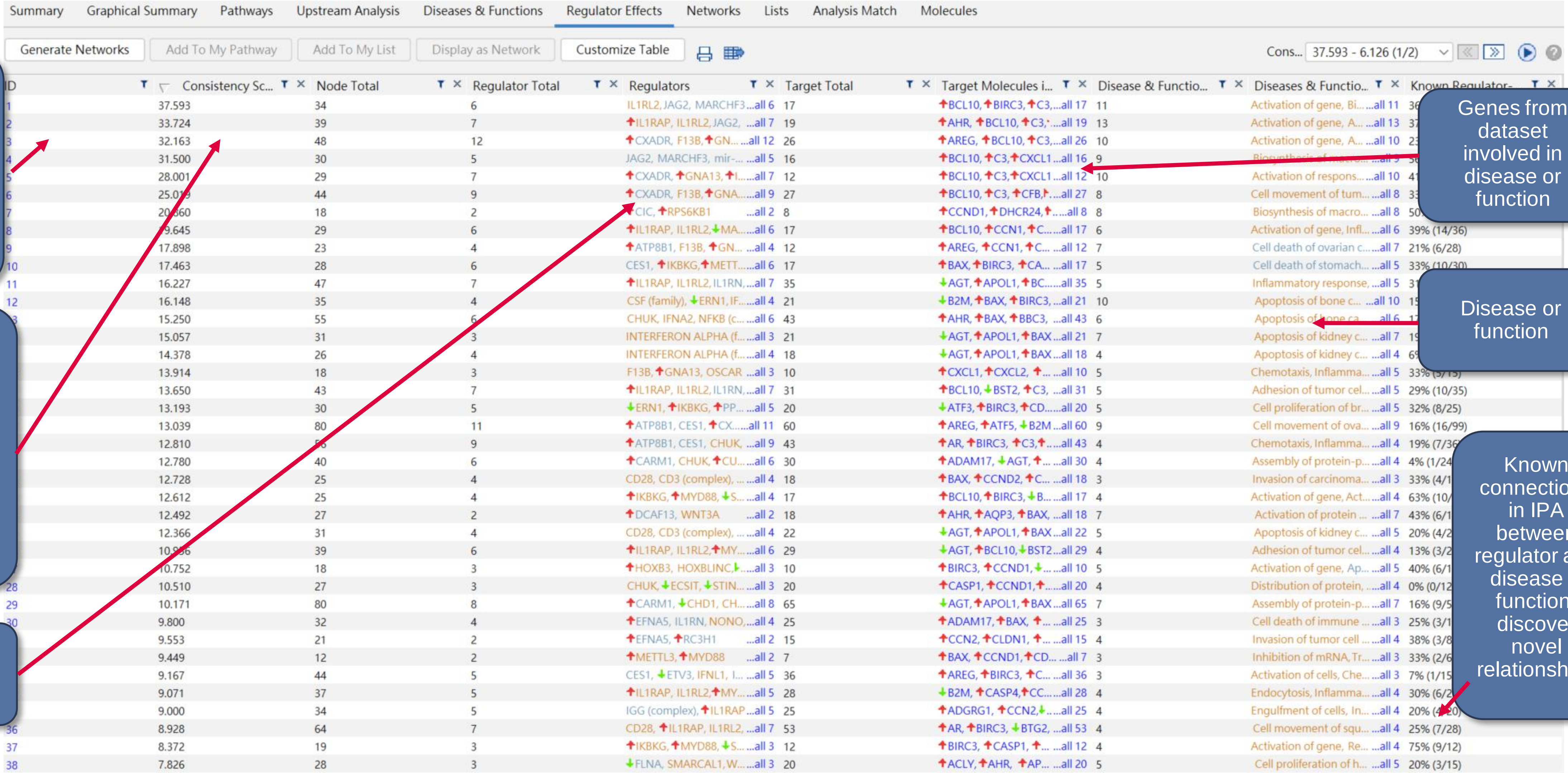
Categories	Diseases or Functions Annotation	p-value	Predicted Activation State	Activation z-score	Molecules	# Molecules
Cancer,Organismal Injury and Abnormali...	Epithelial neoplasm	4.12E-98		-0.390	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1931	1931
Cancer,Organismal Injury and Abnormali...	Carcinoma	4.89E-96		0.053	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1927	1927
Cancer,Organismal Injury and Abnormali...	Head and neck tumor	3.10E-88		-0.896	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1768	1768
Cancer,Organismal Injury and Abnormali...	Solid tumor	1.54E-85		-0.113	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1967	1967
Cancer,Organismal Injury and Abnormali...	Abdominal carcinoma	6.44E-85		0.277	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1825	1825
Cancer,Organismal Injury and Abnormali...	Cancer	5.56E-84	Increased	2.311	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1963	1963
Cancer,Organismal Injury and Abnormali...	Head and neck cancer	6.58E-82			↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1675	1675
Cancer,Organismal Injury and Abnormali...	Head and neck carcinoma	2.35E-79			↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1626	1626
Cancer,Organismal Injury and Abnormali...	Abdominal neoplasm	2.09E-78		-0.149	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1869	1869
Organismal Injury and Abnormalities	Abdominal lesion	6.27E-78		1.147	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1871	1871
Cancer,Organismal Injury and Abnormali...	Abdominal cancer	7.97E-77		-0.087	↓A2M, ↑AACS, ↑AAK1, ↑ABC... ...all 1856	1856

Selected 0 / 1000

Highlight row and click to display at network map

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

Regulator Effects Tab



ID	Consistency Sc...	Node Total	Regulator Total	Regulators	Target Total	Target Molecules i...	Disease & Functio...	Diseases & Functio...	Known Regulator-
1	37.593	34	6	IL1RL2, JAG2, MARCHF3 ...all 6	17	↑BCL10, ↑BIRC3, ↑C3, ...all 17	11	Activation of gene, Bi... ...all 11	36
2	33.724	39	7	↑IL1RAP, IL1RL2, JAG2, ...all 7	19	↑AHR, ↑BCL10, ↑C3, ...all 19	13	Activation of gene, A... ...all 13	37
3	32.163	48	12	↑CXADR, F13B, ↑GN... ...all 12	26	↑AREG, ↑BCL10, ↑C3, ...all 26	10	Activation of gene, A... ...all 10	23
4	31.500	30	5	JAG2, MARCHF3, mir-... ...all 5	16	↑BCL10, ↑C3, ↑CXCL1 ...all 16	9	Biosynthesis of macro... ...all 9	56
5	28.001	29	7	↑CXADR, ↑GNA13, ↑I... ...all 7	12	↑BCL10, ↑C3, ↑CXCL1 ...all 12	10	Activation of respons... ...all 10	41
6	25.019	44	9	↑CXADR, F13B, ↑GNA... ...all 9	27	↑BCL10, ↑C3, ↑CFB, ↑... ...all 27	8	Cell movement of tum... ...all 8	33
7	20.860	18	2	↑CIC, ↑RPS6KB1 ...all 2	8	↑CCND1, ↑DHCR24, ↑... ...all 8	8	Biosynthesis of macro... ...all 8	50
8	19.645	29	6	↑IL1RAP, IL1RL2, ↓MA... ...all 6	17	↑BCL10, ↑CCN1, ↑C... ...all 17	6	Activation of gene, Infl... ...all 6	39% (14/36)
9	17.898	23	4	↑ATP8B1, F13B, ↑GN... ...all 4	12	↑AREG, ↑CCN1, ↑C... ...all 12	7	Cell death of ovarian c... ...all 7	21% (6/28)
10	17.463	28	6	CES1, ↑IKBKG, ↑METT... ...all 6	17	↑BAX, ↑BIRC3, ↑CA... ...all 17	5	Cell death of stomach... ...all 5	33% (10/30)
11	16.227	47	7	↑IL1RAP, IL1RL2, IL1RN, ...all 7	35	↓AGT, ↑APOL1, ↑BC... ...all 35	5	Inflammatory response, ...all 5	31
12	16.148	35	4	CSF (family), ↓ERN1, IF... ...all 4	21	↓B2M, ↑BAX, ↑BIRC3, ...all 21	10	Apoptosis of bone c... ...all 10	15
3	15.250	55	6	CHUK, IFNA2, NFKB (c... ...all 6	43	↑AHR, ↑BAX, ↑BBC3, ...all 43	6	Apoptosis of bone ca... ...all 6	17
	15.057	31	3	INTERFERON ALPHA (f... ...all 3	21	↓AGT, ↑APOL1, ↑BAX ...all 21	7	Apoptosis of kidney c... ...all 7	19
	14.378	26	4	INTERFERON ALPHA (f... ...all 4	18	↓AGT, ↑APOL1, ↑BAX ...all 18	4	Apoptosis of kidney c... ...all 4	69
	13.914	18	3	F13B, ↑GNA13, OSCAR ...all 3	10	↑CXCL1, ↑CXCL2, ↑... ...all 10	5	Chemotaxis, Inflamma... ...all 5	33% (5/15)
	13.650	43	7	↑IL1RAP, IL1RL2, IL1RN, ...all 7	31	↑BCL10, ↓BST2, ↑C3, ...all 31	5	Adhesion of tumor cel... ...all 5	29% (10/35)
	13.193	30	5	↓ERN1, ↑IKBKG, ↑PP... ...all 5	20	↓ATF3, ↑BIRC3, ↑CD... ...all 20	5	Cell proliferation of br... ...all 5	32% (8/25)
	13.039	80	11	↑ATP8B1, CES1, ↑CX... ...all 11	60	↑AREG, ↑ATF5, ↓B2M ...all 60	9	Cell movement of ova... ...all 9	16% (16/99)
	12.810	56	9	↑ATP8B1, CES1, CHUK, ...all 9	43	↑AR, ↑BIRC3, ↑C3, ↑... ...all 43	4	Chemotaxis, Inflamma... ...all 4	19% (7/36
	12.780	40	6	↑CARM1, CHUK, ↑CU... ...all 6	30	↑ADAM17, ↓AGT, ↑... ...all 30	4	Assembly of protein-p... ...all 4	4% (1/24
	12.728	25	4	CD28, CD3 (complex), ...all 4	18	↑BAX, ↑CCND2, ↑C... ...all 18	3	Invasion of carcinoma... ...all 3	33% (4/1
	12.612	25	4	↑IKBKG, ↑MYD88, ↓S... ...all 4	17	↑BCL10, ↑BIRC3, ↓B... ...all 17	4	Activation of gene, Act... ...all 4	63% (10/
	12.492	27	2	↑DCAF13, WNT3A ...all 2	18	↑AHR, ↑AQP3, ↑BAX, ...all 18	7	Activation of protein ... ...all 7	43% (6/1
	12.366	31	4	CD28, CD3 (complex), ...all 4	22	↓AGT, ↑APOL1, ↑BAX ...all 22	5	Apoptosis of kidney c... ...all 5	20% (4/2
	10.936	39	6	↑IL1RAP, IL1RL2, ↑MY... ...all 6	29	↓AGT, ↑BCL10, ↓BST2 ...all 29	4	Adhesion of tumor cel... ...all 4	13% (3/2
	10.752	18	3	↑HOXB3, HOXBLINC, ↓... ...all 3	10	↑BIRC3, ↑CCND1, ↓... ...all 10	5	Activation of gene, Ap... ...all 5	40% (6/1
28	10.510	27	3	CHUK, ↓ECSIT, ↓STIN... ...all 3	20	↑CASP1, ↑CCND1, ↑... ...all 20	4	Distribution of protein, ...all 4	0% (0/12
29	10.171	80	8	↑CARM1, ↓CHD1, CH... ...all 8	65	↓AGT, ↑APOL1, ↑BAX ...all 65	7	Assembly of protein-p... ...all 7	16% (9/5
30	9.800	32	4	↑EFNA5, IL1RN, NONO, ...all 4	25	↑ADAM17, ↑BAX, ↑... ...all 25	3	Cell death of immune ... ...all 3	25% (3/1
	9.553	21	2	↑EFNA5, ↑RC3H1 ...all 2	15	↑CCN2, ↑CLDN1, ↑... ...all 15	4	Invasion of tumor cell ... ...all 4	38% (3/8
	9.449	12	2	↑METTL3, ↑MYD88 ...all 2	7	↑BAX, ↑CCND1, ↑CD... ...all 7	3	Inhibition of mRNA, Tr... ...all 3	33% (2/6
	9.167	44	5	CES1, ↓ETV3, IFNL1, I... ...all 5	36	↑AREG, ↑BIRC3, ↑C... ...all 36	3	Activation of cells, Che... ...all 3	7% (1/15
	9.071	37	5	↑IL1RAP, IL1RL2, ↑MY... ...all 5	28	↓B2M, ↑CASP4, ↑CC... ...all 28	4	Endocytosis, Inflamma... ...all 4	30% (6/2
	9.000	34	5	IGG (complex), ↑IL1RAP ...all 5	25	↑ADGRG1, ↑CCN2, ↓... ...all 25	4	Engulfment of cells, In... ...all 4	20% (4/20)
36	8.928	64	7	CD28, ↑IL1RAP, IL1RL2, ...all 7	53	↑AR, ↑BIRC3, ↓BTG2, ...all 53	4	Cell movement of squ... ...all 4	25% (7/28)
37	8.372	19	3	↑IKBKG, ↑MYD88, ↓S... ...all 3	12	↑BIRC3, ↑CASP1, ↑... ...all 12	4	Activation of gene, Re... ...all 4	75% (9/12)
38	7.826	28	3	↓FLNA, SMARCAL1, W... ...all 3	20	↑ACLY, ↑AHR, ↑AP... ...all 20	5	Cell proliferation of h... ...all 5	20% (3/15)

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

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

Regulators involved in network

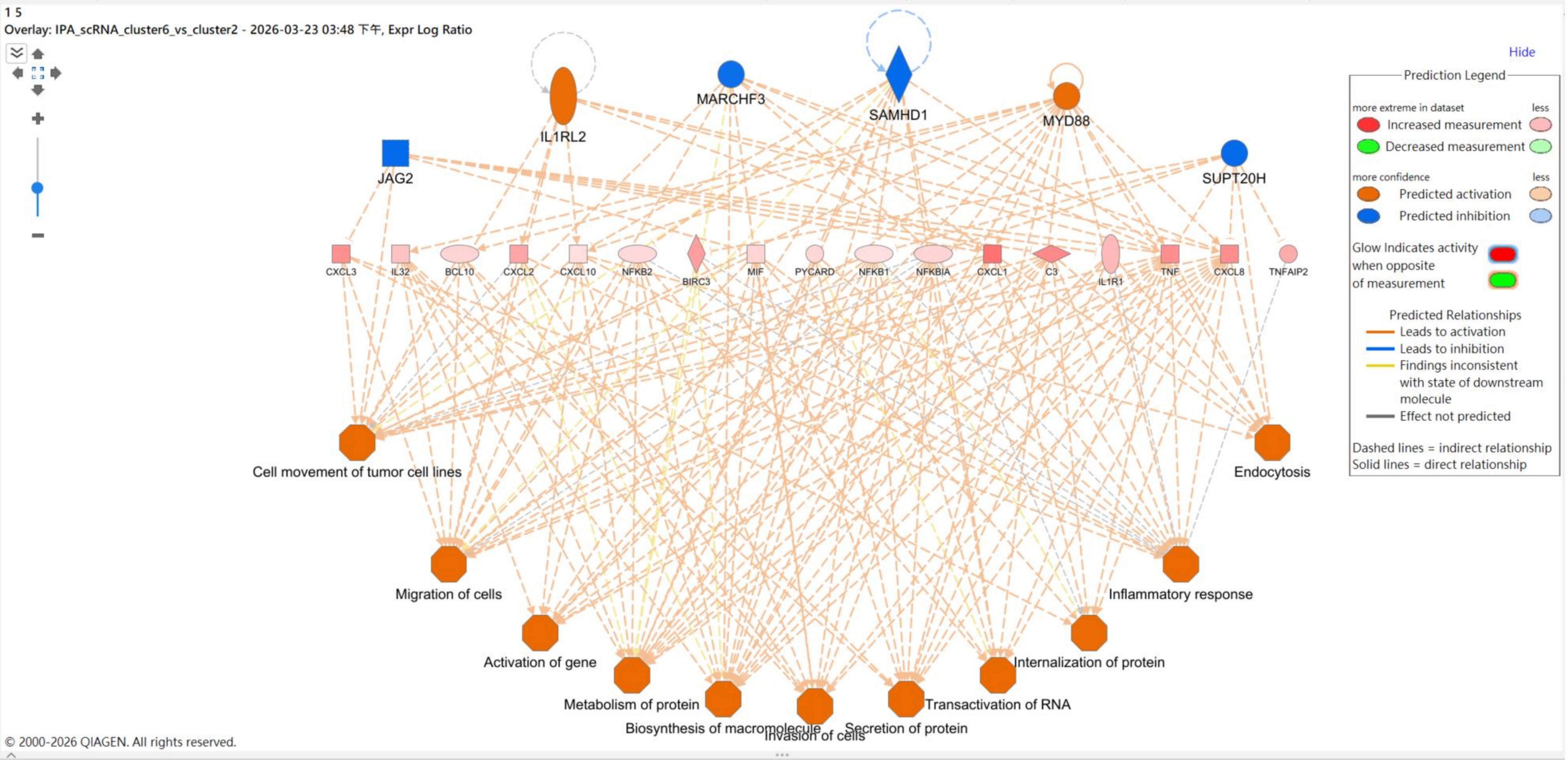
Genes from dataset involved in disease or function

Disease or function

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

Ties dataset molecules and regulators to a predicted phenotypic outcome

Regulate Effect



1 5

Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Log Ratio

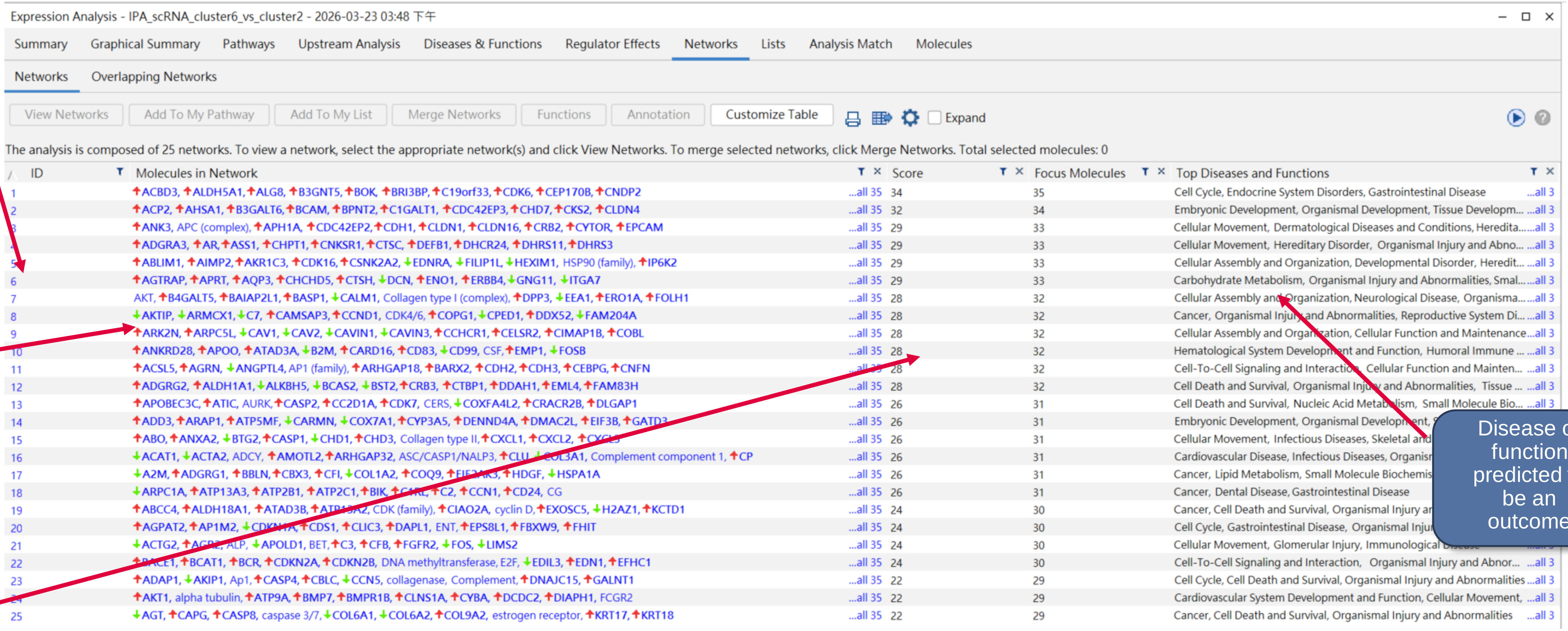
Networks Tab

Network of highly connected molecules, click to open network map

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

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

Disease or function predicted to be an outcome

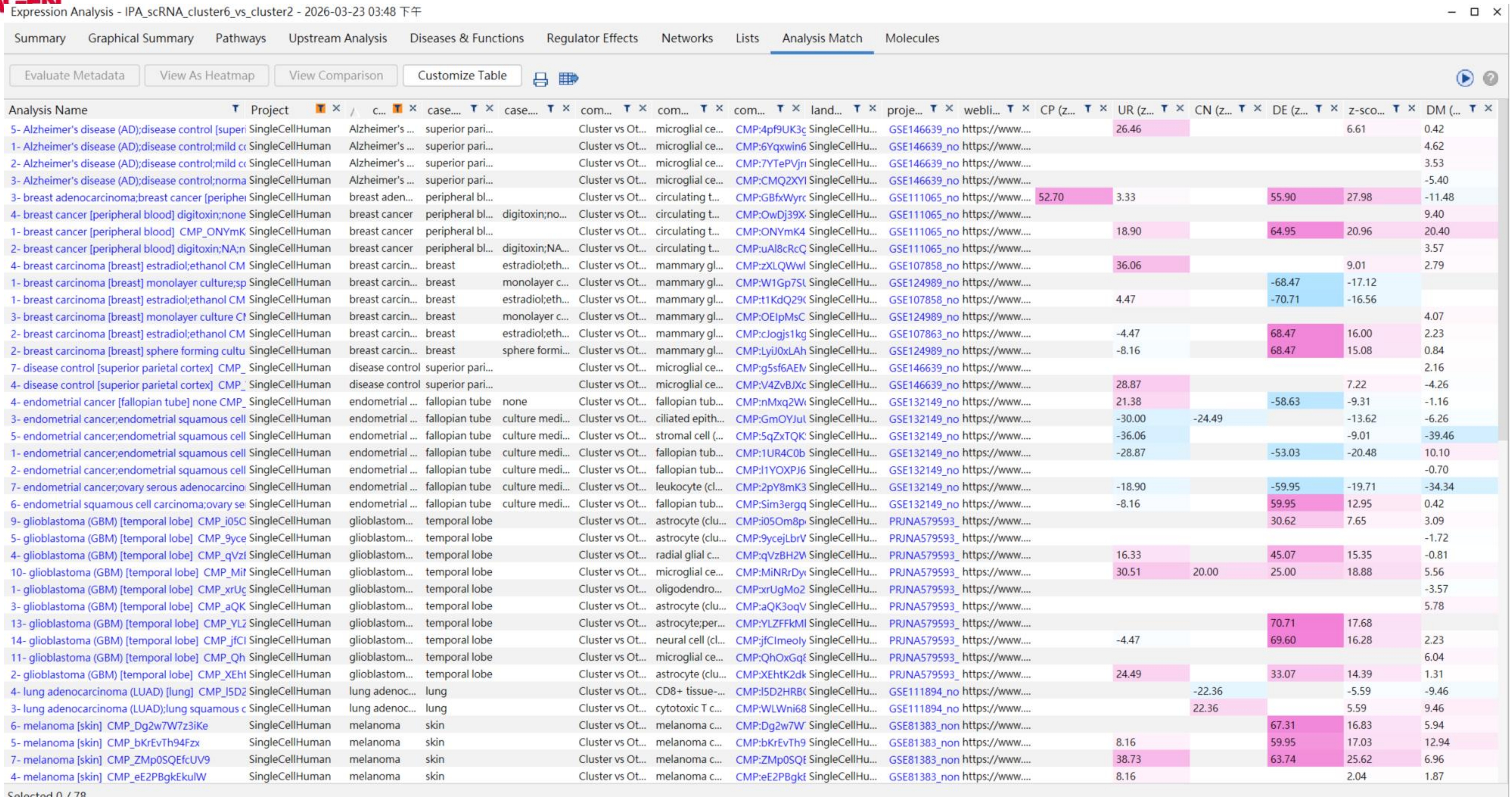


The analysis is composed of 25 networks. To view a network, select the appropriate network(s) and click View Networks. To merge selected networks, click Merge Networks. Total selected molecules: 0

ID	Molecules in Network	Score	Focus Molecules	Top Diseases and Functions
1	↑ACBD3, ↑ALDH5A1, ↑ALG8, ↑B3GNT5, ↑BOK, ↑BRI3BP, ↑C19orf33, ↑CDK6, ↑CEP170B, ↑CNDP2 ...all 35	34	35	Cell Cycle, Endocrine System Disorders, Gastrointestinal Disease ...all 3
2	↑ACP2, ↑AHSA1, ↑B3GALT6, ↑BCAM, ↑BPNT2, ↑C1GALT1, ↑CDC42EP3, ↑CHD7, ↑CKS2, ↑CLDN4 ...all 35	32	34	Embryonic Development, Organismal Development, Tissue Developm... ...all 3
3	↑ANK3, APC (complex), ↑APH1A, ↑CDC42EP2, ↑CDH1, ↑CLDN1, ↑CLDN16, ↑CRB2, ↑CYTOR, ↑EPCAM ...all 35	29	33	Cellular Movement, Dermatological Diseases and Conditions, Heredita... ...all 3
4	↑ADGRA3, ↑AR, ↑ASS1, ↑CHPT1, ↑CNKSR1, ↑CTSC, ↑DEFB1, ↑DHCR24, ↑DHRS11, ↑DHRS3 ...all 35	29	33	Cellular Movement, Hereditary Disorder, Organismal Injury and Abno... ...all 3
5	↑ABLIM1, ↑AIMP2, ↑AKR1C3, ↑CDK16, ↑CSNK2A2, ↓EDNRA, ↓FILIP1L, ↓HEXIM1, HSP90 (family), ↑IP6K2 ...all 35	29	33	Cellular Assembly and Organization, Developmental Disorder, Heredit... ...all 3
6	↑AGTRAP, ↑APRT, ↑AQP3, ↑CHCHD5, ↑CTSH, ↓DCN, ↑ENO1, ↑ERBB4, ↓GNG11, ↓ITGA7 ...all 35	29	33	Carbohydrate Metabolism, Organismal Injury and Abnormalities, Smal... ...all 3
7	AKT, ↑B4GALT5, ↑BAIAP2L1, ↑BASP1, ↓CALM1, Collagen type I (complex), ↑DPP3, ↓EEA1, ↑ERO1A, ↑FOLH1 ...all 35	28	32	Cellular Assembly and Organization, Neurological Disease, Organisma... ...all 3
8	↓AKTIP, ↓ARMCX1, ↓C7, ↑CAMSAP3, ↑CCND1, CDK4/6, ↑COPG1, ↓CPED1, ↑DDX52, ↓FAM204A ...all 35	28	32	Cancer, Organismal Injury and Abnormalities, Reproductive System Di... ...all 3
9	↑ARK2N, ↑ARPC5L, ↓CAV1, ↓CAV2, ↓CAVIN1, ↓CAVIN3, ↑CCHCR1, ↑CELSR2, ↑CIMAP1B, ↑COBL ...all 35	28	32	Cellular Assembly and Organization, Cellular Function and Maintenance ...all 3
10	↑ANKRD28, ↑APOO, ↑ATAD3A, ↓B2M, ↑CARD16, ↑CD83, ↓CD99, CSF, ↑EMP1, ↓FOSB ...all 35	28	32	Hematological System Development and Function, Humoral Immune ... ...all 3
11	↑ACSL5, ↑AGRN, ↓ANGPTL4, AP1 (family), ↑ARHGAP18, ↑BARX2, ↑CDH2, ↑CDH3, ↑CEBPG, ↑CNFN ...all 35	28	32	Cell-To-Cell Signaling and Interaction, Cellular Function and Mainten... ...all 3
12	↑ADGRG2, ↑ALDH1A1, ↓ALKBH5, ↓BCAS2, ↓BST2, ↑CRB3, ↑CTBP1, ↑DDAH1, ↑EML4, ↑FAM83H ...all 35	28	32	Cell Death and Survival, Organismal Injury and Abnormalities, Tissue ... ...all 3
13	↑APOBEC3C, ↑ATIC, AURK, ↑CASP2, ↑CC2D1A, ↑CDK7, CERS, ↓COXFA4L2, ↑CRACR2B, ↑DLGAP1 ...all 35	26	31	Cell Death and Survival, Nucleic Acid Metabolism, Small Molecule Bio... ...all 3
14	↑ADD3, ↑ARAP1, ↑ATP5MF, ↓CARMN, ↓COX7A1, ↑CYP3A5, ↑DENND4A, ↑DMAC2L, ↑EIF3B, ↑GATD3 ...all 35	26	31	Embryonic Development, Organismal Development,
15	↑ABO, ↑ANXA2, ↓BTG2, ↑CASP1, ↓CHD1, ↑CHD3, Collagen type II, ↑CXCL1, ↑CXCL2, ↑CXCL5 ...all 35	26	31	Cellular Movement, Infectious Diseases, Skeletal and
16	↓ACAT1, ↓ACTA2, ADCY, ↑AMOTL2, ↑ARHGAP32, ASC/CASP1/NALP3, ↑CLU, ↓COL3A1, Complement component 1, ↑CP ...all 35	26	31	Cardiovascular Disease, Infectious Diseases, Organism
17	↓A2M, ↑ADGRG1, ↑BBLN, ↑CBX3, ↑CFI, ↓COL1A2, ↑COQ9, ↑EIF2AK3, ↑HDGF, ↓HSPA1A ...all 35	26	31	Cancer, Lipid Metabolism, Small Molecule Biochemis
18	↓ARPC1A, ↑ATP13A3, ↑ATP2B1, ↑ATP2C1, ↑BIK, ↑C1RL, ↑C2, ↑CCN1, ↑CD24, CG ...all 35	26	31	Cancer, Dental Disease, Gastrointestinal Disease
19	↑ABCC4, ↑ALDH18A1, ↑ATAD3B, ↑ATP13A2, CDK (family), ↑CIAO2A, cyclin D, ↑EXOSC5, ↓H2AZ1, ↑KCTD1 ...all 35	24	30	Cancer, Cell Death and Survival, Organismal Injury ar
20	↑AGPAT2, ↑AP1M2, ↓CDKN1A, ↑CDS1, ↑CLIC3, ↑DAPL1, ENT, ↑EPS8L1, ↑FBXW9, ↑FHIT ...all 35	24	30	Cell Cycle, Gastrointestinal Disease, Organismal Inju
21	↓ACTG2, ↑AGR2, ALP, ↓APOLD1, BET, ↑C3, ↑CFB, ↑FGFR2, ↓FOS, ↓LIMS2 ...all 35	24	30	Cellular Movement, Glomerular Injury, Immunological Disease
22	↑BACE1, ↑BCAT1, ↑BCR, ↑CDKN2A, ↑CDKN2B, DNA methyltransferase, E2F, ↓EDIL3, ↑EDN1, ↑EFHC1 ...all 35	24	30	Cell-To-Cell Signaling and Interaction, Organismal Injury and Abnor... ...all 3
23	↑ADAP1, ↓AKIP1, Ap1, ↑CASP4, ↑CBLC, ↓CCN5, collagenase, Complement, ↑DNAJC15, ↑GALNT1 ...all 35	22	29	Cell Cycle, Cell Death and Survival, Organismal Injury and Abnormalities ...all 3
24	↑AKT1, alpha tubulin, ↑ATP9A, ↑BMP7, ↑BMPR1B, ↑CLNS1A, ↑CYBA, ↑DCDC2, ↑DIAPH1, FCGR2 ...all 35	22	29	Cardiovascular System Development and Function, Cellular Movement, ...all 3
25	↓AGT, ↑CAPG, ↑CASP8, caspase 3/7, ↓COL6A1, ↓COL6A2, ↑COL9A2, estrogen receptor, ↑KRT17, ↑KRT18 ...all 35	22	29	Cancer, Cell Death and Survival, Organismal Injury and Abnormalities ...all 3

Networks constructed from your dataset with level of connectivity prioritized

Analysis Match



Expression Analysis - IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午

Analysis Name	Project	c...	case....	case....	com...	com...	com...	land...	proje...	webli...	CP (z...	UR (z...	CN (z...	DE (z...	z-sco...	DM (...
5- Alzheimer's disease (AD);disease control [superi	SingleCellHuman	Alzheimer's ...	superior pari...		Cluster vs Ot...	microglial ce...	CMP:4pf9UK3g	SingleCellHu...	GSE146639_no	https://www....		26.46			6.61	0.42
1- Alzheimer's disease (AD);disease control;mild c	SingleCellHuman	Alzheimer's ...	superior pari...		Cluster vs Ot...	microglial ce...	CMP:6Yqxwin6	SingleCellHu...	GSE146639_no	https://www....						4.62
2- Alzheimer's disease (AD);disease control;mild c	SingleCellHuman	Alzheimer's ...	superior pari...		Cluster vs Ot...	microglial ce...	CMP:7YTePVjn	SingleCellHu...	GSE146639_no	https://www....						3.53
3- Alzheimer's disease (AD);disease control;norma	SingleCellHuman	Alzheimer's ...	superior pari...		Cluster vs Ot...	microglial ce...	CMP:CMQ2XYI	SingleCellHu...	GSE146639_no	https://www....						-5.40
3- breast adenocarcinoma;breast cancer [periphe	SingleCellHuman	breast aden...	peripheral bl...		Cluster vs Ot...	circulating t...	CMP:GBfxWyrc	SingleCellHu...	GSE111065_no	https://www....	52.70	3.33		55.90	27.98	-11.48
4- breast cancer [peripheral blood] digitoxin;none	SingleCellHuman	breast cancer	peripheral bl...	digitoxin;no...	Cluster vs Ot...	circulating t...	CMP:OwDj39X	SingleCellHu...	GSE111065_no	https://www....						9.40
1- breast cancer [peripheral blood] CMP_ONYmK	SingleCellHuman	breast cancer	peripheral bl...		Cluster vs Ot...	circulating t...	CMP:ONYmK4	SingleCellHu...	GSE111065_no	https://www....		18.90		64.95	20.96	20.40
2- breast cancer [peripheral blood] digitoxin;NA;n	SingleCellHuman	breast cancer	peripheral bl...	digitoxin;NA...	Cluster vs Ot...	circulating t...	CMP:uAl8cRcQ	SingleCellHu...	GSE111065_no	https://www....						3.57
4- breast carcinoma [breast] estradiol;ethanol CM	SingleCellHuman	breast carcin...	breast	estradiol;eth...	Cluster vs Ot...	mammary gl...	CMP:zXLQWwl	SingleCellHu...	GSE107858_no	https://www....		36.06			9.01	2.79
1- breast carcinoma [breast] monolayer culture;sp	SingleCellHuman	breast carcin...	breast	monolayer c...	Cluster vs Ot...	mammary gl...	CMP:W1Gp7SL	SingleCellHu...	GSE124989_no	https://www....				-68.47	-17.12	
1- breast carcinoma [breast] estradiol;ethanol CM	SingleCellHuman	breast carcin...	breast	estradiol;eth...	Cluster vs Ot...	mammary gl...	CMP:t1KdQ29	SingleCellHu...	GSE107858_no	https://www....		4.47		-70.71	-16.56	
3- breast carcinoma [breast] monolayer culture CI	SingleCellHuman	breast carcin...	breast	monolayer c...	Cluster vs Ot...	mammary gl...	CMP:OEIpMsC	SingleCellHu...	GSE124989_no	https://www....						4.07
2- breast carcinoma [breast] estradiol;ethanol CM	SingleCellHuman	breast carcin...	breast	estradiol;eth...	Cluster vs Ot...	mammary gl...	CMP:cJogjs1kg	SingleCellHu...	GSE107863_no	https://www....		-4.47		68.47	16.00	2.23
2- breast carcinoma [breast] sphere forming cultu	SingleCellHuman	breast carcin...	breast	sphere formi...	Cluster vs Ot...	mammary gl...	CMP:LyiJ0xLAh	SingleCellHu...	GSE124989_no	https://www....		-8.16		68.47	15.08	0.84
7- disease control [superior parietal cortex] CMP_	SingleCellHuman	disease control	superior pari...		Cluster vs Ot...	microglial ce...	CMP:g5sf6AEN	SingleCellHu...	GSE146639_no	https://www....						2.16
4- disease control [superior parietal cortex] CMP_	SingleCellHuman	disease control	superior pari...		Cluster vs Ot...	microglial ce...	CMP:V4ZvBJXc	SingleCellHu...	GSE146639_no	https://www....		28.87			7.22	-4.26
4- endometrial cancer [fallopian tube] none CMP_	SingleCellHuman	endometrial ...	fallopian tube	none	Cluster vs Ot...	fallopian tub...	CMP:nMxq2W	SingleCellHu...	GSE132149_no	https://www....		21.38		-58.63	-9.31	-1.16
3- endometrial cancer;endometrial squamous cell	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	ciliated epith...	CMP:GmOYJul	SingleCellHu...	GSE132149_no	https://www....		-30.00	-24.49		-13.62	-6.26
5- endometrial cancer;endometrial squamous cell	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	stromal cell (...	CMP:5qZxTQK	SingleCellHu...	GSE132149_no	https://www....		-36.06			-9.01	-39.46
1- endometrial cancer;endometrial squamous cell	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	fallopian tub...	CMP:1UR4C0b	SingleCellHu...	GSE132149_no	https://www....		-28.87		-53.03	-20.48	10.10
2- endometrial cancer;endometrial squamous cell	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	fallopian tub...	CMP:l1YOXPJ6	SingleCellHu...	GSE132149_no	https://www....						-0.70
7- endometrial cancer;ovary serous adenocarcino	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	leukocyte (cl...	CMP:2pY8mK3	SingleCellHu...	GSE132149_no	https://www....		-18.90		-59.95	-19.71	-34.34
6- endometrial squamous cell carcinoma;ovary se	SingleCellHuman	endometrial ...	fallopian tube	culture medi...	Cluster vs Ot...	fallopian tub...	CMP:Sim3ergq	SingleCellHu...	GSE132149_no	https://www....		-8.16		59.95	12.95	0.42
9- glioblastoma (GBM) [temporal lobe] CMP_i05C	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	astrocyte (clu...	CMP:i05Om8p	SingleCellHu...	PRJNA579593_	https://www....				30.62	7.65	3.09
5- glioblastoma (GBM) [temporal lobe] CMP_9yce	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	astrocyte (clu...	CMP:9ycejLbrV	SingleCellHu...	PRJNA579593_	https://www....						-1.72
4- glioblastoma (GBM) [temporal lobe] CMP_qVzI	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	radial glial c...	CMP:qVzBH2W	SingleCellHu...	PRJNA579593_	https://www....		16.33		45.07	15.35	-0.81
10- glioblastoma (GBM) [temporal lobe] CMP_Mi	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	microglial ce...	CMP:MiNRrDy	SingleCellHu...	PRJNA579593_	https://www....		30.51	20.00	25.00	18.88	5.56
1- glioblastoma (GBM) [temporal lobe] CMP_xrUc	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	oligodendro...	CMP:xrUgMo2	SingleCellHu...	PRJNA579593_	https://www....						-3.57
3- glioblastoma (GBM) [temporal lobe] CMP_aQK	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	astrocyte (clu...	CMP:aQK3oqV	SingleCellHu...	PRJNA579593_	https://www....						5.78
13- glioblastoma (GBM) [temporal lobe] CMP_YLZ	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	astrocyte;per...	CMP:YLZFFkMI	SingleCellHu...	PRJNA579593_	https://www....				70.71	17.68	
14- glioblastoma (GBM) [temporal lobe] CMP_jfCI	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	neural cell (cl...	CMP:jfCImeoly	SingleCellHu...	PRJNA579593_	https://www....		-4.47		69.60	16.28	2.23
11- glioblastoma (GBM) [temporal lobe] CMP_Qh	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	microglial ce...	CMP:QhOxGq	SingleCellHu...	PRJNA579593_	https://www....						6.04
2- glioblastoma (GBM) [temporal lobe] CMP_XEh	SingleCellHuman	glioblastom...	temporal lobe		Cluster vs Ot...	astrocyte (clu...	CMP:XEhtK2dk	SingleCellHu...	PRJNA579593_	https://www....		24.49		33.07	14.39	1.31
4- lung adenocarcinoma (LUAD) [lung] CMP_I5D2	SingleCellHuman	lung adenoc...	lung		Cluster vs Ot...	CD8+ tissue-...	CMP:I5D2HRB	SingleCellHu...	GSE111894_no	https://www....			-22.36		-5.59	-9.46
3- lung adenocarcinoma (LUAD);lung squamous c	SingleCellHuman	lung adenoc...	lung		Cluster vs Ot...	cytotoxic T c...	CMP:WLWni68	SingleCellHu...	GSE111894_no	https://www....			22.36		5.59	9.46
6- melanoma [skin] CMP_Dg2w7W7z3iKe	SingleCellHuman	melanoma	skin		Cluster vs Ot...	melanoma c...	CMP:Dg2w7W	SingleCellHu...	GSE81383_non	https://www....				67.31	16.83	5.94
5- melanoma [skin] CMP_bKrEvTh94Fzx	SingleCellHuman	melanoma	skin		Cluster vs Ot...	melanoma c...	CMP:bKrEvTh9	SingleCellHu...	GSE81383_non	https://www....		8.16		59.95	17.03	12.94
7- melanoma [skin] CMP_ZMp0SQEfcUV9	SingleCellHuman	melanoma	skin		Cluster vs Ot...	melanoma c...	CMP:ZMp0SQ	SingleCellHu...	GSE81383_non	https://www....		38.73		63.74	25.62	6.96
4- melanoma [skin] CMP_eE2PBgkEkulW	SingleCellHuman	melanoma	skin		Cluster vs Ot...	melanoma c...	CMP:eE2PBgk	SingleCellHu...	GSE81383_non	https://www....		8.16			2.04	1.87

Selected 0 / 78

Spatial RNA-seq

nature communications

Article

https://doi.org/10.1038/s41467-024-47271-y

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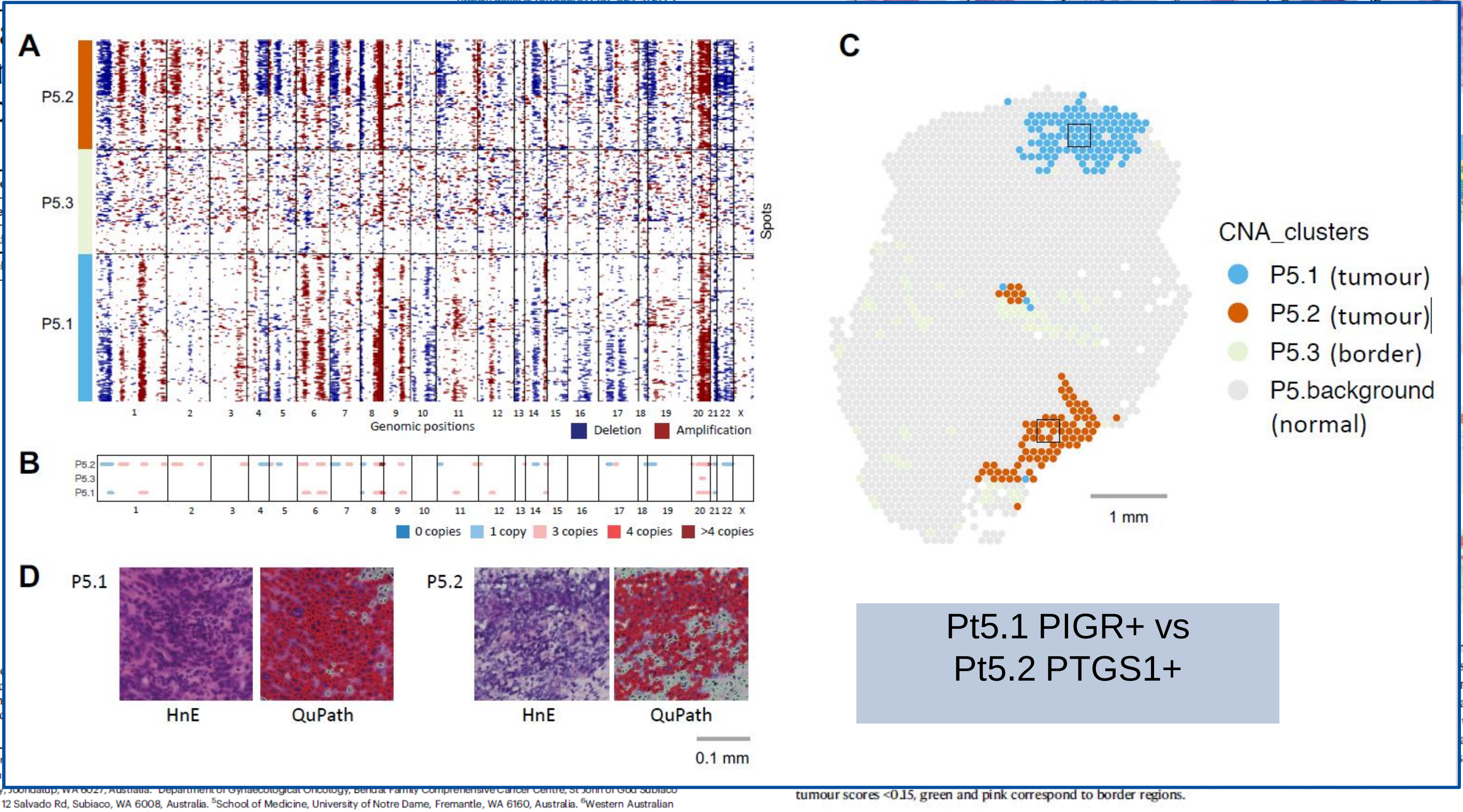
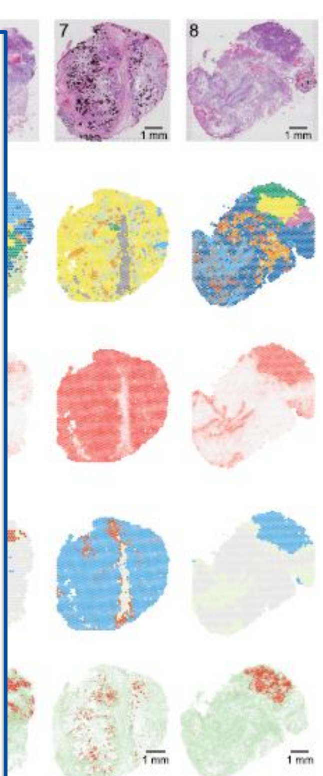


Pt5.1 PIGR+ vs
Pt5.2 PTGS1+



notation of the tissue sections using QuPath[67]. Red
s, green corresponds to stroma. Scale bar = 1 mm.
n **b** are arbitrary but highlight that unsupervised
ata using Seurat (**b**), and clustering of inferCNV
with spatial patterns that largely reflected the mor-
athology shown in **e**. Supplementary Fig. S19 shows
s summarising the relationship between the clusters

tumour scores <0.15, green and pink correspond to border regions.

Ovarian
worldwi
common
ovarian

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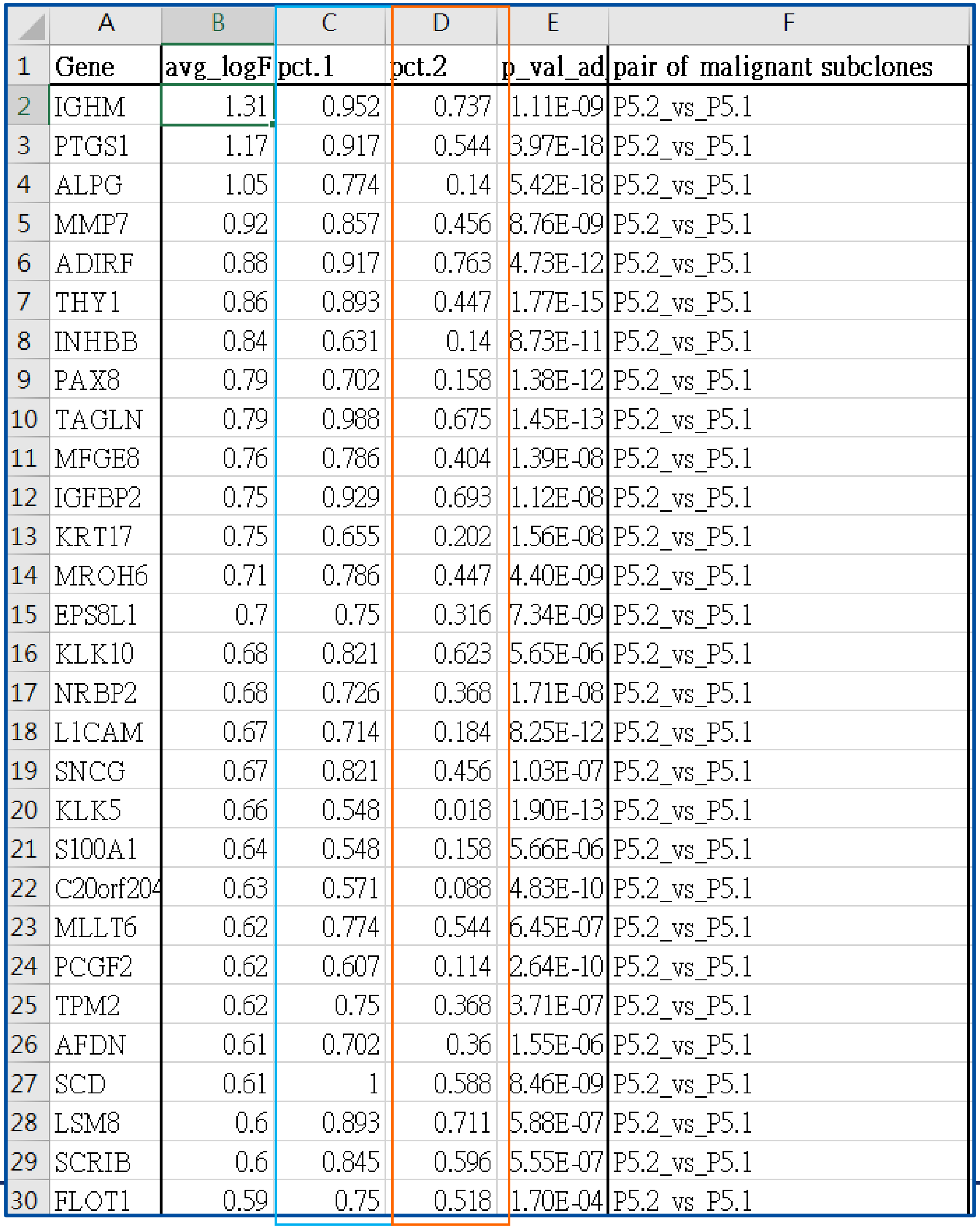
Nature Communications | (2024)15:2860 1

Case study – upload dataset

PIGR+ 腫瘤亞群

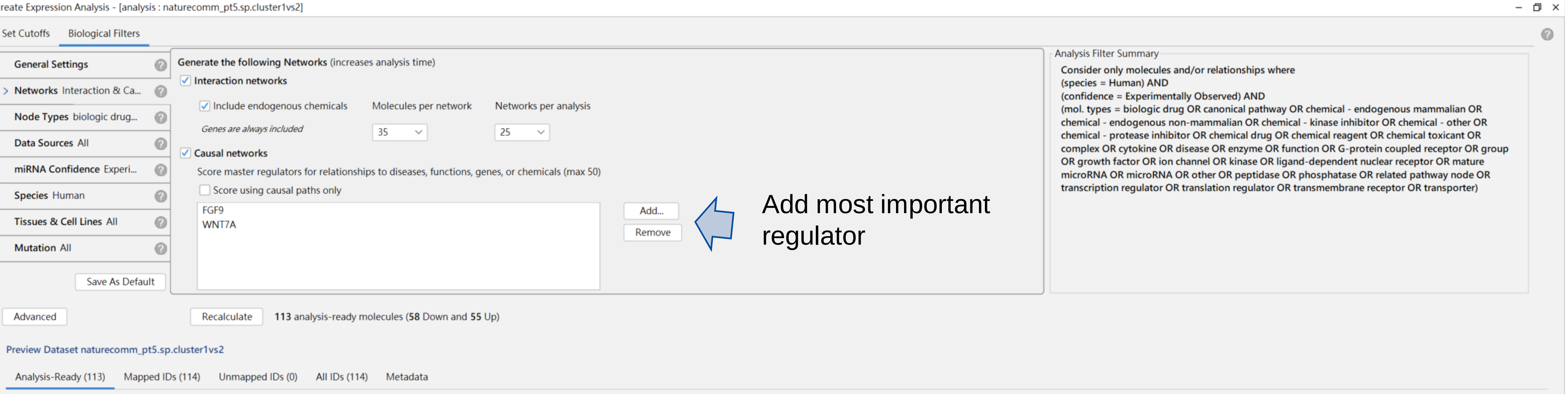
PTGS1+ 腫瘤亞群



	A	B	C	D	E	F
1	Gene	avg_logF	pct.1	pct.2	p_val_ad	pair of malignant subclones
2	IGHM	1.31	0.952	0.737	1.11E-09	P5.2_vs_P5.1
3	PTGS1	1.17	0.917	0.544	3.97E-18	P5.2_vs_P5.1
4	ALPG	1.05	0.774	0.14	5.42E-18	P5.2_vs_P5.1
5	MMP7	0.92	0.857	0.456	8.76E-09	P5.2_vs_P5.1
6	ADIRF	0.88	0.917	0.763	4.73E-12	P5.2_vs_P5.1
7	THY1	0.86	0.893	0.447	1.77E-15	P5.2_vs_P5.1
8	INHBB	0.84	0.631	0.14	8.73E-11	P5.2_vs_P5.1
9	PAX8	0.79	0.702	0.158	1.38E-12	P5.2_vs_P5.1
10	TAGLN	0.79	0.988	0.675	1.45E-13	P5.2_vs_P5.1
11	MFGE8	0.76	0.786	0.404	1.39E-08	P5.2_vs_P5.1
12	IGFBP2	0.75	0.929	0.693	1.12E-08	P5.2_vs_P5.1
13	KRT17	0.75	0.655	0.202	1.56E-08	P5.2_vs_P5.1
14	MROH6	0.71	0.786	0.447	4.40E-09	P5.2_vs_P5.1
15	EPS8L1	0.7	0.75	0.316	7.34E-09	P5.2_vs_P5.1
16	KLK10	0.68	0.821	0.623	5.65E-06	P5.2_vs_P5.1
17	NRBP2	0.68	0.726	0.368	1.71E-08	P5.2_vs_P5.1
18	L1CAM	0.67	0.714	0.184	8.25E-12	P5.2_vs_P5.1
19	SNCG	0.67	0.821	0.456	1.03E-07	P5.2_vs_P5.1
20	KLK5	0.66	0.548	0.018	1.90E-13	P5.2_vs_P5.1
21	S100A1	0.64	0.548	0.158	5.66E-06	P5.2_vs_P5.1
22	C20orf204	0.63	0.571	0.088	4.83E-10	P5.2_vs_P5.1
23	MLLT6	0.62	0.774	0.544	6.45E-07	P5.2_vs_P5.1
24	PCGF2	0.62	0.607	0.114	2.64E-10	P5.2_vs_P5.1
25	TPM2	0.62	0.75	0.368	3.71E-07	P5.2_vs_P5.1
26	AFDN	0.61	0.702	0.36	1.55E-06	P5.2_vs_P5.1
27	SCD	0.61	1	0.588	8.46E-09	P5.2_vs_P5.1
28	LSM8	0.6	0.893	0.711	5.88E-07	P5.2_vs_P5.1
29	SCRIB	0.6	0.845	0.596	5.55E-07	P5.2_vs_P5.1
30	FLOT1	0.59	0.75	0.518	1.70E-04	P5.2_vs_P5.1

Casual Network

To find the Root nodes



reate Expression Analysis - [analysis : naturecomm_pt5.sp.cluster1vs2]

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

Generate the following Networks (increases analysis time)

☑ **Interaction networks**

☑ Include endogenous chemicals

Genes are always included

Molecules per network: 35

Networks per analysis: 25

☑ **Causal networks**

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

☐ Score using causal paths only

FGF9
WNT7A

Add most important regulator

Analysis Filter Summary

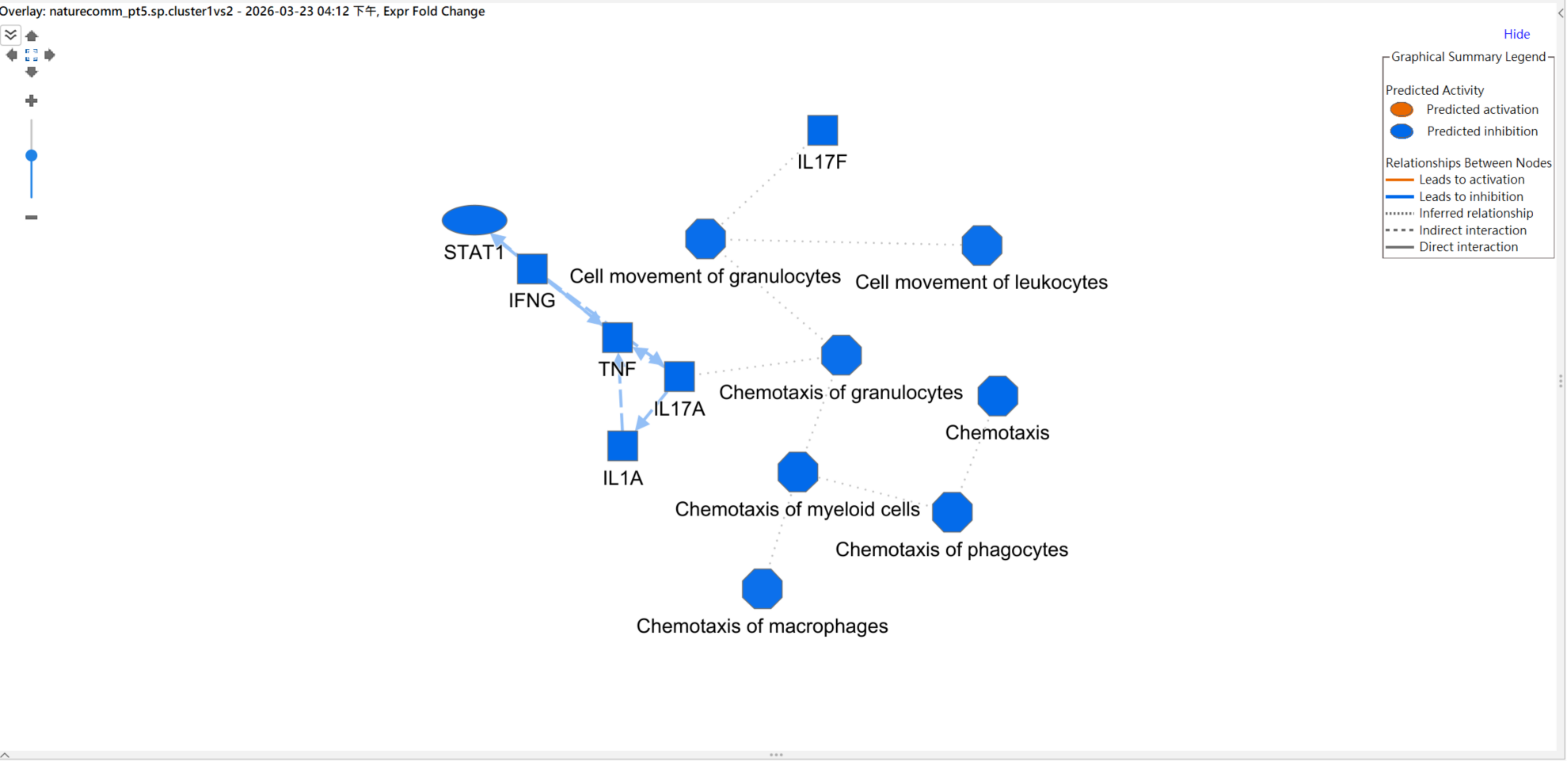
Consider only molecules and/or relationships where (species = Human) AND (confidence = Experimentally Observed) AND (mol. types = biologic drug OR canonical pathway OR chemical - endogenous mammalian OR chemical - endogenous non-mammalian OR chemical - kinase inhibitor OR chemical - other OR chemical - 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)

113 analysis-ready molecules (**58** Down and **55** Up)

Preview Dataset naturecomm_pt5.sp.cluster1vs2

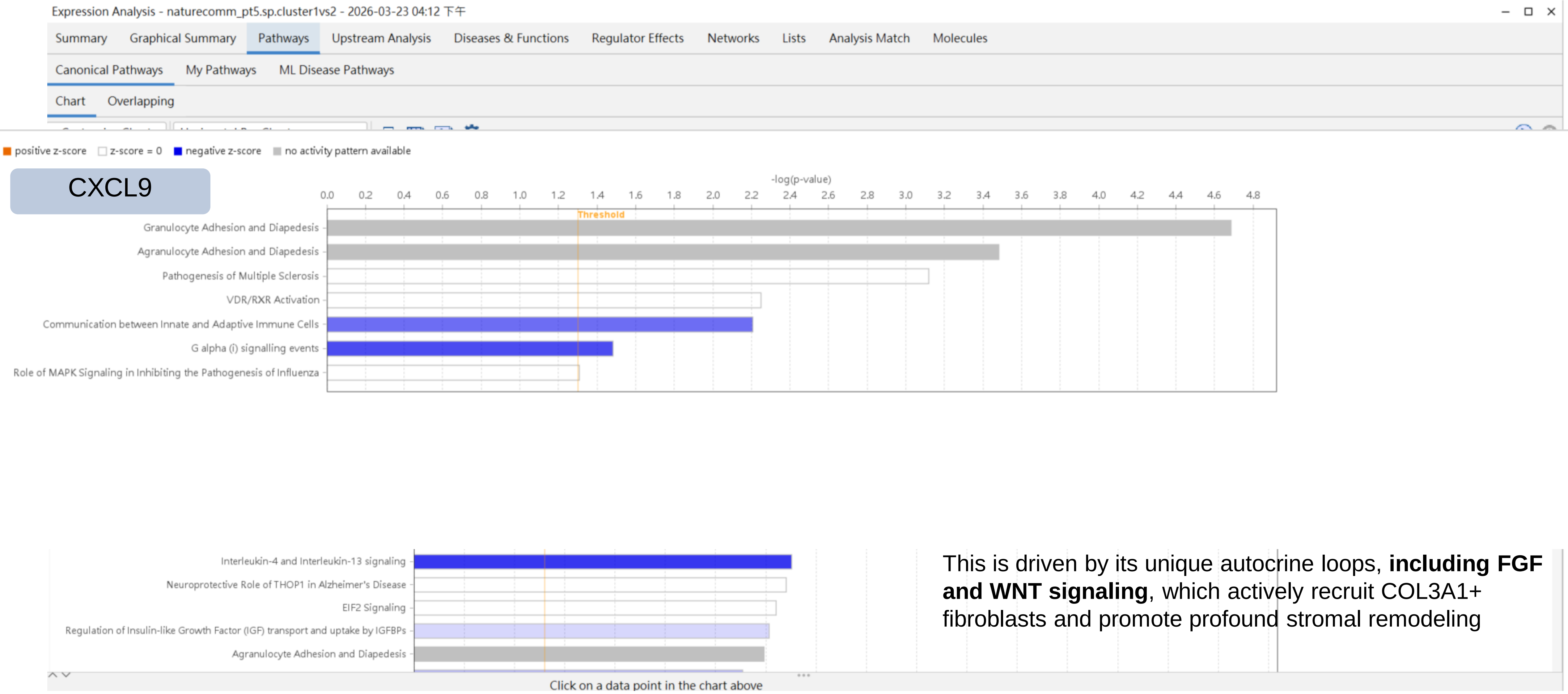
PTGS+ activate FGF9/FGF18 -> FGFR1/2/3
FGF18 and FGFR1/2 poorly survival and implicated in cisplatin resistant

Graphical summary



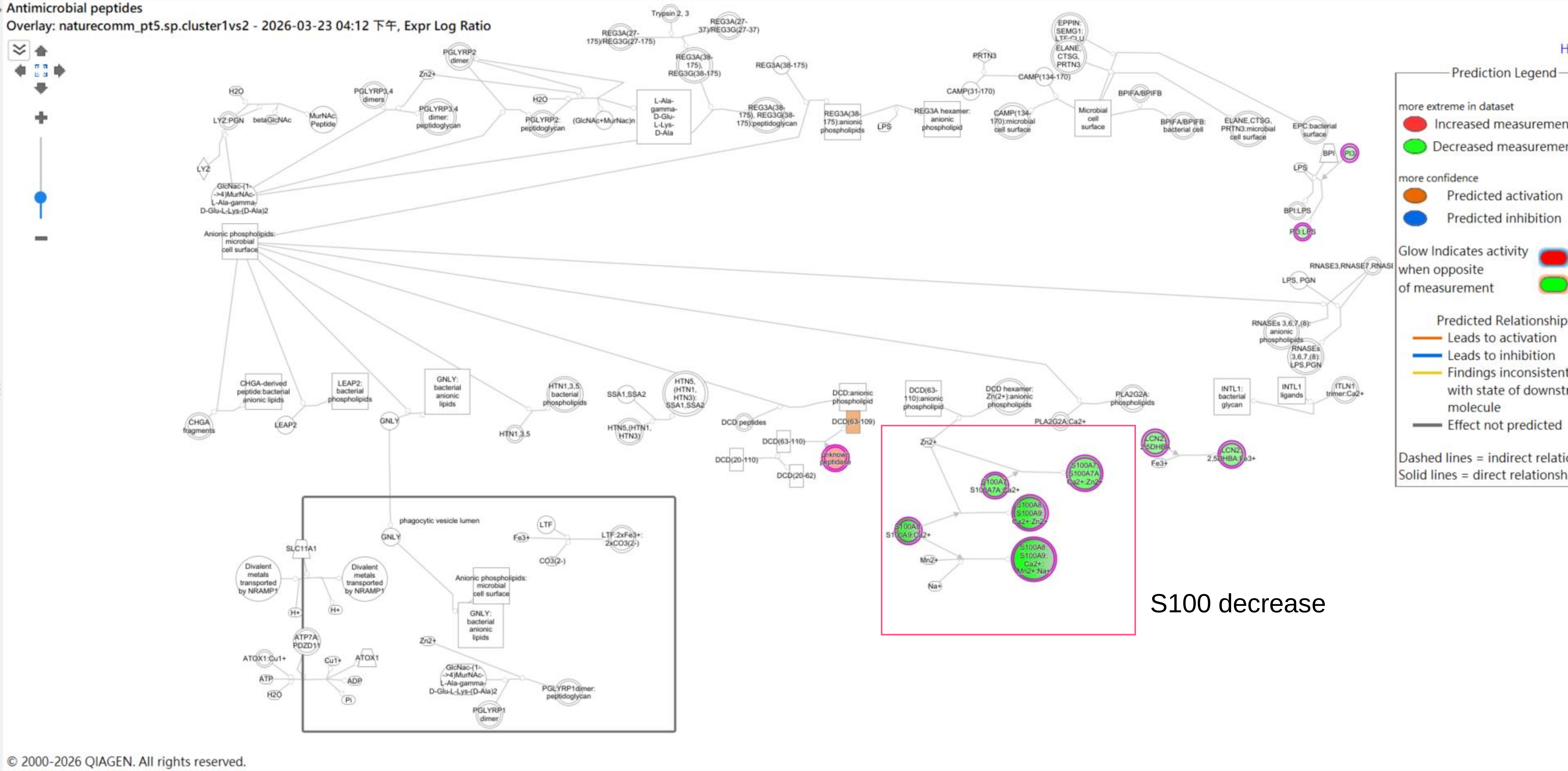
Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Fold Change

Canonical Pathway



Expression Analysis - naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午

This is driven by its unique autocrine loops, **including FGF and WNT signaling**, which actively recruit COL3A1+ fibroblasts and promote profound stromal remodeling

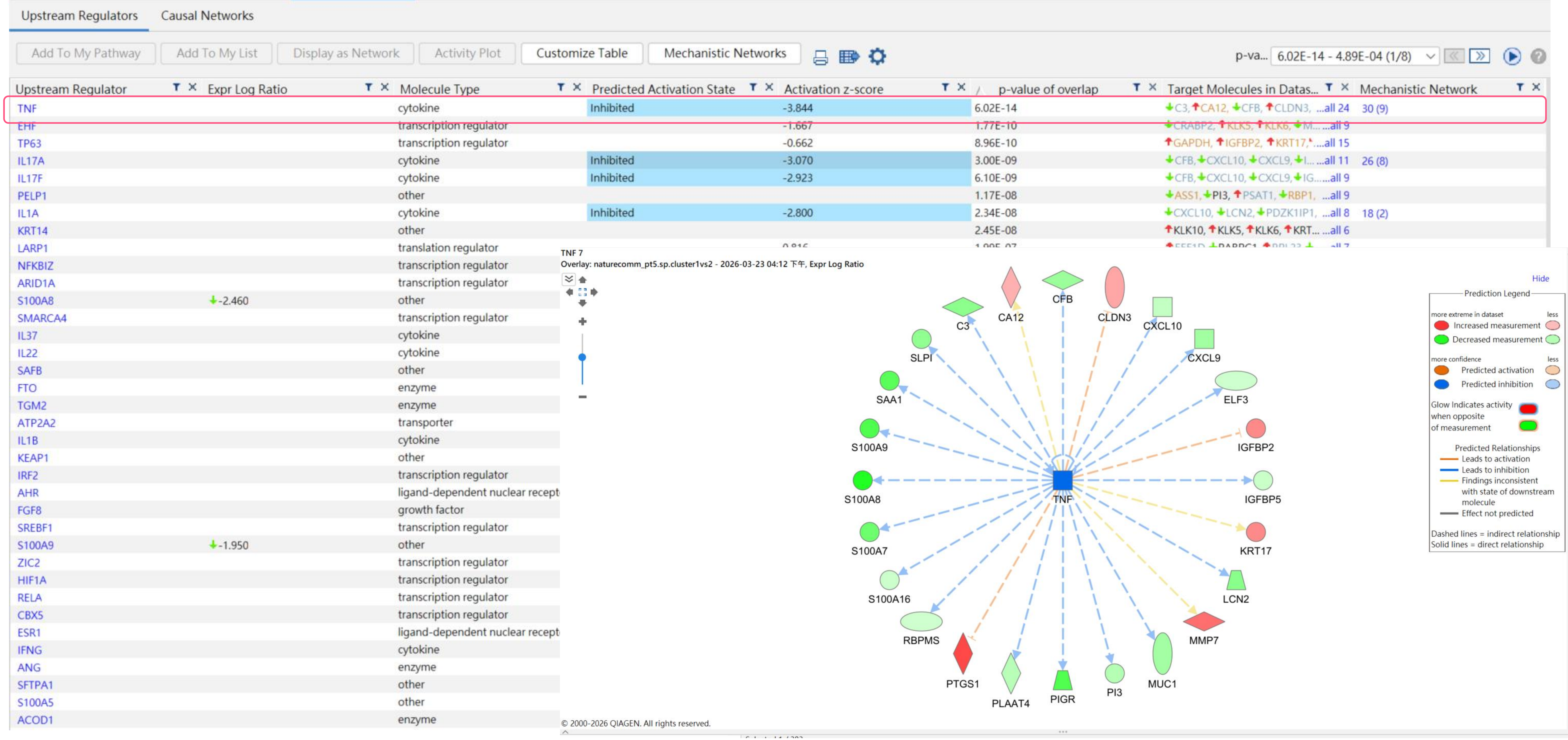


Antimicrobial peptides

Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Log Ratio

S100 decrease

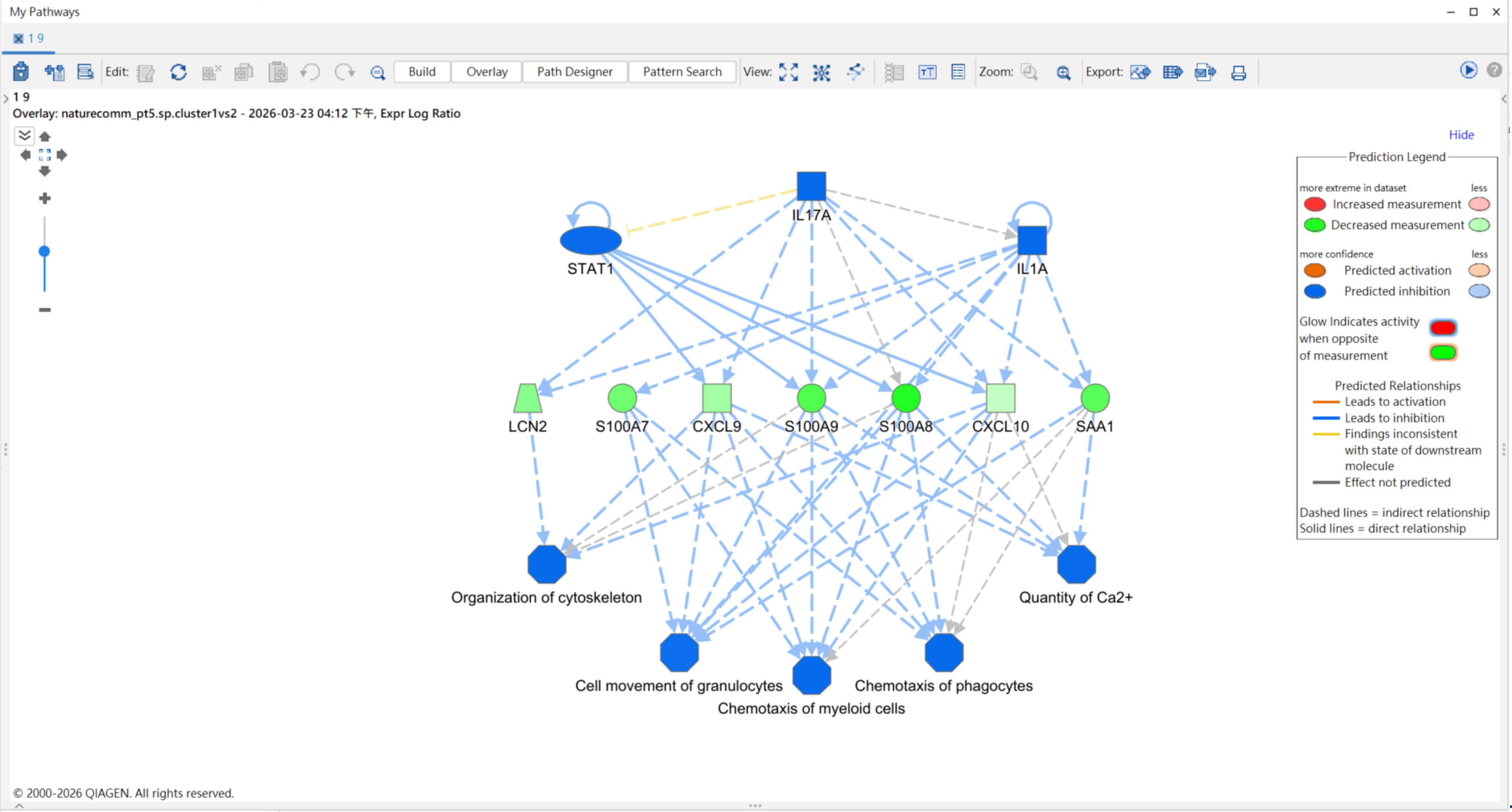
Upstream regulator



Upstream Regulator	Expr Log Ratio	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap	Target Molecules in Datas...	Mechanistic Network
TNF		cytokine	Inhibited	-3.844	6.02E-14	↓C3, ↑CA12, ↓CFB, ↑CLDN3, ...all 24	30 (9)
EHF		transcription regulator		-1.667	1.77E-10	↓CRABP2, ↑KLK5, ↑KLK6, ↓M... ...all 9	
TP63		transcription regulator		-0.662	8.96E-10	↑GAPDH, ↑IGFBP2, ↑KRT17, ...all 15	
IL17A		cytokine	Inhibited	-3.070	3.00E-09	↓CFB, ↓CXCL10, ↓CXCL9, ↓I... ...all 11	26 (8)
IL17F		cytokine	Inhibited	-2.923	6.10E-09	↓CFB, ↓CXCL10, ↓CXCL9, ↓IG... ...all 9	
PELP1		other			1.17E-08	↓ASS1, ↓PI3, ↑PSAT1, ↓RBP1, ...all 9	
IL1A		cytokine	Inhibited	-2.800	2.34E-08	↓CXCL10, ↓LCN2, ↓PDZK1IP1, ...all 8	18 (2)
KRT14		other			2.45E-08	↑KLK10, ↑KLK5, ↑KLK6, ↑KRT... ...all 6	
LARP1		translation regulator		0.816	1.09E-07	...all 7	
NFKBIZ		transcription regulator					
ARID1A		transcription regulator					
S100A8	↓-2.460	other					
SMARCA4		transcription regulator					
IL37		cytokine					
IL22		cytokine					
SAFB		other					
FTO		enzyme					
TGM2		enzyme					
ATP2A2		transporter					
IL1B		cytokine					
KEAP1		other					
IRF2		transcription regulator					
AHR		ligand-dependent nuclear recept					
FGF8		growth factor					
SREBF1		transcription regulator					
S100A9	↓-1.950	other					
ZIC2		transcription regulator					
HIF1A		transcription regulator					
RELA		transcription regulator					
CBX5		transcription regulator					
ESR1		ligand-dependent nuclear recept					
IFNG		cytokine					
ANG		enzyme					
SFTPA1		other					
S100A5		other					
ACOD1		enzyme					

TNF 7
Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Log Ratio

Regular effect



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Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Log Ratio

Prediction Legend

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

more confidence		less
🟠	Predicted activation	●
🔵	Predicted inhibition	●

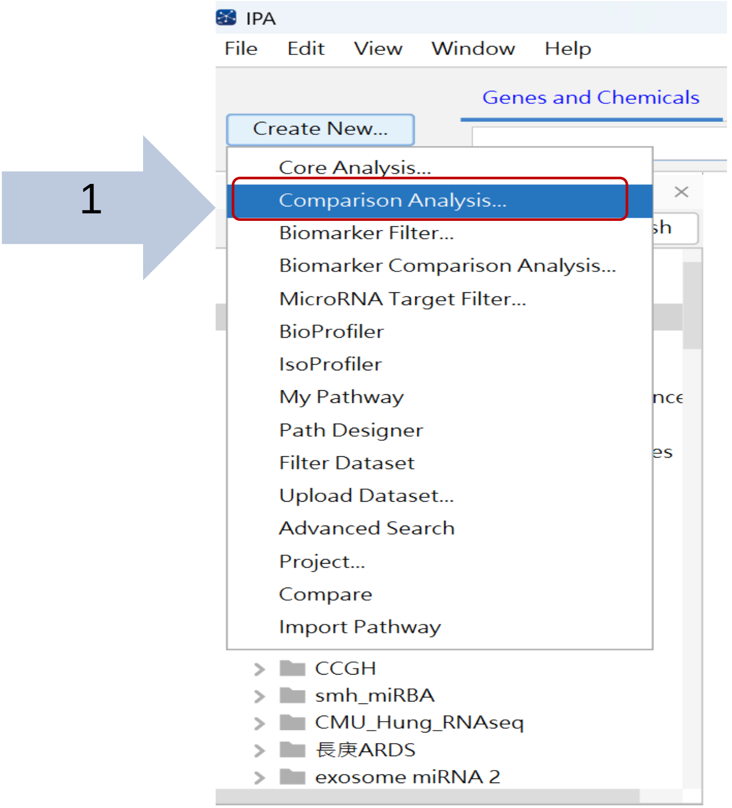
Glow Indicates activity when opposite of measurement

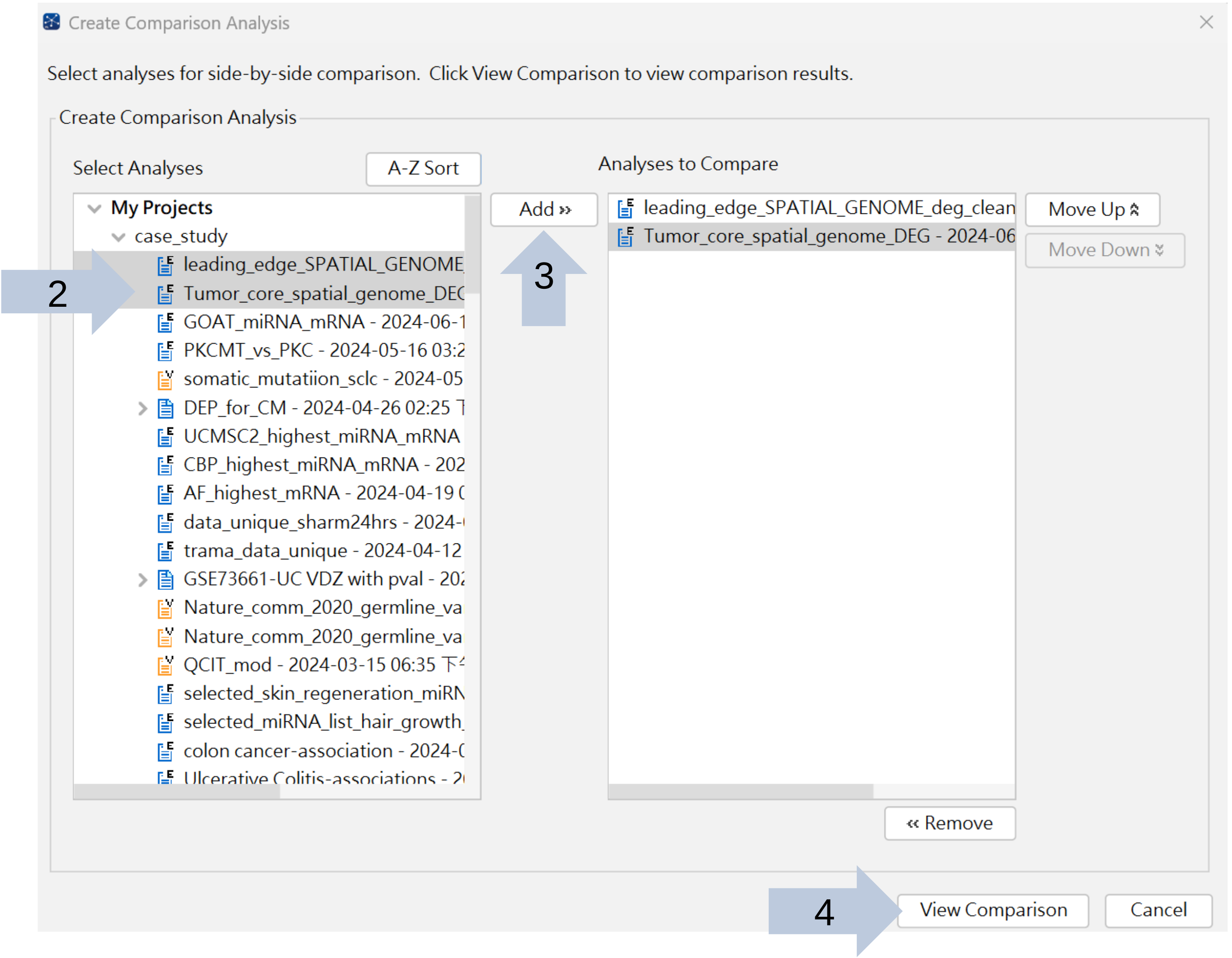
Predicted Relationships
- Leads to activation
- Leads to inhibition
- Findings inconsistent with state of downstream molecule
- Effect not predicted

Dashed lines = indirect relationship
Solid lines = direct relationship

Compare Analysis

Step for You to do your compared analysis





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

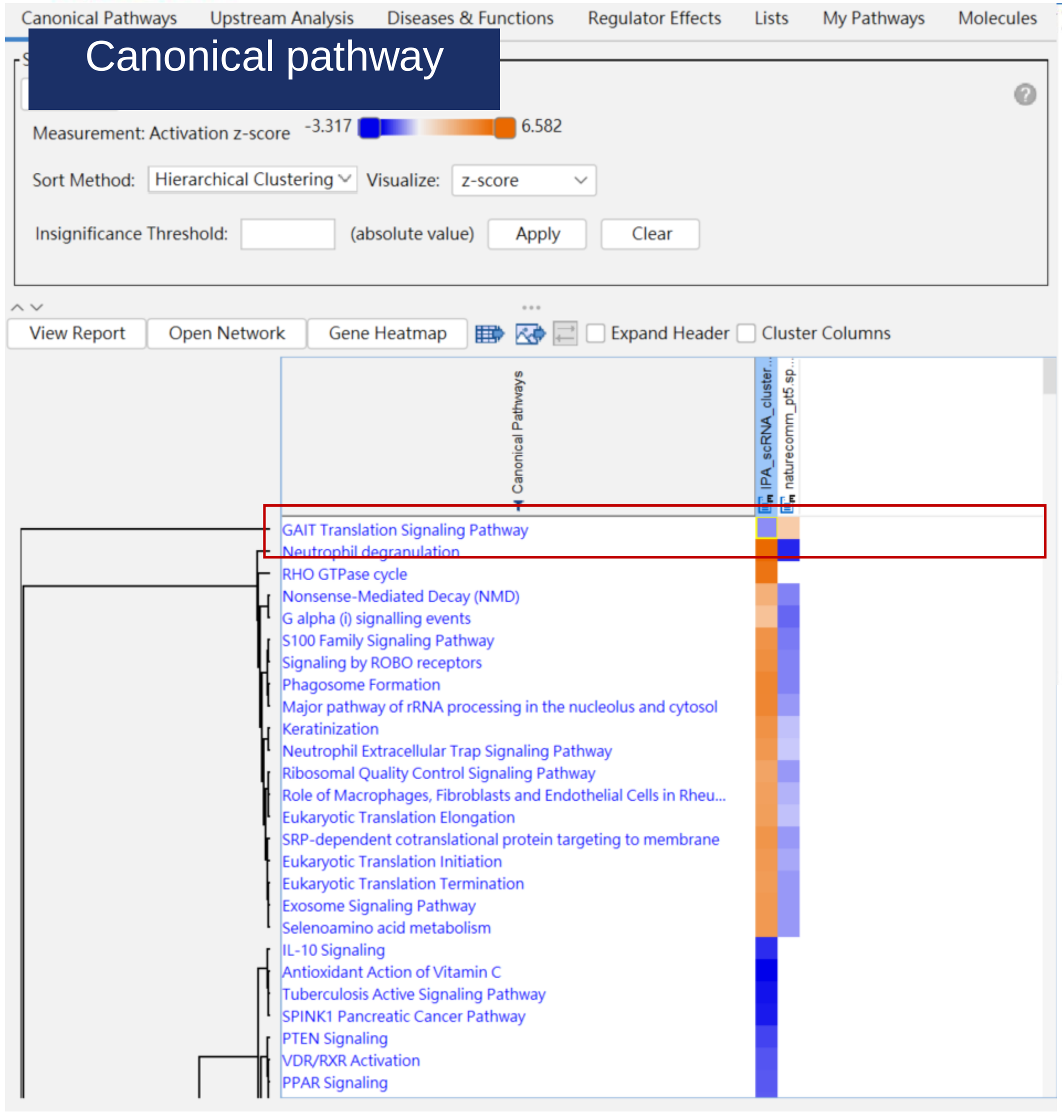
Select Analyses:

- My Projects
  - case_study
    - leading_edge_SPATIAL_GENOME
    - Tumor_core_spatial_genome_DEG
    - GOAT_miRNA_mRNA - 2024-06-1
    - PKCMT_vs_PKC - 2024-05-16 03:2
    - somatic_mutatiion_sclc - 2024-05
    - DEP_for_CM - 2024-04-26 02:25
    - UCMSC2_highest_miRNA_mRNA
    - CBP_highest_miRNA_mRNA - 202
    - AF_highest_mRNA - 2024-04-19
    - data_unique_sharm24hrs - 2024-
    - trama_data_unique - 2024-04-12
    - GSE73661-UC VDZ with pval - 202
    - Nature_comm_2020_germline_va
    - Nature_comm_2020_germline_va
    - QCIT_mod - 2024-03-15 06:35 下
    - selected_skin_regeneration_miRN
    - selected_miRNA_list_hair_growth_
    - colon cancer-association - 2024-
    - Ulcerative Colitis-associations - 2

Analyses to Compare:

- leading_edge_SPATIAL_GENOME_deg_clean
- Tumor_core_spatial_genome_DEG - 2024-06

Compare Analysis Result



Canonical pathway

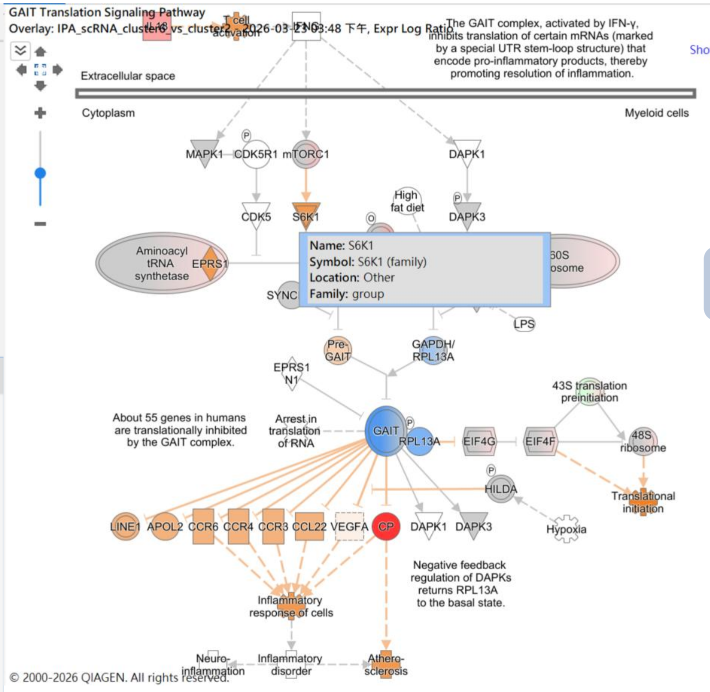
Measurement: Activation z-score -3.317 6.582

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value)

- GAIT Translation Signaling Pathway
- Neutrophil degranulation
- RHO GTPase cycle
- Nonsense-Mediated Decay (NMD)
- G alpha (i) signalling events
- S100 Family Signaling Pathway
- Signaling by ROBO receptors
- Phagosome Formation
- Major pathway of rRNA processing in the nucleolus and cytosol
- Keratinization
- Neutrophil Extracellular Trap Signaling Pathway
- Ribosomal Quality Control Signaling Pathway
- Role of Macrophages, Fibroblasts and Endothelial Cells in Rheu...
- Eukaryotic Translation Elongation
- SRP-dependent cotranslational protein targeting to membrane
- Eukaryotic Translation Initiation
- Eukaryotic Translation Termination
- Exosome Signaling Pathway
- Selenoamino acid metabolism
- IL-10 Signaling
- Antioxidant Action of Vitamin C
- Tuberculosis Active Signaling Pathway
- SPINK1 Pancreatic Cancer Pathway
- PTEN Signaling
- VDR/RXR Activation
- PPAR Signaling



GAIT Translation Signaling Pathway

Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Log Ratio

The GAIT complex, activated by IFN-γ, inhibits translation of certain mRNAs (marked by a special UTR stem-loop structure) that encode pro-inflammatory products, thereby promoting resolution of inflammation.

Show Legend

Name: S6K1
Symbol: S6K1 (family)
Location: Other
Family: group

About 55 genes in humans are translationally inhibited by the GAIT complex.

Negative feedback regulation of DAPKs returns RPL13A to the basal state.

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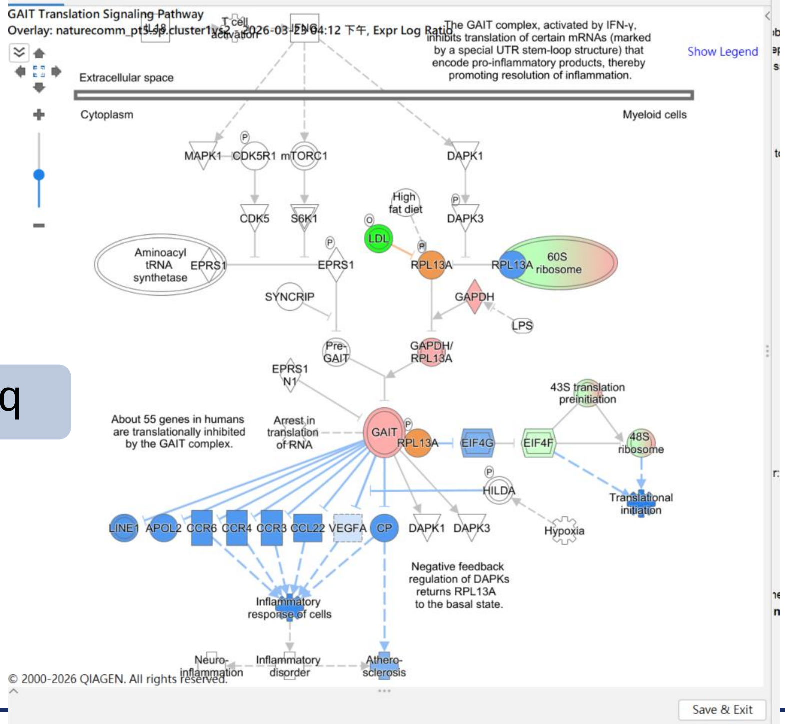
scRNA



GAIT Translation Signaling Pathway

Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Log Ratio

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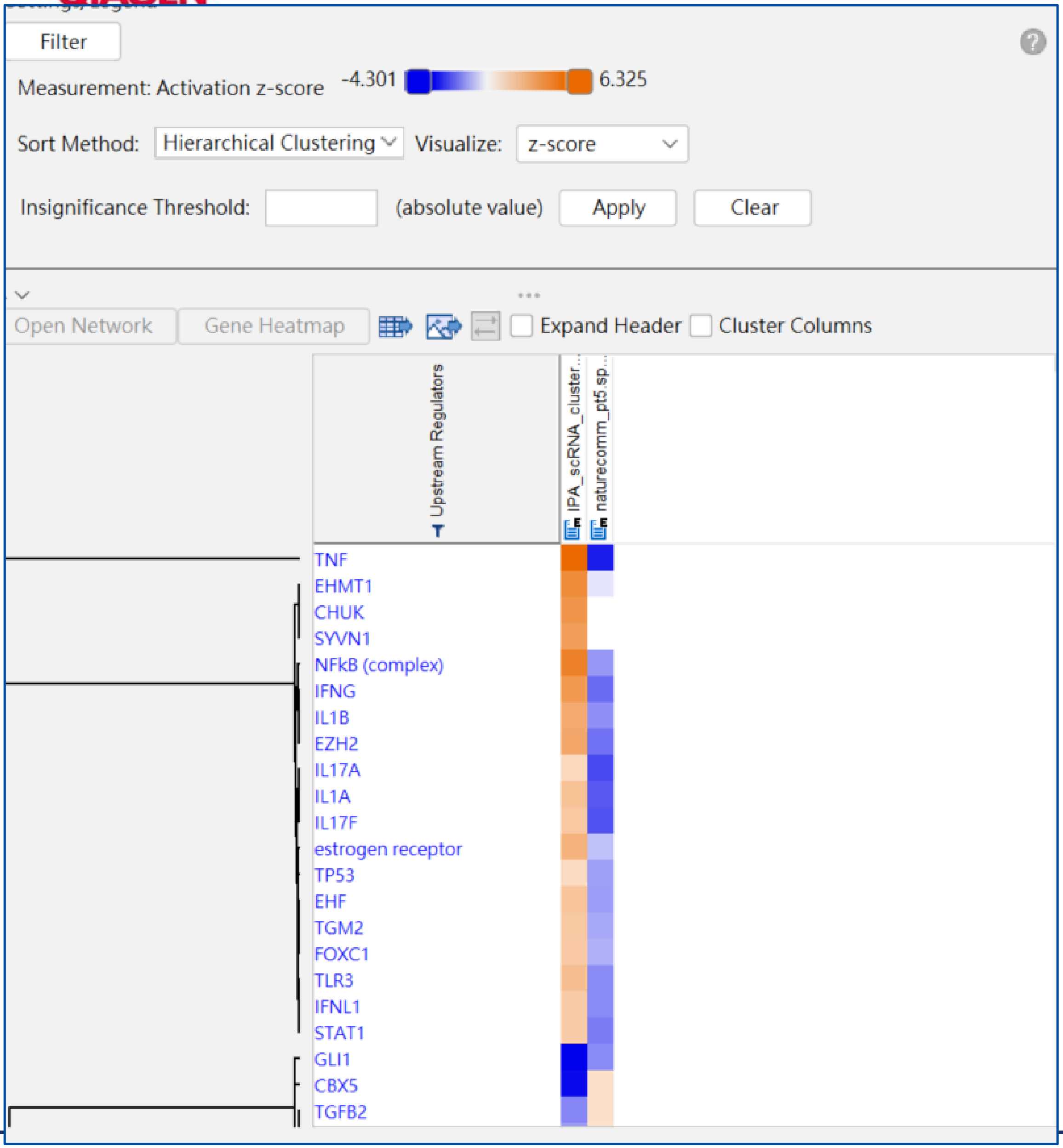
Spatial RNA-seq

QIAGEN

Upstream regulator

訊聯基因數位



Filter

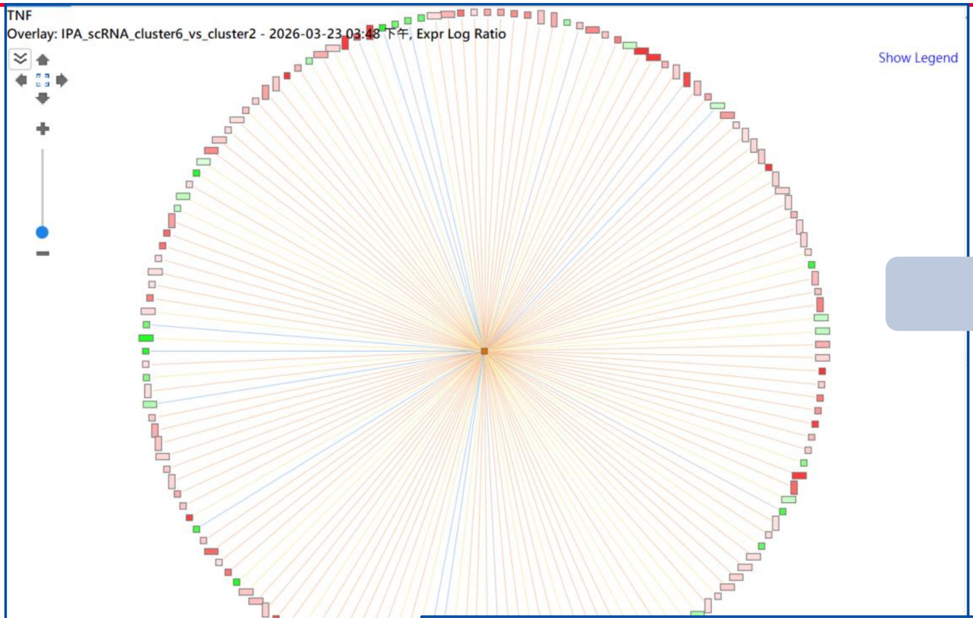
Measurement: Activation z-score -4.301 6.325

Sort Method: Hierarchical Clustering

Visualize: z-score

Insignificance Threshold: (absolute value)

TNF
EHMT1
CHUK
SYVN1
NFkB (complex)
IFNG
IL1B
EZH2
IL17A
IL1A
IL17F
estrogen receptor
TP53
EHF
TGM2
FOXC1
TLR3
IFNL1
STAT1
GLI1
CBX5
TGFB2

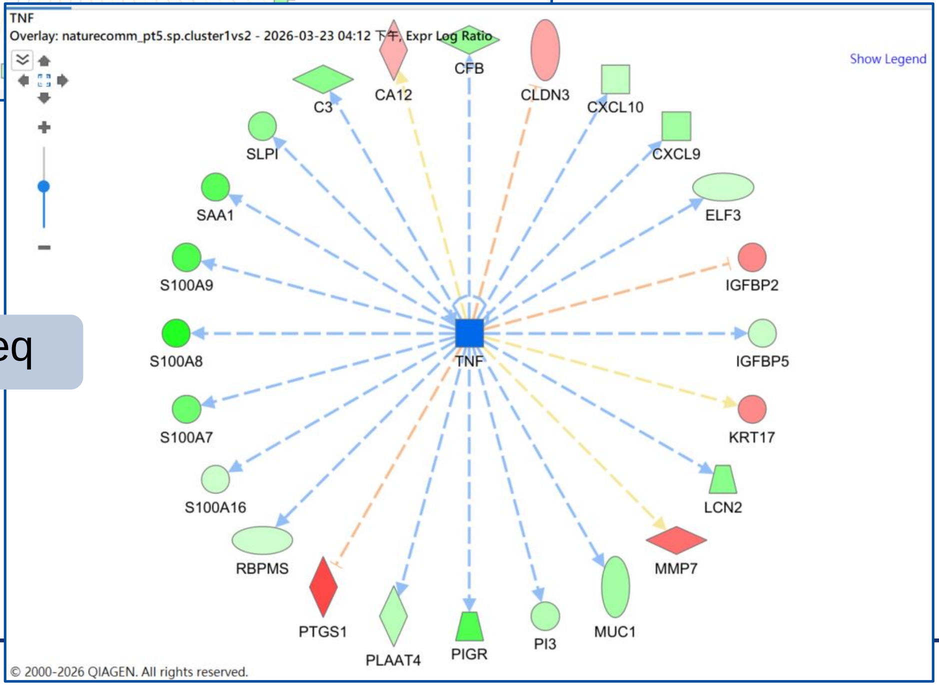


TNF

Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Log Ratio

scRNA

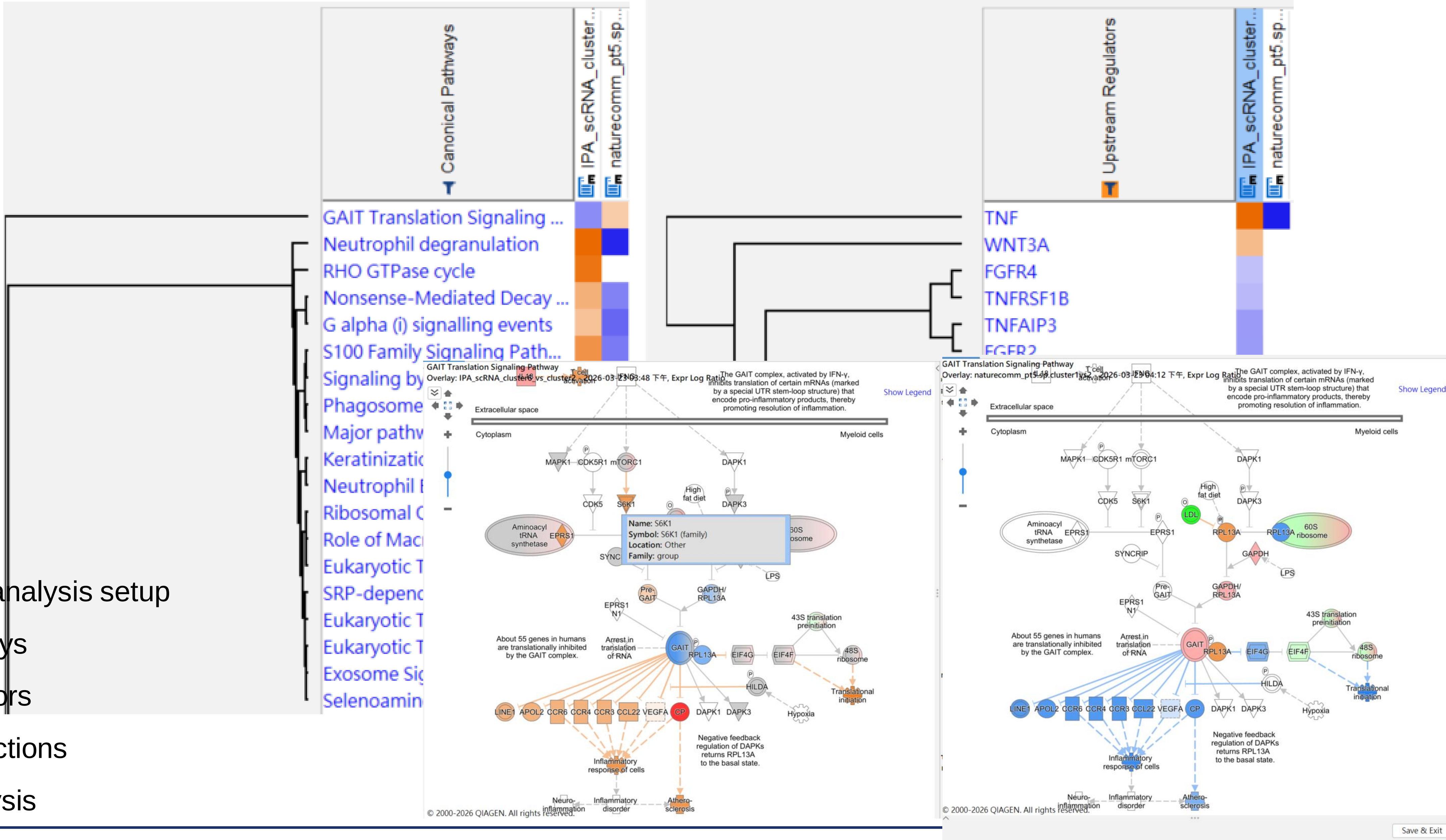
Spatial RNA-seq



TNF

Overlay: naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午, Expr Log Ratio

Summary: Evaluating your ′omics data using IPA



Canonical Pathways	IPA_scRNA_cluster…	naturecomm_pt5.sp…
GAIT Translation Signaling ...		
Neutrophil degranulation		
RHO GTPase cycle		
Nonsense-Mediated Decay ...		
G alpha (i) signalling events		
S100 Family Signaling Path...		
Signaling by		
Phagosome		
Major pathw		
Keratinizatic		
Neutrophil I		
Ribosomal (		
Role of Mac		
Eukaryotic T		
SRP-depend		
Eukaryotic T		
Eukaryotic T		
Exosome Sic		
Selenoamin		

Upstream Regulators	IPA_scRNA_cluster…	naturecomm_pt5.sp…
TNF		
WNT3A		
FGFR4		
TNFRSF1B		
TNFAIP3		
FGFR2		

GAIT Translation Signaling Pathway
Overlay: IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午, Expr Log Ratio

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