

Translating Multi-Omics Data into Target Discovery and Translational Medicine



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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.

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 \(ingenuity.com\)](https://analysis.ingenuity.com/pa/installer/select)

Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

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

Module 1 | IPA in Drug Discovery and Translational Medicine

Module 2 | Transcriptomics and Drug Mechanism of Action

- Case Study: BOLD-100 in Colorectal Cancer

Module 3 | miRNA Regulation and Natural Compound Mechanisms

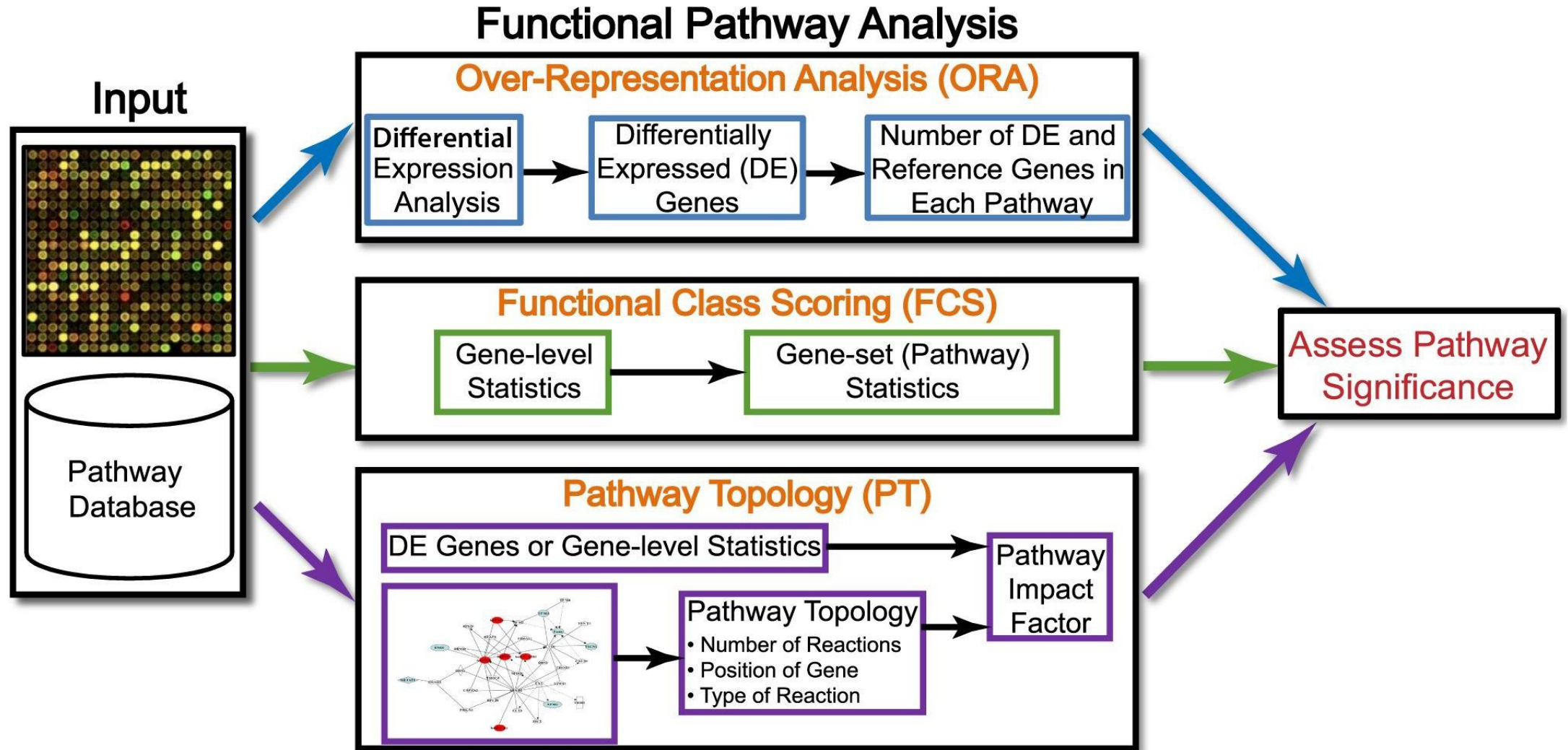
- Case Study: Ugonin V in Chondrosarcoma

Module 4 | Comparative Analysis and Candidate Target Discovery

- Case Studies: Immunotherapy Resistance and Single-Cell Heterogeneity

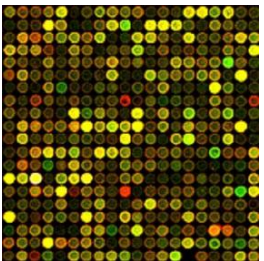
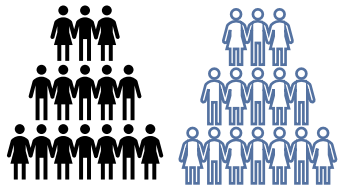
Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer



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

Your dataset



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

Drugs and chemicals

Pathway

Disease

Function

Network

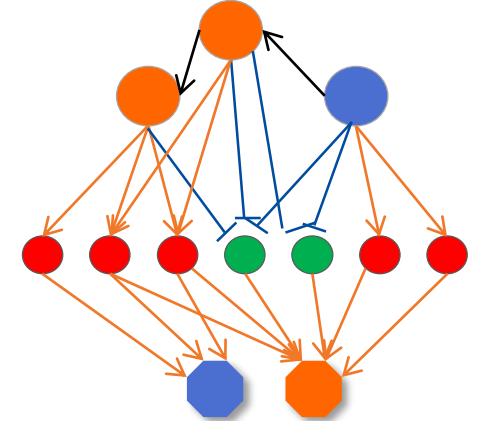
ORA/FCS/Topology
Pathway Analysis

Public
/commercial
database



Machine
learning

What do they
relate to each
other?



What are the
relationship
between each
molecules?

From 2020-2026
1,698 literatures

> 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.

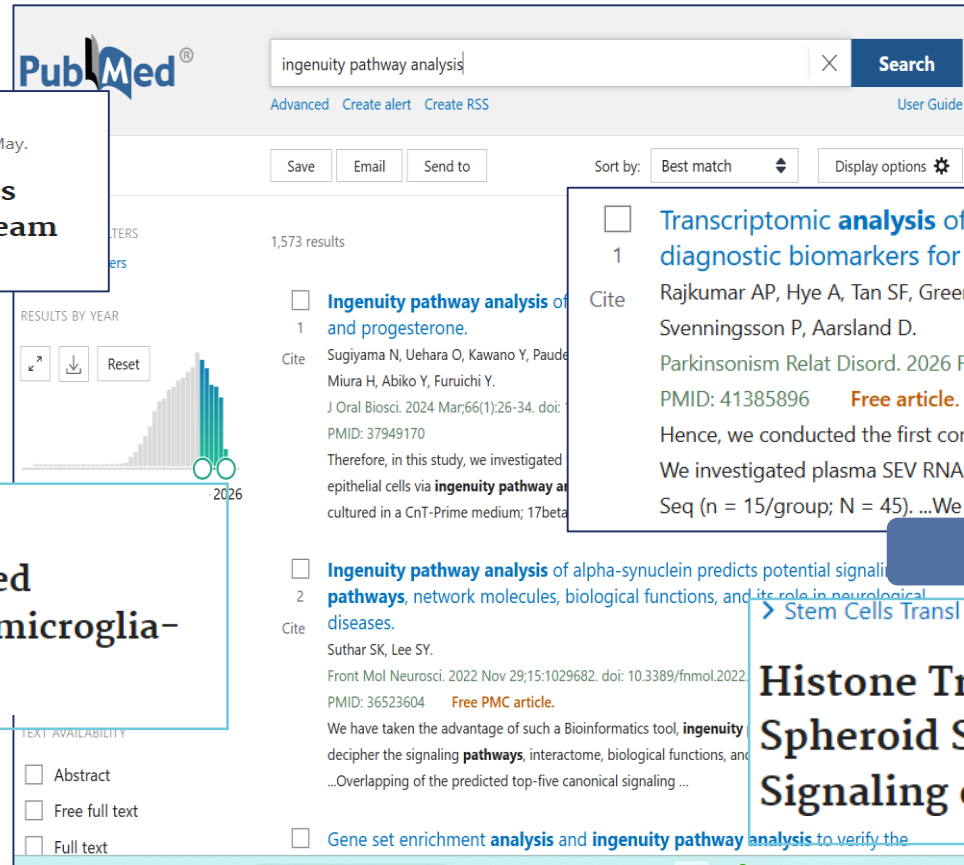
Deletion of Slc9a1 in Cx3cr1⁺ cells stimulated microglial subcluster CREB1 signaling and microglia-oligodendrocyte crosstalk

transcriptomic

> 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

proteomics



Transcriptomic analysis of plasma small extracellular vesicles identifies potential diagnostic biomarkers for Parkinson's disease dementia.

Cite Rajkumar AP, Hye A, Tan SF, Green H, Killick R, Nizamudeen Z, Isik FB, Figueredo G, Ballard C, Svenningsson P, Aarsland D. Parkinsonism Relat Disord. 2026 Feb;143:108150. doi: 10.1016/j.parkreldis.2025.108150. Epub 2025 Dec 9. PMID: 41385896 **Free article.** Hence, we conducted the first comprehensive transcriptomic **analysis** of PDD plasma SEV. METHODS: We investigated plasma SEV RNA of PDD, PD, and people without PD or dementia (Controls) using RNA-Seq (n = 15/group; N = 45). ...We identified differentially expressed genes (DE ...

exosome

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

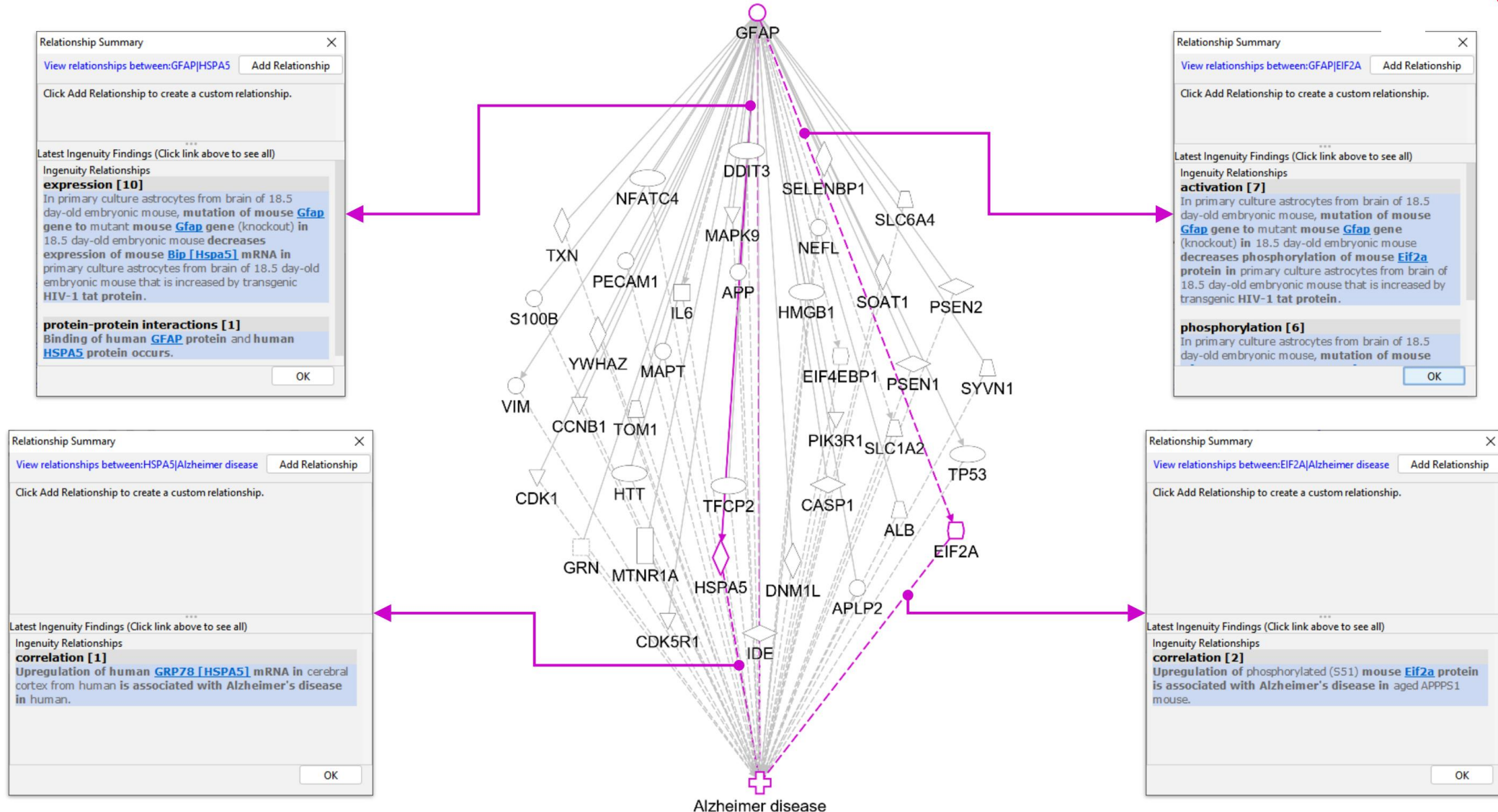
Histone Trimethylations and HDAC5 Regulate Spheroid Subpopulation and Differentiation Signaling of Human Adipose-Derived Stem Cells

Single-cell RNA-seq

> 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



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

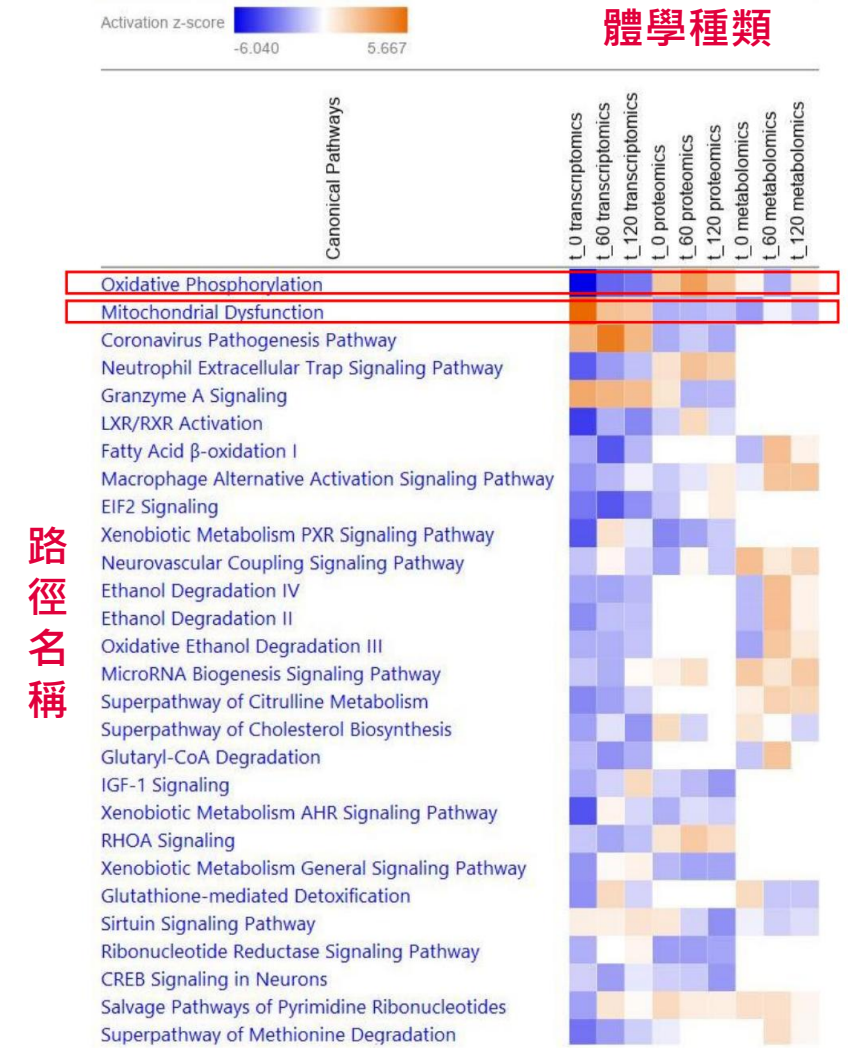
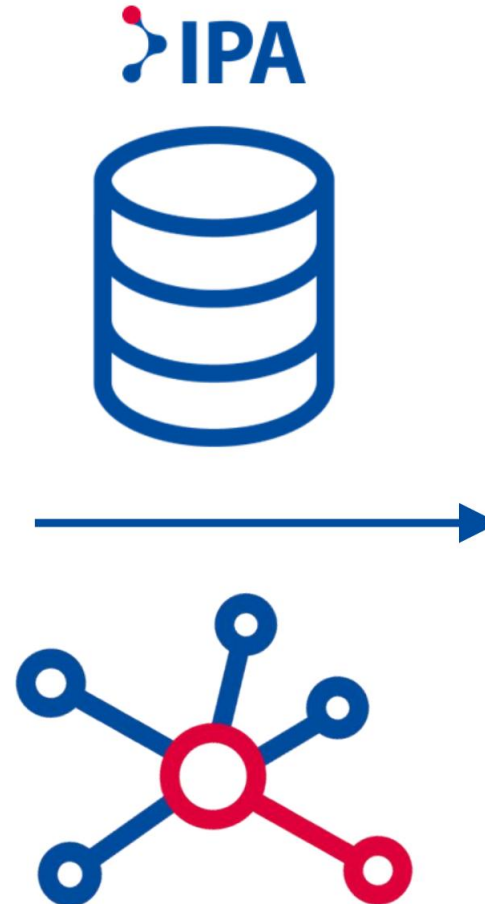
Orthologs Gene from NCBI Eukaryotic Genome
Annotation Pipeline

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					

Omics data type

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



IPA

File Edit View Window Help

Genes and Chemicals

Diseases and Functions

Pathways and Lists

Datasets and Analyses

Create New...

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

Search

Advanced Search

Process RNA-seq data

QIAGEN Land Explorer

Project Manager

Search Results

Provide Feedback | Support

Gene Chen

Close IPA

Molecule Annotations

Add To My Pathway

Add To My List

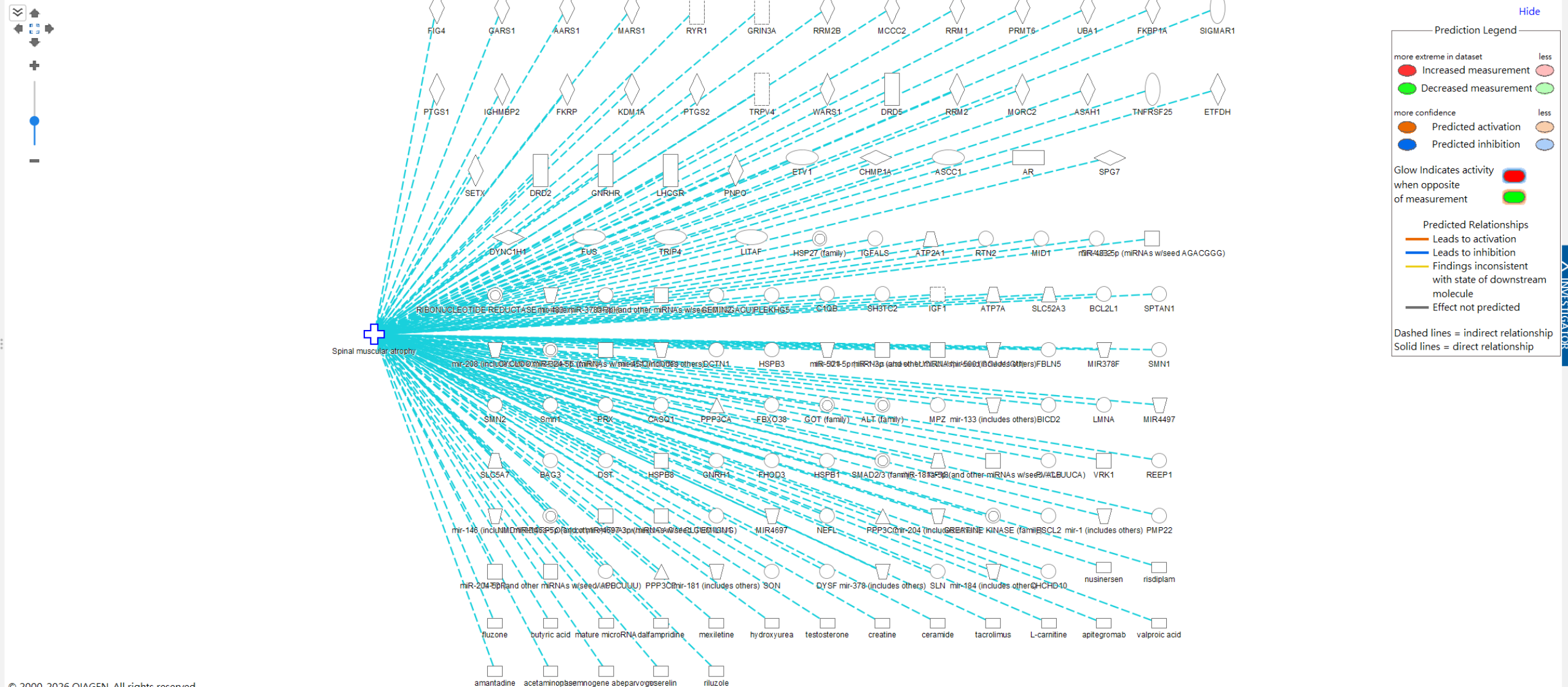
Create Dataset

Customize Table

Symbol AARS1 - NEFL (1/2)

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

Selected/Total molecules: 0/144



Machine Learning pathway

Other pathway type

Genes and Chemicals

Diseases and Functions

Pathways and Lists

Datasets and Analyses

Create New...

spinal

Type

Select row(s) to be filtered in table.

☐ Select/Deselect all

☒ ML Disease Pathways

☐ Metabolic pathway

☐ My List

☐ My aop

☐ My pathway

☐ Reactome pathway

☐ Signaling pathway

☐ Tox List

OK

Cancel

Search Results

Pathways and Lists

Add To My Pathway

Add To My List

View Report

Activity Plot

Customize Table



The search for spinal matched 16 items.

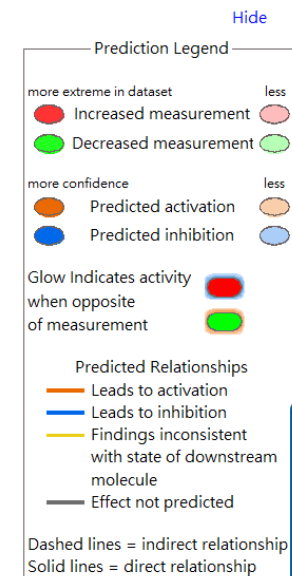
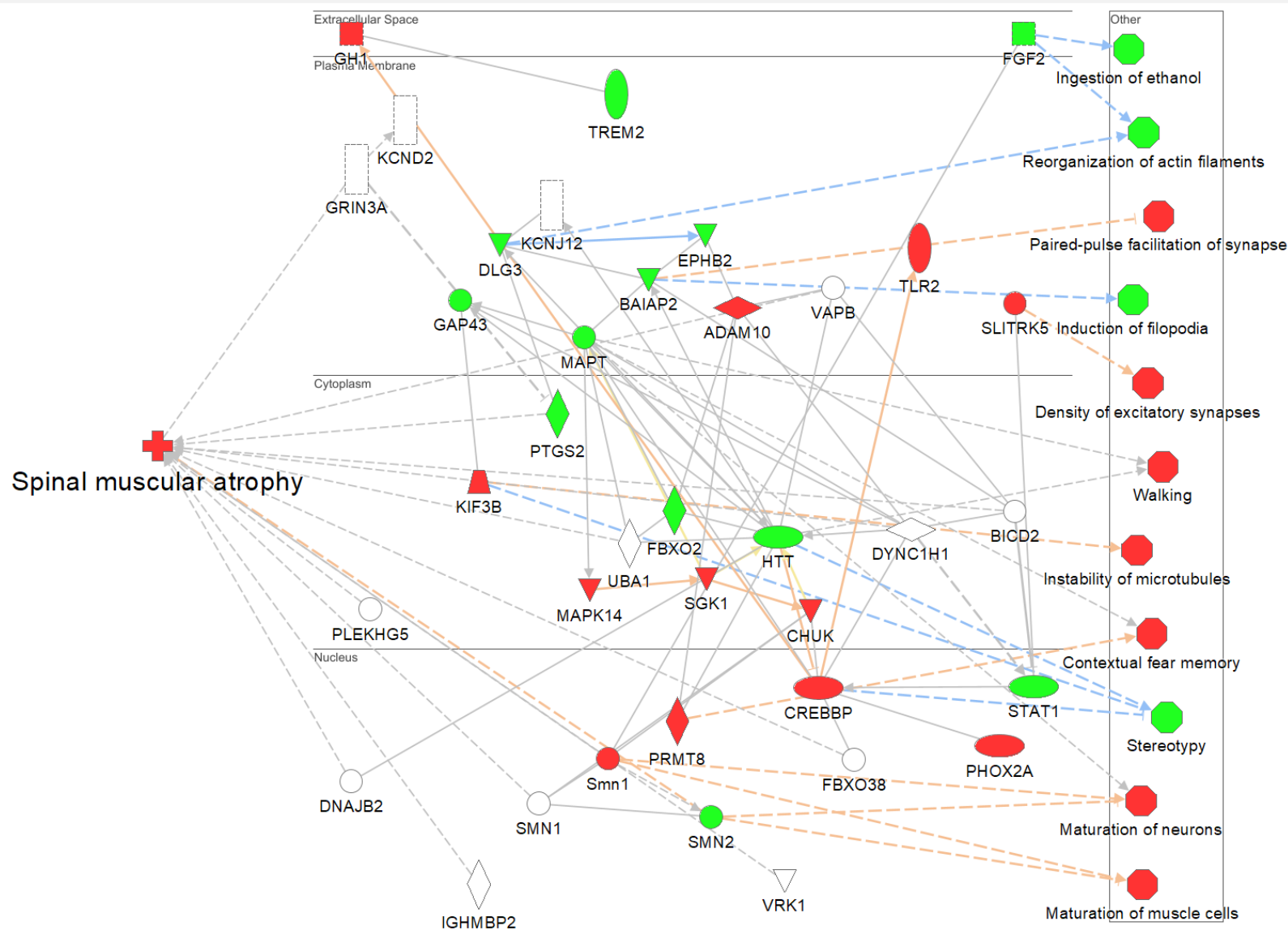
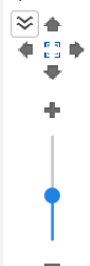
☐	#	Name	Matched Term	Pathway Category	Type	Location
☐	0	Spinal muscular atrophy	Spinal muscular atrophy	My pathway	My pathway	My Pro
☐	1	Spinal muscular atrophy	Spinal muscular atrophy	ML Disease Pathways	ML Disease Pathways	Librarie
☐	2	Oxytocin in Spinal Neurons Signaling Pathway		Neurotransmitters and Ot	Signaling pathway	ingenu
☐	3	SMN growrh SMA	diagnosis - spinal muscular atrophy,Spinal muscular atrophy	My pathway	My pathway	My Pro
☐	4	Path Designer SMN1 SMA	Spinal muscular atrophy	My pathway	My pathway	My Pro
☐	5	SMN1 SMA	Spinal muscular atrophy	My pathway	My pathway	My Pro
☐	6	SMN_SMA	Spinal muscular atrophy	My pathway	My pathway	My Pro
☐	7	Gastrointestinal dysmotility	Activation of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	8	RAR Activation	Development of spinal cord,Neurogenesis of spinal cord	Ingenuity Toxicity List Path	Signaling pathway	ingenu
☐	9	Behavioral deficit	Quantity of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	10	Dyssomnia	Quantity of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	11	Chorea	Activation of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	12	Familial neurological disorder	Activation of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	13	Degenerative brain disorder	Activation of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	14	Familial insulin resistance	Quantity of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie
☐	15	Familial psychiatric disease	Activation of spinal neuron	ML Disease Pathways	ML Disease Pathways	Librarie

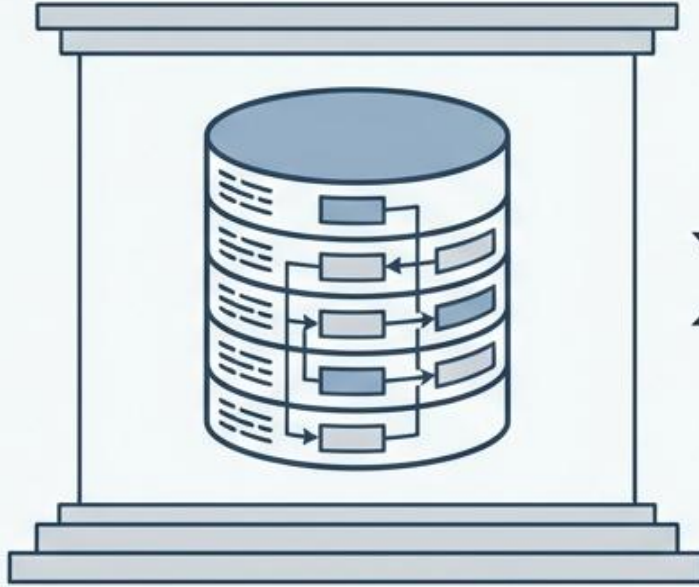


Spinal muscu...



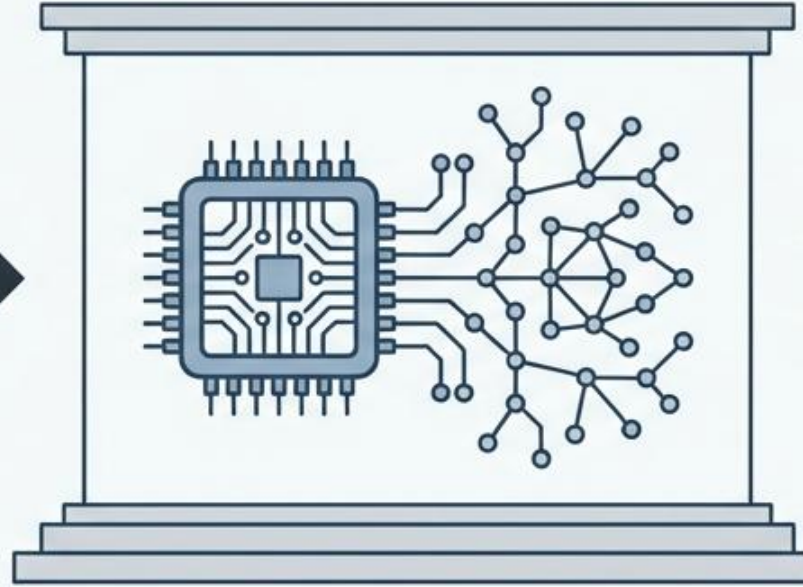
Spinal muscular atrophy





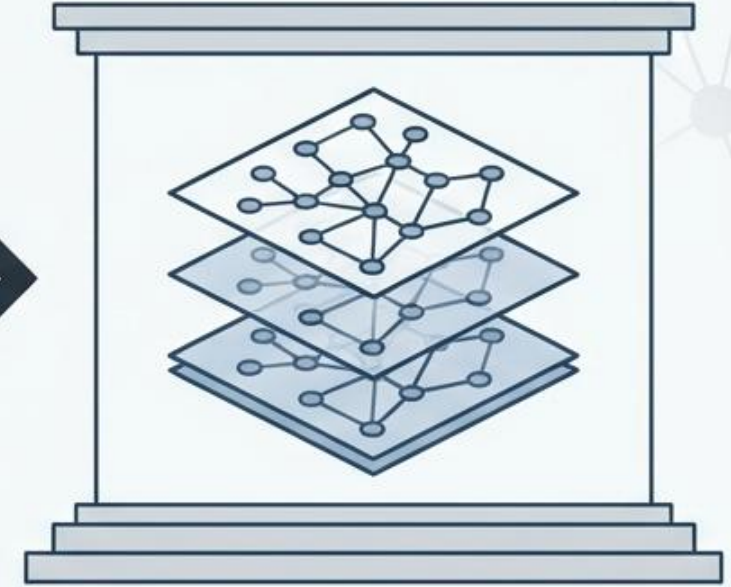
The Source: QIAGEN Knowledge Base

Mining decades of **causal findings**.



The Engine: Machine Learning Generation

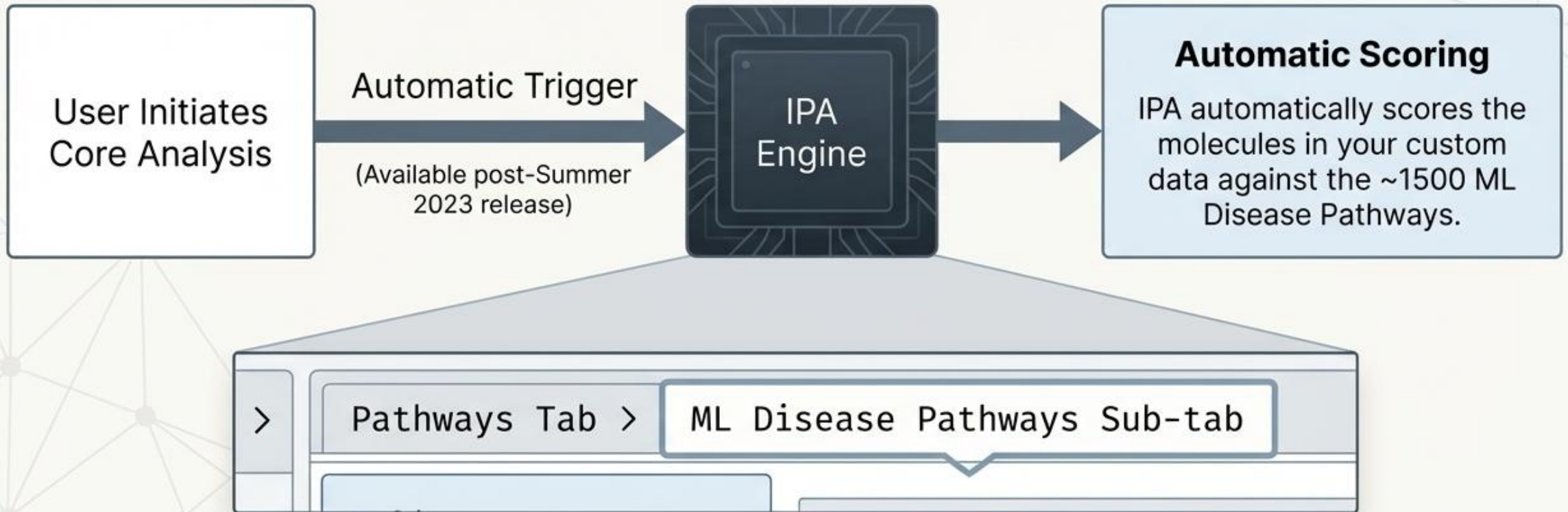
Automated creation of **~1500 disease, phenotype, and function pathways** to prioritize **key causal genes**.



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**.





Prioritized Causal Focus

~1500 pathways built purely on automated KB mining, independent of expression data.



Predictive Power

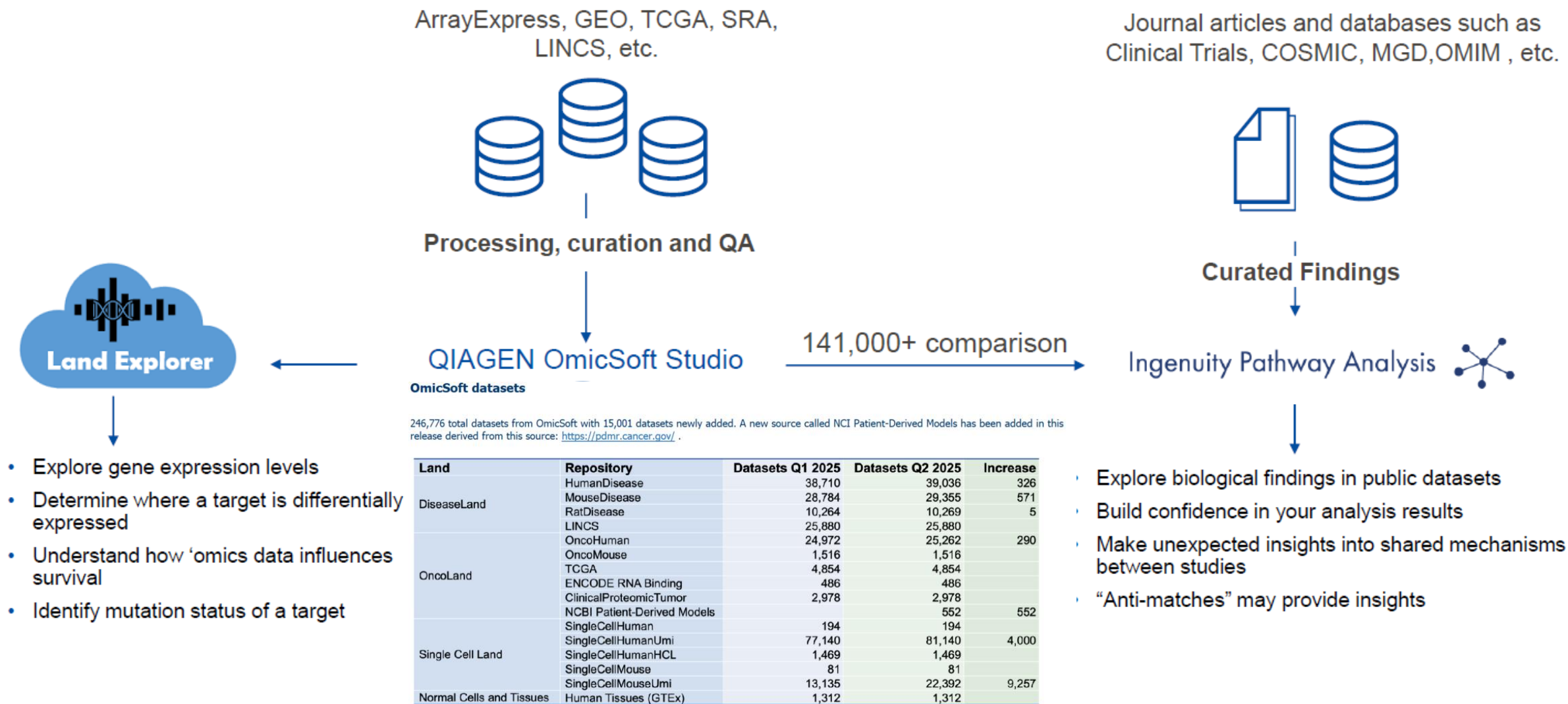
Red/Green activity nodes hypothesize novel participants through shared regulatory patterns.



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.

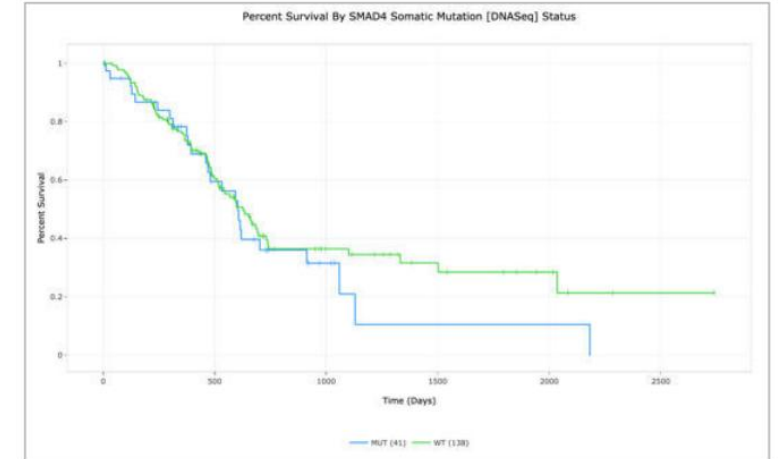




Expression in Rat, Mouse, and Human Disease



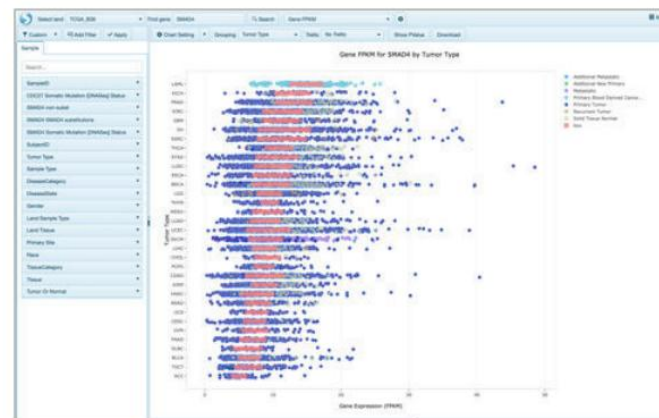
Mutation frequency



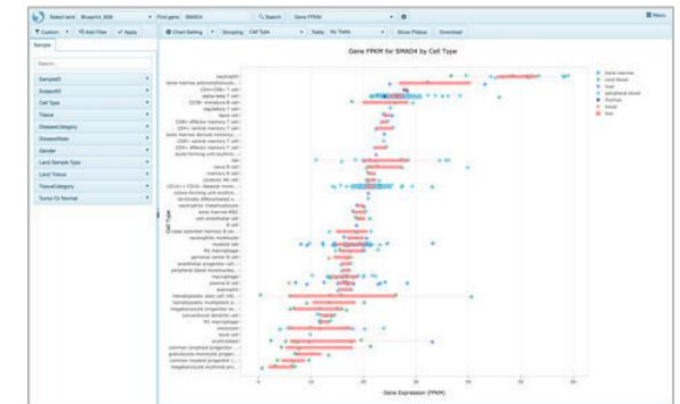
Survival plots



Cell line expression



Tumor expression



Hematopoietic expression (BluePrint)

QIAGEN Land Explorer

Genes and Chemicals | Diseases and Functions | Pathways and Lists | Datasets and Analyses

Create New... | Search | Advanced Search

Project Manager | Search Results

My Projects

- smh_miRBA
- CMU_Hung_RNAseq
- QDARDS
- exosome miRNA 2
- exosome miRNA
- 2023-demo
- Isoform
- HTCH_Dr.Liu_2022-12-16
- NDMC1020
- CGU_20221018
- TMU0816
- BIONET
- CMUHuang

Search Results

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, Erb1, ERBP, HER1, HER1 (EGFR), MENA, NISBD2, PIG61, wa-2, Wa5	epidermal growth factor receptor	Plasma Membran

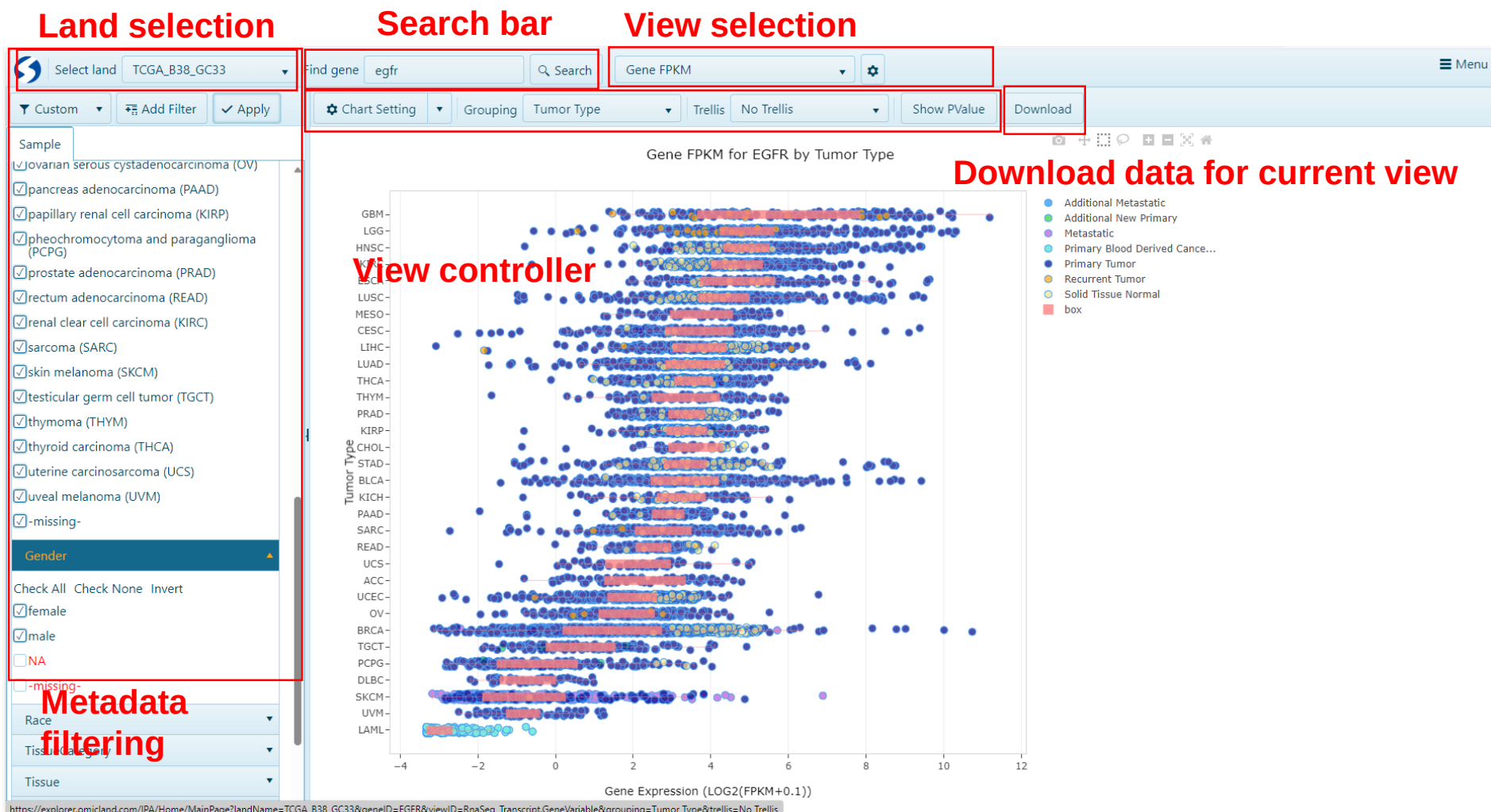
Choose which you want

OmicSoft Land Explorer: Sample-level experimental data

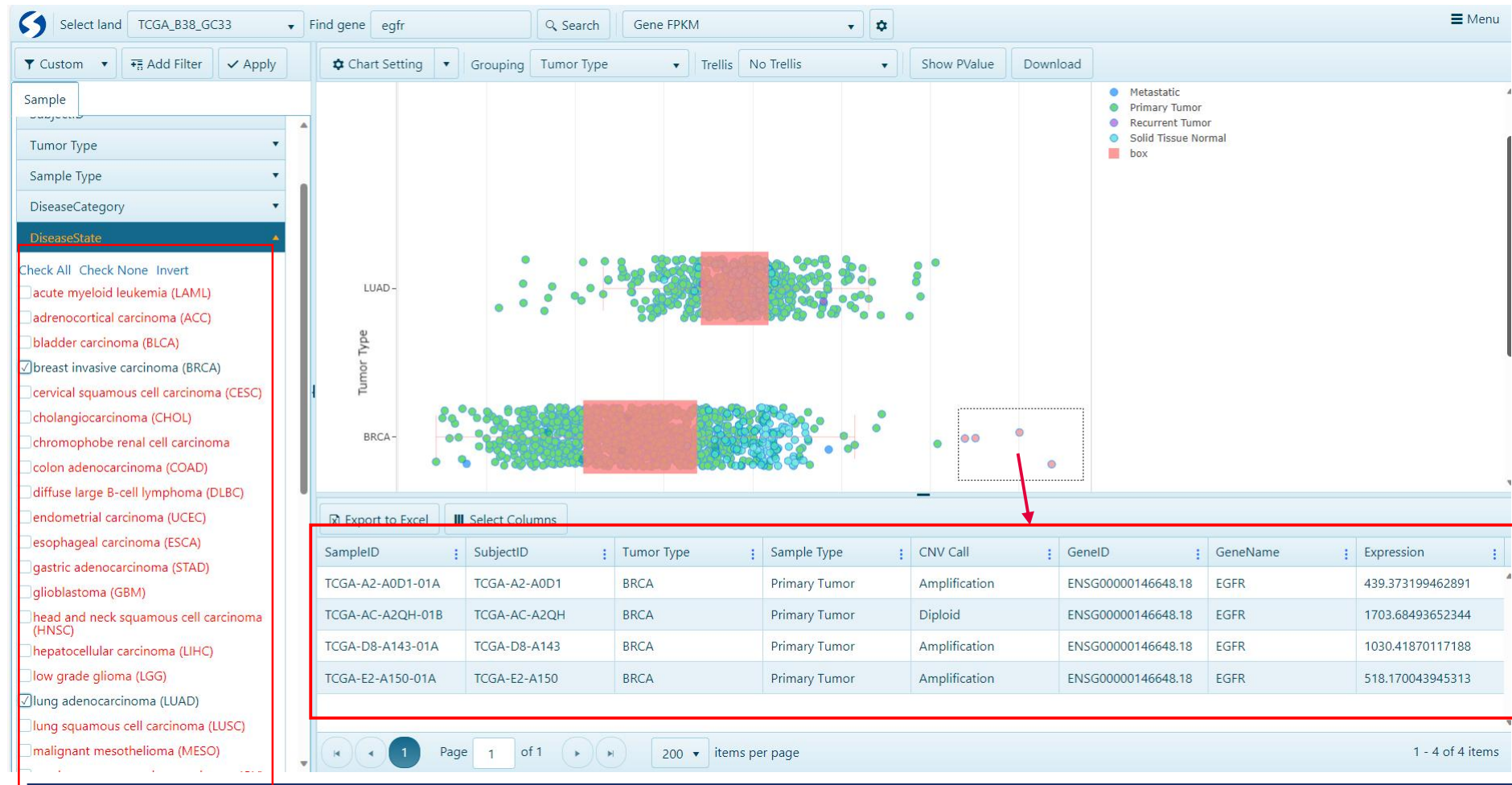
Data Type / Data Source	Normal Tissue	Cell Lines	Oncology Consortia	Oncology Studies	Disease Studies
RNA-seq expression:	Solid tissue (GTEx), Solid tissue (HPA), Blueprint	Cancer cell lines (CCLE)	TCGA, TARGET, BeatAML, ICGC, CGCI, CCLE+GTEx+TCGA, ENCODE RNA-associated gene knockdown	General oncology, 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

- TCGA-B38-G33



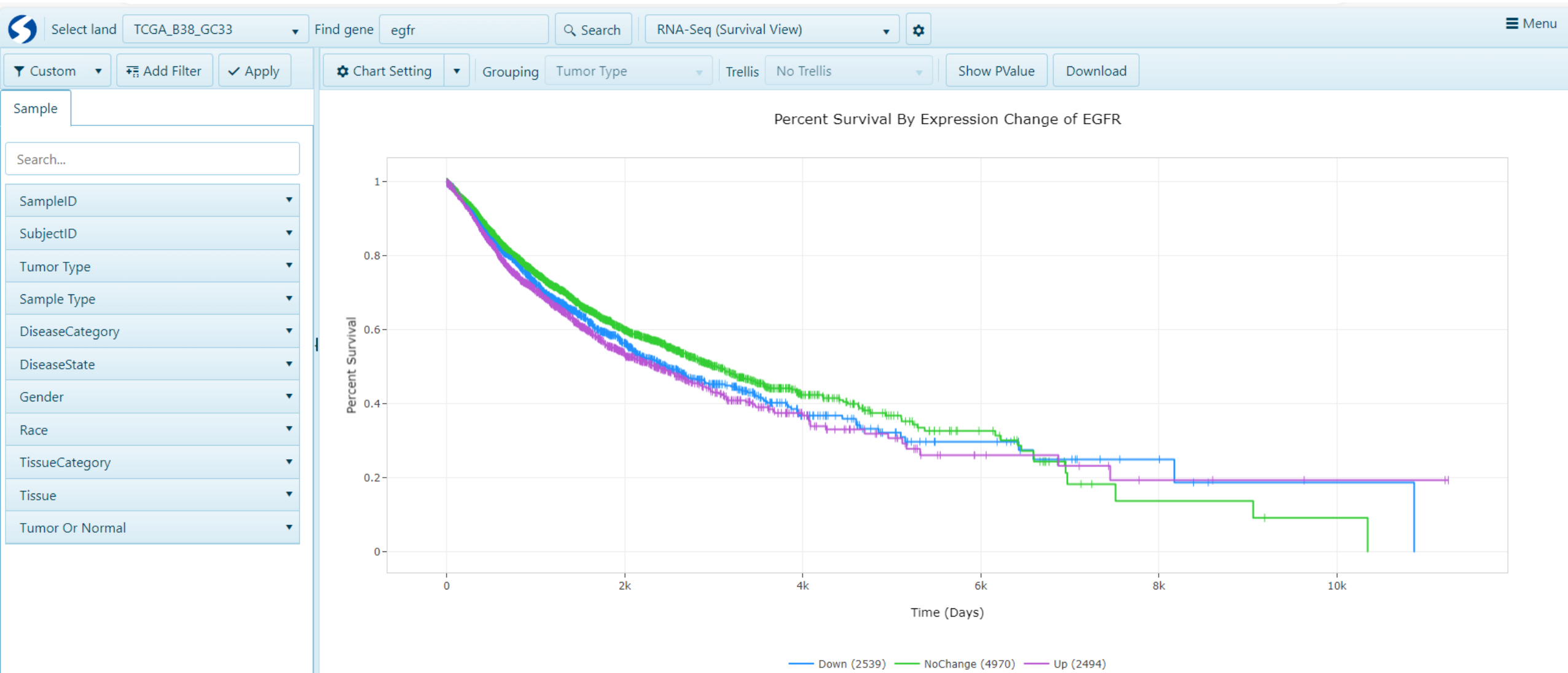
- Through DiseaseState filter, to observe the expression difference of EGFR gene in cancer type in TCGA
- Select a specific experimental group to view more detailed information.



The screenshot shows the OmicSoft Land Explorer interface. The top bar includes a search bar with 'egfr' and a 'Gene FPKM' dropdown. The left sidebar shows a 'DiseaseState' filter with a list of cancer types. The main plot area displays a scatter plot of EGFR expression across different cancer types, with a red box highlighting a specific group of samples. A red arrow points from this box to a detailed table view at the bottom.

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

TCGA_B38_GC33



Find projects by curated metadata

Experiment themes

Data types

Database groups

Add keywords to build the search query

Project distribution

Group by Therapeutic area

Subgroup by Data type

See 11421 projects

Oncology

Microarray

RNA-seq

Single Cell

Sequence...

miRNA-seq

Ot

Proteomics

Neurology

Microarray

RNA-seq

Single Cell

miR...

Pulmonary

Microarray

RNA-seq

Singl...

S

Rheumatology

Microarray

RNA-seq

Dermatology

Microarray

RNA-seq

Endocrinology/Metabolism/Bone

Microarray

RNA-seq

Sin

mi

Hematology/Coagulation

Microarray

RNA-seq

Seque...

Sin...

mi

Immunomodulators

Microarray

RNA-seq

Infectious Disease (...)

Microarray

RNA-s...

Renal Disease

Microarray

RNA-seq

Si

Psychiatry

Microarray

RNA-seq

Gastroenterology

Microarray

RNA-seq

Si...

m

p

Cardiovascular Disease

Microarray

RNA-seq

Urologic

Microarray

RNA-seq

NA

RNA-s...

Microa...

S

Ophthalmology

RNA-seq

Micro...

Si...

Infectious Diseases...

Microarray

RN...

Example searches:

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

Explore RNA-seq data specifically curated for normal human tissue expression.

Try search

Experiments in normal human lung tissue (clinical samples)

Discover experiments focused on normal human lung tissue and pathologic lung tissues using clinical samples.

Try search



Filter project

Unsaved search TCGA_BRCA x

TCGA_BRCA

Breast cancer starts in the tissues of the breast and is the most frequently diagnosed cancer and the second cause of cancer deaths in women. Men can also have breast cancer, although male breast cancer is rare. Due to early detection through use of mammograms and improvements in treatment, breast cancer deaths have steadily decreased since the 1990s. TCGA focused mainly on two types of invasive breast cancer: ductal carcinoma and lobular carcinoma. Invasive ductal...

[View more](#)

Database tcga_b38_gc33
Samples 2253
Therapeutic Area Oncology
Keywords breast;breast invasive car...
Metadata 696

[View more](#)

Data type RNA-seq;Sequence variat...
Database group Oncology Consortium
Disease breast invasive carcinom...
OmicSoft 2014R2
release
Theme No value

399 Comparisons

[Download differential expression table](#)

Comparison index	Comparison name	Comparison category	Experiment assay	Case sample size	Control sam
Filter	Filter	Filter	Filter	≥ Filter	≥ Filter
CMP:0eit7j6FLf1L	Compare DNaseqSomaticMutationStatus[ESR1]...	Other	RnaSeq_Transcript	10	972
CMP:0fztdolhajZa	Compare DNaseqSomaticMutationStatus[ATR]:...	Other	MirnaSeq_Count	27	939
CMP:0JFNO8dWXYR3	Compare HER2[Status][IHC]:positive vs negativ...	Phenotype1 vs. Phenotype2	RnaSeq_Transcript	23	55
CMP:0KeKNQfwbUsc	Compare DNaseqSomaticMutationStatus[PDGF...	Other	MirnaSeq_Count	9	957
CMP:0R7GvVZJDUhi	Compare DNaseqSomaticMutationStatus[SUZ1...	Other	MirnaSeq_Count	5	961
CMP:0RcaPE38vNEP	Compare DNaseqSomaticMutationStatus[EPHA...	Other	RnaSeq_Transcript	12	970
CMP:0Teuxe42legR	Compare PR[Status][IHC]:positive vs negative in...	Phenotype1 vs. Phenotype2	RnaSeq_Transcript	704	346
CMP:0XYIliKHgjy8	Compare DNaseqSomaticMutationStatus[RB1]:...	Other	MirnaSeq_Count	21	945
CMP:1aveA4z5MO19	Compare DNaseqSomaticMutationStatus[HGF]...	Other	RnaSeq_Transcript	5	977
CMP:1dmoffgXTGzy	Compare DNaseqSomaticMutationStatus[CYLD...	Other	RnaSeq_Transcript	6	976
CMP:1DopPtz63PYC	Compare DNaseqSomaticMutationStatus[CAR...	Other	RnaSeq_Transcript	10	972

Project is part of the selected data set.

[Select project](#)

[Deselect project](#)

Search Filters

Show all projects that include

Themes, 1 v

Oncology multiomics x

Data types, 1 v

RNA-seq x

Database group, 1 v

Oncology Consortium x

EXCLUDED Project id, 16 v

TCGA_UCS x TCGA_LUSC x TCGA_BLCA x
TCGA_PCPG x TCGA_OV x TCGA_COAD x
TCGA_TGCT x TCGA_ESCA x TCGA_DLBC x
BeatAML x

[Show all](#)

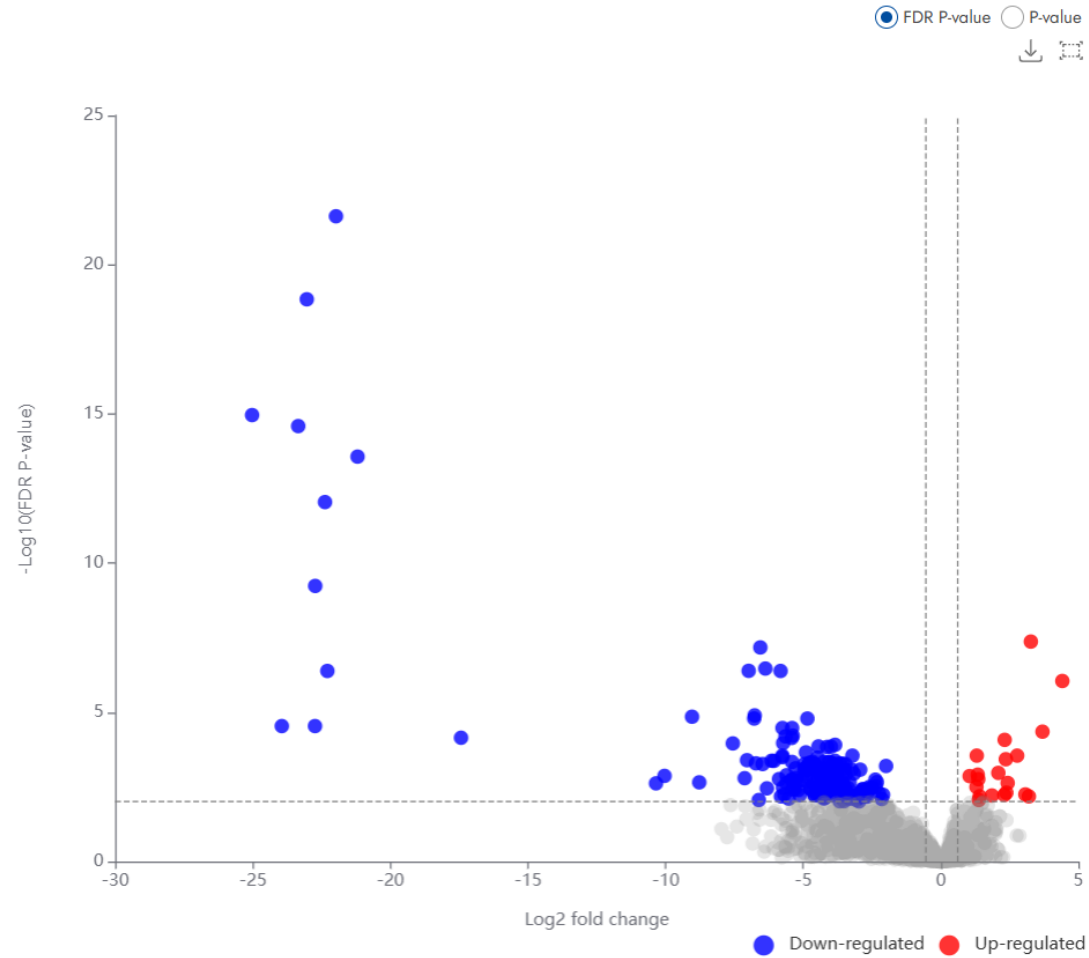
[Clear](#)

[Share search](#)

[Save search](#)

Compare DNaseSeqSomaticMutationStatus[ESR1]:positive vs negative

Experiment details



FDR P-value

0.01

Log2 fold change <

-0.58

Log2 fold change >

0.58

Reset

Significant genes: 213 of 26053

[Download differential expression table](#)

Name	Log2 fold change	FDR P-value
Filter	≥ Filter	≤ Filter
S100G	-21.976	2.38e-22
RSC1A1	-23.036	1.44e-19
LALBA	-25.025	1.10e-15
CT83	-23.349	2.56e-15
AC058822.1	-21.192	2.70e-14
AC007068.1	-22.375	9.02e-13
TBC1D3	-22.731	5.82e-10
SGCA	3.272	4.27e-8
COL2A1	-6.558	6.70e-8
ZIC1	-6.375	3.41e-7
WIF1	-6.982	4.07e-7
KRT81	-5.822	4.11e-7
AC005786.3	-22.289	4.11e-7
C2orf27B	4.416	8.91e-7

Colored by:

Fold change

[Back](#)

[Get SQL query](#)

[Share experiment](#)

[Save experiment](#)

[Find similar experiments](#)

[Open in IPA Interpret](#)

Search Filters

AI Summary

Differential Expression Summary

This volcano plot shows differential expression of genes between positive and negative from TCGA_BRCA. Statistical significance is plotted on the Y-axis, with more significant differential expression (DESeq2.v.0.0.5_DESeq2[1.42.1]) higher up.

Up-regulated genes such as SGCA, C2orf27B, PKHD1, JMJD1C-AS1, FA2H, FMOD, SLC14A1, AC023302.2, LSMEM2, and AOC1 are to the right, down-regulated genes such as S100G, RSC1A1, LALBA, CT83, AC058822.1, AC007068.1, TBC1D3, COL2A1, ZIC1, and WIF1 are to the left.

Since there are few differentially-expressed genes in this experiment, interpret any downstream analyses such as Differential Expression Match with caution.

Note that the magnitude of fold change is not large, which may be due to limitations of the assay.

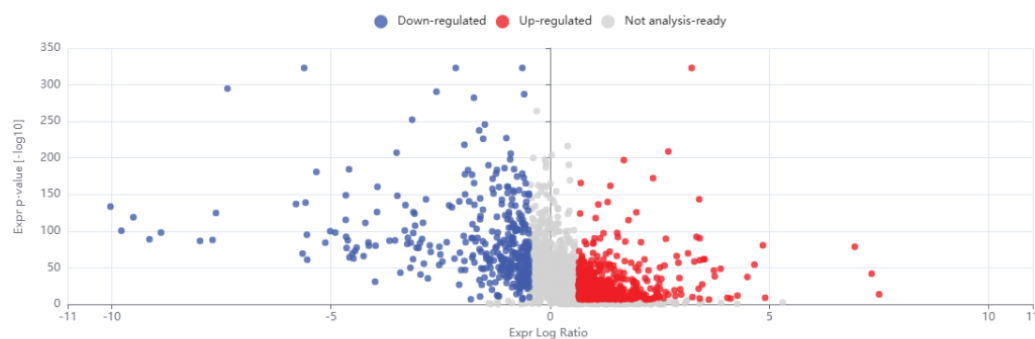
Common next steps include exploring the predicted biological functions and pathways that might explain this differential expression using IPA (click "Open in IPA Interpret"), or searching for other experiments that share patterns of differential expression (click "Find similar experiments"). You can also click on a gene of interest to see other experiments where this gene was significantly up- or down-regulated (click "View expression across projects"). You might also want to inspect other experiments from the same project.

Dataset

992 genes passed cutoffs (356 down and 636 up)

Cutoffs: Expr Other >1.0

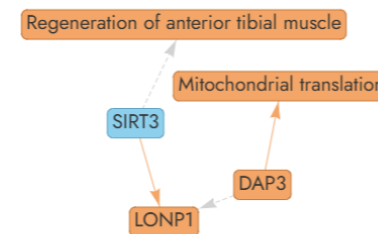
X Axis: Choose an option Y Axis: Choose an option



Dataset molecules

Name	Entrez Gene	Identifier	Expr p-value	Expr Log Ratio	Molecule Type
Filter	Filter	Filter	Filter ≤	Filter abs. ≥	Select or type to filter
A2M	alpha-2-macroglobulin	ENSG00000175899.14	1.32e-26	0.59	other
A2MAS1	A2M antisense RNA 1	ENSG00000245105.4	0.20	0.69	other
AAK1	AP2 associated kinase 1	ENSG00000115977.19	2.15e-34	0.37	kinase
ABCA1	ATP binding cassette subfamily A member 1	ENSG00000165029.16	6.37e-4	0.49	transporter
ABI3	ABI family member 3	ENSG00000108798.9	1.28e-33	-0.67	other
ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase	ENSG00000143322.21	4.13e-6	-1.20	kinase

Graphical Summary



AI suggestion

Mitochondrial Proteostasis and Muscle Regeneration: A DAP3-SIRT3-LONP1 Axis

Mitochondrial Translation Control via DAP3

The network directly links increased DAP3 activity to increased mitochondrial translation, indicating that DAP3 acts as a positive regulator of protein synthesis within mitochondria. This is consistent with DAP3's known role as a component of the mitochondrial ribosome, where it influences assembly and function of the translation machinery. The directional edge from DAP3 to mitochondrial translation suggests that changes in DAP3 levels upstream can modulate the rate or efficiency of mitochondrial protein production, thereby shaping respiratory chain biogenesis and overall mitochondrial function.

Mitochondrial Proteostasis Regulation through LONP1

Both increased DAP3 and decreased SIRT3 converge on increased LONP1 activity, highlighting LONP1 as a central node in mitochondrial proteostasis. LONP1 is a key ATP-dependent protease that degrades misfolded or damaged mitochondrial proteins. The DAP3 → LONP1 connection suggests that enhanced mitochondrial translation may necessitate higher protease activity to maintain protein quality control. The SIRT3 → LONP1 relationship indicates a separate regulatory route whereby loss of the deacetylase SIRT3 relieves repression or alters post-translational modification of LONP1,

Canonical pathway

Canonical Pathways ⓘ

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

Pathway ⓘ	P-value ^ ⓘ	Activation z-score ⚡ ⓘ	Percentage overlap ⚡ ⓘ
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Antimicrobial peptides	1.25e-6	-2.45	16.22%
Keratinization	2.25e-5	-2.65	7.87%
Role of IL-17A in Psoriasis	1.75e-4	..	25.00%
Arachidonate metabolism	6.71e-4	-2.00	9.52%
Atorvastatin ADME	8.85e-4	..	40.00%
Tyrosine Degradation I	8.85e-4	..	40.00%
Atherosclerosis Signaling	9.36e-4	-2.45	5.08%

[View Details →](#)

Upstream Regulators

Upstream Regulators ⓘ

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

Regulator ⓘ	P-value ^ ⓘ	Activation z-score ⚡ ⓘ	Percentage overlap ⚡ ⓘ
Filter	Filter ≤	Filter abs. ≥	Filter ≥
estradiol-17beta-benzoate	8.46e-10	-0.57	7.69%
IL17A	2.77e-6	-2.28	3.91%
IL22	2.67e-5	-1.92	7.87%
IL17C	3.80e-5	-1.97	20.00%
Ca2	5.78e-5	-1.16	4.18%
diethylstilbestrol	9.79e-5	-0.79	3.94%
EFNA5	1.26e-4	-1.34	10.00%

[View Details →](#)

Diseases and Functions ⓘ

Diseases and biological functions that are

Disease and Function

Disease or Function ⓘ	P-value ^ ⓘ	Activation z-score ⚡ ⓘ	Percentage overlap ⚡ ⓘ
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Hereditary palmoplantar keratoderma	2.71e-7	..	20.69%
Familial cornification disorder	2.30e-6	..	8.89%
Focal or diffuse nonepidermolytic palmoplantar keratoderma	2.49e-6	..	36.36%
Cornification disorder	2.62e-6	..	5.67%
Congenital erythroderma with palmoplantar keratoderma, hypotrichosis, and hyper-IgE	3.37e-6	..	75.00%
Focal palmoplantar keratoderma	8.37e-6	..	60.00%
Metabolism of coumarin	8.37e-6	..	60.00%

[View Details →](#)

Tox Function

Tox Functions ⓘ

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

Tox Function ⓘ	P-value ^ ⓘ	Activation z-score ⚡ ⓘ	Percentage overlap ⚡ ⓘ
Filter	Filter ≤	Filter abs. ≥	Filter ≥
Combined hepatocellular carcinoma and cholangiocarcinoma	2.57e-3	..	5.05%
Calcification of aortic valve	2.58e-3	..	2.75%
Proximal tubular toxicity	4.94e-3	..	5.56%
End-stage chronic kidney disease	5.59e-3	..	16.67%
End-stage renal failure	5.59e-3	..	16.67%
Severe acute renal failure	5.59e-3	..	16.67%
Arrhythmia of heart ventricle	8.45e-3	..	3.26%

[View Details →](#)

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

Summary Graphical Summary Pathways Upstream Analysis Diseases & Functions Regulator Effects Networks Lists **Analysis Match** Molecules

Evaluate Metadata View As Heatmap View Comparison Customize Table

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

Analysis Name	Project	case...	case.t...	case.t...	case.t...	comp...	comp...	comp...	webli...	CP (z...	UR (z...	CN (z...	DE (z...	z...	DM (z...
1358- normal control [hepatocellular carcinoma] 3-D culture	SingleCellHuman...	normal control	kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GSE111091.GPL1	https://www...	50.00	52.09	46.93	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	46.93	15.79		
671- normal control [bronchial epithelium] air liq	SingleCellHuman...	normal control	bronchial epi...	air liquid int...	Cell Type vs ...	pulmonary io...	GSE102580.UN	https://www...	55.90	48.99	30.00	51.57	13.41		
654- normal control [bronchial epithelium] 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	13.41		
25- hepatocellular carcinoma (LIHC) [liver] NA 116	OncoHuman	hepatocellul...	liver	NA	Treatment1 v...	CellLine:Infec...	GSE20948.GPL1	https://www...	55.90	52.92	26.46	50.53	16.87		
5349- intrahepatic cholangiocarcinoma [liver] 53	SingleCellHuman...	intrahepatic ...	liver		Cell Type vs ...	cytotoxic T ce...	GSE14278		55.90	51.12	24.49	53.59	31.02		
13- normal control [skeletal muscle] NA 8919	RatDisease	normal control	skeletal muscle	NA	Treatment vs...	TreatTime[da...	GSE14278		55.90	57.45	30.00	45.13	15.11		
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cluster vs Ot...	embryonic st...	GSE14278		55.90	56.67	31.62	44.96	27.78		
3682- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cell Type vs ...	embryonic st...	GSE14278		55.90	56.67	31.62	44.96	27.78		
87- disease [airway epithelium] NA 6093	HumanDisease	disease contr...	airway epith...		Treatment1 v...	SamplingTim...	GSE411091		55.90	50.99	30.00	45.38	18.48		
8219- normal control [retina] NA 20248	SingleCellHuman...	normal control	retina	NA	Cluster vs Ot...	retinal rod ce...	GSE411091		55.90	40.00	31.62	53.59	18.65		
20- normal control [skeletal muscle] NA 8925	RatDisease	normal control	skeletal muscle	NA	Treatment vs...	TreatTime[da...	GSE57816.GPL1	https://www...	55.90	50.14	30.00	45.25	14.43		
6657- normal control [osteoarthritis] NA 2522	SingleCellHuman...	osteoarthritis...	synovial mem...		Cluster vs Ot...	synovial fibr...	GSE14278		55.90	53.85	31.62	45.16	16.44		
23- normal control [fore skin] 4-thiouridine	HumanDisease	normal control	fore skin	4-thiouridine	Treatment1 v...	SampleMat...	GSE5919		55.90	53.96	30.00	46.13	15.61		
1- prostate cancer [prostate] NA 1141	MetastaticCancer	prostate can...	prostate	NA	Disease vs. N...	LandSam...	GSE6919.GPL1	https://www...	50.00	57.45	33.17	38.59	34.62		
2- nephrolithiasis [papillary duct] NA 1141	HumanDisease	nephrolithiasis	papillary duct				GSE73680		50.00	53.85	30.00	44.96	24.88		
8878- normal control [colorectal cancer] NA 1141	SingleCellHuman...	colorectal ca...	colon rectu...				GSE73680		50.00	58.31	33.17	37.19	33.85		
1388- normal control [embryo] NA 1141	SingleCellMouse...	normal control	embryo				GSE73680		50.00	56.57	22.36	46.13	13.38		
10818- normal control [bladder] NA 1141	SingleCellHuman...	normal control	bladder				GSE73680		50.00	54.77	22.36	46.13	26.44		
216- normal control [breast cancer] NA 1141	OncoHuman	breast carcin...	breast				GSE73680		50.00	41.46	20.00	43.02	8.39		
1- normal control [lung] NA 1141	MouseDisease	normal control	lung	NA	Treatment vs...	ExperimentG...	GSE73680		50.00	44.91	22.36	48.38	12.46		
161- lung adenocarcinoma [lung] NA 1141	SingleCellHuman...	lung adenoc...	lung	NA	Cell Type vs ...	unassigned c...	E-M...		50.00	41.46	26.46	42.88	25.93		
5368- normal control [fetal testis] 5367	SingleCellHuman...	normal control	fetal testis		Cluster vs Ot...	unassigned c...	GSE73680		50.00	61.64	47.96	61.89	21.80		
23- normal control [heart] NA 6093	RatDisease	normal control	heart	NA	Treatment vs...	TreatTime:Su...	GSE73680		50.00	42.00	36.06	42.76	12.79		
3- diet induced obesity [lung] NA 20248	MouseDisease	diet induced ...	lung	NA	Disease vs. N...	DiseaseState...	GSE3680		50.00	45.83	33.57	41.26	10.20		
7902- normal control [fore skin] pellet culture; TGF	SingleCellHuman...	normal control	fore skin	pellet culture...	Cell Type vs ...	chondrocyte ...	GSE160625.UN	https://www...	40.82	46.00	30.00	53.59	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	10.05		
7781- normal control [fore skin] pellet culture; TGF	SingleCellHuman...	normal control	fore skin	pellet culture...	Cluster vs Ot...	chondrocyte ...	GSE160625		50.00	50.00	26.46	42.53	20.41		
6271- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cell Type vs ...	chondrogeni...	GSE14278		50.00	41.46	30.00	47.27	14.89		
135- normal control [liver] cerivastatin 6363	RatDisease	normal control	liver	cerivastatin	Treatment vs...	TreatTime[da...	GSE57816.GPL1	https://www...	50.00	45.83	26.46	45.13	8.52		
7640- idiopathic pulmonary fibrosis [bronchoalve	SingleCellHuman...	idiopathic p...	bronchoalve...		Cluster vs Ot...	epithelial cell...	GSE1519		50.00	56.57	24.49	42.06	27.33		
10- non-small cell lung carcinoma [lung] NA 1141	OncoHuman	non-small cel...	lung	NA	Other Comp...	SmokingStat...	GSE1519		50.00	37.71	20.00	42.05	13.28		
EEC P32 Tumor vs Norm RPKM - 2018-09-28 04:03 AS123									50.00	57.45		42.04			
EEC P32 Tumor vs Norm RPKM - 2020-02-13 11:12 NDMC-0212									50.00	45.39		41.93			
28- colon carcinoma [colon] recombinant hTGF al	OncoHuman	colon carcin...	colon	recombinant ...	Treatment1 v...	CellLine:Trea...	GSE101091		50.00	38.38	31.62	41.82	9.24		
1- normal control [umbilical cord vein] mechanica	HumanDisease	normal control	umbilical cor...	mechanical s...	Treatment vs...	Treatment:Tr...	GSE17814		50.00	43.59	26.46	35.73	7.59		
EEC P32 Tumor vs Norm RPKM123 - 2020-02-14 11 NDMC-0212									50.00	86.60		37.52	41.64		
3- normal control [small airway epithelium] 3132	HumanDisease	normal control	small airway ...		Other Comp...	SmokingStat...	GSE77658.GPL1	https://www...	50.00	48.99	26.46	39.95	41.35		
MetastaticMelanoma mRNA_vs_Normal PMID_204 CT20190116									50.00	61.24	44.72	59.25	41.30		

Selected 0 / 140569

Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project

Cell & Tissue

Datasets
information

similar

opposite

The screenshot displays the OmicSoft IPA Analysis Match interface. On the left, a 'Project' selection panel shows a tree view of 'Libraries' including 'OmicSoft', 'OncoLand', 'DiseaseLand', 'SingleCellLand', and 'Normal Cells and Tissues'. The main window is divided into two panes. The left pane, titled 'Analysis Match', shows a table with columns for 'Project', 'Cell & Tissue', and 'Datasets information'. The right pane, titled 'Analysis Match', shows a table of 'z-scores' for various datasets. A red dashed box highlights the 'z-scores' table.

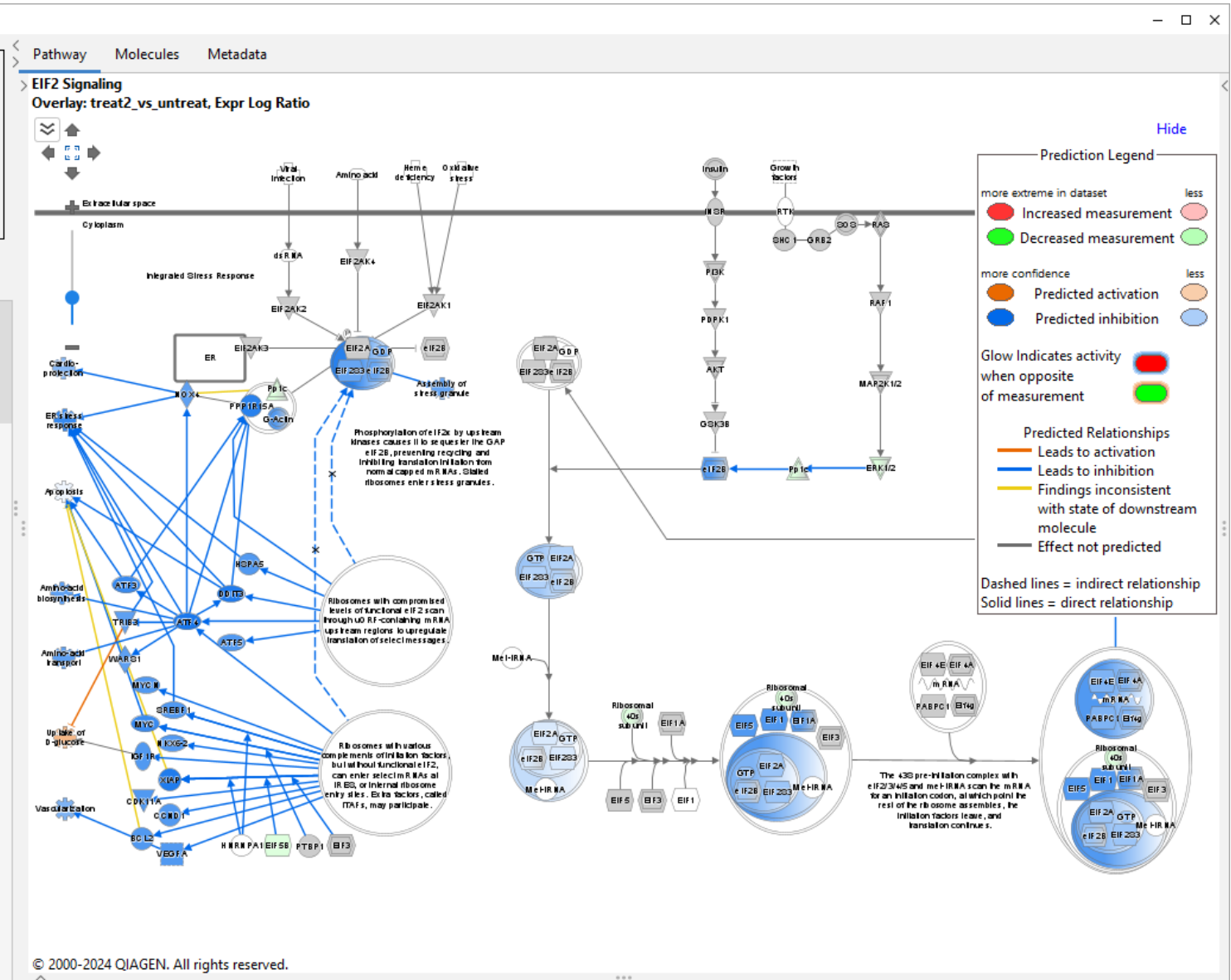
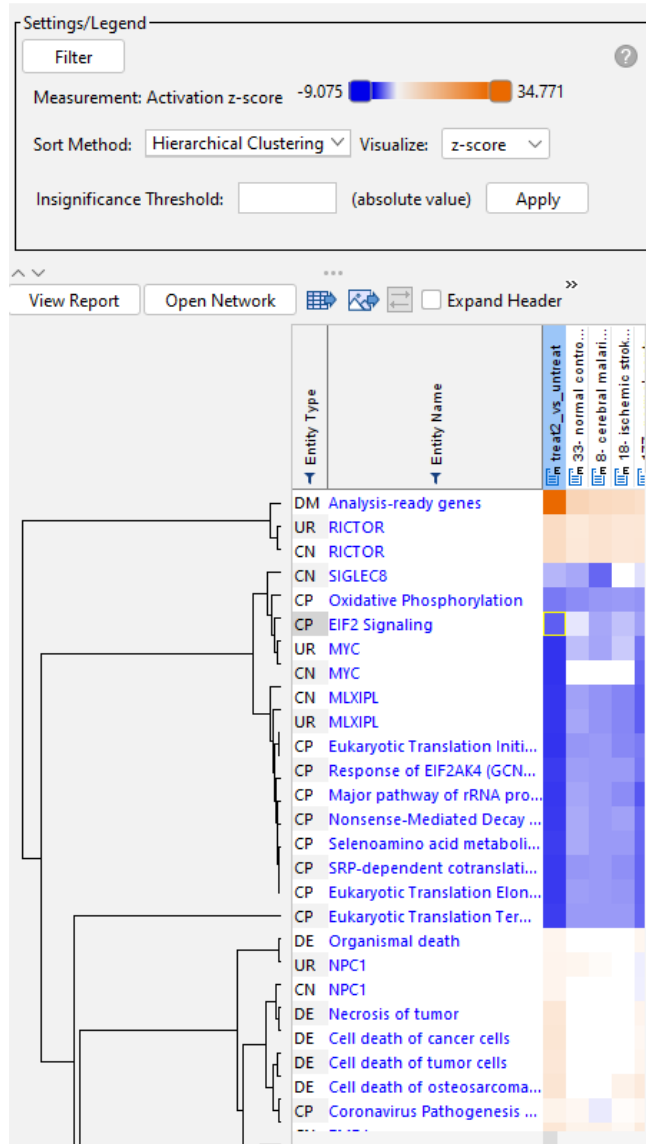
Project	Cell & Tissue	Datasets information	CP (z-s...)	UR (z-s...)	CN (z-s...)	DE (z-s...)	z-score...	D...
127- breast carcinoma [breast] human marrow strom HumanDisease	breast	case.di... case.tar... case.tis...	23.33	22.36	11.42	12.45		
67- breast carcinoma [breast] human marrow strom HumanDisease	breast	breast carcino...	55.90	42.43	30.00	30.94	39.82	9.96
129- breast carcinoma [breast] IL-6;siltuximab 27511 HumanDisease	breast	breast carcino...		20.00	33.17		13.29	8.65
101- breast carcinoma [breast] IL-6;siltuximab 27481 HumanDisease	breast	breast carcino...		41.23	28.28		27.37	7.33
east carcino...	breast	IL-6;siltuximab			-20.00		-5.00	6.65
east carcino...	breast	Treatment1 vs. ... CellLine:Sampli...		43.59	24.49		29.17	24.31
east carcino...	breast	none CellType1 vs. C... SamplingTime...		10.00	10.00		35.73	13.93
east carcino...	breast	ethanol Treatment1 vs. ... Treatment:Tra...		47.96	20.00		35.73	25.92
east carcino...	breast	IL-6 Treatment vs. ... CellLine:Sampli...		-18.86	10.00		-34.21	-10.77
east carcino...	breast	IL-6 Treatment vs. ... CellLine:Sampli...		-11.34	-20.00		3.90	-6.86
east carcino...	breast	ethanol Treatment1 vs. ... Treatment:Tra...		42.43	22.36		30.94	23.93
east carcino...	breast	IL-6;siltuximab Treatment1 vs. ... CellLine:Sampli...		20.00	28.28		12.07	-1.05
east carcino...	breast	IL-6;siltuximab Treatment vs. ... CellLine:Sampli...		-28.40	14.14		-25.26	-9.88
east carcino...	breast	human marro... Treatment vs. ... CellLine:Sampli...		-38.38	6.32		-27.29	-14.84
east carcino...	breast	none Treatment1 vs. ... CellLine:Sampli...		-37.42	-24.49		-23.06	-21.24
east carcino...	breast	human marro... Treatment1 vs. ... CellLine:Sampli...		-38.73	-20.00		-25.26	-21.00
east carcino...	breast	none Treatment1 vs. ... CellLine:Sampli...		-42.43	-22.36		-32.62	-24.35

Datasets

data

z-scores

Match Analyses Heatmap: treat2_vs_untreat



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File

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Genes and Chemicals

Diseases and Functions

Pathways and Lists

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lung cancer

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QIAGEN Land Explorer

QIAGEN

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Diseases and Functions

Datasets and Analyses

Search Results

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

Folder Types

dataset (17090)

analysis (16031)

VariantLossGain (8)

Open

Add to Comparison

Customize Table

Crea... 2024/... - 2024/... (1/125)

Name

Type

Creation Date

case.diseasestate

colon cancer-association - 2024-03-05 03:36 下午

analysis

2024/03/04 23:36:43

colon cancer-association

1294- breast cancer [breast] 1293

analysis

2024/01/12 09:20:15

breast cancer

263- normal control [bladder;bone;bone marrow;brain;embryo...

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

2446- normal control;pulmonary fibrosis [lung] 2445

analysis

2024/01/12 09:16:59

normal control;pulmonary fibrosis [lung] 2445

6615- hepatocellular carcinoma (LIHC);intrahepatic cholangiocarc...

analysis

2024/01/12 09:16:30

hepatocellular carcinoma (LIHC);intrahepatic cholangiocarcinoma (LIHC) 6615

314- normal control [testis] 313

analysis

2024/01/12 09:16:24

normal control [testis] 313

1240- normal control [fetal lung] 1239

analysis

2024/01/12 09:16:13

normal control [fetal lung] 1239

3918- breast cancer [breast] 3917

analysis

2024/01/12 09:15:24

breast cancer [breast] 3917

4042- chronic obstructive pulmonary disease (COPD);disease co...

analysis

2024/01/12 09:14:00

chronic obstructive pulmonary disease (COPD);disease co...

8970- colorectal cancer [colonrectum] 8969

analysis

2024/01/12 08:40:25

colorectal cancer [colonrectum] 8969

8975- colorectal cancer [colonrectum] 8974

analysis

2024/01/12 08:40:15

colorectal cancer [colonrectum] 8974

1- acute myeloid leukemia (LAML) [bone marrow] NA 168

analysis

2024/01/09 02:17:06

acute myeloid leukemia (LAML) [bone marrow] NA 168

1- acute myeloid leukemia (LAML) [bone marrow] NA 213

analysis

2024/01/09 02:16:46

acute myeloid leukemia (LAML) [bone marrow] NA 213

1- breast cancer [breast;lymph node;peripheral blood] 0

analysis

2024/01/09 02:13:03

breast cancer [breast;lymph node;peripheral blood] 0

1- breast cancer [breast] 68

analysis

2024/01/09 02:12:49

breast cancer [breast] 68

1- breast cancer [peripheral blood] NA 8

analysis

2024/01/09 02:12:37

breast cancer [peripheral blood] NA 8

1- breast carcinoma [breast] estradiol;ethanol 0

analysis

2024/01/09 02:12:21

breast carcinoma [breast] estradiol;ethanol 0

1- breast carcinoma [breast] estradiol;ethanol 4

analysis

2024/01/09 02:12:05

breast carcinoma [breast] estradiol;ethanol 4

1- germ cell cancer [ovary] NA 4

analysis

2024/01/09 02:09:17

germ cell cancer [ovary] NA 4

1- kidney clear cell sarcoma (CCSK) [kidney] NA 14

analysis

2024/01/09 02:07:58

kidney clear cell sarcoma (CCSK) [kidney] NA 14

1- kidney rhabdoid cancer [kidney] Transfection_BAF47 442

analysis

2024/01/09 02:07:40

kidney rhabdoid cancer [kidney] Transfection_BAF47 442

1- childhood acute lymphocytic leukemia [hematopoietic tissue]...

analysis

2024/01/09 02:02:21

childhood acute lymphocytic leukemia [hematopoietic tissue]...

1- endometrial cancer;endometrial squamous cell carcinoma;ova...

analysis

2024/01/09 02:01:04

endometrial cancer;endometrial squamous cell carcinoma;ova...

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

We can type

1. Disease name

2. GEO profile number

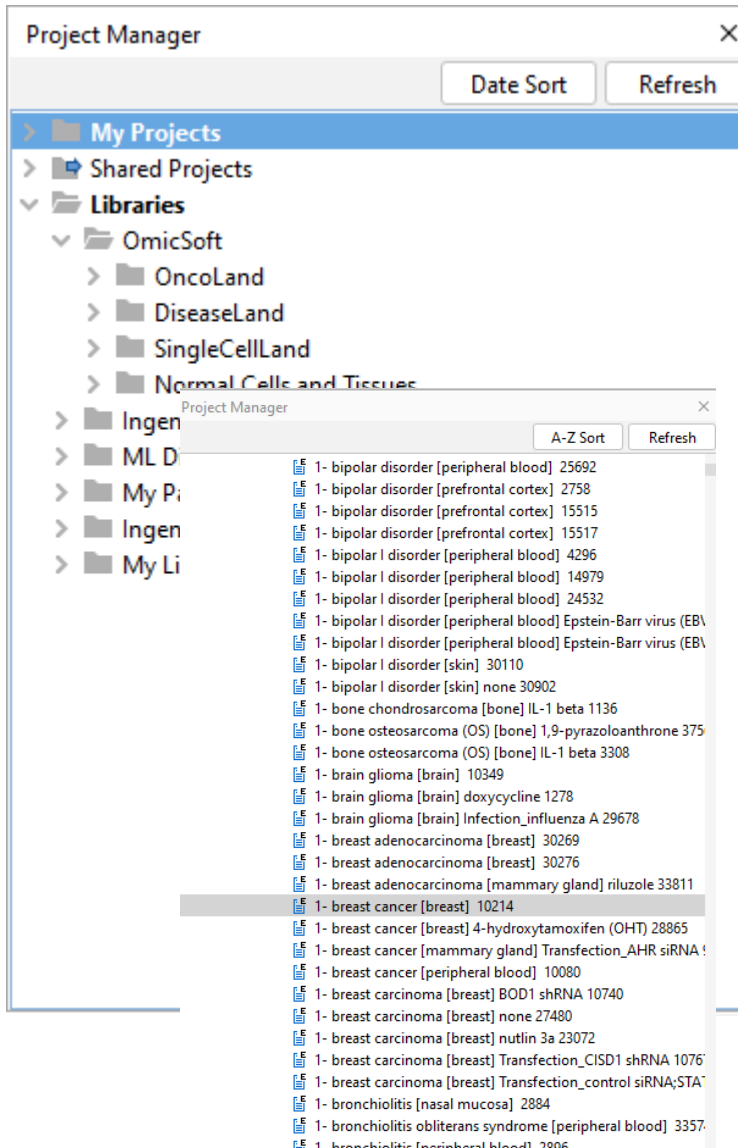
4

Add to Comparison

3

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

Graphical summary



Project Manager

My Projects

Shared Projects

Libraries

OmicSoft

OncoLand

DiseaseLand

SingleCellLand

Normal Cells and Tissues

Ingen

ML D

My P

Ingen

My Li

Project Manager

A-Z Sort

Refresh

1- bipolar disorder [peripheral blood] 25692

1- bipolar disorder [prefrontal cortex] 2758

1- bipolar disorder [prefrontal cortex] 15515

1- bipolar disorder [prefrontal cortex] 15517

1- bipolar I disorder [peripheral blood] 4296

1- bipolar I disorder [peripheral blood] 14979

1- bipolar I disorder [peripheral blood] 24532

1- bipolar I disorder [peripheral blood] Epstein-Barr virus (EBV)

1- bipolar I disorder [peripheral blood] Epstein-Barr virus (EBV)

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

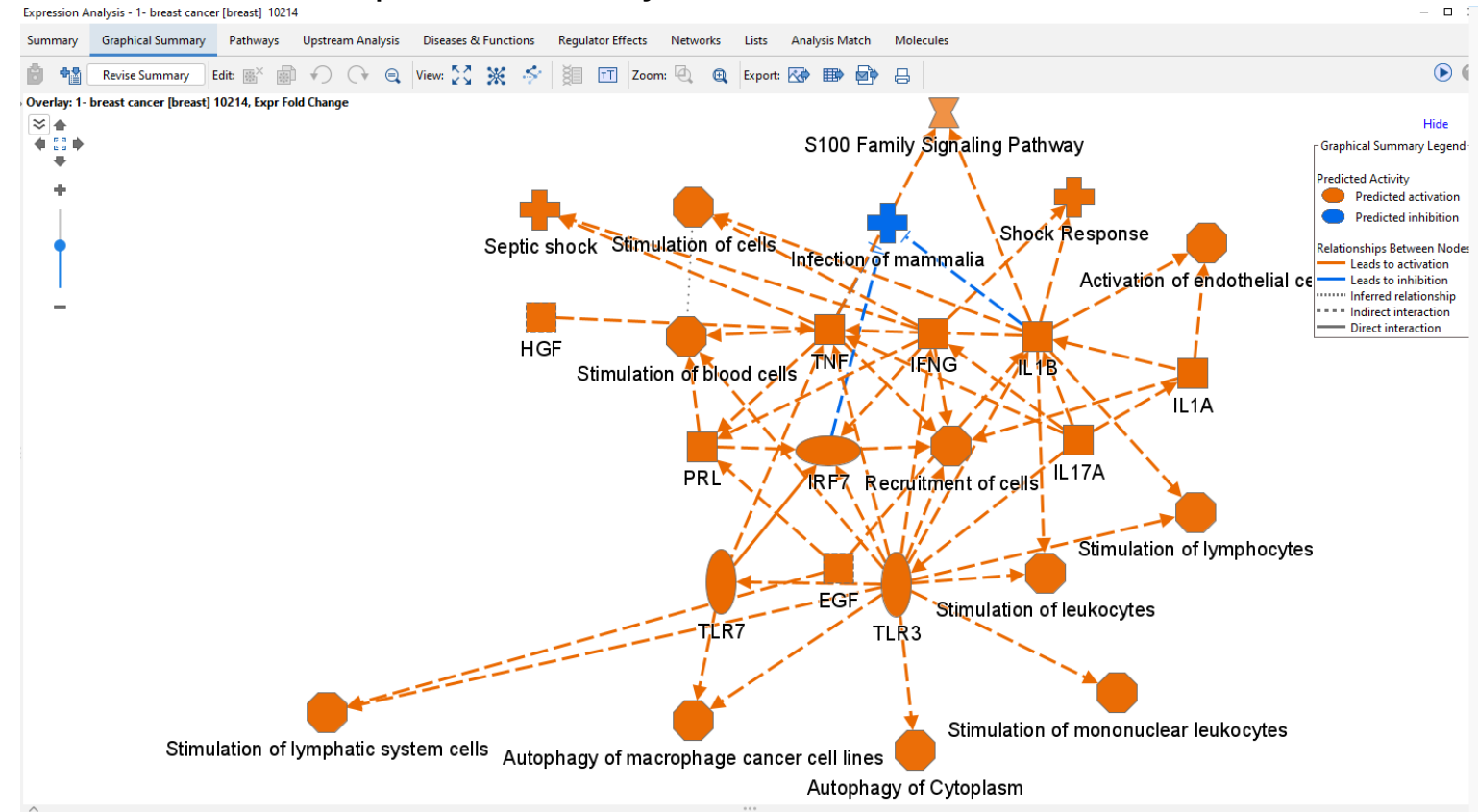
1- breast carcinoma [breast] Transfection_CISD1 shRNA 1076

1- breast carcinoma [breast] Transfection_control siRNA;STA

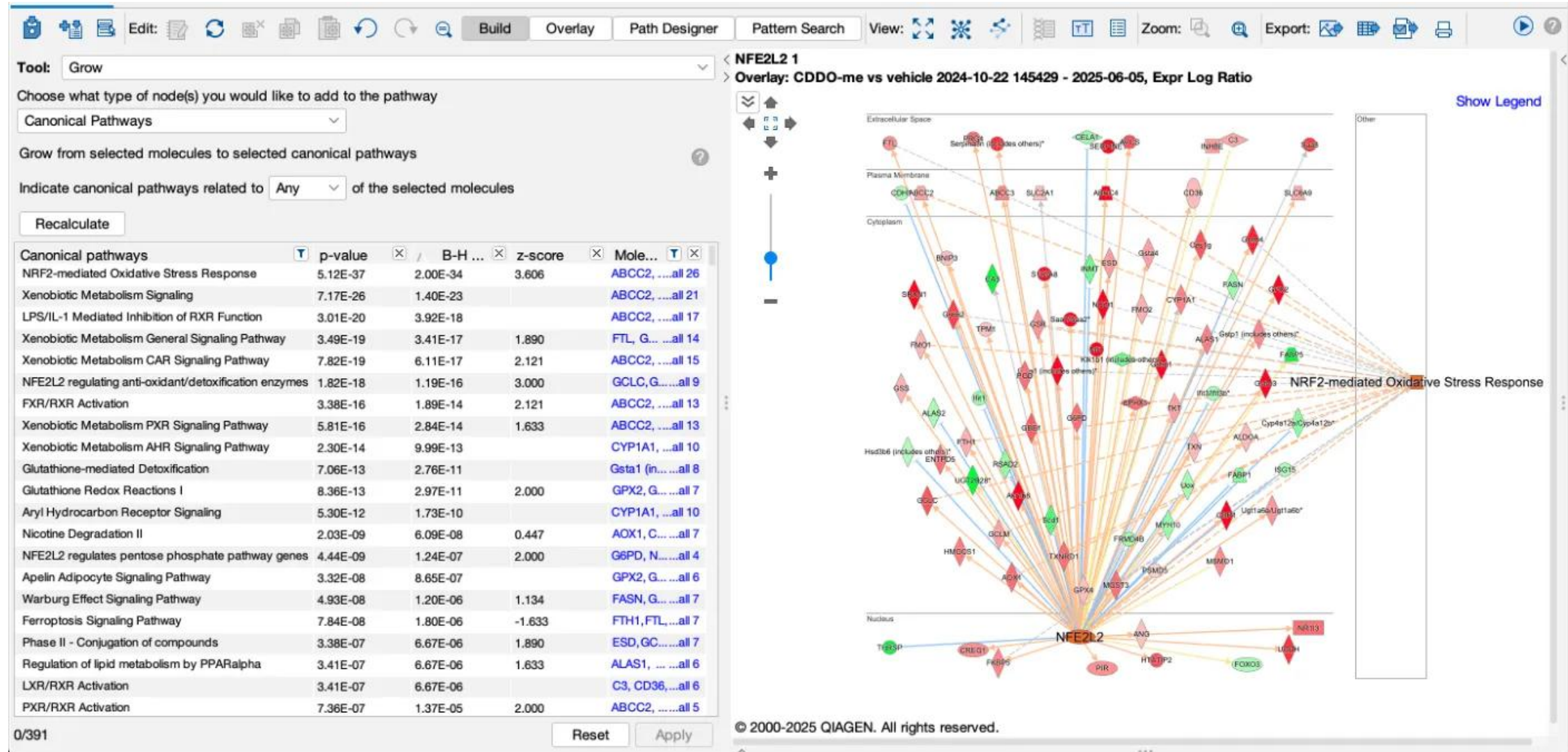
1- bronchiolitis [nasal mucosa] 2884

1- bronchiolitis obliterans syndrome [peripheral blood] 3357

1- bronchiolitis [peripheral blood] 2806



Grow function





HOME

Welcome to IPA Interpret

Transform complex omics data into meaningful biological insights

Available Analyses

 Analyses

Showing all **317** analyses

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

Getting Started

What is IPA Interpret? >

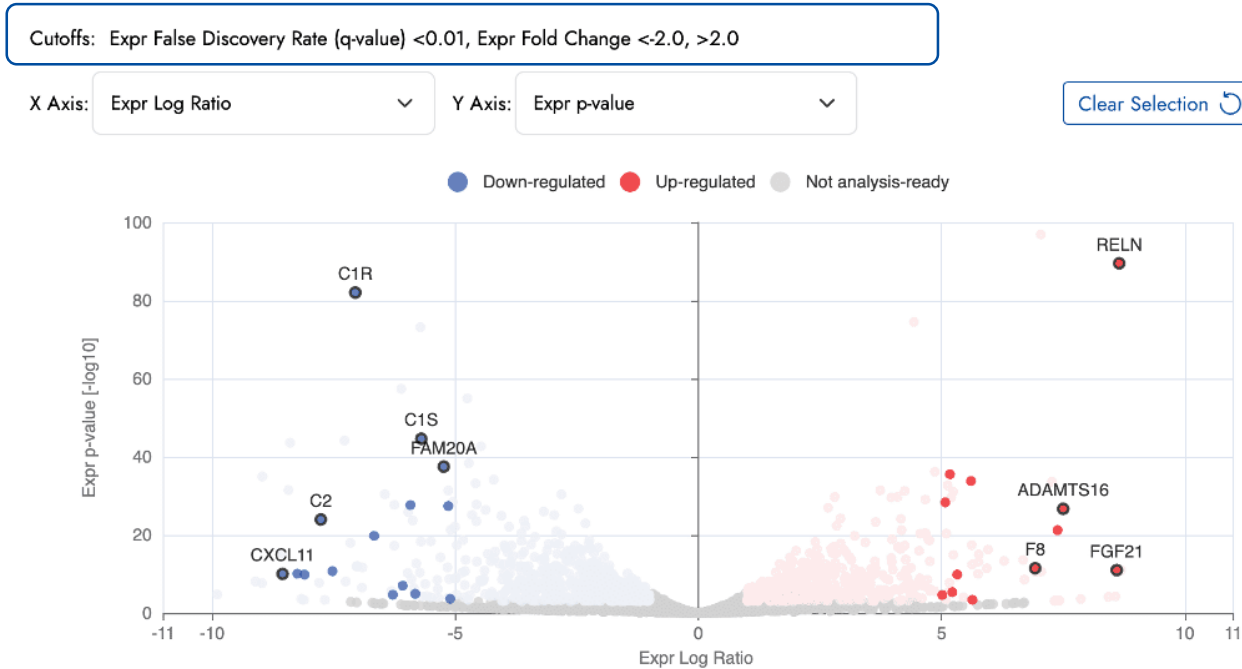
QIAGEN IPA Interpret is a shareable overview of the key analyses and actionable insights from a QIAGEN

Introduction to IPA Interpret for QIAGEN IPA

CDDO-me treatment of mice (liver)



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



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 metalloproteinase with thrombospondin type 1 motif 16

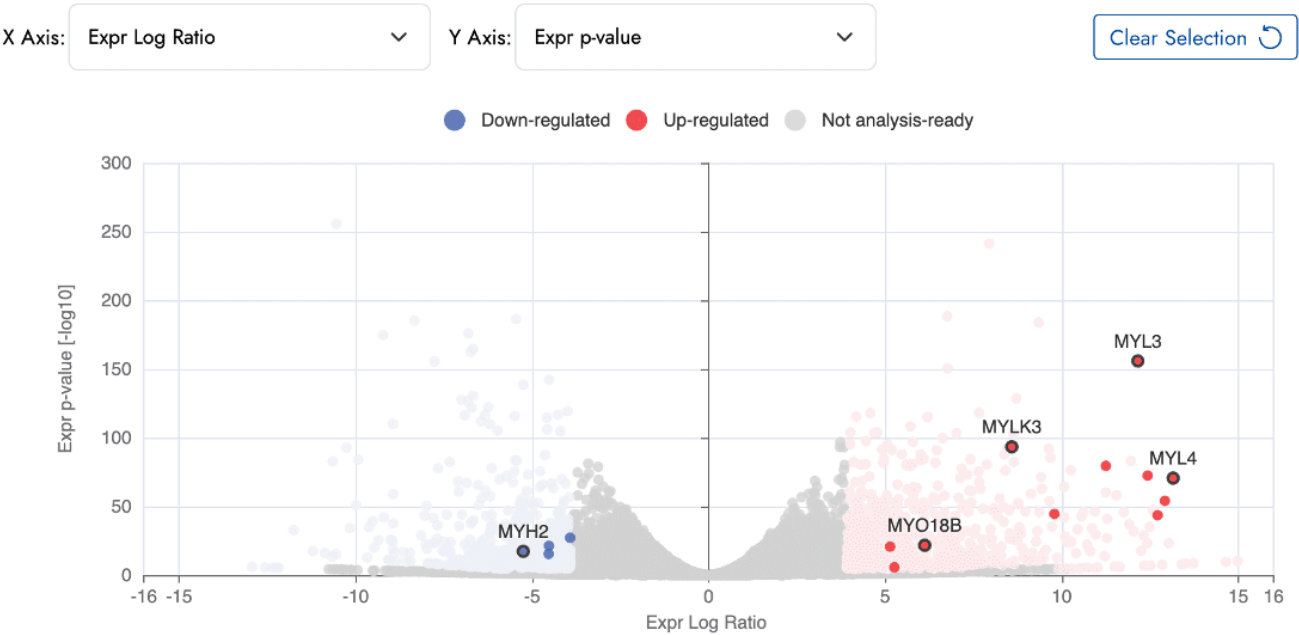
Dataset molecules

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



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-IV/sb, Mylc, Mylc1v, myosin light chain 3, myosin, light polypeptide 3, rVMLC1, VELC, Ventricular Myosin Essential Light Chain, VLC1, VLCI

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

M-B / Canonical Pathways / Bubble Chart

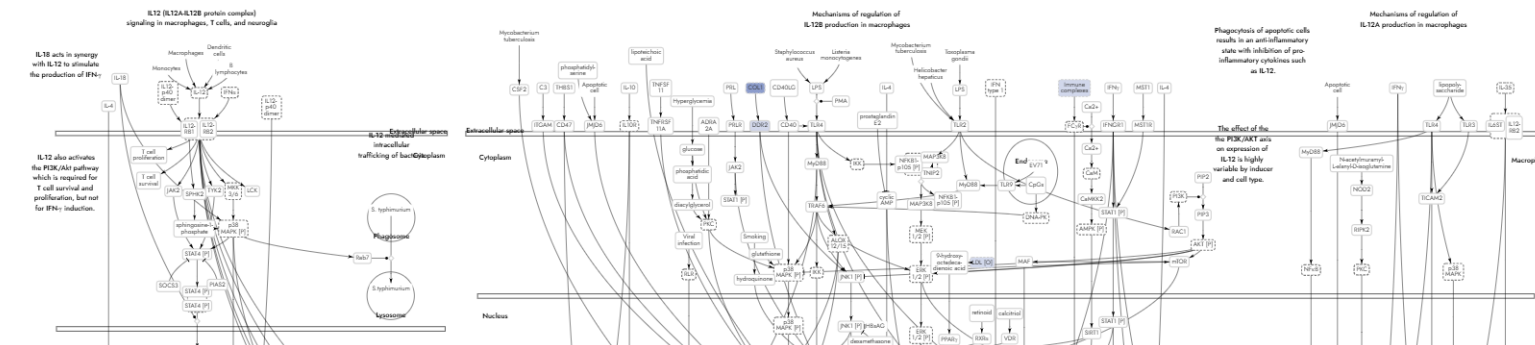
Canonical Pathways

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



Pathway representation

IL-12 Signaling and Production in Macrophages Figure Legend OFF



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 $\beta 1$ and $\beta 2$ 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-12RB1 thereby increasing the number of IL-12 binding sites expressed on macrophages. Autocrine production

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

Table Bar Chart Bubble Chart

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
Intrinsic cell surface interactions	9.22e-17	9.22e-15	4.15	24.71%	21	85

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](#)

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	(黃)-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	Asparaginy-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

Raw Data (487) Dataset Summary (274) Metadata							
Edit Observation Names		Infer Observations					
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...	5.06793999999999...	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	0.205101024999999...	3.72625799999999...	M-D
54	2-(Methylthiomethyl...	-	-	193.0677_1.5	0.239687147999999...	4.49547299999999...	M-D
55	2-[[hydroxy(1-oxo-1...	-	-	246.0415_9.7	-0.16949968900000...	7.22580000000000...	M-D
56	2-[[hydroxy(5-hydrox...	-	-	233.0564_5.1	-0.77596192100000...	3.96179999999999...	M-D
57	2-Decylfuran	HMDB0032215	-	209.1896_9.7	-4.75624190000000...	2.42859999999999...	M-D
58	2-Deoxy-2-Amino Gl...	HMDB0001504	C06605	260.0533_3.1	-0.193207566	5.90249999999999...	M-D
59	2-Methoxyxanthone	HMDB0032998	-	225.055_7.9	0.290501863000000...	3.90629999999999...	M-D
60	2-oxo-3-(3,4,5-trihy...	-	-	211.0247_8.9	-0.12797825800000...	3.03852200000000...	M-D
61	2-Pyrrolidinone	HMDB0002039	C11118	86.06_1.8	-0.13496873100000...	1.37650000000000...	M-D
62	2,4-Diamino-6-[N-(2...	-	-	340.177_6.6	-0.19252112499999...	2.59653299999999...	M-D
63	2,4,6-Triethyl-1,3,5-...	-	-	207.0877_1.2	-0.13045403799999...	3.54621999999999...	M-D

Comparison Analysis

Trend Analysis Summary of this Comparison AI-Suggested

Robust Activation of Pro-inflammatory Pathways

IL1B (Upstream Regulator), **lipopolysaccharide**, and **TNF** show high positive z-scores (8.686, 11.318, 9.719, respectively), indicating cross-analysis activation. Coupled with elevated $-\log_{10}(\text{BH } p\text{-values})$, this pattern reflects dominant innate immune signaling and suggests a pronounced inflammatory response across the datasets....

[View Full AI Summary](#)

Bubble size

Bubble color

Sort by

Data display

$-\log[\text{P-value}]$

Activation z-score

Activation z-score (sum of absolute scores across the row) ▾

Active Filters: BH P-value, Z-score, Entity types ▾

☐ Expand labels

Figure legend: ☒ ON

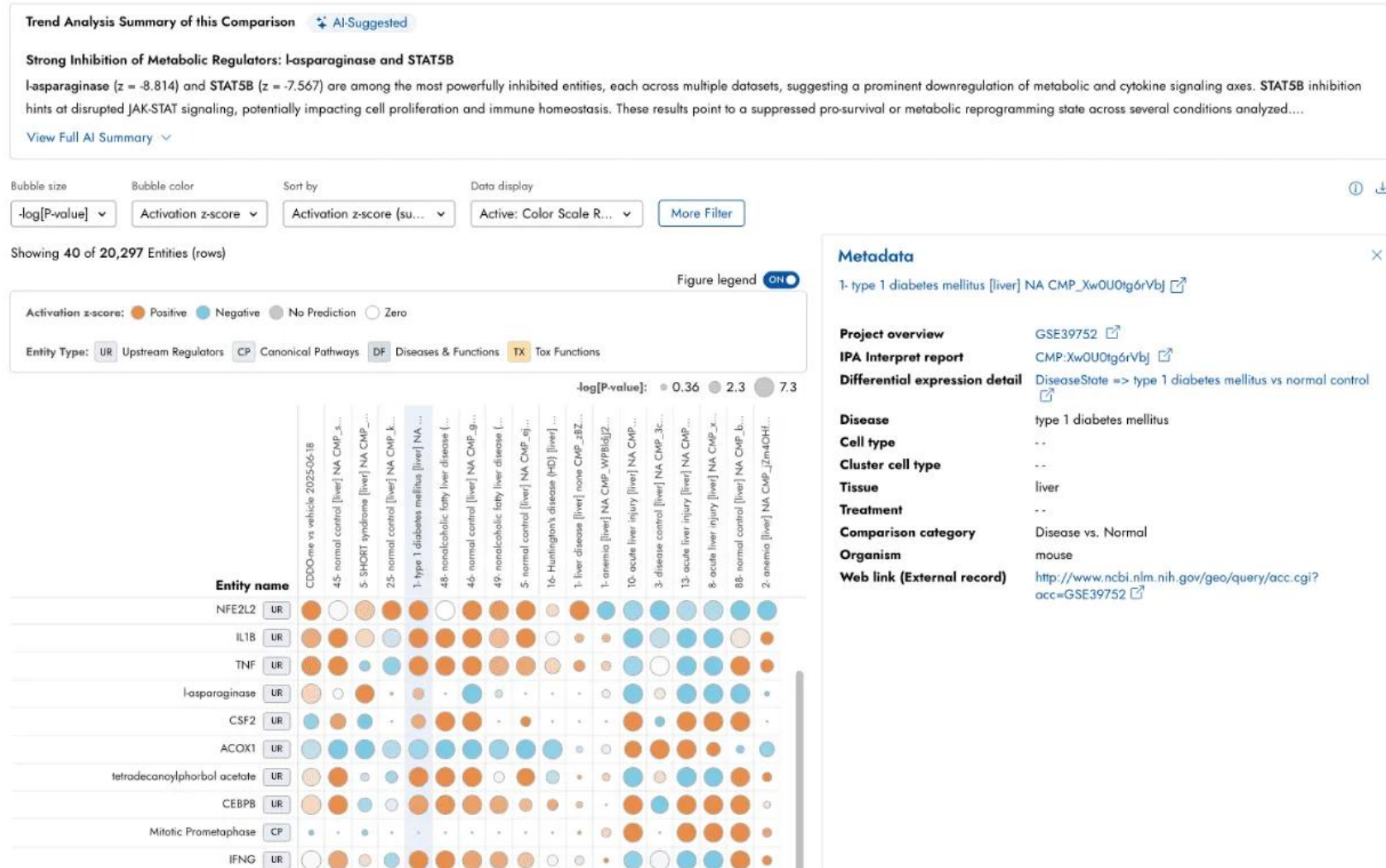
Activation z-score: ■ Positive ■ Negative ■ Zero ■ Neutral / No Prediction Entity Type: ■ UR Upstream Regulators ■ CP Canonical Pathways ■ DF Diseases & Functions

-log[P-value]: ● 0.37 ● 2.3 ● 7.6

[illegible]

Make discoveries by including OmicSoft analyses in a Comparison Analysis

Comparison Analysis



What's new in the QIAGEN® Ingenuity Pathway Analysis Summer Release (2026)

How to build your comparison

Choose which you want to compared and add to Compare Builder

From omicsoft similar analysis, choose and add to Compare Builder

QIAGEN IPA Interpret

Welcome to IPA Interpret
Transform complex omics data into meaningful biological insights

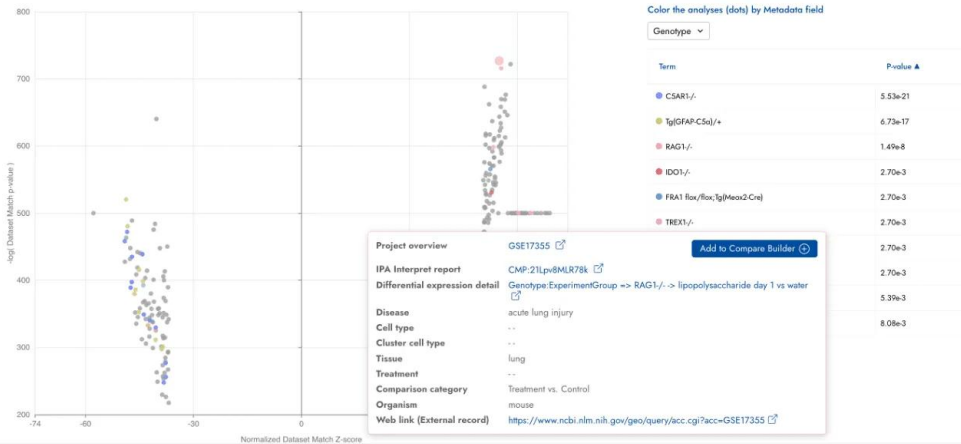
Available Analyses
2 analyses selected

Showing all 49 analyses

Project	Analysis Name	Type	Analyzed Genes	Reference Set	Owner	Last Activity
Welding	4 hr blood	Expression	20	MouseRef-8 v2.0	Me	Tue May 19 07:30:54 GMT-7 2026
Welding	28 d aorta	Expression	3	MouseRef-8 v2.0	Me	Tue May 19 07:12:58 GMT-7 2026
Welding	28 d lung	Expression	527	MouseRef-8 v2.0	Me	Tue May 19 07:12:58 GMT-7 2026
Welding	28 d blood	Expression	10	MouseRef-8 v2.0	Me	Tue May 19 07:12:58 GMT-7 2026
Welding	4 hr aorta	Expression	8	MouseRef-8 v2.0	Me	Tue May 19 07:12:58 GMT-7 2026
Welding	4 hr lung	Expression	702	MouseRef-8 v2.0	Me	Tue May 19 07:12:58 GMT-7 2026

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.



Choose multiple analysis to compared builder

5 analyses selected

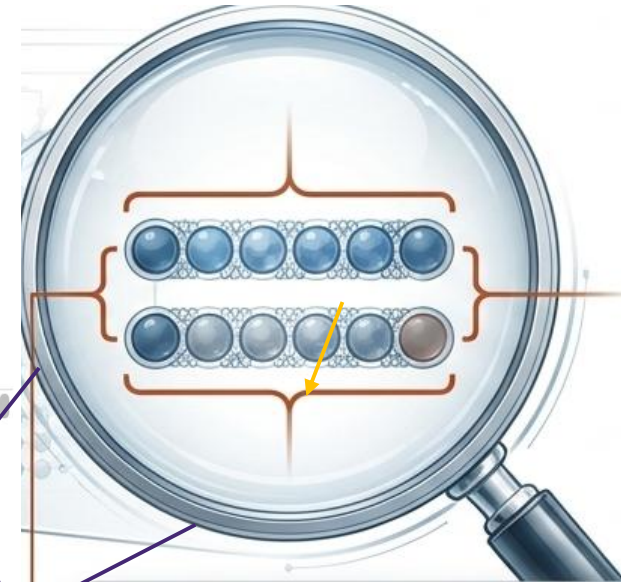
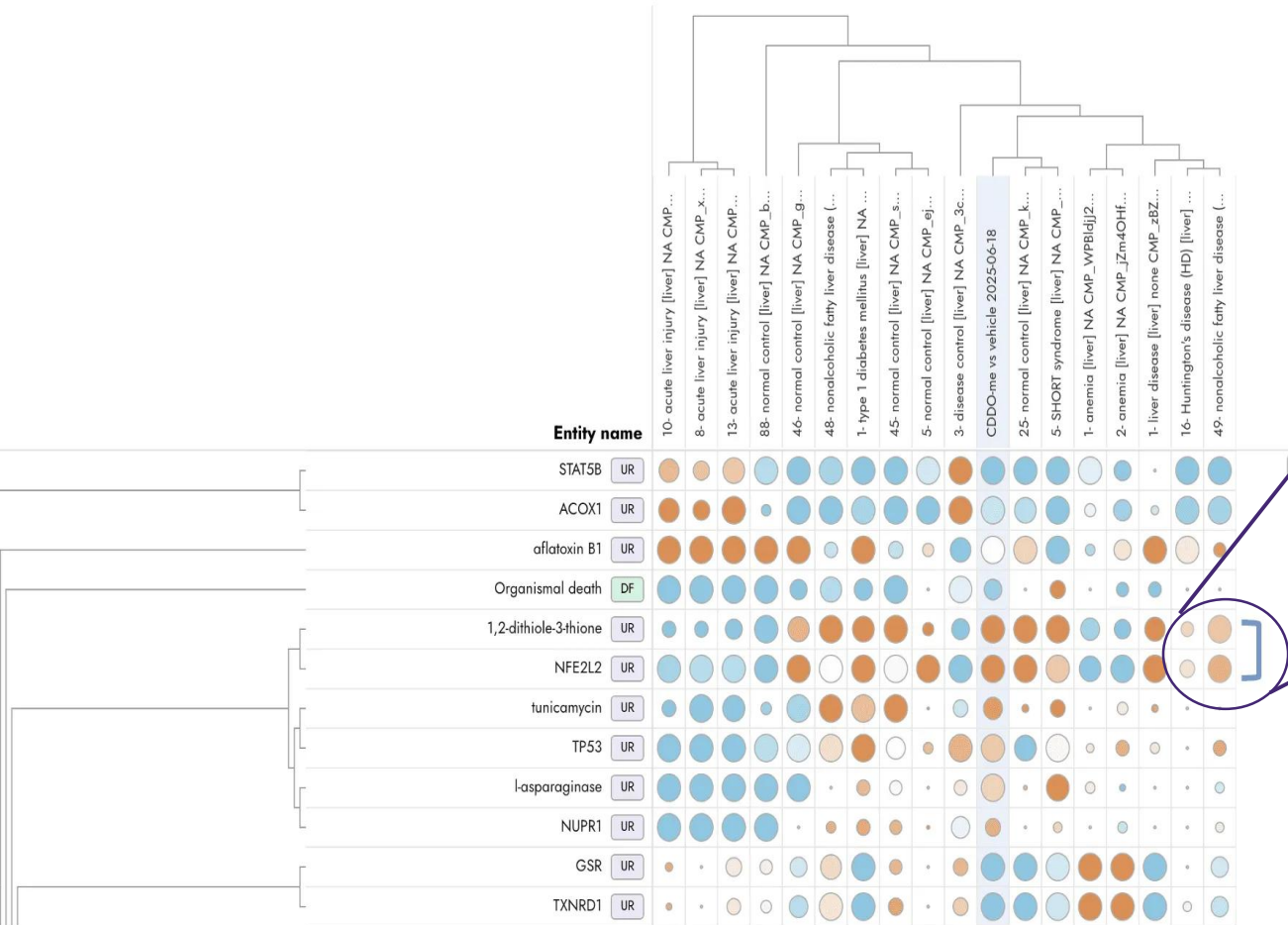
Showing 5 of 200 analyses

Issue	Treatment	Comparison category	Organism	Genotype	All treatment	Dosage	Subject treatment	-log p-value	Normalized z-score	Web link
ing	--	Treatment vs. Control	mouse	--	influenza A expressing HA D222G [SubjectInfection]	10 ⁻⁶ TCID50	SubjectInfection_influenza A expressing HA D222G	500.00	69.01	Web link
ing	--	Treatment vs. Control	mouse	--	influenza A expressing HA D222G [SubjectInfection]	10 ⁻⁶ TCID50	SubjectInfection_influenza A expressing HA D222G	500.00	68.27	Web link
ing	--	Treatment vs. Control	mouse	--	influenza A expressing HA D222G [SubjectInfection]	10 ⁻⁶ TCID50	SubjectInfection_influenza A expressing HA D222G	500.00	67.73	Web link
ing	--	Treatment vs. Control	mouse	--	influenza A expressing HA D222G [SubjectInfection]	10 ⁻⁶ TCID50	SubjectInfection_influenza A expressing HA D222G	500.00	66.62	Web link

Discover biological patterns by hierarchically clustering the rows and/or columns

Activation z-score: Positive Negative No Prediction Zero Entity Type: UR Upstream Regulators CP Canonical Pathways DF Diseases & Functions TX Tox Functions

-log[P-value]: 0.36 2.3 7.3



The NFE2L2 Example

- **The Pattern:** The chemical 1,2-dithiole-3-thione clusters tightly with the upstream regulator NFE2L2.
- **The Biology:** They do not just share genes; they share the same predicted activity pattern across analyses, driving similar downstream expression impacts.
- **The Outcome:** Immediate identification of shared activation mechanisms and novel pattern discovery.

Cluster up to 7,000 entities to discover hidden similarities across subsets of pathways and regulators.

Precision Control & Data Display

Filters

>

^

≥

▼

1

>

▼

≥

▼

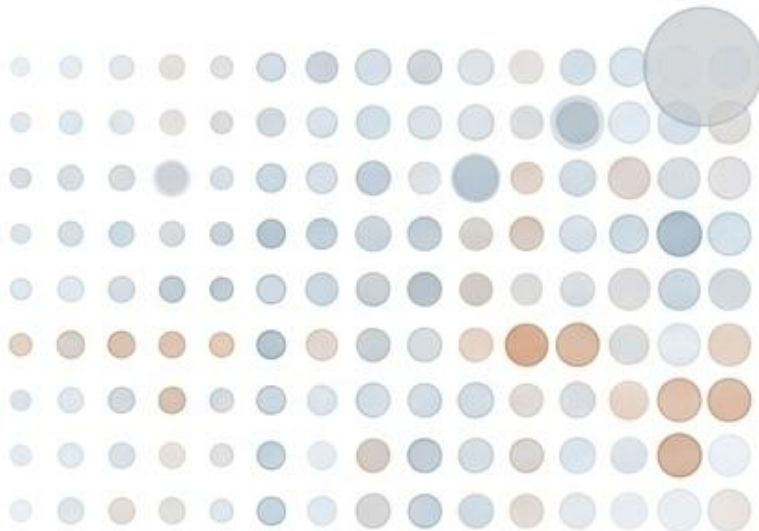
Entity Type: Cytokines ▼

Visual

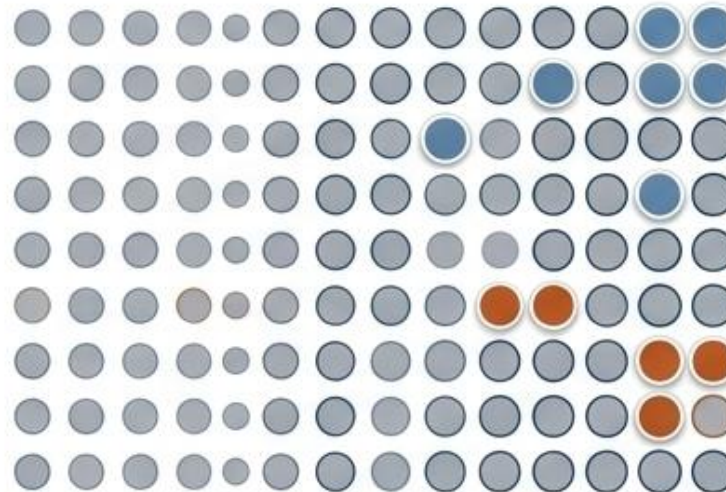
Color

Size

Before

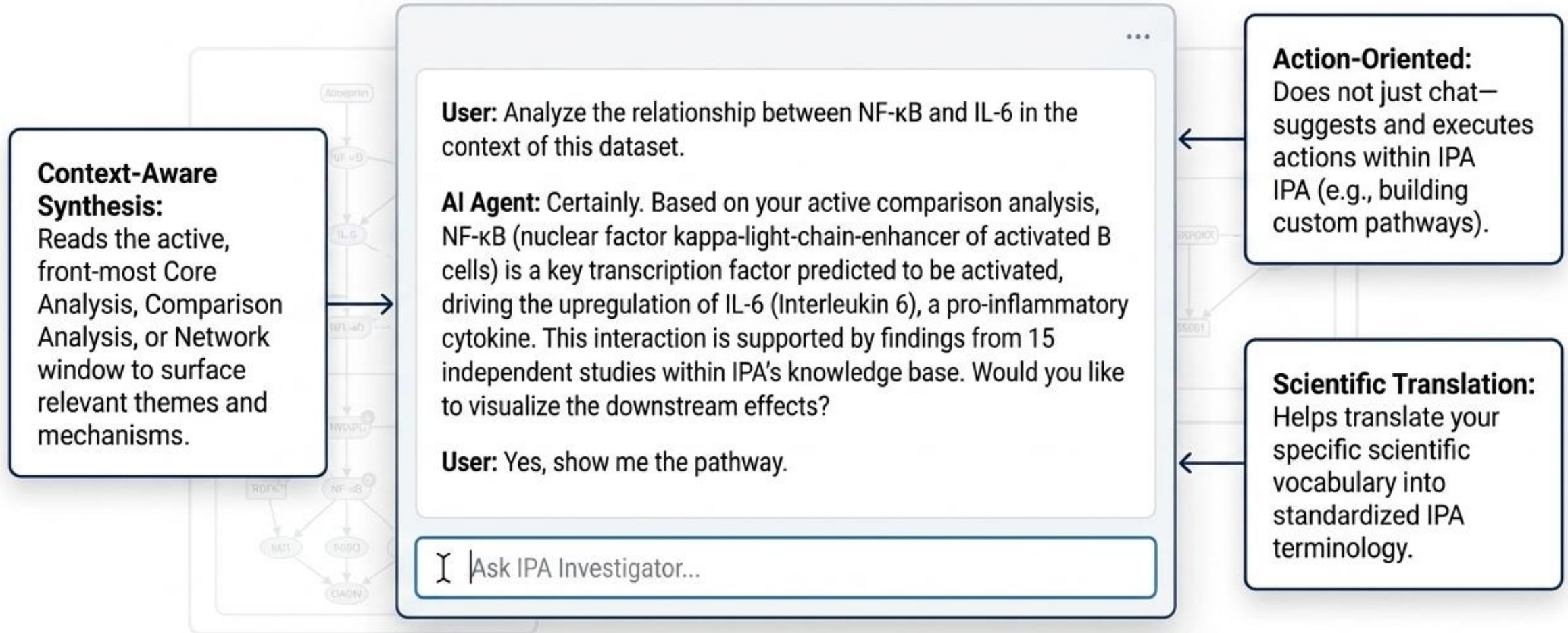


After

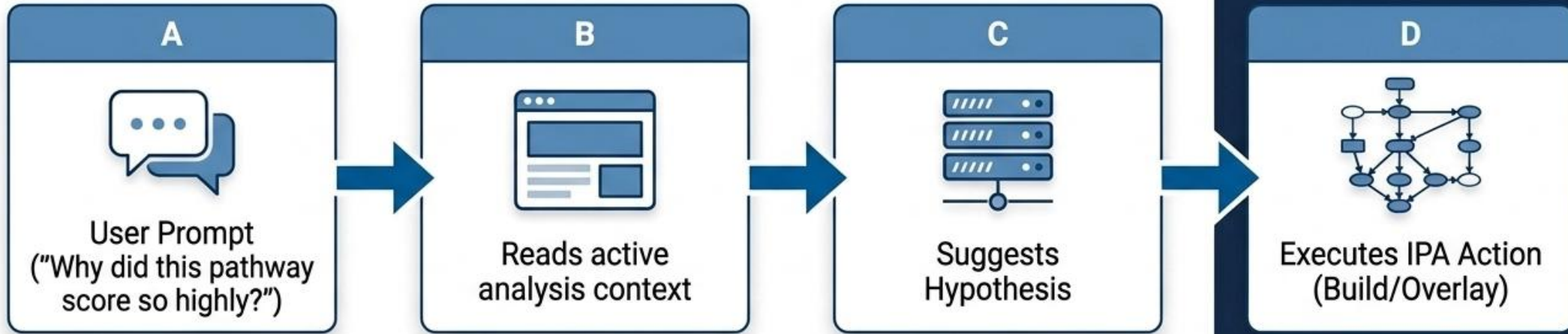


- **Exact Cutoffs:** New operator precision ($>$, $\geq$) and entity type filtering (e.g., isolate only Cytokines).
- **Visual Sliders:** Manually adjust bubble size and color intensity to correct for large value outliers washing out the map.
- **Signal vs. Noise:** Set an insignificance threshold (e.g., z-score < 2) to gray out statistically insignificant bubbles.
- **Publication Ready:** Fully customize fonts, colors, and aspect ratios for direct export to journals.

Introducing of IPA Investigator [Beta]



AI Action Architecture



How AI works with IPA deterministic tools

1. AI Suggests: The Investigator provides hypotheses based on your data context.

2. IPA Computes: Actions (like creating an 'AnalysisTheme' or executing a 'GrowToBioFunctions' causal analysis) are powered purely by IPA's built-in tools.

3. No Hallucinated Networks: All generated visual networks use relationship information sourced strictly from the QIAGEN Knowledge Base.

Enterprise AI Security & Compliance

Security Dimension	Public Generative AI	IPA Investigator [Enterprise]
AI Model	Standard Public Models	Enterprise GPT 5.1 hosted securely via Microsoft Azure.
Data Training	✗	✓ Prompts and interactions are NEVER retained or used to train general or specific AI models.
Access Protocol	Always On / Public	✓ Opt-in strictly required. Feature is turned OFF by default globally.
Data Input Policy	Unrestricted	✓ Strictly Research Use Only (RUO). NO patient-identifiable data, PHI, or biometric data allowed.
Oversight	Automated Output	✓ Outputs remain subject to human review and independent verification.

You can now activate the AI by accepting terms in the UI



IPA
INVESTIGATOR AI Beta

Email Feedback

Copy

Reset

✓ IPA Investigator is Enabled

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When you have full access, you can type your questions here.

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Formatting 'omics data before uploading to IPA

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

Analyte identifier **REQUIRED** to explore enrichment

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

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

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

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

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

Accepted file formats:

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

Multiple comparisons or observations may be uploaded in one file

Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)

	A	B	C	D
	Proteins	Fold change	P_value	P_value_adjust
1				
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	AGQTQPNPILPIQPALT(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/>

Multiple ID columns

Ratio, fold change, etc. (recommended)

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

Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

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- What's new in Ingenuity Pathway Analysis

Module 1 | IPA in Drug Discovery and Translational Medicine

Module 2 | Transcriptomics and Drug Mechanism of Action

- Case Study: BOLD-100 in Colorectal Cancer

Module 3 | miRNA Regulation and Natural Compound Mechanisms

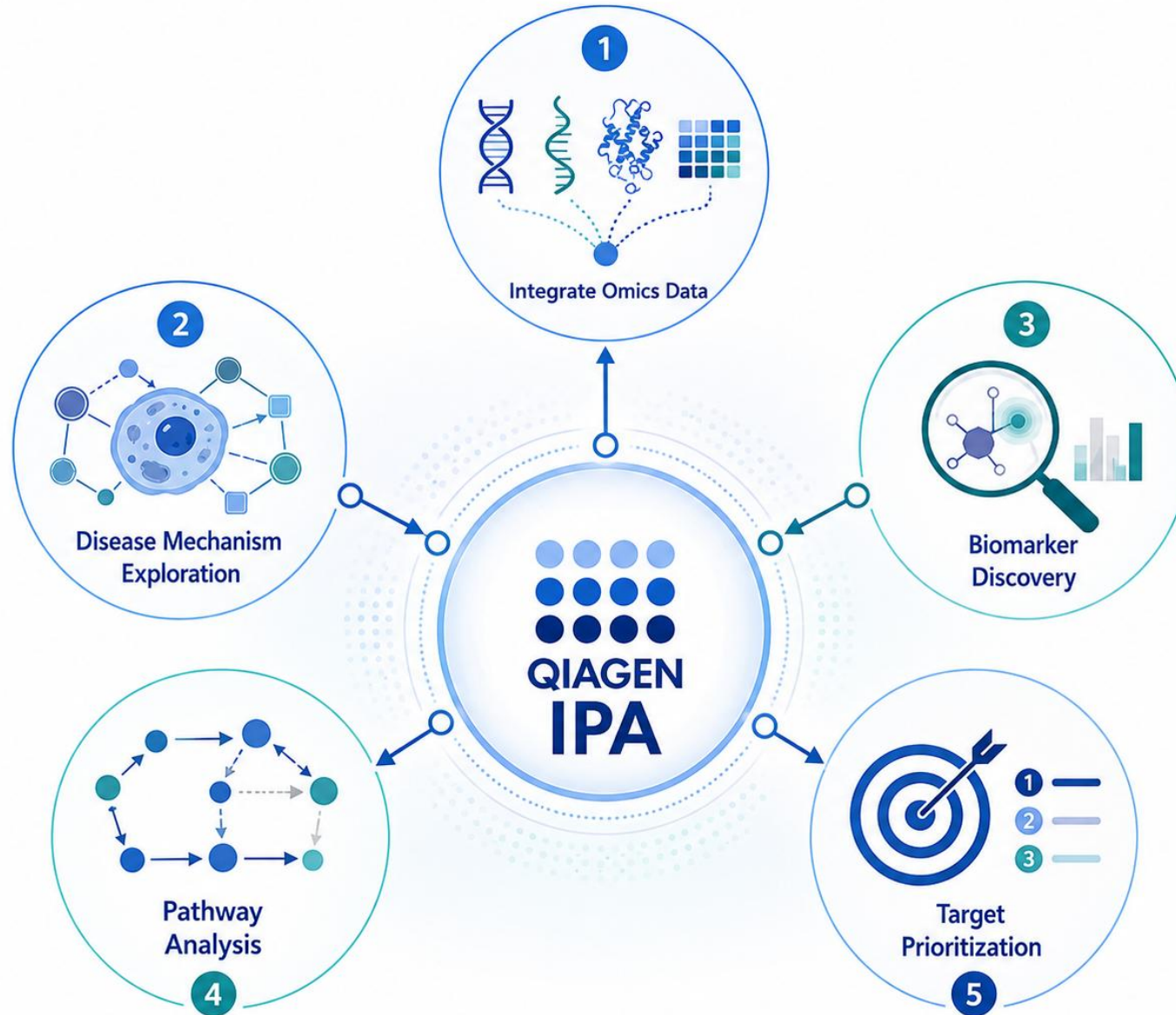
- Case Study: Ugonin V in Chondrosarcoma

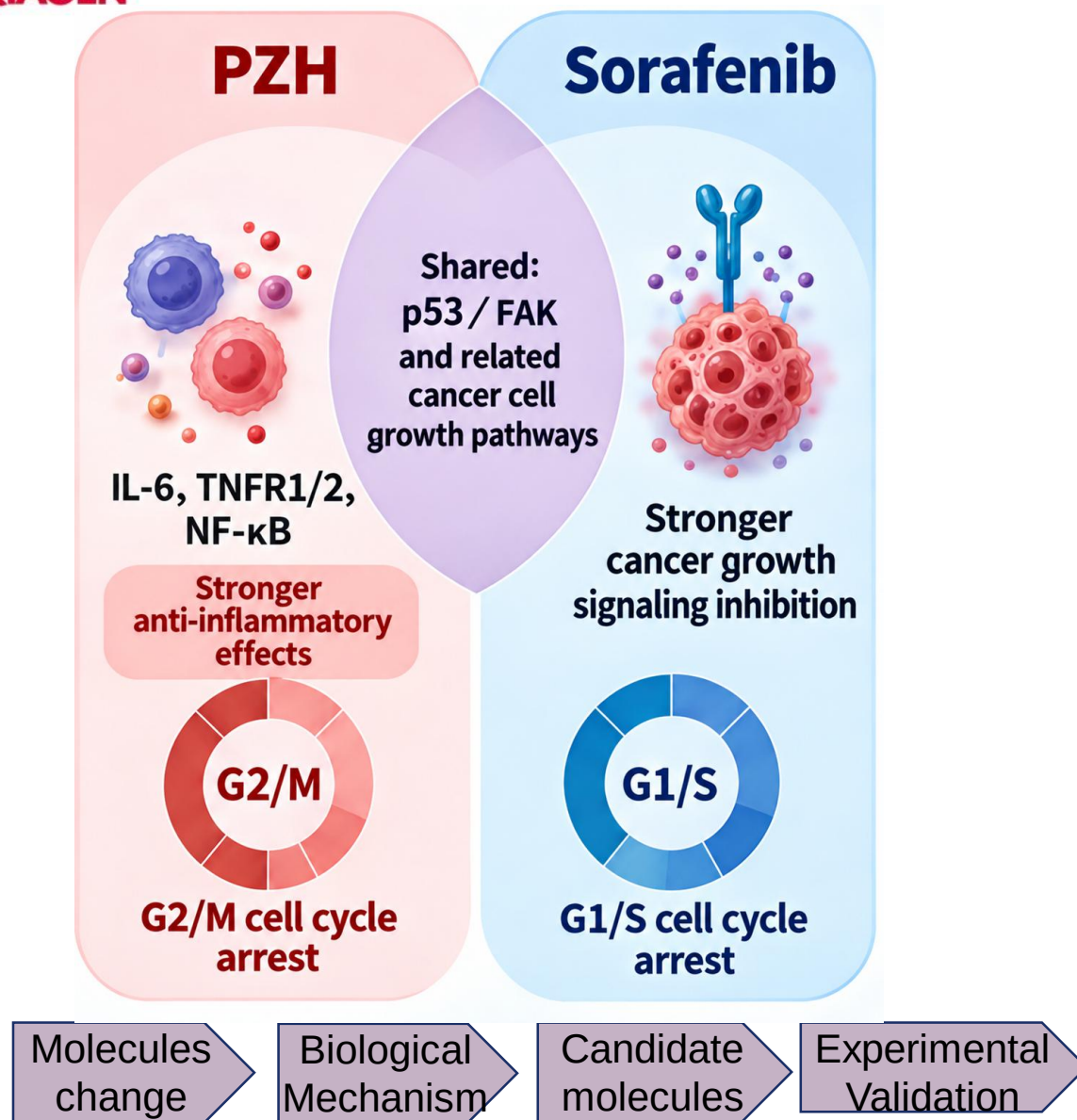
Module 4 | Comparative Analysis and Candidate Target Discovery

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Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer





<https://doi.org/10.1155/2020/4876251>

Research Article

Deciphering Antitumor Mechanism of Pien Tze Huang in Mice of Hepatocellular Carcinoma Based on Proteomics

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The Chinese formula Pien Tze Huang (PZH) has been used to treat hepatocellular carcinoma (HCC) and showed positive clinical effects. However, the antitumor mechanism of PZH in HCC remains unclear. In this study, HCC xenograft Balb/c mice were treated with PZH; then, proteomics detection and Ingenuity Pathway Analysis (IPA) were used to analyze the differentiated phosphorylated proteins in tumor tissues. The results indicated that PZH could inhibit tumor weight by 50.76%. Eighty-four upregulated and 11 downregulated phosphorylated proteins were identified in PZH-treated mice. Twenty signaling pathways were associated with inflammation (including the IL-6 and TNFR1/2 pathways), cancer growth (including the p53 and FAK pathways), and the cell cycle (including the G2/M and G1/S checkpoint regulation pathways). Moreover, TNF-α, IL-6, and several typical differentially expressed phosphorylated proteins (such as p-CCNB1, p-FOXO3, and p-STAT3) in tumor tissues, tumor cell viability, and cell cycle arrest assay *in vitro* further verify the results of IPA. These results revealed that PZH achieved antitumor activity in HCC; the underlying mechanisms of which were mainly through regulating the inflammation-associated cytokine secretion, cancer growth pathways, and induction of G2/M arrest. These data provided the potential molecular basis for PZH to act as a therapeutic drug or a supplement to chemotherapy drugs for human HCC in the future.

1. Introduction

Liver cancer, the fourth leading cause of cancer death worldwide, is one of the most common cancers in China [1, 2]. It is estimated to be responsible for more than 700,000 deaths in one year; the age-standardized 5-year relative survival rate of liver cancer is only 10.1% [3]. The most predominant type of liver cancer is hepatocellular carcinoma (HCC) [4]. Although there are various risk factors for inducing HCC, including viral infections, alcohol abuse, autoimmune hepatitis, diabetes mellitus, and obesity, these factors, especially

hepatitis, point to induce chronic inflammation or even injury in the liver [1]. The mechanism of HCC has been shown to involve several pathways mainly related to cancer growth in HCC progression. In this context, previous studies have reported that inactivation of the tumor suppressor p53 pathway and alterations in the cell cycle are major defects in HCC [4–6]. Recently, increasing research has focused on inflammation, especially chronic inflammation and cytokines, in HCC. In the etiology and pathogenesis of HCC, persistent inflammation has been proven to exacerbate HCC, and most HCC cases arise in the context

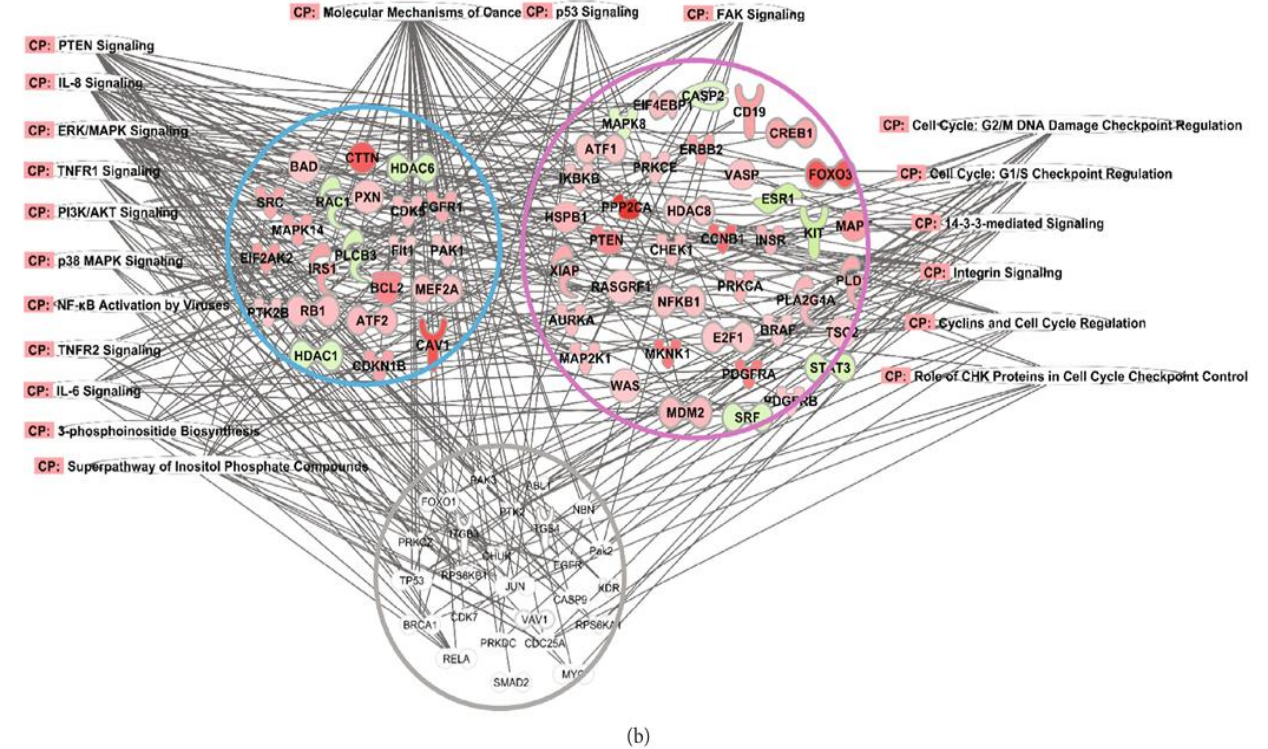
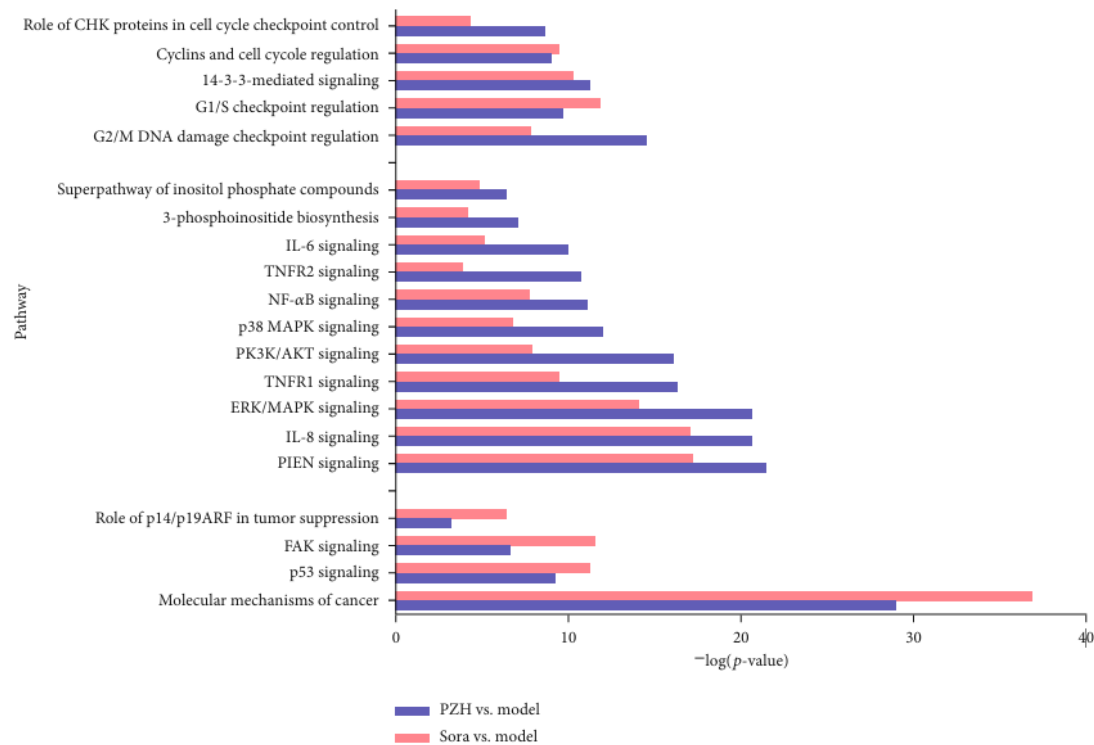
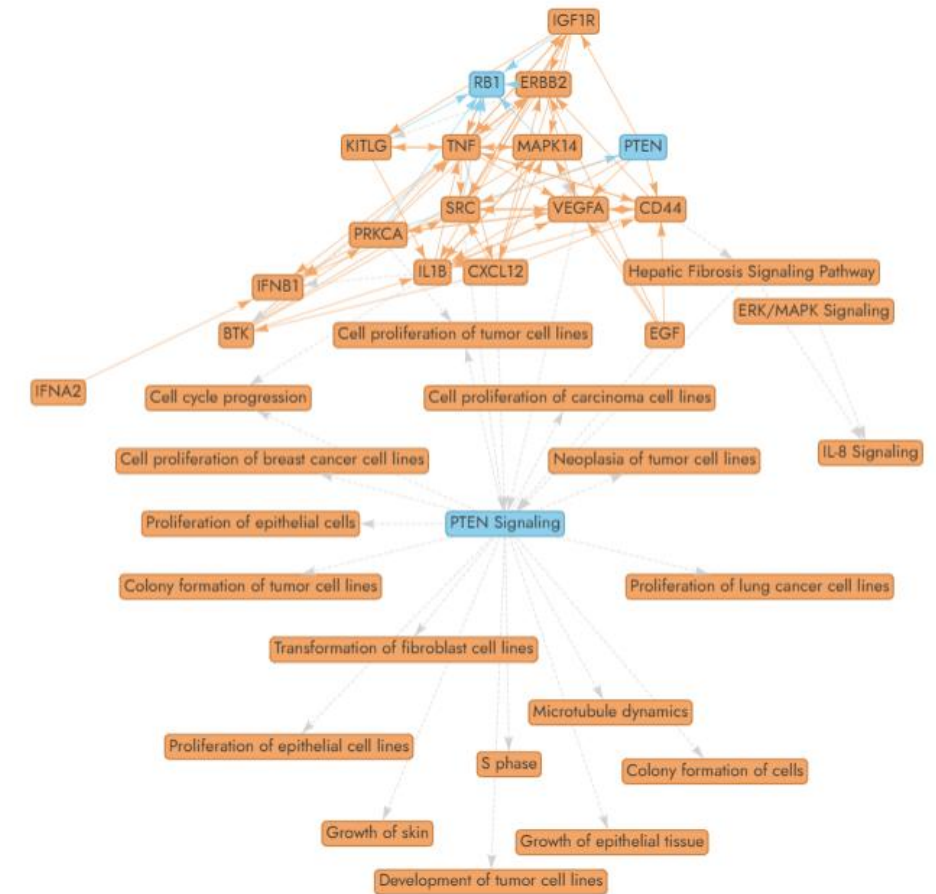
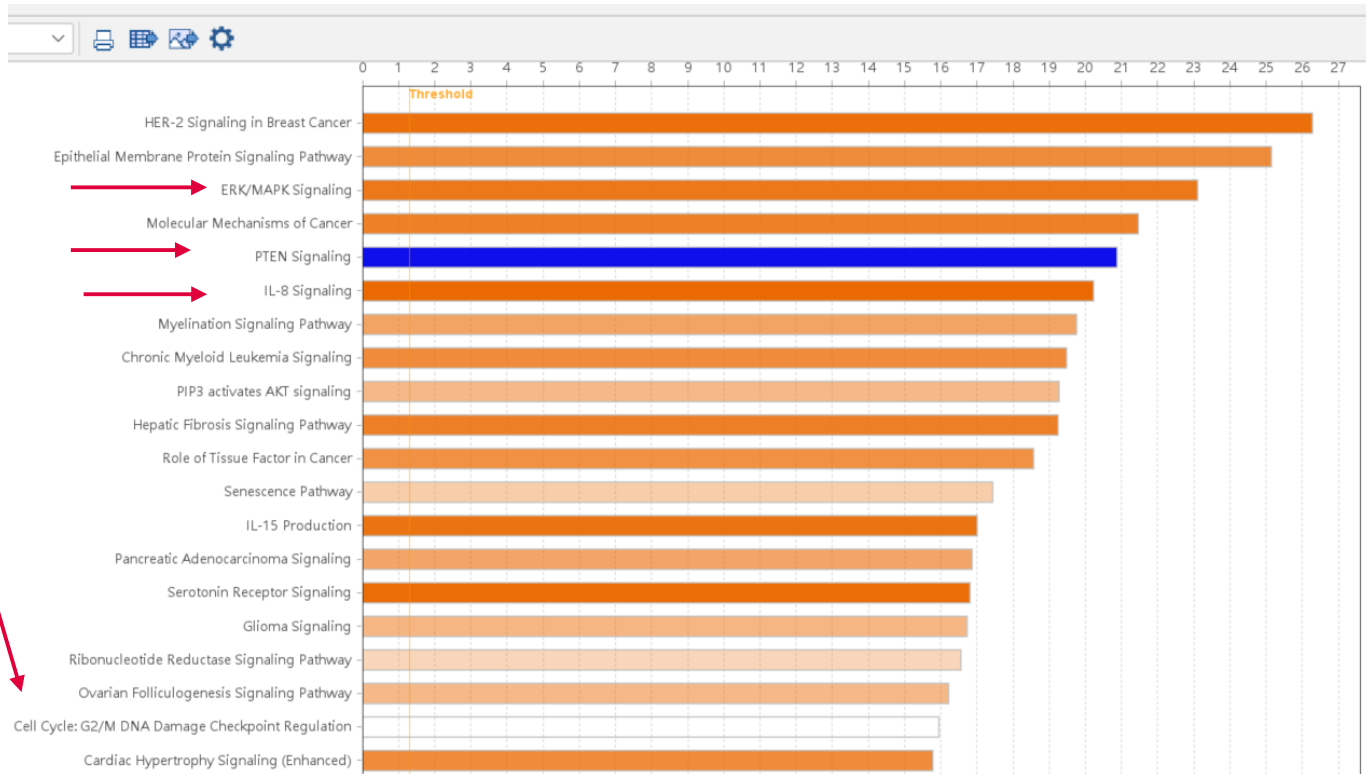
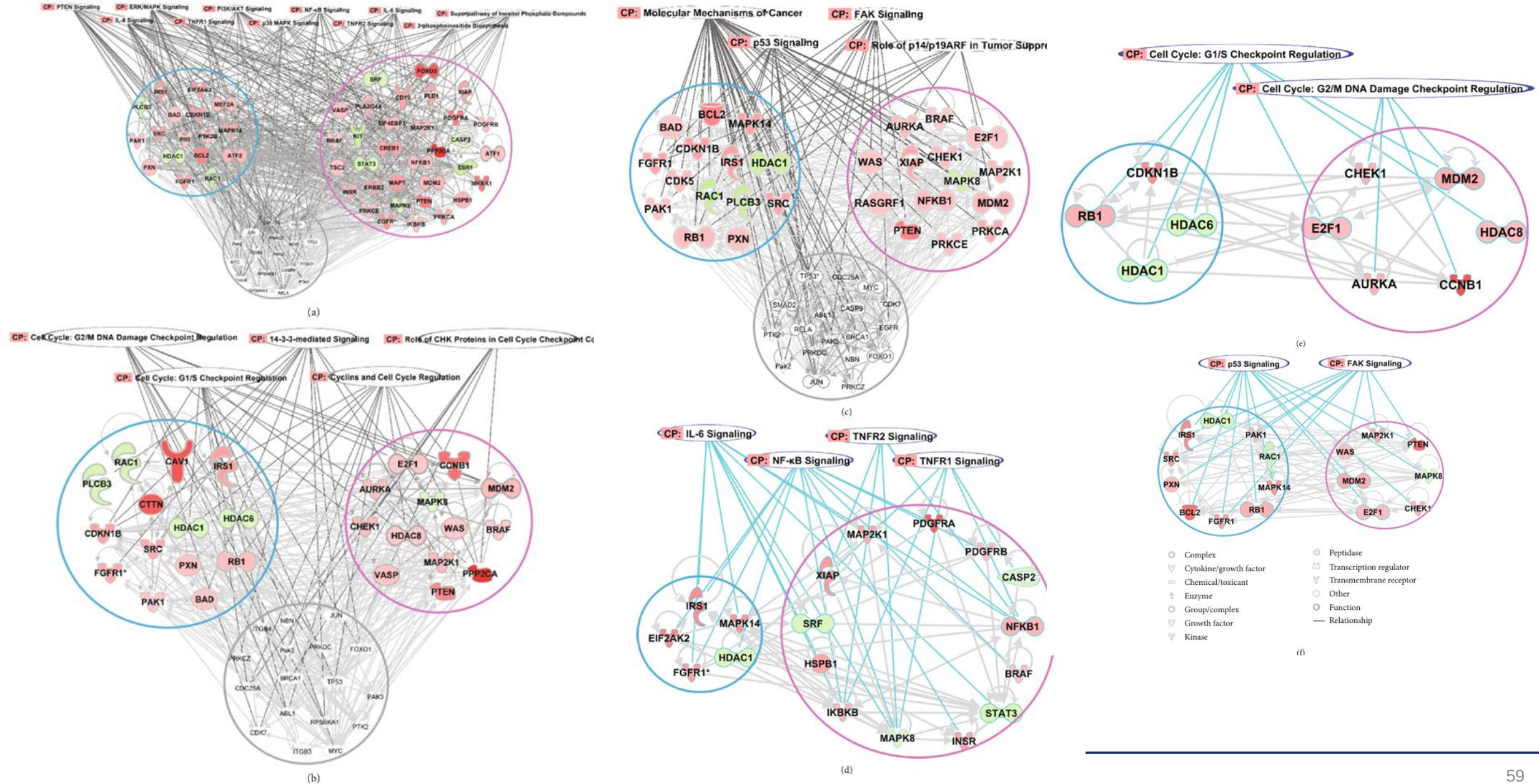


Figure 3: Comparison of involved pathways between PZH and Sora treatment. (a) The-log (p value) value of involved pathways in PZH and Sora groups. (b) The molecular network involved in those pathways regulated by PZH and Sora treatment.

PZH remodels tumor-associated phospho-signaling networks





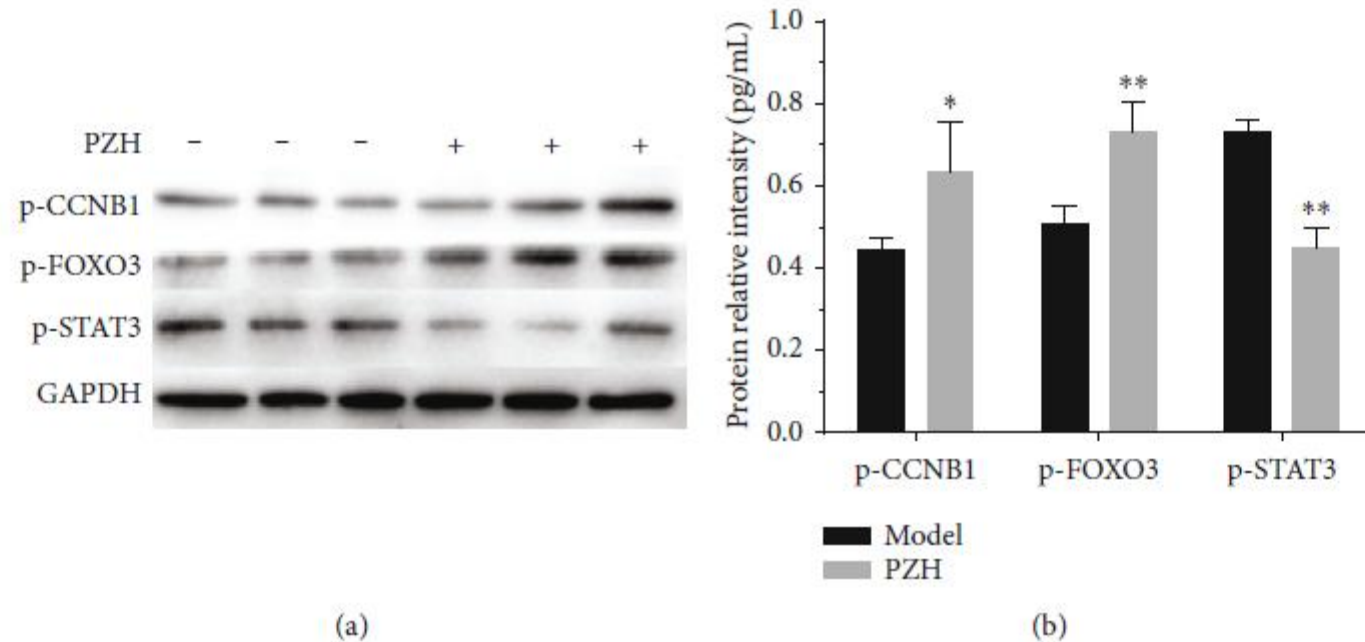


FIGURE 7: PZH upregulates the expression of p-CCNB1 and p-FOXO3 and downregulates the expression of p-STAT3 in tumor tissue of HCC mice. (a) Representative Western blot bands of p-CCNB1, p-FOXO3, and p-STAT3. (b) Analysis of relative protein levels. * $p < 0.05$, ** $p < 0.01$ vs. model group.

Proteomics + Ingenuity Pathway Analysis (IPA)



Fan et al. | Journal of Immunology Research | 2020
Deciphering Antitumor Mechanism of Pien Tze Huang in Mice of Hepatocellular Carcinoma Based on Proteomics



KEY FINDINGS

- ✓ Tumor weight reduced by **50.76%**
- ✓ **95** differential phosphoproteins identified
- ✓ **84** upregulated | **11** downregulated
- ✓ **20** signaling pathways involved



MAJOR PATHWAY THEMES



Inflammation: IL-6, TNF-alpha, TNFR1/2 signaling



Cancer growth: p53 and FAK-related pathways



Cell cycle: G2/M arrest and G1/S checkpoint regulation



TAKE-HOME MESSAGE

PZH shows antitumor activity in HCC by modulating inflammation-associated cytokine signaling, suppressing tumor-growth pathways, and promoting cell-cycle arrest.

Source: Fan D. et al., J Immunol Res. 2020; Article ID 4376251.

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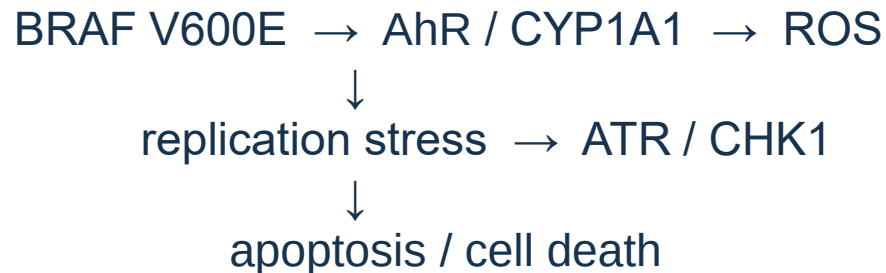
- Case Studies: Immunotherapy Resistance and Single-Cell Heterogeneity

Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer

KEY MESSAGE FROM THE PAPER

BOLD-100 is a pre-formed Ru(III) coordination drug. The study demonstrates that a metal-based drug can induce ROS-linked stress in cancer cells.



VACO432: IC₅₀ 30.69 μM | VT1: IC₅₀ 119.67 μM

24 h exploratory DEG: VACO432 423↑ / 231↓; VT1 50↑ / 13↓

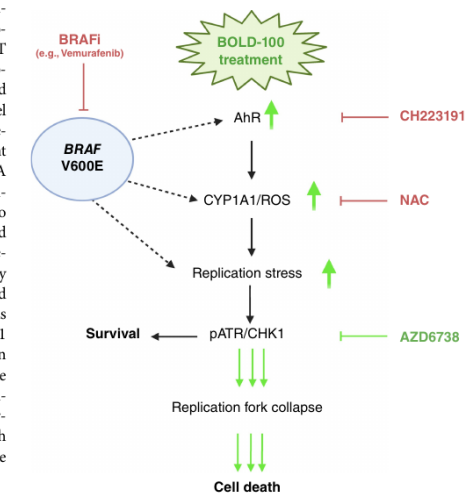
Shivakshi Karella, Richard Kennedy, Kieran I. Savage, Simon McDade, Adam Carie, Jim Pankovitch, Mark Bazett⁶, and Sandra Van Schaeybroeck¹

ABSTRACT

Patients with class 1 ^{V600E}BRAF-mutant (MT) colorectal cancer exhibit a poor prognosis, and their response to combined anti-BRAF/EGFR inhibition remains limited. An unmet need exists for further understanding the biology of ^{V600E}BRAFMT colorectal cancer. We used differential gene expression of BRAFWT and MT colorectal cancer cells to identify pathways underpinning BRAFMT colorectal cancer. We tested a panel of molecularly/genetically subtyped colorectal cancer cells for their sensitivity to the unfolded protein response (UPR) activator BOLD-100. To identify novel combination strategies for BOLD-100, we performed RNA sequencing and high-throughput drug screening. Pathway enrichment analysis identified significant enrichment of the UPR and DNA repair pathways in BRAFMT colorectal cancer. We found that oncogenic BRAF plays a crucial role in mediating the response to BOLD-100. Using a systems biology approach, we identified ^{V600E}BRAFMT-dependent activation of the replication stress response kinase ataxia telangiectasia and Rad3-related (ATR) as a key mediator of resistance to BOLD-100. Further analysis identified acute increases in BRAFMT-dependent reactive oxygen species levels following treatment with BOLD-100, which promoted ATR/CHK1 activation and apoptosis. Furthermore, activation of reactive oxygen species/ATR/CHK1 following BOLD-100 was mediated through the AhR transcription factor and CYP1A1. Importantly, pharmacological blockade of this resistance pathway with ATR inhibitors synergistically increased BOLD-100-induced apoptosis and growth inhibition in BRAFMT models. These results highlight a possible novel therapeutic opportunity for BRAFMT colorectal cancer.

Implications: BOLD-100 induces BRAFMT-dependent replication stress, and targeted strategies against replication stress (e.g.,

by using ATR inhibitors) in combination with BOLD-100 may serve as a potential novel therapeutic strategy for clinically aggressive BRAFMT colorectal cancer.



Introduction

BRAF mutations are found in approximately 10% of metastatic colorectal cancer tumors, and around 90% of these tumors harbor a

T1799A transversion in exon 15, resulting in a valine amino acid substitution (V600E; ref. 1). The ^{V600E}BRAF (class I) mutation identifies a distinct subgroup of colorectal cancer, often associated

¹Patrick G. Johnston Centre for Cancer Research, School of Medicine, Dentistry, and Biomedical Science, Queen's University Belfast, Belfast, United Kingdom.

Queen's University Belfast, 97 Lisburn Road, Belfast BT9 7AE, United Kingdom. E-mail: s.vanschaeybroeck@qub.ac.uk

Analysis – Set Cutoff & Biological Filter

Create Expression Analysis - [analysis : VACO432_24h_DEG_full]

Set Cutoffs Biological Filters

Use cutoffs to select a set of molecules from your dataset to analyze. Ideally choose between 100 and 3000

Load Volcano Plot

Set Cutoffs Biological Filters

General Settings

> Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species All

Tissues & Cell Lines All

Mutation All

Save As Default

Generate the following Networks (increases analysis time)

☒ Interaction networks☒ Include endogenous chemicals

Molecules per network

Networks per analysis

Genes are always included

35

25

☒ Causal networks

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

☐ Score using causal paths only

Synthesis of reactive oxygen species [ROS synthesis,synthesis of ROS]

Accumulation of lipid reactive oxygen species [accumulation of lipid ROS,accrual of lipid RO

Accumulation of reactive oxygen species [ROS accrual,ROS concentration,...]

Add...

Remove

0.653	2.93E-02	1.66E-01	ABO	ABO	ABO, alpha 1-3-N-acetylgala...	Cytoplasm	enzyme
0.751	1.12E-02	1.25E-01	ADCY4	ADCY4	adenylate cyclase 4	Plasma Membrane	enzyme

0 / 582

Flags:

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

"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.

"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with italic text.

"A" - Gene/Protein/Chemical ID marked as Absent. The gene/protein/chemical will not be used as a focus molecule or appear in networks unless you also explicitly override this flag with the Override column.

Run Analysis

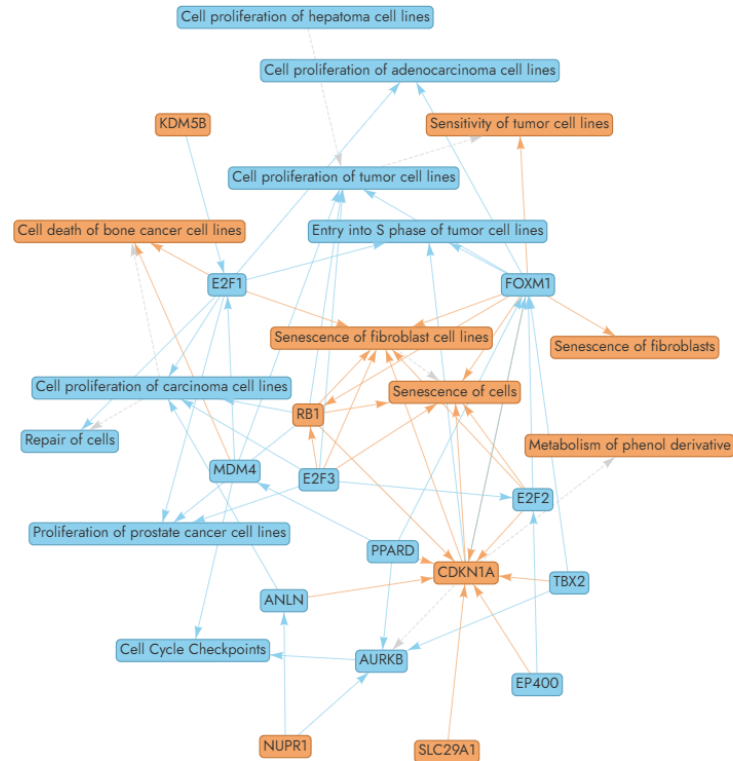
Cancel

VACO432_24h_DEG_full · 2026-08-05 11:01 下午 / Graphical Summary

VACO432_24h_DEG_full - 2026-08-05 11:01 下午

Created on August 5, 2026, from dataset VACO432_24h_DEG_full

VACO432_24h_DEG_full - 2026-08-05 11:01 下午 Figure Legend ☐ OFF



RB–E2F–p21 Axis Orchestrating Cell-Cycle Arrest, Senescence, and Therapy Sensitization in Tumor Cells

AI-Suggested

RB–E2F–FOXM1 Core Cell-Cycle Control Module

The network centers on the classical RB–E2F pathway, extended by FOXM1, as a master regulator of cell-cycle progression in cancer cells. Decreases in E2F1, E2F2, and E2F3 uniformly lead to reduced cell proliferation across carcinoma, adenocarcinoma, and prostate cancer cell lines, as well as reduced entry into S phase and impaired cell repair. FOXM1 is tightly integrated: its decrease mirrors E2F loss, causing reduced tumor cell proliferation and S-phase entry, and increasing RB1. This is consistent with RB1 restraining E2Fs and FOXM1, such that increased RB1 activity decreases cell proliferation (tumor and carcinoma) and prostate cancer cell growth. Upstream regulators such as EP400, PPARD, TBX2, and KDM5B modulate this axis by reducing E2F and FOXM1 activity, thereby reinforcing cell-cycle arrest. Overall, the directionality shows a coherent module where RB1, E2F family members, and FOXM1 coordinate the commitment to cell division in tumor contexts.

CDKN1A (p21)–Driven Cell-Cycle Arrest and Senescence Program

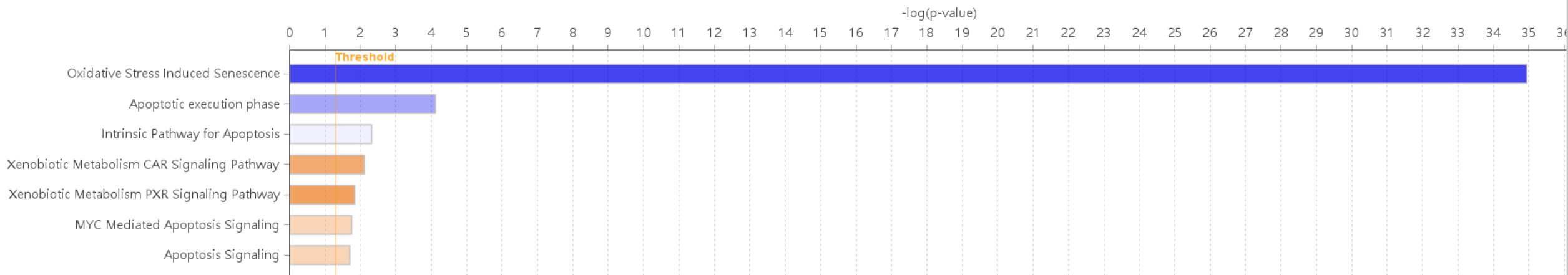
CDKN1A (p21) emerges as a central effector that converts upstream regulatory changes into durable cell-cycle exit and senescence. Multiple inputs (decrease of ANLN, E2F2, EP400, PPARD, FOXM1, TBX2, and increased RB1, SLC29A1) converge to increase CDKN1A. In turn, elevated CDKN1A decreases AURKB (a mitotic kinase), FOXM1, and tumor cell entry into S phase, directly enforcing cell-cycle arrest. Crucially, increased CDKN1A drives senescence in both general cell populations and fibroblast cell lines, and this fibroblast senescence feeds back to increase overall cellular senescence. The network therefore depicts p21 as the key node linking upstream transcriptional and chromatin regulators to a stable, senescent state rather than transient quiescence, particularly in tumor and fibroblast contexts.

AURKB and MDM4 as Mitotic Checkpoint and Survival Nodes Undermined by p21/RB Signaling

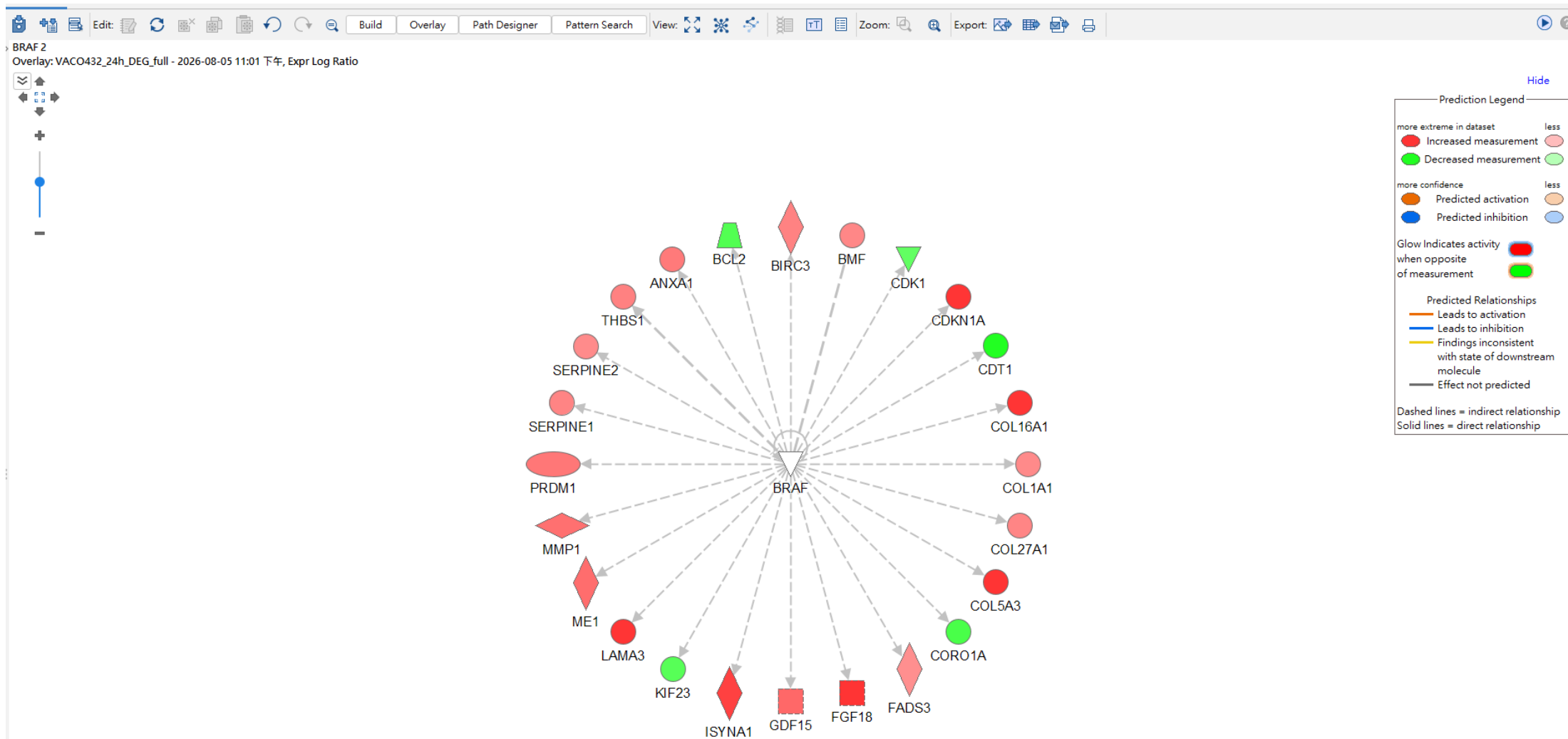
AURKB and MDM4 function as downstream pro-proliferative and pro-survival factors that are suppressed when the RB–p21 axis is engaged. Decreased AURKB leads to reduced cell-cycle checkpoints, highlighting its role in mitotic progression and genomic surveillance; CDKN1A directly inhibits AURKB, and NUPR1 and PPARD also decrease AURKB, reinforcing this checkpoint failure from multiple upstream pressures. MDM4, a key regulator of p53 signaling, is decreased by PPARD, which in turn reduces tumor cell proliferation and cell-cycle checkpoints and promotes cell death in bone cancer cell lines via lowered E2F1. Together, AURKB and MDM4 represent critical nodes where cell-cycle and DNA damage checkpoint signaling intersect; their suppression in this network strengthens the transition from active cycling to arrest and death.

Pathway results

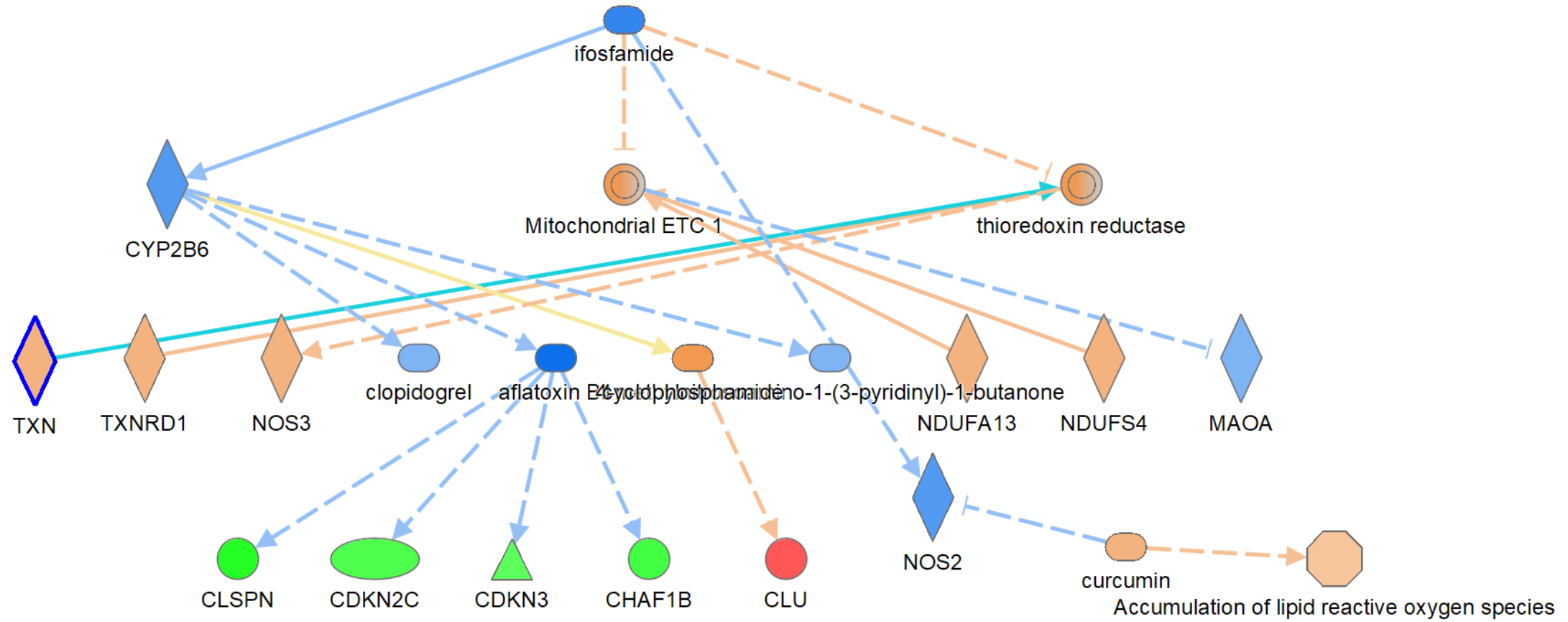
■ positive z-score ■ z-score = 0 ■ negative z-score ■ no activity pattern available



Upstream regulator



Causal relationship



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What is QIAGEN Ingenuity Pathway Analysis

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

Module 1 | IPA in Drug Discovery and Translational Medicine

Module 2 | Transcriptomics and Drug Mechanism of Action

- Case Study: BOLD-100 in Colorectal Cancer

Module 3 | miRNA Regulation and Natural Compound Mechanisms

- Case Study: Ugonin V in Chondrosarcoma

Module 4 | Comparative Analysis and Candidate Target Discovery

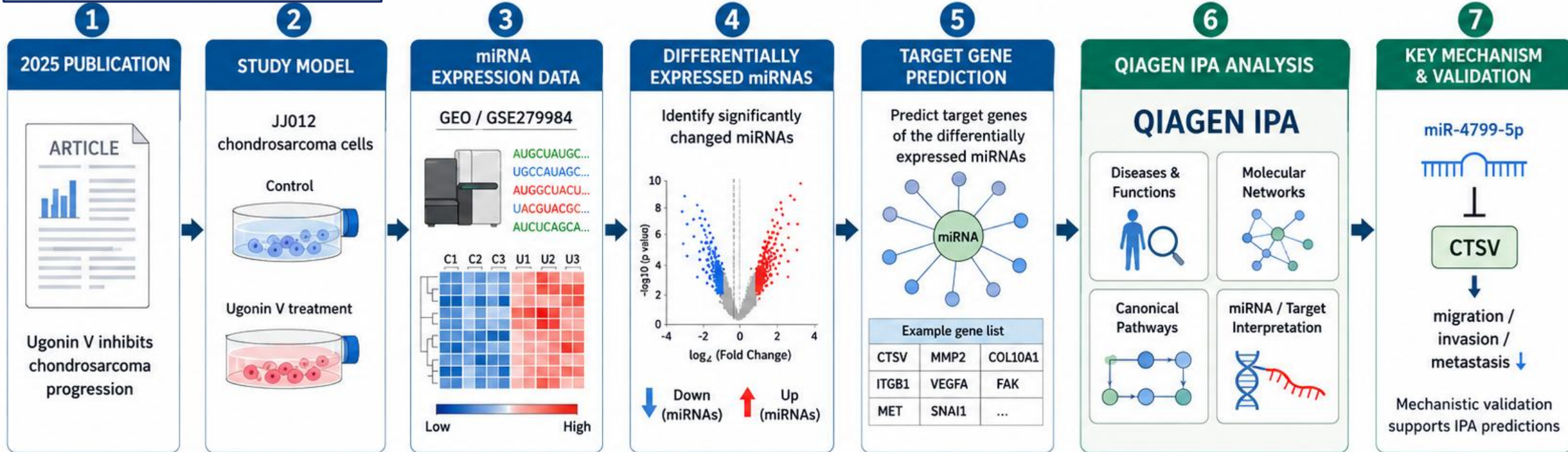
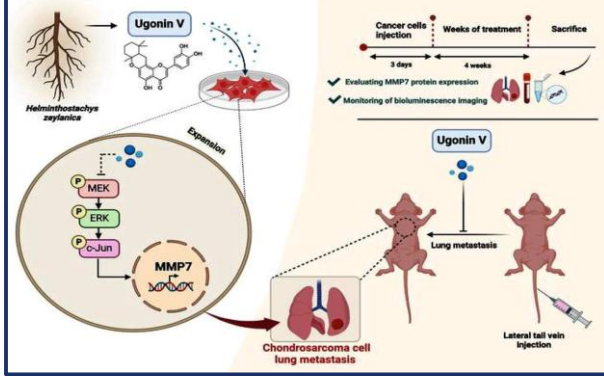
- Case Studies: Immunotherapy Resistance and Single-Cell Heterogeneity

Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer

2025 LITERATURE CASE EXAMPLE & IPA RE-ANALYSIS CONCEPT MAP

Using Ugonin V and Chondrosarcoma miRNA Data as an Example



KEY TAKEAWAYS FROM RE-ANALYSIS



REPRODUCIBLE WITH PUBLIC DATA

Utilizing GEO public data ensures transparency and reproducibility of the analysis pipeline.



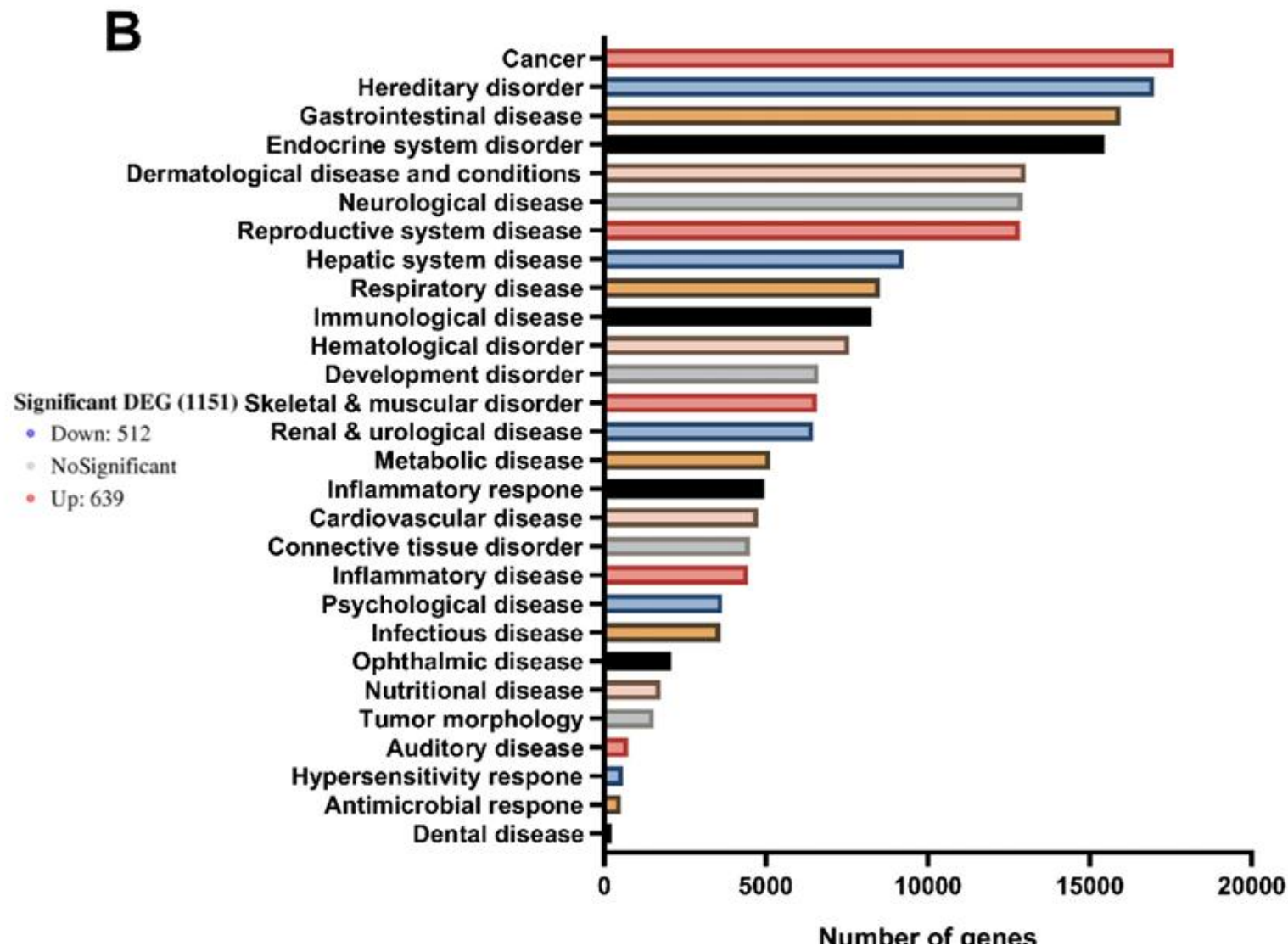
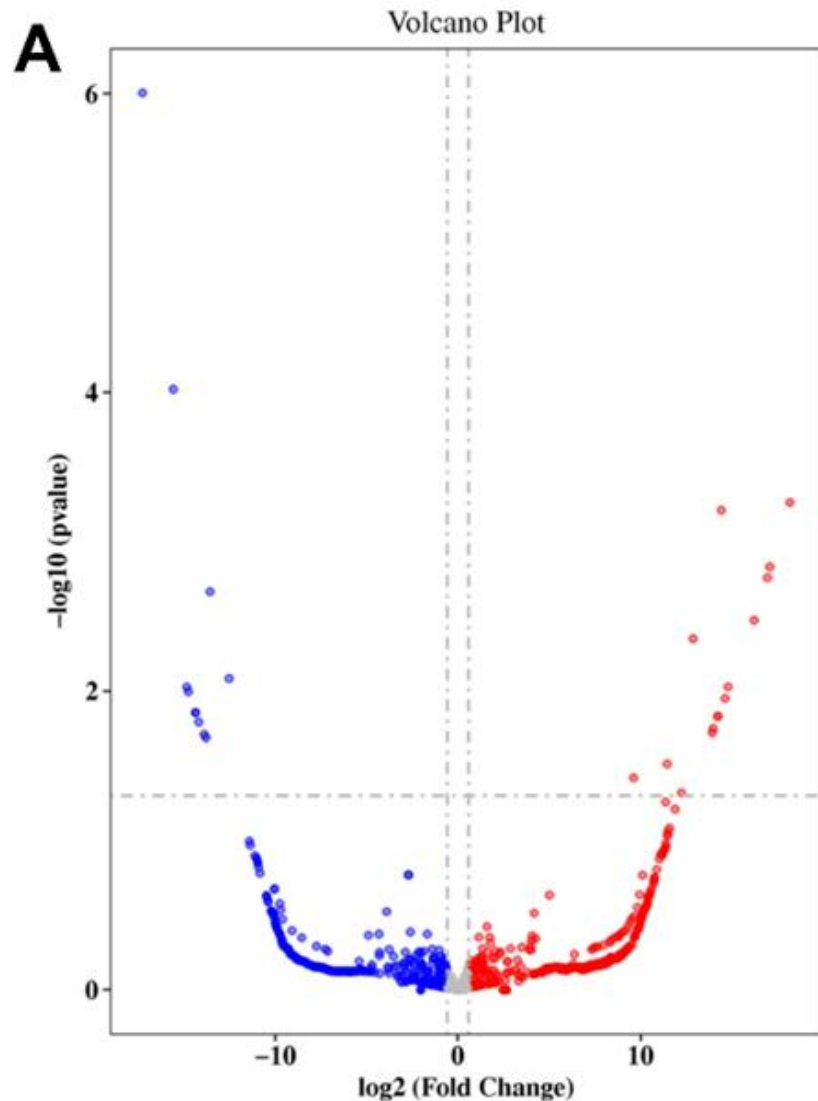
DISEASE & PATHWAY INSIGHTS

Integrating differential miRNA and target genes reveals key disease mechanisms and signaling pathways.



ACTIONABLE FOR FUTURE RESEARCH

Establish a framework for analysis and validation to support future drug discovery and experimental design.



Ugonin V treatment Differential expression

	A	B	C	D	E	F	G	H	I	J	K
1	gene_id	length	Control_mean_TPM	Treatment_mean_TPM	Control_mean_norm_count	Treatment_mean_norm_count	log2FoldChange	pvalue	padj_BH	tested	significance
2	NovelmiRNA-368	21.000	0.000	398.480	0.000	2649.871	12.372	3.35E-04	1.61E-01	☒	Not significant
3	hsa-miR-3912-3p	21.000	2.735	0.000	19.013	0.000	-5.286	1.95E-03	4.70E-01	☒	Not significant
4	NovelmiRNA-12	22.000	0.000	51.040	0.000	337.323	9.400	7.70E-03	7.60E-01	☒	Not significant
5	hsa-miR-548au-3p	22.000	0.000	20.165	0.000	133.536	8.066	6.22E-03	7.60E-01	☒	Not significant
6	NovelmiRNA-155	23.000	0.000	8.105	0.000	53.618	6.758	9.48E-03	7.60E-01	☒	Not significant
7	hsa-miR-222-3p	23.000	12569.520	20970.735	87270.825	139665.775	0.678	8.80E-03	7.60E-01	☒	Not significant
8	NovelmiRNA-554	23.000	869.080	0.000	6053.420	0.000	-13.564	1.24E-02	7.74E-01	☒	Not significant
9	NovelmiRNA-371	24.000	0.000	12.305	0.000	82.657	7.378	1.45E-02	7.74E-01	☒	Not significant
10	hsa-miR-145-5p	23.000	808.955	432.415	5622.889	2883.519	-0.963	1.39E-02	7.74E-01	☒	Not significant
11	hsa-miR-4521	25.000	2796.855	0.000	19511.475	0.000	-15.252	1.75E-02	8.40E-01	☒	Not significant
12	NovelmiRNA-190	22.000	219.440	0.000	1517.937	0.000	-11.568	2.14E-02	8.92E-01	☒	Not significant
13	NovelmiRNA-120	22.000	6.705	0.000	46.471	0.000	-6.554	2.23E-02	8.92E-01	☒	Not significant
14	NovelmiRNA-491	21.000	0.000	13.705	0.000	89.370	7.490	3.00E-02	9.70E-01	☒	Not significant
15	hsa-miR-3661	22.000	0.000	3.365	0.000	22.058	5.496	3.03E-02	9.70E-01	☒	Not significant
16	hsa-miR-324-3p	23.000	151.185	99.540	1050.605	659.282	-0.672	2.75E-02	9.70E-01	☒	Not significant
17	NovelmiRNA-513	18.000	0.000	141.995	0.000	908.639	10.828	4.40E-02	1.00E+00	☒	Not significant
18	NovelmiRNA-230	18.000	108.545	0.000	745.200	0.000	-10.542	8.91E-02	1.00E+00	☒	Not significant
19	NovelmiRNA-736	18.000	0.000	43.235	0.000	312.934	9.292	2.31E-01	1.00E+00	☒	Not significant
20	hsa-miR-4435	22.000	0.055	64.670	0.376	401.966	8.844	1.01E-01	1.00E+00	☒	Not significant

miRNA target mRNA

IPA

File Edit View Window Help

Genes and Chemicals Diseases and Functions Pathways and Lists **Datasets and Analyses**

Create New...

GSE279984

Search

Advanced Search

Provide Feedback | Support

Gene Chen

Close IPA

Annotated Dataset: Ugonin_V_upload

Preview Dataset Ugonin_V_upload

Mapped IDs (398) Unmapped IDs (83) All IDs (481) Metadata

Add To My Pathway

Add To My List

Create Dataset

Customize Table

Symbol

let-7a-5p (and o... (1/4)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
0.996	1.86E-01	hsa-let-7c-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
0.287	2.13E-01	hsa-miR-98-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.287	2.87E-01	hsa-let-7d-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.281	2.48E-01	hsa-let-7e-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.205	8.29E-02	hsa-let-7a-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.201	5.03E-01	hsa-let-7g-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.119	6.81E-01	hsa-let-7f-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.085	7.22E-01	hsa-let-7i-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.014	9.09E-01	hsa-let-7b-5p	D	let-7a-5p (and other miRNAs w/see		Cytoplasm	mature microRNA	
-0.532	9.63E-01	hsa-miR-1-3p		miR-1-3p (and other miRNAs w/see		Cytoplasm	mature microRNA	
0.591	1.77E-01	hsa-miR-100-5p	D	miR-100-5p (and other miRNAs w/s		Cytoplasm	mature microRNA	
0.257	6.03E-01	hsa-miR-99a-5p	D	miR-100-5p (and other miRNAs w/s		Cytoplasm	mature microRNA	
0.007	9.75E-01	hsa-miR-101-3p		miR-101-3p (and other miRNAs w/s		Cytoplasm	mature microRNA	
-0.464	2.03E-01	hsa-miR-107		miR-103-3p (and other miRNAs w/s		Cytoplasm	mature microRNA	
-0.307	6.77E-01	hsa-miR-1908-5p		miR-10396b-5p (and other miRNAs		Cytoplasm	mature microRNA	
0.370	9.70E-01	hsa-miR-10399-3p		miR-10399-3p (miRNAs w/seed UCL		Cytoplasm	mature microRNA	
-0.463	9.60E-02	hsa-miR-105-5p		miR-105-5p (and other miRNAs w/s		Cytoplasm	mature microRNA	
-2.340	3.41E-01	hsa-miR-10523-5p		miR-10523-5p (miRNAs w/seed AC		Cytoplasm	mature microRNA	
-4.479	6.00E-01	hsa-miR-10526-3p		miR-10526-3p (miRNAs w/seed AA		Cytoplasm	mature microRNA	
-0.243	6.14E-01	hsa-miR-10b-5p	D	miR-10a-5p (and other miRNAs w/s		Cytoplasm	mature microRNA	
-0.187	6.96E-01	hsa-miR-10a-5p	D	miR-10a-5p (and other miRNAs w/s		Cytoplasm	mature microRNA	
-0.146	7.36E-01	hsa-miR-1180-3p		miR-1180-3p (miRNAs w/seed UUC		Cytoplasm	mature microRNA	
4.977	2.48E-01	hsa-miR-3679-5p		miR-1185-5p (and other miRNAs w/		Cytoplasm	mature microRNA	
0.025	9.99E-01	hsa-miR-12135		miR-12135 (miRNAs w/seed AAAGG		Cytoplasm	mature microRNA	
-0.515	5.68E-01	hsa-miR-942-5p		miR-12202-3p (and other miRNAs w		Cytoplasm	mature microRNA	
0.273	9.86E-01	hsa-miR-1226-3p		miR-1226-3p (miRNAs w/seed CAC		Cytoplasm	mature microRNA	
-1.720	8.85E-01	hsa-miR-1228-3p		miR-1228-3p (miRNAs w/seed CAC		Cytoplasm	mature microRNA	
2.339	4.77E-01	hsa-miR-1229-3p	D	miR-1229-3p (miRNAs w/seed UCU		Cytoplasm	mature microRNA	
1.333	1.79E-01	hsa-miR-2110	D	miR-1229-3p (miRNAs w/seed UCU		Cytoplasm	mature microRNA	
0.702	2.82E-01	hsa-miR-1249-3p		miR-1249-3p (and other miRNAs w/		Cytoplasm	mature microRNA	

0 / 398

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.

Core Analysis

Biomarker Filter

Filter Dataset

microRNA Target Filter

BioProfiler

IsoProfiler

Edit Dataset Settings

Analyze/Filter Dataset

Close

Sample to Insight

73

324 miRNA
↓
1567 mRNA

microRNA Target Filter

324 microRNA have targeting information available.
Filtered to 133 microRNAs targeting 1567 mRNAs.

[Details](#)
[Summary](#)

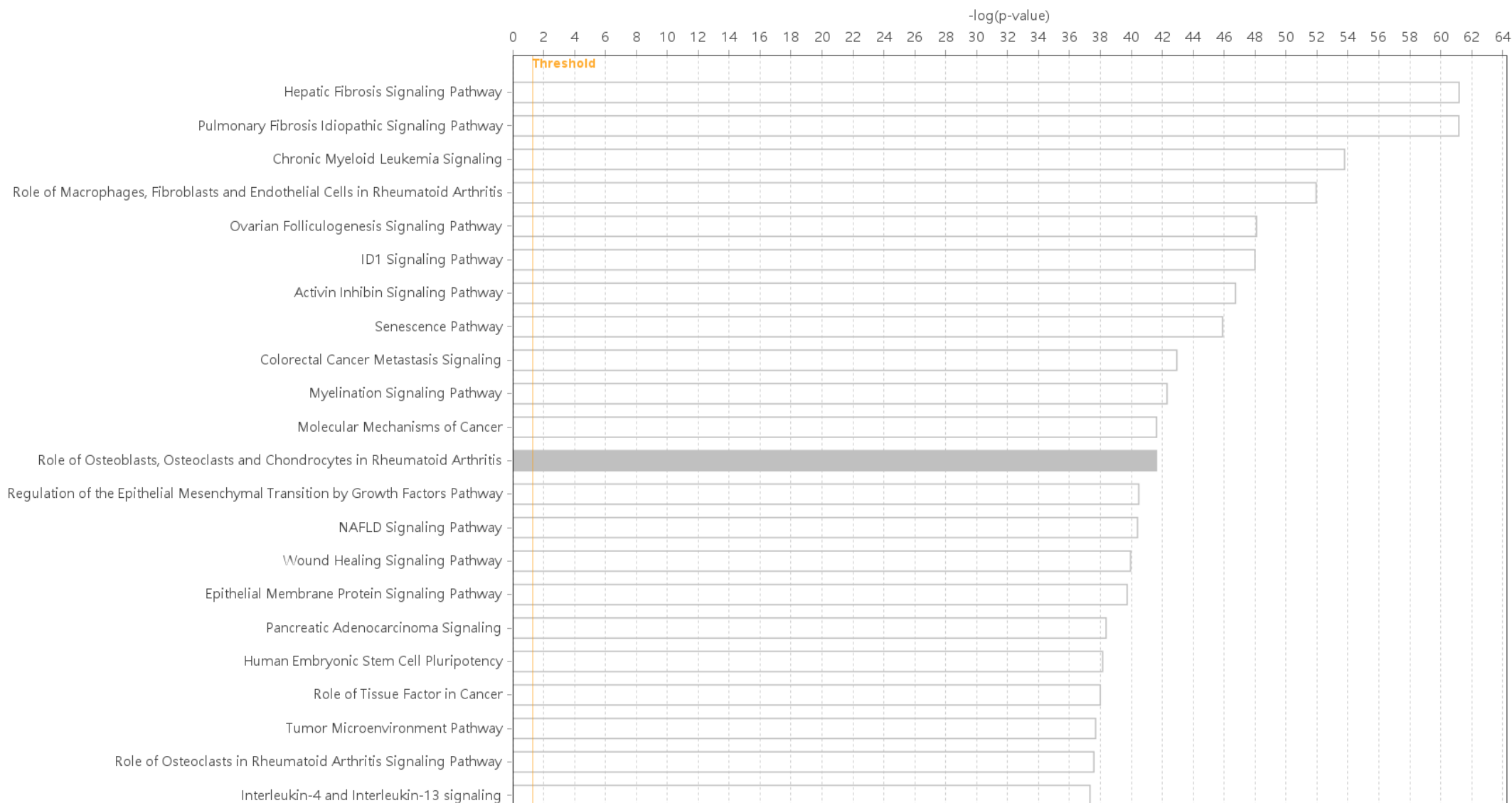
[Add/Replace mRNA dataset](#)
[Expression Pairing ↕](#)

[Add To My Pathway](#)
[Add To My List](#)
[Create Dataset](#)
[Display As Network](#)

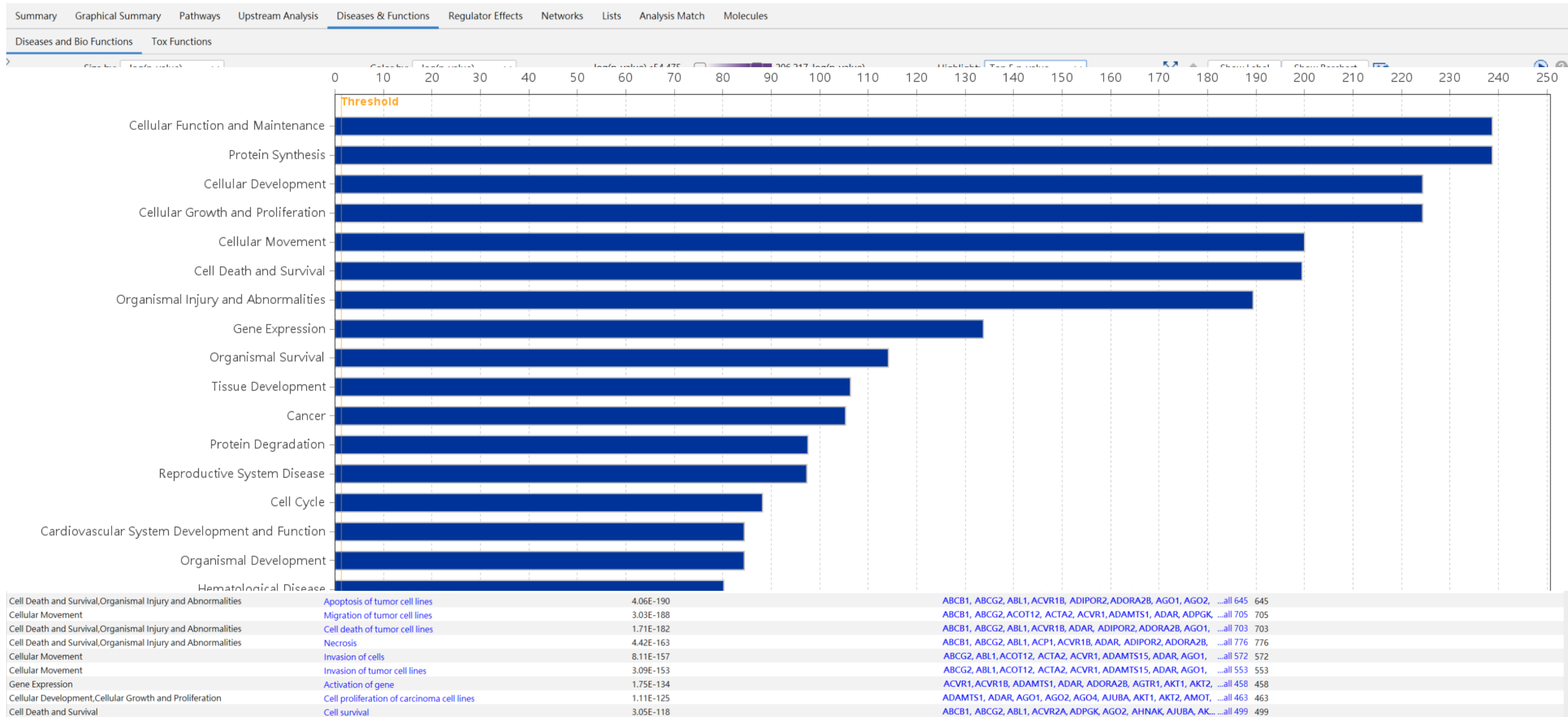
Use to filter a column. Edit columns using .

☐	microRNA dataset: Ugonin_V_upload		Edit columns	Relationship	Edit columns	mRNA	Edit columns
☐	ID	Symbol	Expr Log Ratio	Source	miRNA Confidence	Symbol	Pathway
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	AARSD1	Heparan Sulfate Bi... all 3
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	miRecords	Experimentally Observed	ACP1	3-phosphoinosit... all 13
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, Ingenui	Experimentally Observed, M	ADAMTS14	Axonal Guidance S... all 3
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, Ingenui	Experimentally Observed, Hi	ADAMTS15	Axonal Guidance S... all 2
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	Ingenuity Expert Findings	Experimentally Observed	ADAMTS2	Axonal Guidance S... all 3
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	ADGRG1	BBSome Signalin... all 12
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TargetS	Experimentally Observed, Hi	AGO4	Beta-catenin ind... all 23
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TarBase	Experimentally Observed, M	AKAP8	Cardiac β-adrener... all 3
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	ANAPC1	Cell Cycle Checkp... all 18
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	ATAD3B	Neutrophil degran... all 1
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	ATP6V0A1	Adrenergic Recep... all 15
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase, TargetScan Humar	Experimentally Observed, Hi	ATP6V1F	Adrenergic Recep... all 15
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase, TargetScan Humar	Experimentally Observed, M	AURKB	Breast Cancer Re... all 13
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, Ingenui	Experimentally Observed, M	BCL2L1	Amyotrophic Late... all 47
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Human, miReco	Experimentally Observed, M	BCL7A	MITF-M-dependen... all 3
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	miRecords	Experimentally Observed	BMP2K	
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, Ingenui	Experimentally Observed, M	BSG	Aspirin ADME, Cell ... all 9
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	CALCOCO2	
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	CAPG	
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	CARHSP1	
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TargetS	Experimentally Observed, Hi	CASP3	Acetylcholine Rec... all 78
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	Ingenuity Expert Findings, T	Experimentally Observed, M	CCND1	AMPK Signaling, ... all 89
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TargetS	Experimentally Observed, Hi	CDC25A	3-phosphoinosit... all 23
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	CDIPT	3-phosphoinositid... all 4
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	miRecords	Experimentally Observed	CDK6	Aryl Hydrocarbon... all 24
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase, TargetScan Humar	Experimentally Observed, M	CDKAL1	
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TarBase	Experimentally Observed, M	CEMIP2	Chondroitin Sulfat... all 2
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TarBase	Experimentally Observed	CHMP2A	Endosomal Sortin... all 9
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TarBase	Experimentally Observed, M	CIAO2A	Iron homeostasis s... all 1
☐	hsa-let-7c-5p	let-7a-5p (and other miRNAs)	↑0.996	TargetScan Mouse, TarBase	Experimentally Observed, Hi	COIL	

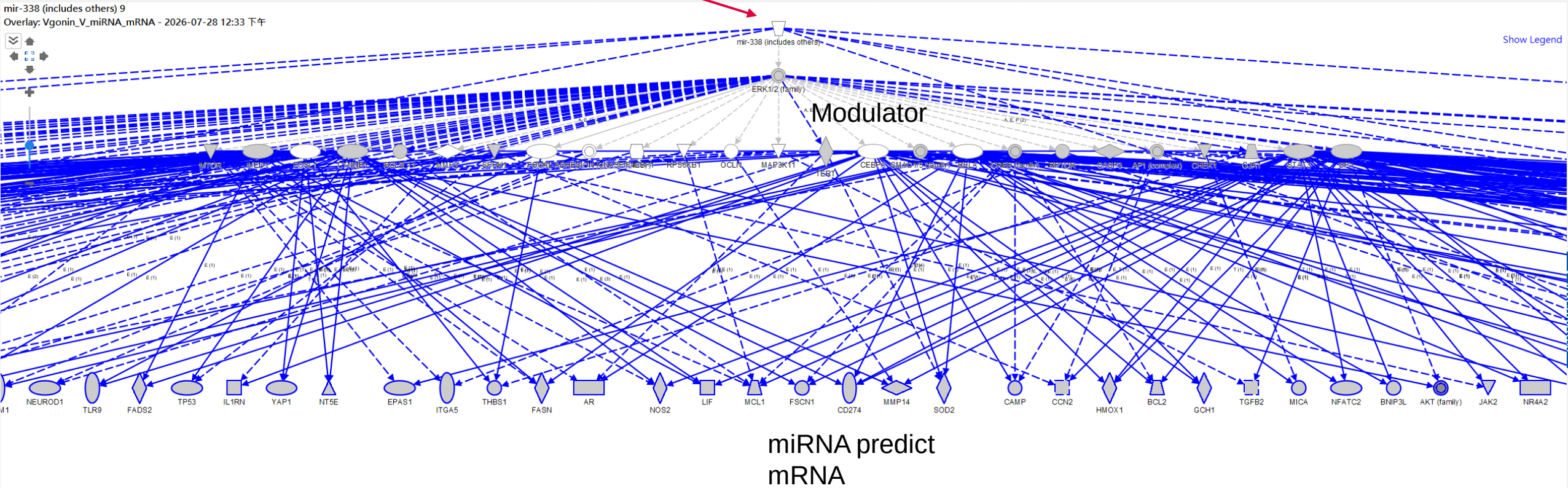
■ positive z-score
 ■ z-score = 0
 ■ negative z-score
 ■ no activity pattern available



Disease and function



Causal network



Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

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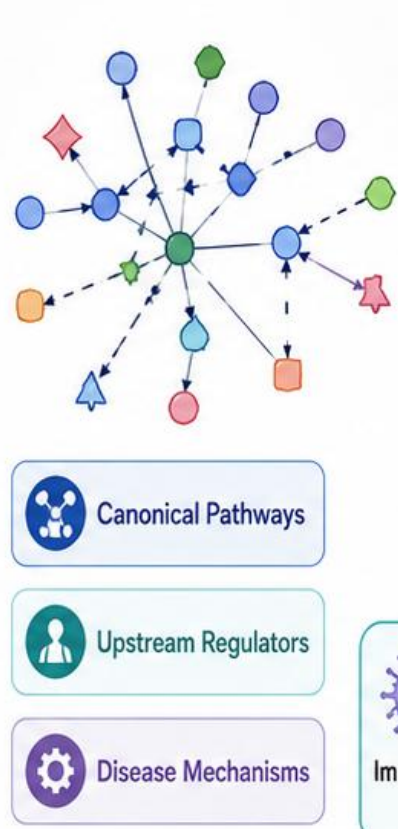
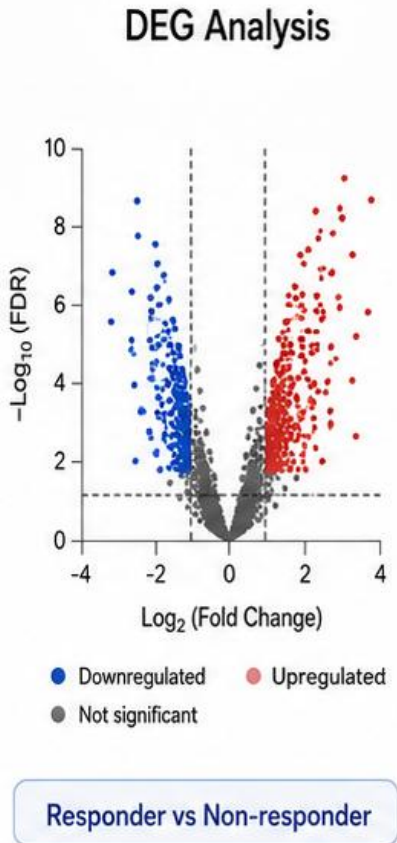
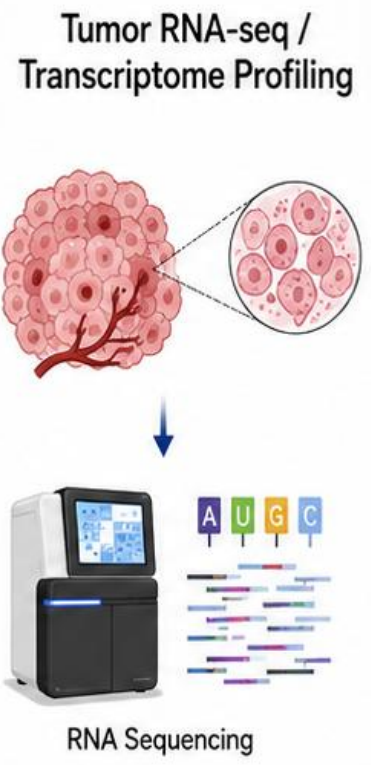
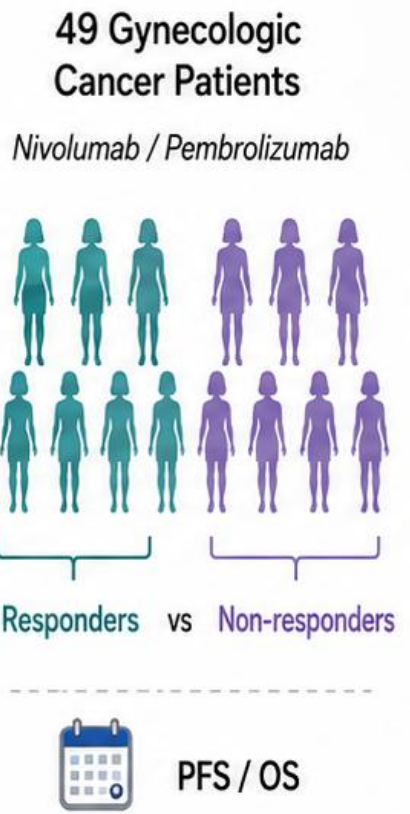
- Case Study: Ugonin V in Chondrosarcoma

Module 4 | Comparative Analysis and Candidate Target Discovery

- Case Studies: Immunotherapy Resistance and Single-Cell Heterogeneity

Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer

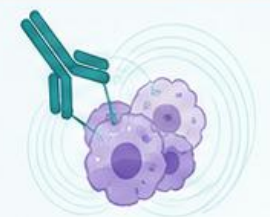


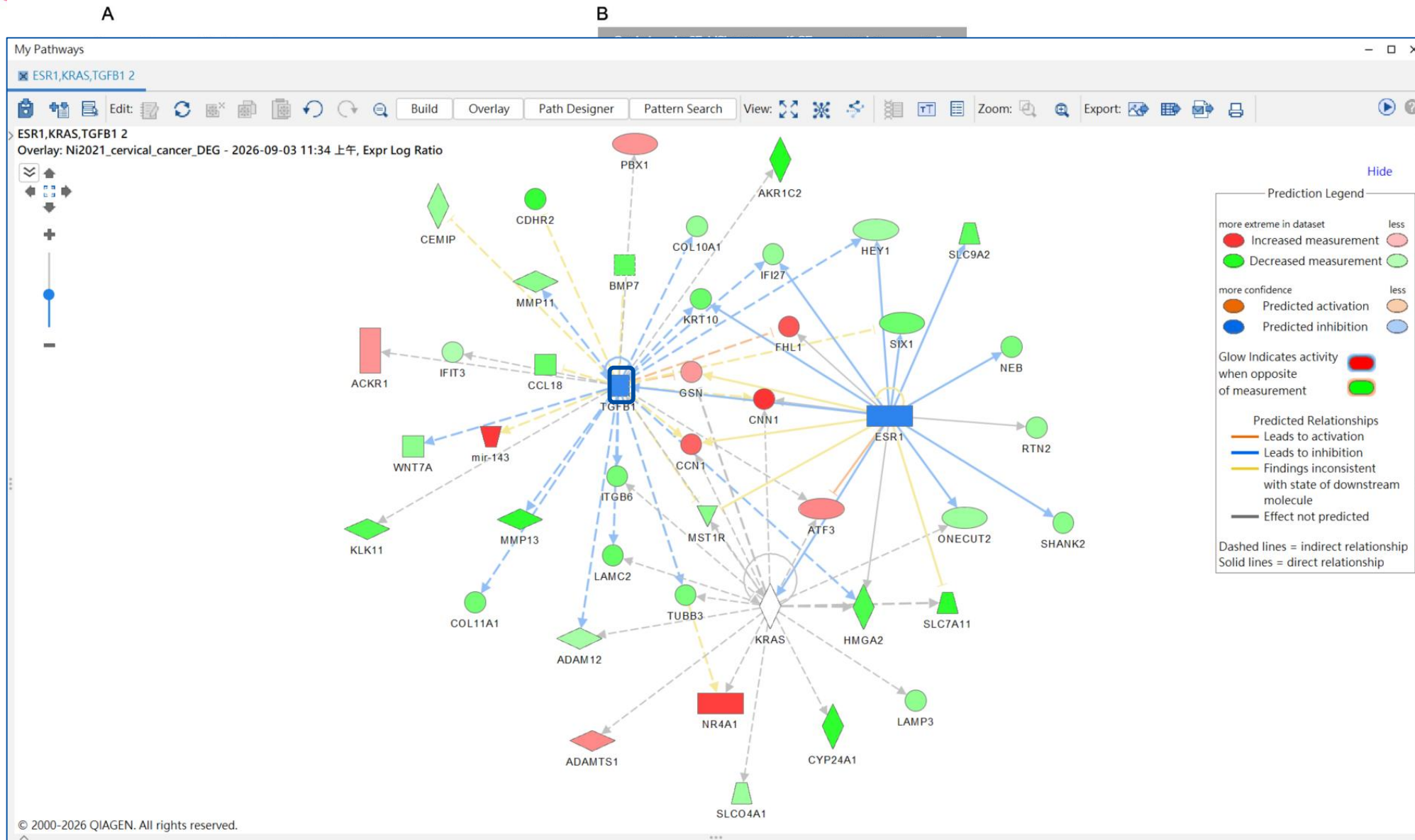
Value of IPA

- Mechanism Discovery
- Biomarker Identification
- Target Prioritization
- Rational Combination Strategy

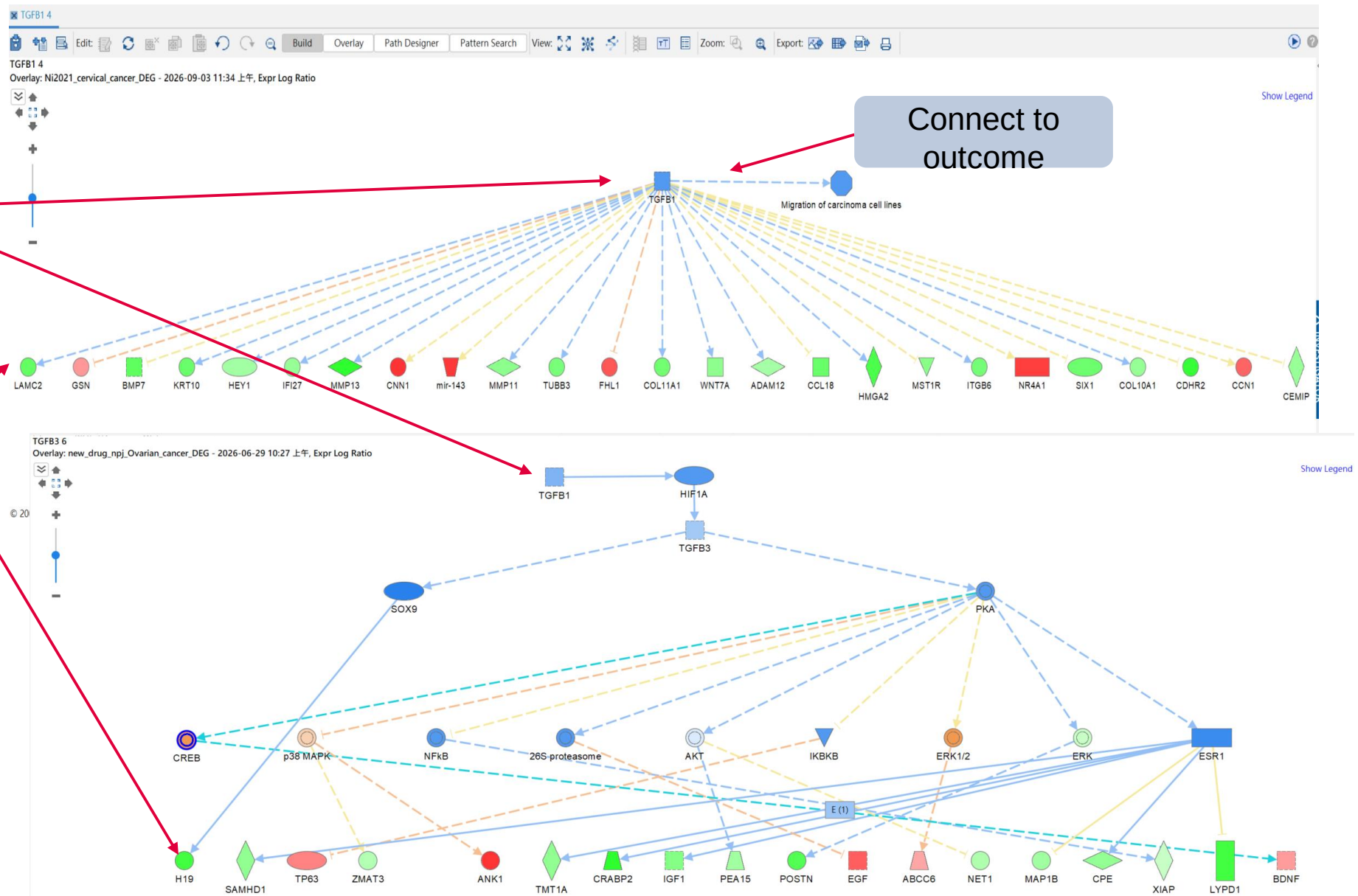


High TGF- β signaling predicts ICI resistance and supports TGF- β -targeted combination approaches.





how transcriptomic
munotherapy
sponders can be
hypotheses using
ting DEGs as
IPA maps them
networks and
s that may drive
his study, shared
B1, KRAS, IGF1,
B provided a
mechanism
development, and
ategies.



Create Comparison Analysis

×

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

Create Comparison Analysis

Select Analyses

A-Z Sort

▼ My Projects

> newdrug_demo

> NTHU_Chen

> NDMU

> KCGH

> VGHTP

> CGUST_test

> CMU_WYC

> techcomm

> CGH_lai

> 北醫_磷酸化蛋白分析_教育訓練

> 耕莘

> NCKU

工研院孫博PD服務案

Anji

> bioasia

> IPA_推廣文章

> presale_practice_case study

> 台大教育訓練_muti_omics

> Lily_data

> 2021_cervical_cancer_DEG - 2026-09-03 1

Add >>

Analyses to Compare

2021_cervical_cancer_DEG - 2026-09-03 1

Move Up ↕

Move Down ⇩

« Remove

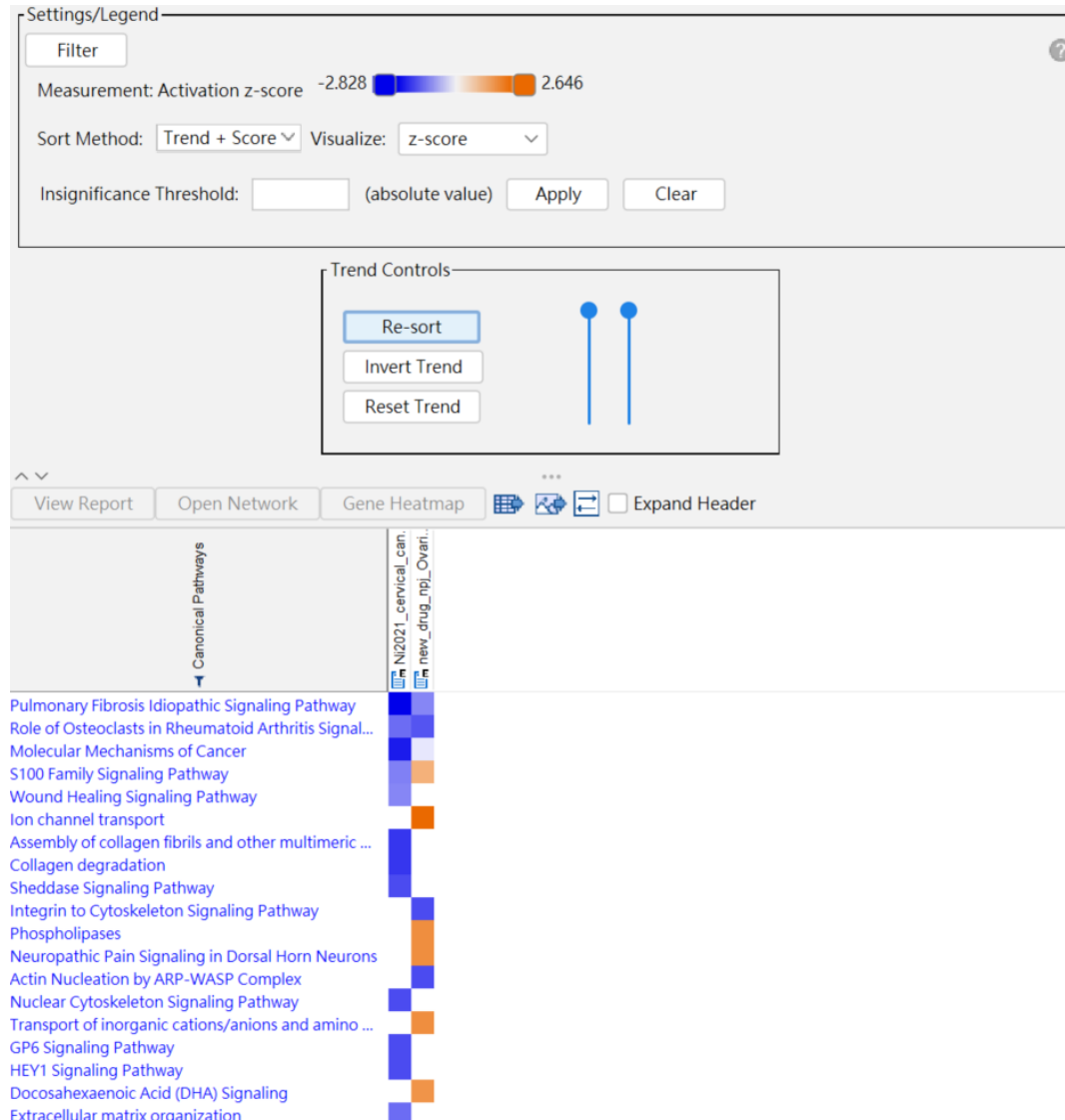
View Comparison

Cancel

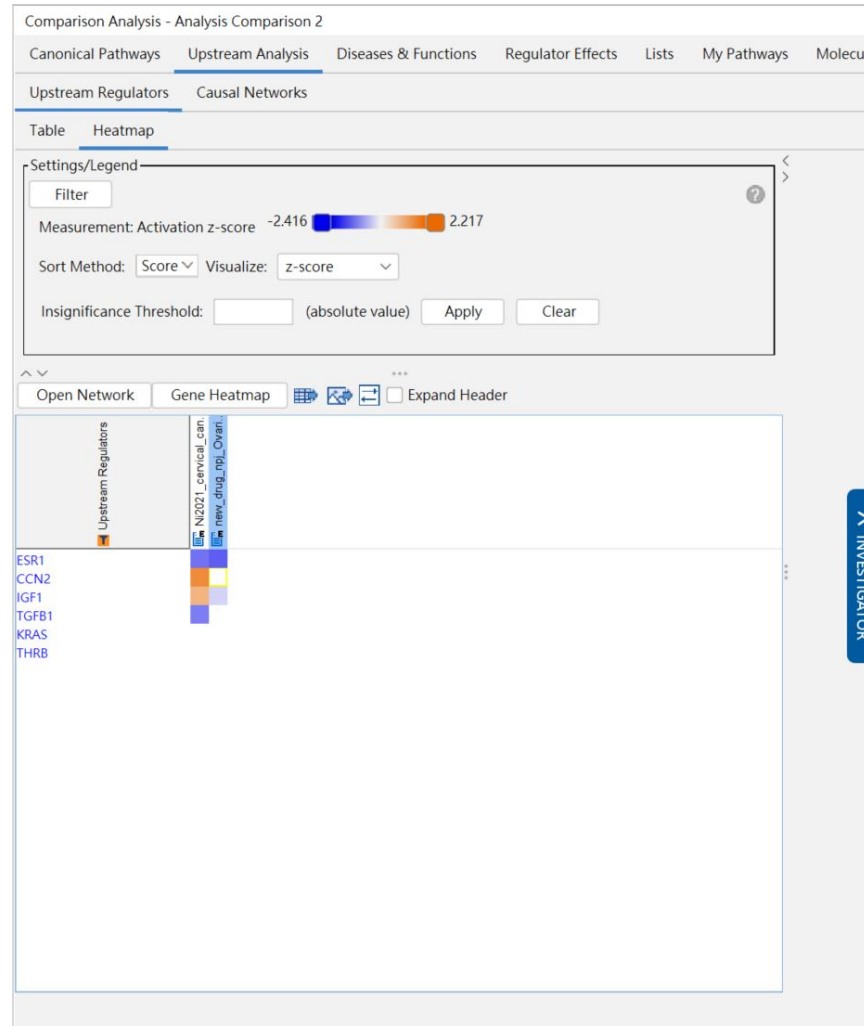
Sample to Insight

82

Canonical Pathway



Upstream regulator



IPA INVESTIGATOR AI Beta
Email Feedback
Copy
Reset

因此，從這切 comparison 看，IGF1 並不像 ESR1 那樣在兩個分析中展現相似趨勢，要把 IGF1 視作「共同 upstream regulator」需要更多證據。

其他值得注意的整體主題
雖然您聚焦在 TGFB1、KRAS、ESR1、IGF1、CCN2、THRB，但這張 comparison 本身呈現幾個可解釋ICI 反應差異的「主題」：

1) 腫瘤細胞 migration / invasion / proliferation 在 Ovarian vs Cervical 中呈反向調控
Migration / Invasion / Proliferation 相關的 Diseases & Functions 幾乎全部是：
Ovarian : z 略微正或接近 0
Cervical : z 顯著負向 (多數 ≤ -2 ，甚至 -4)
例如：
Migration of tumor cell lines : 0.199 vs -4.44
Migration of cells : 0.536 vs -4.404
Invasion of tumor cell lines : 0.991 vs -3.747
Cell proliferation of tumor cell lines : 1.001 vs -3.133

這顯示在 Cervical cancer 這個分析裡，免疫檢查點抑制劑反應差異與明顯「抑制腫瘤細胞遷移、侵襲、增殖」相關，而 Ovarian 的 responder vs non-responder 間則較不顯著。這種截然不同的 z-score pattern 顯示兩種癌別中，調控腫瘤細胞動態的 upstream regulators、pathways 可能不同，也可能是同一套 regulators 在兩個腫瘤微環境中被「反向運用」。

建議在 IPA 中：
您可以先以這一群功能 (Migration of tumor cell lines, Migration of cells, Invasion of tumor cell lines, Cell proliferation of tumor cell lines, Invasion of carcinoma cell lines, Binding of tumor cell lines) 作為「主題」，把 Ovarian 與 Cervical 兩個分析分成不同 cluster，讓 IPA 自動構建顯示哪些 upstream regulators (包括 TGFB1、KRAS、CCN2、THRB 是否牽涉其中) 在兩癌別間有相似或相反模式。

ComparisonTheme

建立以腫瘤細胞動態為主題的跨癌別比較路徑圖，找出共同與差異性調控

FilterComparisonScores

在 comparison 介面中只顯示腫瘤細胞動態相關功能，便於檢視 z-score 趨勢

2) ESR1 相關的「癌與上皮組織增生」共同負向趨勢
除了 ESR1 本身是負向，與上皮細胞增生和「Cancer」「Solid tumor」「Neoplasia of cells」等 Diseases & Functions 也一致負向，且在 Cervical 分析更顯著：
Proliferation of epithelial cells : -0.645 vs -1.744
Growth of epithelial tissue : -0.456 vs -1.47
Cancer : -0.547 vs -2.003
Solid tumor : -0.467 vs -2.283
Neoplasia of cells : -0.156 vs -2.577

這一整串 z-score 顯示「上皮增生/腫瘤性變化」在兩癌別中都趨向被抑制，但 Cervical 的抑制更大，且可能與 ESR1 相關的網絡有關，這與臨床 Cervical cancer 在免疫治療中有時比 Ovarian 更明顯的腫瘤負荷下降相符。
要檢驗 ESR1 是否是跨癌別的「共同負向 upstream regulator」，可以以 ESR1 加上這些功能作為主題，讓 IPA 建一條顯示兩個分析中 ESR1 下游及其與免疫檢查點相關分子的路徑。

Ask

Ask a scientific question or tell me what you'd like do today

Asking about comparison "Analysis Comparison 2"

The information within this panel is generated by AI, which can make mistakes. Learn More

You can choose which term you want to do



My Pathways

TumorDynamics

Build Overlay Path Designer Pattern Search

Tool: Grow

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

Upstream Expression Regulators

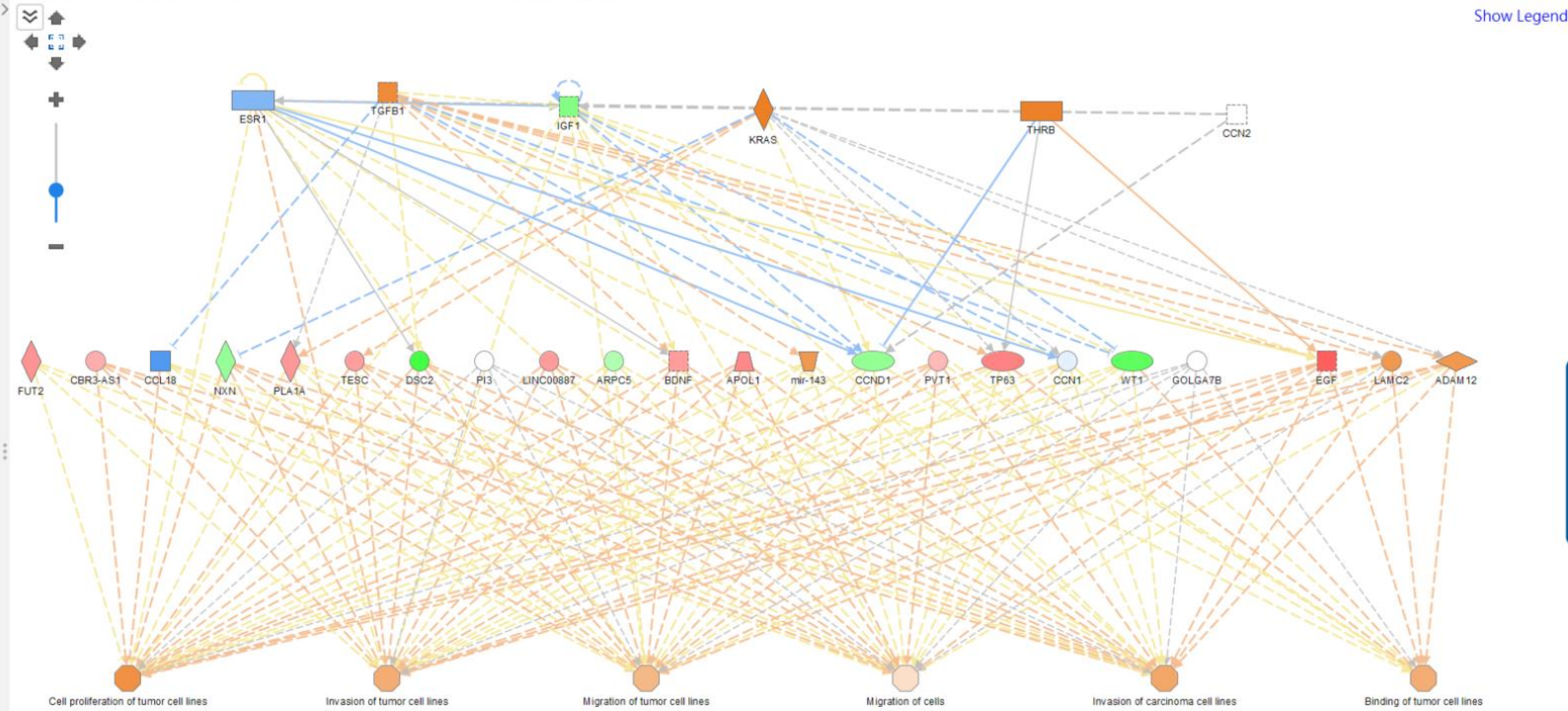
Grow from selected molecules to selected regulators

Indicate regulators related to Any of the selected molecules

Recalculate

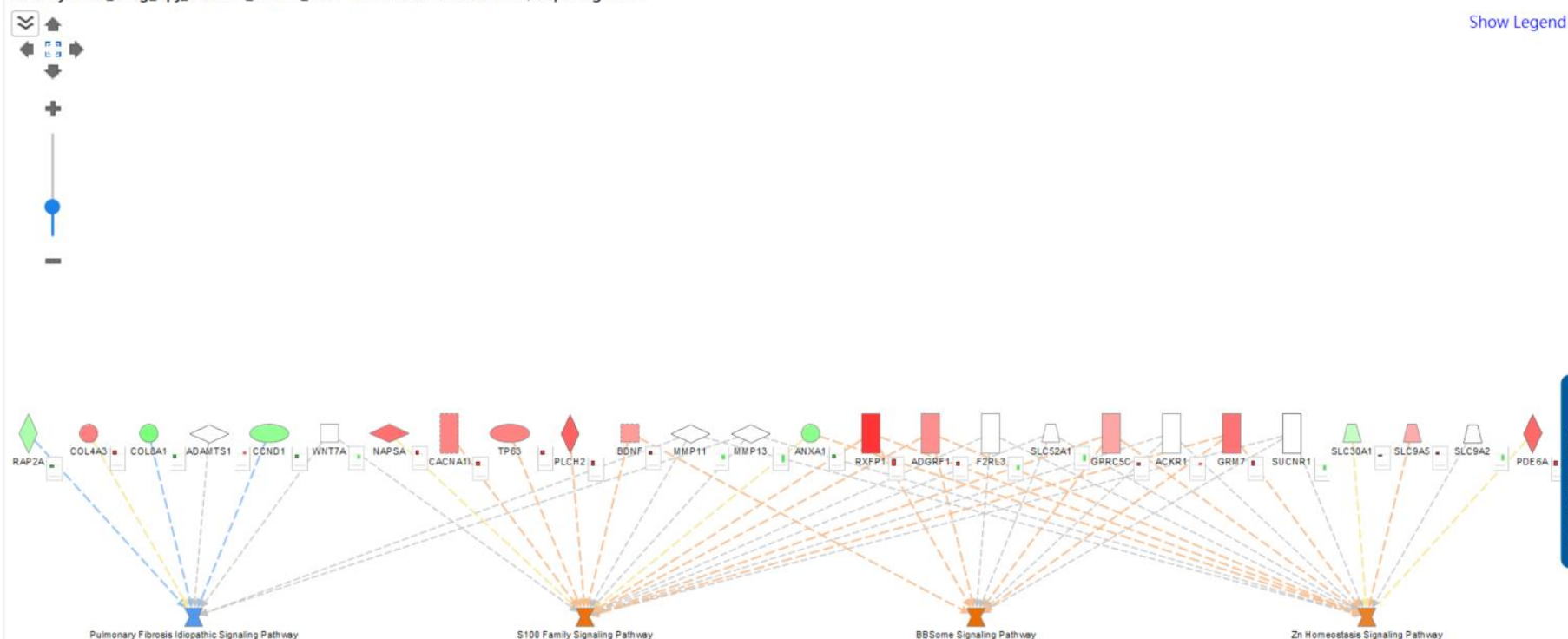
Regulators	Molecule Ty...	p-value	B-H corrected p...	z-score	Molecules
TGFB1	growth factor	1.70E-09	2.56E-06	1.212	ADAM12, BDNF, ...all 13
KRAS	enzyme	9.21E-08	3.08E-05	1.432	ADAM12, CCN1, ...all 9
IGF1	growth factor	3.69E-07	7.43E-05	0.454	BDNF, CCN1, C, ...all 7
CCN2	growth factor	1.13E-04	1.81E-03		CCND1, ESR1, L, ...all 3
ESR1	ligand-dependent n...	2.59E-04	3.22E-03	-0.656	BDNF, CCN1, C, ...all 7
THRB	ligand-dependent n...	1.69E-03	8.99E-03		CCND1, EGF, T, ...all 3

Overlay: new_drugnpj_Ovarian_cancer_DEG - 2026-06-29 10:27 上午, Expr Log Ratio

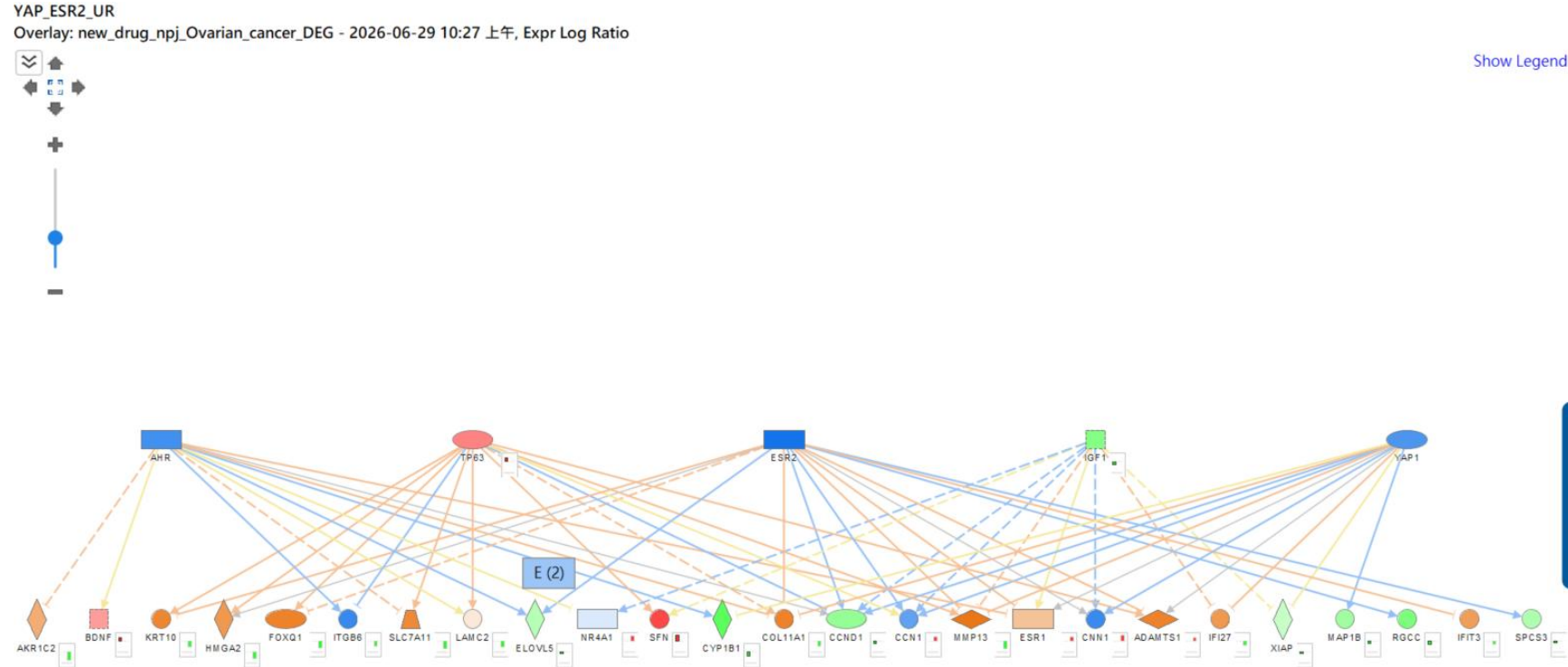


The theme is 「Integrated regulation of tumor cell proliferation、migration、invasion and adhesion」. When EGF、TP63、PVT1、BDNF、LAMC2 and others increase or have influential activity, they promote tumor cell proliferation、migration and invasion; conversely, decreases in IGF1、WT1、CCND1、ARPC5、NXN、DSC2 are also associated with increases in these malignant behaviors, indicating that 「tumor suppressors being switched off + oncogenes/long non-coding RNAs being switched on」 jointly drive tumor dynamics. ESR1、CCN1、ADAM12、CCL18、GOLGA7B、PLA1A and others serve as regulatory nodes that promote interactions between tumor cells and stromal/immune-related factors, enhancing adhesion and infiltration capabilities.

Zn_S100_Pathways
Overlay: new_drugnpj_Ovarian_cancer_DEG - 2026-06-29 10:27 上午, Expr Log Ratio



This network theme named Zn_S100_Pathways is 「Integrated regulation of metal ion homeostasis and S100/fibrosis pathways in tumor and pulmonary fibrosis microenvironments」. The activation of BDNF、TP63、GRM7、RXFP1、GPRC5C、ADGRF1 and others collectively promotes S100 family signaling、BBSome and Zn homeostasis pathways, suggesting that neurotrophic factors and GPCR/ion channels play important roles in regulating inflammation and the tumor microenvironment; at the same time, the downregulation of MMP11/MMP13、WNT7A、ADAMTS1 and collagen-related genes (COL4A3、COL8A1) and the cell-cycle factor CCND1 is associated with 「Idiopathic pulmonary fibrosis pathway inhibition」, indicating a dynamic balance between ECM remodeling and antifibrotic signaling. Metal/ion transporters such as SLC30A1、SLC9A5、PDE6A are directly linked to the regulation of Zn homeostasis, potentially affecting the function and survival of immune cells and tumor cells.



This network theme named YAP_ESR2_UR is the “axis through which YAP1 / ESR2 / IGF1 / AHR / TP63 jointly regulate epithelial differentiation, the cell cycle, and ECM/invasion genes”. Decreases in IGF1 、YAP1 、ESR2 generally lead to downregulation of cell cycle and contraction-related genes such as CCND1 、CNN1 、NR4A1, accompanied by upregulation of invasion and matrix remodeling genes such as ESR1 、MMP13 、COL11A1 、LAMC2 ; a decrease in AHR, meanwhile, relieves the repression of ESR1 、AKR1C2 、BDNF 、SLC7A11 and others, favoring the activation of antioxidant/ferroptosis regulation and neuron-like signaling. An increase in TP63 suppresses CCND1 、ITGB6 on the one hand, while promoting epithelial differentiation and tumor matrix/invasion genes such as KRT10 、LAMC2 、MMP13 、HMGA2 on the other, shaping a tumor phenotype of “atypical proliferation + high invasiveness and reprogramming”

McCann et al., STTT 2025: Workflow and Value of IPA

Proliferative diabetic retinopathy subtypes defined by immune defense and endothelial mitochondrial dysfunction

1 Clinical Samples



End-stage PDR



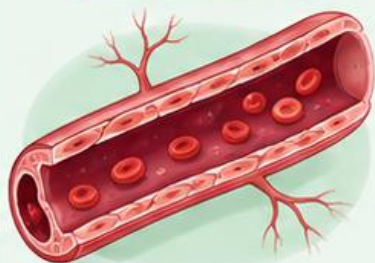
Vitrectomy samples



± Pre-op anti-VEGF

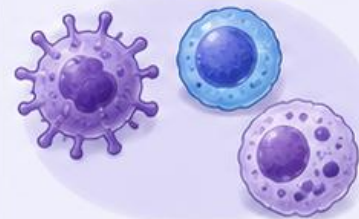
2 Cell-Enriched Profiles

CD31 high



Endothelial-rich

CD31 low

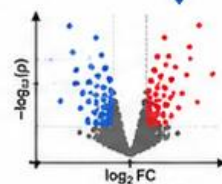


Immune-rich

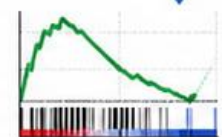
3 Omics Analysis



RNA-seq



DEGs



GSEA



IPA

4 IPA Insights

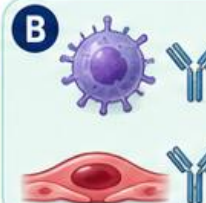
A



Disease Mechanism

- Immune-defense subtype
- Endothelial mitochondrial dysfunction

B



Treatment Effect

- Anti-VEGF affects immune cells
- Anti-VEGF affects endothelial cells

C

Pathway Changes



↓ Suppressed in immune-rich samples after anti-VEGF
↑ Increased in endothelial-related anti-VEGF signatures

5 IPA Value



Define PDR subtypes



Explain anti-VEGF response



Reveal alternative targets



Guide translational strategy

Key Takeaways

1



PDR is heterogeneous

2



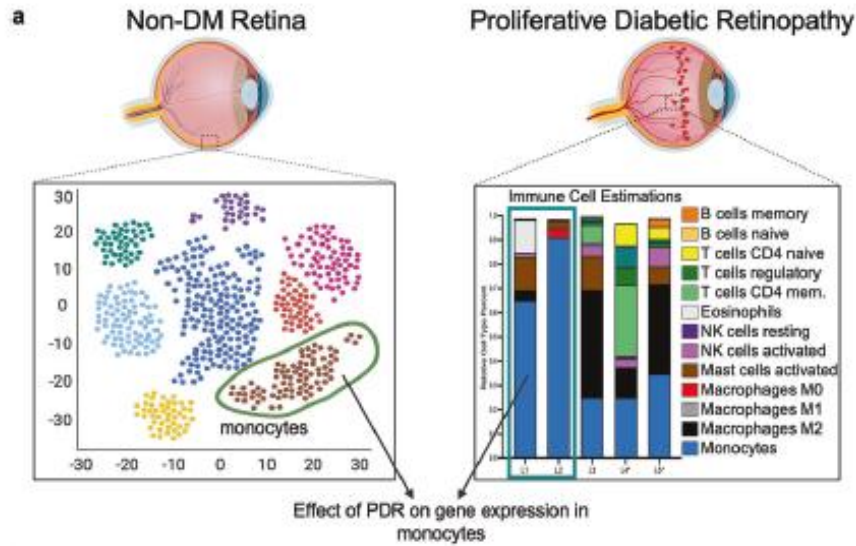
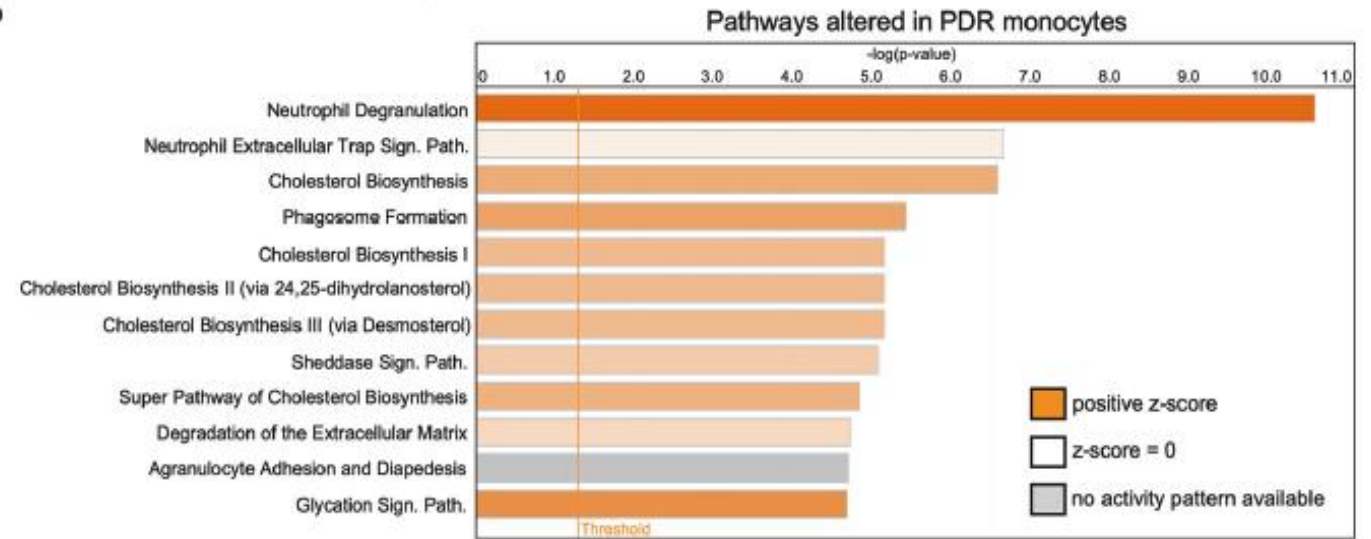
Anti-VEGF acts beyond vasculature

3



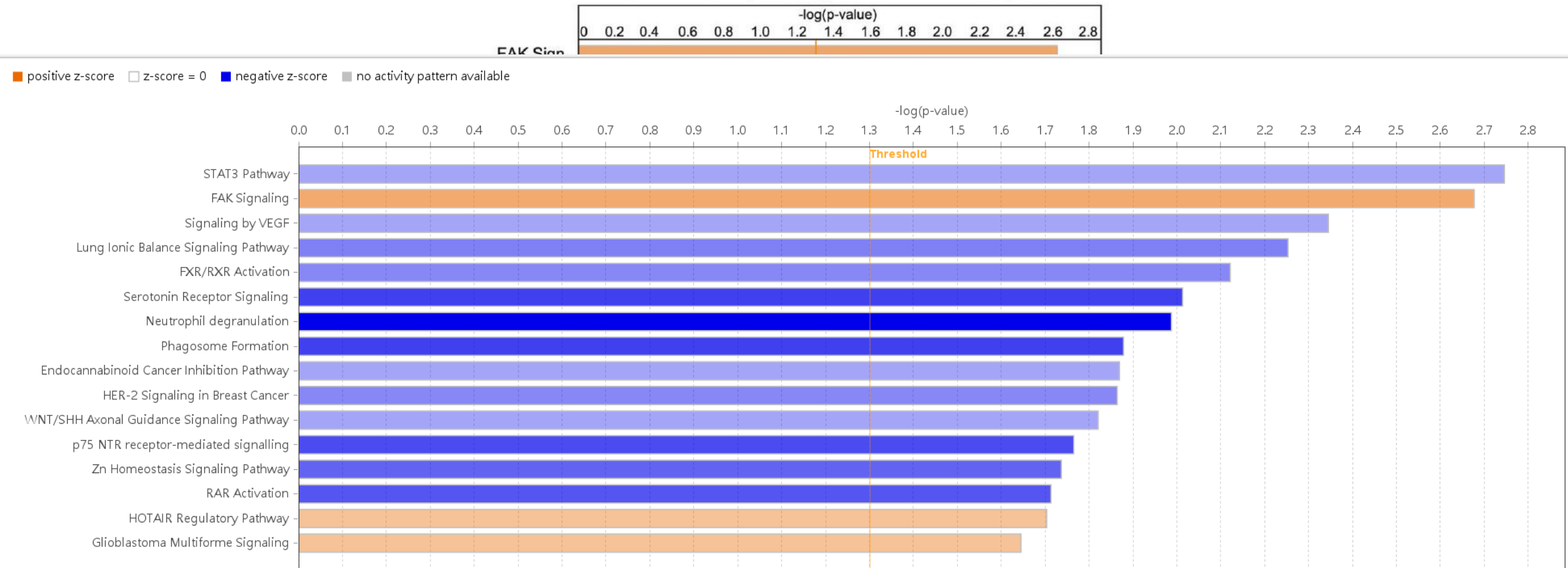
IPA converts transcriptomics into actionable biology

6

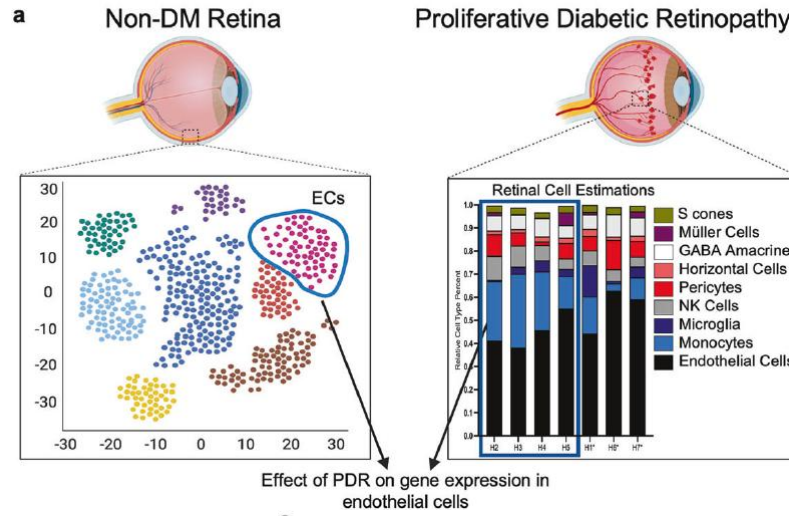
**b**

PDR samples were stratified into CD31-high endothelial-rich and CD31-low immune-rich profiles by comparing gene expression signatures with non-diabetic retinal reference cells. This reveals that PDR is not a uniform angiogenic disease, but contains distinct vascular and immune-dominant biological states.

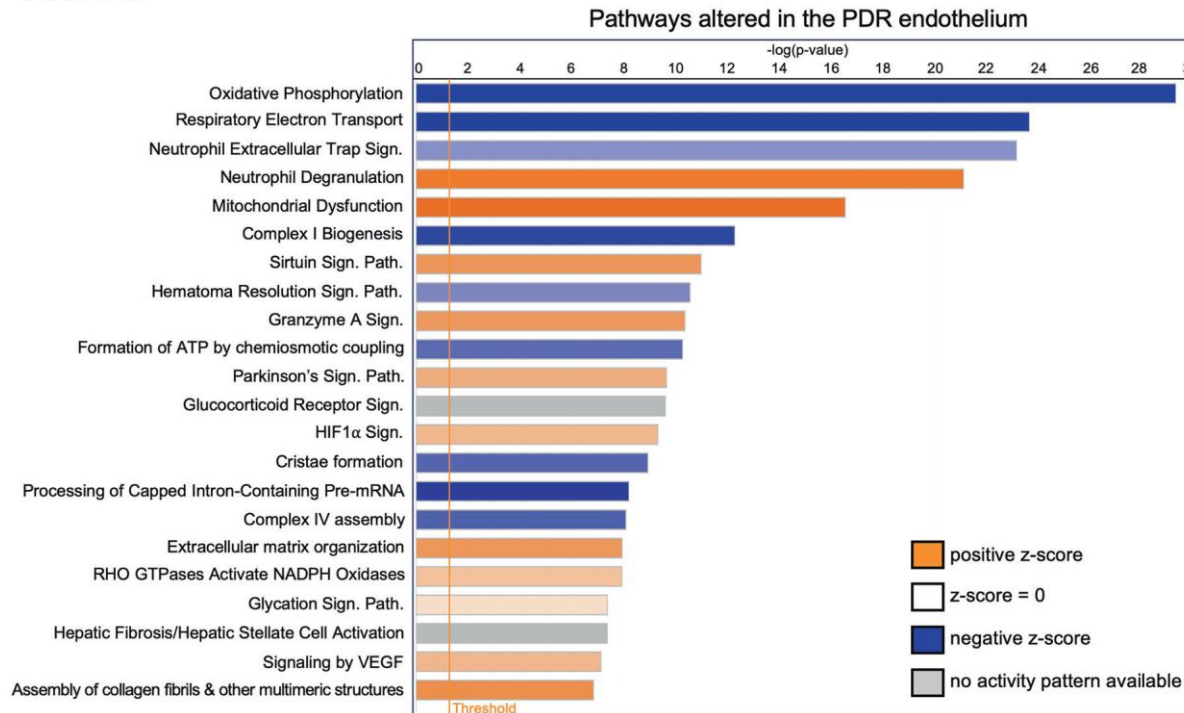
b

Anti-VEGF pathways in CD31^{low} samples

In CD31-low immune-rich PDR samples, IPA showed that anti-VEGF treatment suppressed VEGF signaling together with inflammatory and phagocytic pathways. This indicates that anti-VEGF therapy affects not only vascular biology, but also immune-related disease mechanisms in PDR.



IPA analysis of CD31-high endothelial-rich PDR samples revealed mitochondrial dysfunction and other disease-associated pathways compared with non-diabetic retinal endothelium. This suggests that PDR endothelium contains VEGF-independent biology, supporting the need to explore complementary therapeutic targets beyond anti-VEGF therapy.



VEGF (family) 5

Overlay: McCann_2025_PDR_CD31low_antiVEGF_DEG - 2026-06-28 11:53 上午, Expr Log Ratio



modulator

VEGF (family)

Link to interested disease

Diabetic retinopathy

SOCS3

HPSE

LEF1

PLAUR

MCM2

CCL20

ANPEP

CDH5

EDA

SCML4

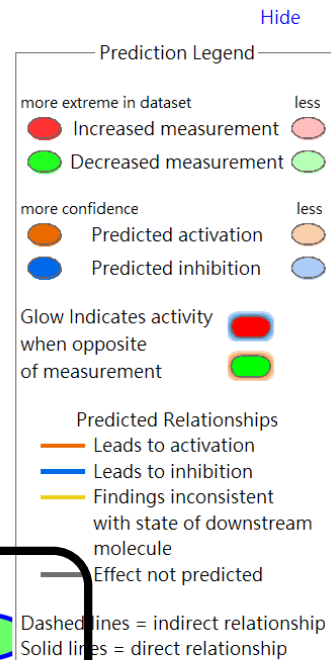
THBD

GEM

IL1A

HES1

DEG

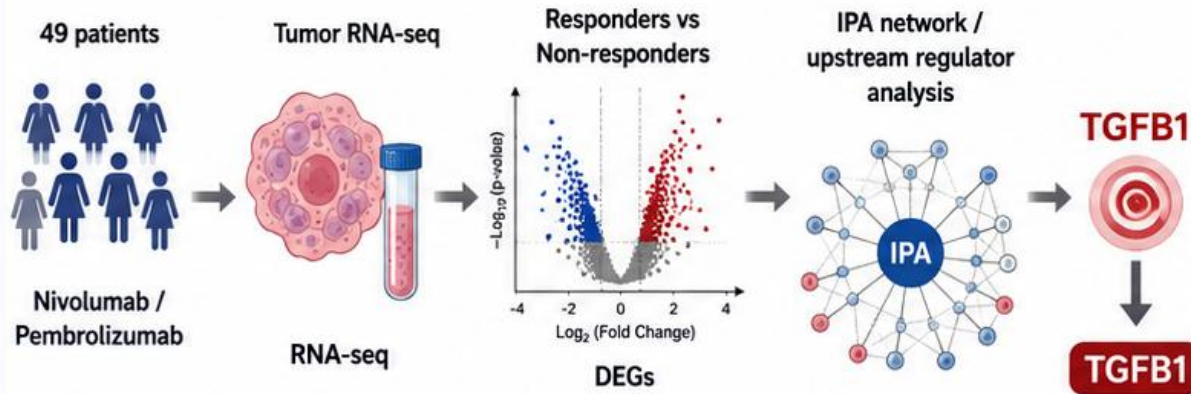


How IPA Supports Drug Development: Two Case Studies

From transcriptomics to mechanism, biomarkers, and target prioritization

Case 1 | Ni et al., npj Precision Oncology (2021)

ICI resistance in gynecologic cancer



Biomarker:
TGF-beta signature



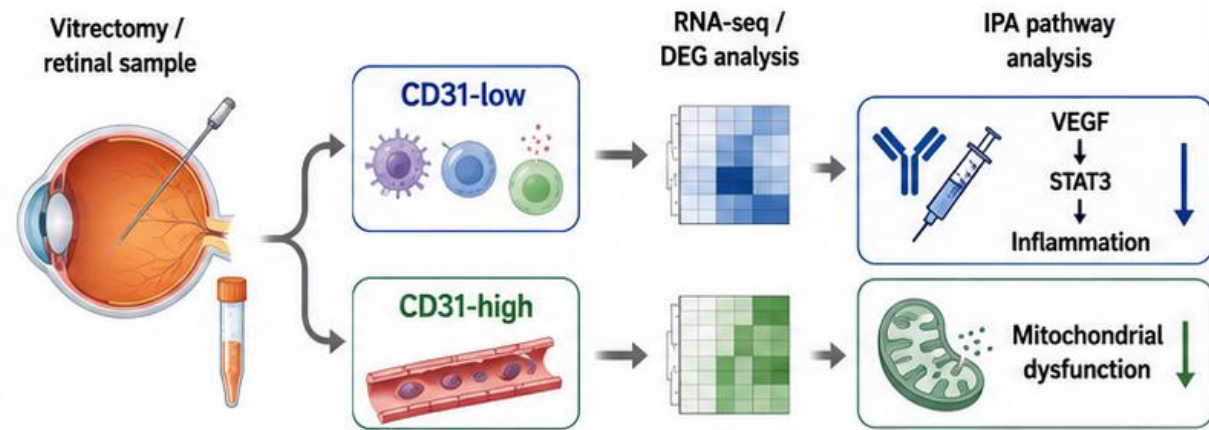
Mechanism:
immunotherapy resistance



Strategy:
target / combination prioritization

Case 2 | McCann et al., STTT (2025)

PDR heterogeneity and anti-VEGF biology



Mechanism:
immune-rich vs endothelial-rich states



MOA:
anti-VEGF effects beyond vasculature



Alternative targets beyond VEGF

IPA Contributions to Drug Development



Integrate Omics Data



Disease Mechanism



Biomarker Discovery



Target Prioritization



Translational Strategy

IPA converts complex omics data into actionable insights for mechanism discovery, biomarker-guided development, and target selection.

Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

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

Module 1 | IPA in Drug Discovery and Translational Medicine

Module 2 | Transcriptomics and Drug Mechanism of Action

- Case Study: BOLD-100 in Colorectal Cancer

Module 3 | miRNA Regulation and Natural Compound Mechanisms

- Case Study: Ugonin V in Chondrosarcoma

Module 4 | Comparative Analysis and Candidate Target Discovery

- Case Studies: Immunotherapy Resistance and Single-Cell Heterogeneity

Module 5 | Translational Applications: Drug Effect Prediction and Biomarker Discovery

- Case Study: BOLD-100 in Colorectal Cancer

With dataset

- Find connections in your data
- Identify novel biomarkers
- Uncover key targets and regulators
- Discover novel disease mechanisms
- Compare across experiments

Without dataset

- Search and explore the QIAGEN Knowledge Base
- Test hypothesis in silico
- Identify degree of novelty in a hypothesis

Search Results

Genes and Chemicals

Diseases and Functions

Add To My Pathway

Add To My List

Create Dataset

BioProfiler

Interaction Network

Activity Plot

IPA

File Edit View Window Help

Genes and Chemicals

Diseases and Functions

Pathways and Lists

Datasets and Analyses

Create New...

BOLD-100

Search

Advanced Search

Search Results

Genes and Chemicals

Add To My Pathway

Add To My List

Create Dataset

BioProfiler

Interaction Network

Activity Plot

The search for BOLD-100 matched 1 items.

☐	☐	#	Symbol	Matched Term	Synonym(s)	Entrez Gene Name	Location
☐	☐	1	NKP-1339	BOLD-100, ruthenium-based small molecule therapeutic BOLD-100	197723-00-5, BOLD-100, C14H12Cl4N4NaRu+, IT-139, KP1339, ruthenate(1-), tetrachlorobis(1H-indazole-kabbaN2)-, sodium ruthenium-based small molecule therapeutic BOLD-100, ruthenium-based transferrin targeting agent NKP-1339, sodium;bis(1H-indazole);tetrachlororuthenium		Other

Drug

Endoplasmic reticulum stress response

cellular response to endoplasmic reticulum stress

response to endoplasmic reticulum stress

389

Cellular Compromise

389

endoplasmic reticulum stress response

389

Endoplasmic reticulum stress response

cellular response to endoplasmic reticulum stress

response to endoplasmic reticulum stress

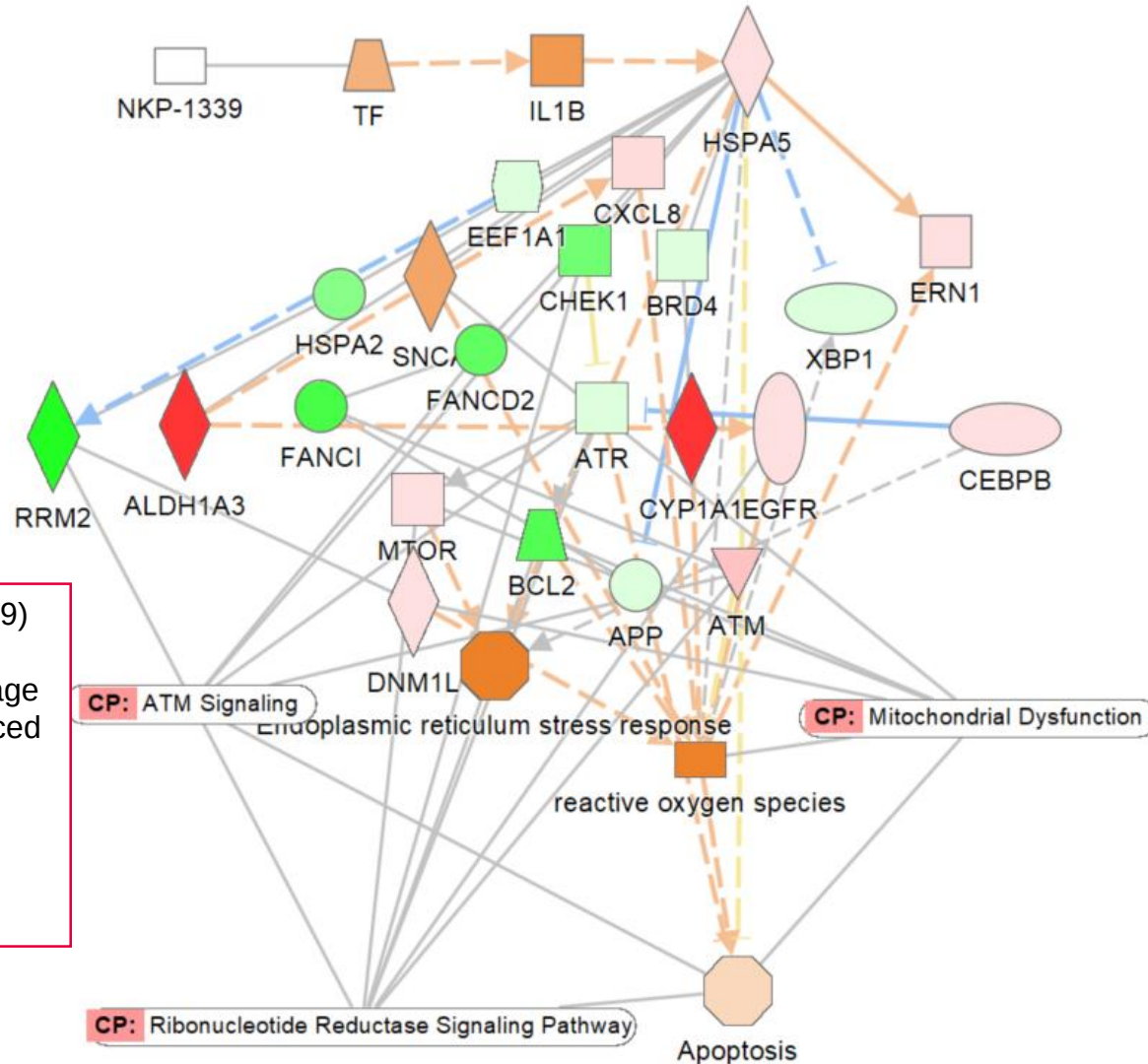
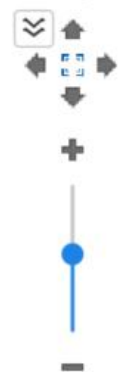
389

Function

96

New My Pathway 10

Overlay: VACO432_24h_DEG_full, Expr Log Ratio



Show Legend

INVESTIGATOR

IPA network modeling of the 24-hour BOLD-100 (NKP-1339) response links **RRM2 downregulation** and increased **reactive oxygen species** to replication stress, DNA-damage signaling, mitochondrial dysfunction, and apoptosis. Reduced RRM2 may limit dNTP availability, while ROS further enhances cellular stress. Together, these effects support BOLD-100-induced apoptosis and highlight the ATR/CHK1 pathway as a potential compensatory survival mechanism and combination-treatment target.

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Analysis -> Biomarker

Annotated Dataset: VT1_24h_DEG_full
Preview Dataset VT1_24h_DEG_full

Mapped IDs (12658) Unmapped IDs (1555) All IDs (14213) Metadata

Add To My Pathway Add To My List Create Dataset Customize Table

Symbol A1BG-AS1 - ACBD4 (1/127)

Expr Log Ratio	Expr Fold Change	Expr p-value	Expr False Discovery Rate ...	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
0.192	1.142	5.40E-01	8.46E-01	A1BG-AS1		A1BG-AS1	A1BG antisense RNA 1	Other	other	
-0.101	0.933	6.62E-02	7.44E-01	AAAS		AAAS	aladin WD repeat nucleoporin	Nucleus	other	
0.144	1.105	2.56E-01	7.55E-01	AACS		AACS	acetoacetyl-CoA synthetase	Cytoplasm	enzyme	
0.101	1.072	7.57E-01	9.28E-01	AACSP1		AACSP1	acetoacetyl-CoA synthetase pseu...	Other	other	
0.187	1.138	4.58E-02	7.44E-01	AADAT		AADAT	aminoadipate aminotransferase	Cytoplasm	enzyme	
-0.021	0.986	8.37E-01	9.59E-01	AAGAB		AAGAB	alpha and gamma adaptin bindi...	Cytoplasm	other	
0.076	1.054	1.23E-01	7.44E-01	AAK1		AAK1	AP2 associated kinase 1	Cytoplasm	kinase	LP-935509, SM1-71
0.126	1.091	3.47E-01	7.81E-01	AAMDC		AAMDC	adipogenesis associated Mth938...	Cytoplasm	other	
0.038	1.027	4.72E-01	8.20E-01	AAMP		AAMP	angio associated migratory cell ...	Plasma Membrane	other	
-0.113	0.925	2.57E-01	7.56E-01	AAR2		AAR2	AAR2 splicing factor	Other	other	
-0.045	0.969	2.92E-01	7.66E-01	AARS1		AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme	
-0.009	0.994	9.48E-01	9.88E-01	AARS2		AARS2	alanyl-tRNA synthetase 2, mitoc...	Cytoplasm	enzyme	
0.442	1.358	7.91E-02	7.44E-01	AARSD1		AARSD1	alanyl-tRNA synthetase domain ...	Nucleus	enzyme	
0.199	1.148	2.16E-01	7.51E-01	AASDH		AASDH	aminoadipate-semialdehyde de...	Other	enzyme	
-0.137	0.910	4.19E-01	8.02E-01	AASDHPPT		AASDHPPT	aminoadipate-semialdehyde de...	Cytoplasm	enzyme	
0.184	1.136	3.24E-01	7.73E-01	AASS		AASS	aminoadipate-semialdehyde syn...	Cytoplasm	enzyme	
-0.070	0.953	1.02E-01	7.44E-01	AATF		AATF	apoptosis antagonizing transcri...	Nucleus	transcription regulator	
0.293	1.225	8.51E-02	7.44E-01	AATK		AATK	apoptosis associated tyrosine ki...	Cytoplasm	kinase	
0.113	1.082	2.64E-01	7.60E-01	ABAT		ABAT	4-aminobutyrate aminotransferase	Cytoplasm	enzyme	theophylline/tretinoin/valproic ...
0.047	1.033	9.09E-01	9.79E-01	ABCA11P		ABCA11P	ATP binding cassette subfamily ...	Other	other	
0.064	1.045	7.28E-01	9.16E-01	CRYM-AS1		ABCA15P	ATP binding cassette subfamily ...	Other	other	
-0.278	0.825	2.14E-01	7.51E-01	ABCA17P		ABCA17P	ATP binding cassette subfamily ...	Other	other	
0.098	1.070	3.05E-01	7.67E-01	ABCA2		ABCA2	ATP binding cassette subfamily ...	Plasma Membrane	transporter	
0.060	1.042	4.03E-01	7.99E-01	ABCA3		ABCA3	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.291	1.224	5.46E-02	7.44E-01	ABCA5		ABCA5	ATP binding cassette subfamily ...	Plasma Membrane	transporter	
0.077	1.055	5.16E-01	8.37E-01	ABCA7		ABCA7	ATP binding cassette subfamily ...	Plasma Membrane	transporter	
0.097	1.070	2.31E-01	7.52E-01	ABCB10		ABCB10	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.425	1.343	7.58E-02	7.44E-01	ABCB6		ABCB6	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.033	1.023	7.07E-01	9.09E-01	ABCB7		ABCB7	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.139	1.101	1.94E-01	7.47E-01	ABCB8		ABCB8	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.177	1.130	2.41E-01	7.53E-01	ABCB9		ABCB9	ATP binding cassette subfamily ...	Cytoplasm	transporter	
0.130	1.094	2.16E-01	7.51E-01	ABCC1		ABCC1	ATP binding cassette subfamily ...	Plasma Membrane	transporter	
0.195	1.145	1.96E-01	7.47E-01	ABCC10		ABCC10	ATP binding cassette subfamily ...	Plasma Membrane	transporter	

0 / 12658

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.

Core Analysis
Biomarker Filter
Filter Dataset
microRNA Target Filter
BioProfiler
IsoProfiler

Edit Dataset Settings Analyze/Filter Dataset Close

Biological Filter and set cutoffs

Create Biomarker Filter - [analysis : VACO432_24h_DEG_full]

Create Biomarker Filter - [analysis : VACO432_24h_DEG_full]

Set Cutoffs

Biological Filter

Use cutoffs to select a set of significantly regulated molecules to obtain causal predictions.

Set Cutoffs

Dataset Column Measure

log2FC Expr Log

pvalue Expr p-

padj_BH Expr Fa

Advanced

Preview Dataset VACO432

Set Cutoffs Biological Filters

Select filters that are most relevant to your biomarker discovery project. An "OR" operation is executed within each filter and an "AND" operation across the filters.

Species Human

Tissues & Cell Lines Caco2 ...

Node Types

Diseases Categories Cance...

Biofluids

> Biomarkers efficacy...

Select Biomarker Applications:

☐ Select all

☐ diagnosis

☐ disease progression

☒ efficacy

☐ not applicable

☐ prognosis

☐ response to therapy

☐ safety

☐ unspecified application

☐ Not a known Biomarker

Select Biomarker Diseases:

☐ Select all

> ☐ Auditory Disease

> ☒ Cancer

> ☐ Cardiovascular Disease

> ☐ Connective Tissue Disorders

> ☐ Dermatological Diseases and Conditions

> ☐ Developmental Disorder

> ☐ Endocrine System Disorders

> ☐ Gastrointestinal Disease

Advanced

Advanced

Recalculate

30 molecules eligible for Biomarker Filter

Preview Dataset VACO432_24h_DEG_full

Biomarker Filter Eligible (30)

Mapped IDs (13216)

Unmapped IDs (1515)

All IDs (14731)

Metadata

Add To My Pathway

Add To My List

Create Dataset

Customize Table

Expr Log Ratio	Expr p-value	Expr False Discovery R...	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
0.948	1.85E-02	1.44E-01	ABCG1		ABCG1	ATP binding cassette subfam...	Plasma Membrane	transporter	
-0.656	2.19E-02	1.49E-01	BCL2		BCL2	BCL2 apoptosis regulator	Cytoplasm	transporter	BP1002, S65487, rosomidnar,...
-0.656	2.06E-03	8.31E-02	BIRC5		BIRC5	baculoviral IAP repeat contain...	Cytoplasm	other	VS-101, gataparsen, EZN 304...
-0.597	2.92E-02	1.66E-01	CDK1		CDK1	cyclin dependent kinase 1	Nucleus	kinase	CGP 74514A, molport-003-7...
1.092	1.09E-02	1.24E-01	CDKN1A		CDKN1A	cyclin dependent kinase inhi...	Nucleus	other	RAG-01
1.302	1.15E-02	1.26E-01	CHI3L1		CHI3L1	chitinase 3 like 1	Extracellular Space	enzyme	
0.882	2.48E-02	1.56E-01	CLU		CLU	clusterin	Cytoplasm	other	clusterin antisense oligonuc...
1.973	1.92E-04	6.87E-02	CYP1B1		CYP1B1	cytochrome P450 family 1 su...	Cytoplasm	enzyme	

0 / 30

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.

Filter Summary

Consider only molecules where
(species = Human) AND
(tissues/cell lines = SW-620 OR HCT-116 OR HCT-15 OR RKO OR HT29 OR KM-12 OR Colon Cancer Cell Lines not otherwise specified OR SW-480 OR COLO205 OR HCC-2998 OR Caco2 cells OR Other Tissues and Primary Cells OR Other Colon Cancer Cell Lines OR Other Organ Systems) AND
(diseases = Cancer) AND
((biomarker applications = efficacy) AND (biomarker diseases = acute lymphocytic leukemia OR acute lymphocytic leukemia, type L3 OR acute myeloid leukemia OR acute myeloid leukemia with inv(16) OR acute myeloid leukemia with t(8;21) OR adenocarcinoma OR adenoma OR adrenal cortex carcinoma OR adrenal cortex neoplasm OR adrenocortical carcinoma OR adult solid tumor OR adult T cell leukemia OR adult T-cell leukemia/lymphoma OR advanced gastric cancer OR AIDS-related lymphoma OR ALK-positive anaplastic large cell lymphoma OR alveolar rhabdomyosarcoma OR anal cancer OR anal neoplasm OR anaplastic thyroid cancer OR anaplastic thyroid carcinoma OR

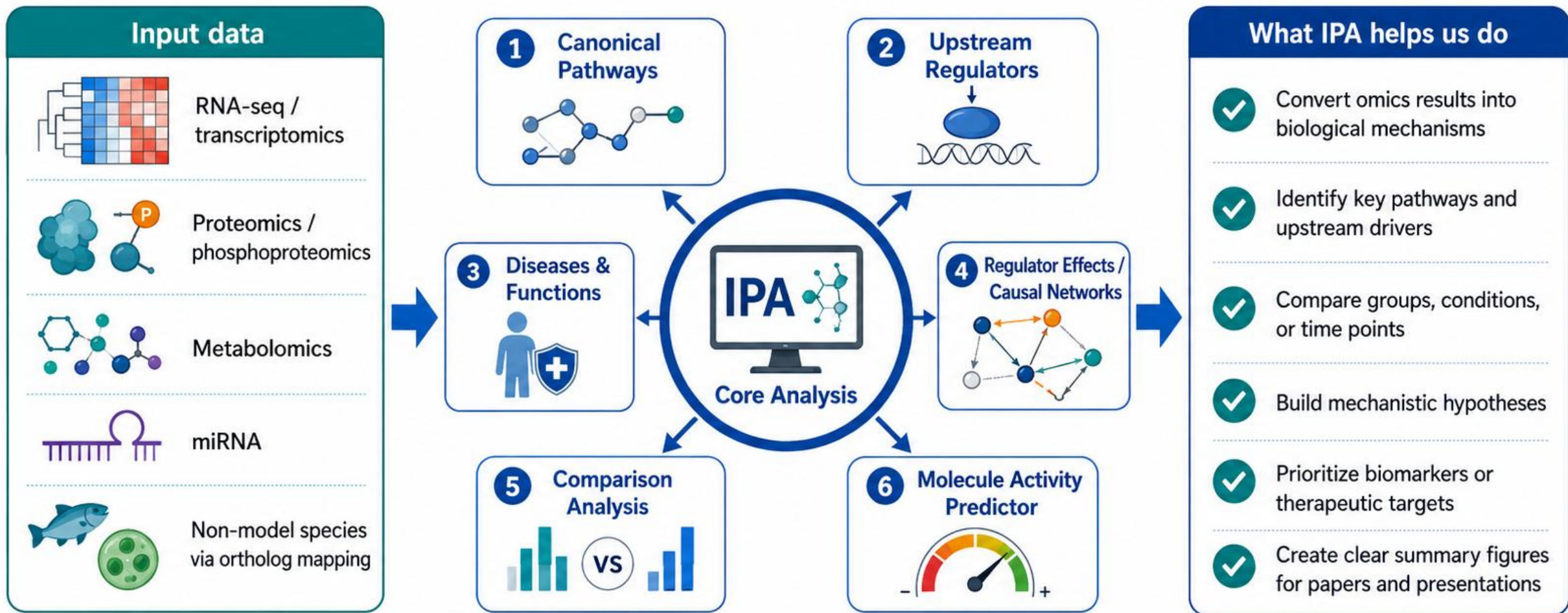
Run Analysis

Cancel

3	Symbol	Entrez Gene	Location	Family	Drug(s)	Gene Sym	Expr Log	Expr p-value	Expr False	Human	Other Org	Other Tiss	Caco2 cell	COLO205	Colon Car	HCC-2998	HCT-116	HCT-15	HT29	KM-12	Other Colo	RKO	SW-480	SW-620	Biomarker Application
4	ABCC3	ATP binding cassette	Plasma Membrane	transporter		ABCC3	0.666	5.02E-03	1.01E-01	x	x	x	x	x		x		x	x					x	diagnosis, prognosis
5	ABCG1	ATP binding cassette	Plasma Membrane	transporter		ABCG1	0.948	1.85E-02	1.44E-01	x	x	x		x					x						efficacy, unspecified
6	AHNAK2	AHNAK	Cytoplasm	other		AHNAK2	1.111	5.91E-04	7.29E-02	x	x						x								unspecified application
7	ALDH1A	aldehyde dehydrogenase	Cytoplasm	enzyme	disulfiram	ALDH1A	1.083	2.56E-02	1.57E-01	x	x	x		x		x			x	x	x				diagnosis, disease progression
8	ALDH1A	aldehyde dehydrogenase	Cytoplasm	enzyme		ALDH1A	1.898	1.97E-03	8.30E-02	x	x				x	x	x	x	x	x				x	unspecified application
9	ALDH3A	aldehyde dehydrogenase	Cytoplasm	enzyme		ALDH3A	1.179	1.42E-02	1.32E-01	x	x	x		x		x		x	x	x				x	diagnosis, unspecified
10	ALPP	alkaline phosphatase	Plasma Membrane	phosphatase	anti-ALP	ALPP	1.45	1.26E-02	1.28E-01	x	x	x													diagnosis, unspecified
11	ANXA1	annexin A	Plasma Membrane	other	hydrocortisone	ANXA1	0.696	3.19E-02	1.71E-01	x	x	x		x		x	x	x	x	x	x	x		x	diagnosis, prognosis
12	BCL2	BCL2 apoptosis	Cytoplasm	transporter	BP1002, SBCL2	BCL2	-0.656	2.19E-02	1.49E-01	x	x	x		x	x	x	x	x	x	x	x	x	x	x	diagnosis, efficacy, prognosis
13	BIRC5	baculoviral inhibitor of	Cytoplasm	other	VS-101, g	BIRC5	-0.656	2.06E-03	8.31E-02	x	x	x	x	x		x	x	x	x		x	x	x	x	diagnosis, disease progression
14	CALB2	calbindin 28k	Cytoplasm	other		CALB2	-0.66	2.82E-02	1.64E-01	x	x			x		x			x	x	x			x	unspecified application
15	CCNF	cyclin F	Nucleus	other		CCNF	-0.693	3.48E-05	6.87E-02	x	x		x	x		x	x	x	x	x	x			x	unspecified application
16	CD22	CD22 molecule	Plasma Membrane	transmembrane	pinatuzumab	CD22	0.831	2.00E-02	1.47E-01	x	x	x		x		x	x	x	x	x	x			x	unspecified application
17	CDK1	cyclin dependent kinase	Nucleus	kinase	CGP 7451	CDK1	-0.597	2.92E-02	1.66E-01	x	x		x			x	x	x	x	x	x			x	efficacy
18	CDKN1A	cyclin dependent kinase	Nucleus	other	RAG-01	CDKN1A	1.092	1.09E-02	1.24E-01	x	x	x		x		x	x	x	x	x	x		x	x	diagnosis, efficacy, prognosis
19	CHI3L1	chitinase 3-like 1	Extracellular	enzyme		CHI3L1	1.302	1.15E-02	1.26E-01	x	x														diagnosis, efficacy, prognosis
20	CLU	clusterin	Cytoplasm	other	clusterin antibody	CLU	0.882	2.48E-02	1.56E-01	x	x	x	x		x	x	x	x	x	x				x	efficacy, unspecified
21	CYP1B1	cytochrome P450 17A1	Cytoplasm	enzyme		CYP1B1	1.973	1.92E-04	6.87E-02	x	x	x							x	x					diagnosis, efficacy, prognosis
22	CYP3A5	cytochrome P450 3A5	Cytoplasm	enzyme		CYP3A5	0.703	1.62E-02	1.37E-01	x	x			x					x		x				efficacy, safety, unspecified
23	E2F1	E2F transcription factor 1	Nucleus	transcription factor		E2F1	-0.643	2.55E-02	1.57E-01	x	x	x	x	x		x	x	x	x	x	x			x	disease progression
24	FADS3	fatty acid synthase	Plasma Membrane	enzyme		FADS3	0.588	2.25E-02	1.50E-01	x	x				x	x	x	x	x	x				x	unspecified application
25	FAS	Fas cell surface	Plasma Membrane	transmembrane	APO010,	FAS	0.766	3.02E-02	1.68E-01	x	x	x				x	x	x	x	x	x		x		diagnosis, disease progression
26	FOXO1	forkhead box O1	Nucleus	transcription factor		FOXO1	-0.661	1.77E-04	6.87E-02	x	x		x	x		x	x	x	x	x	x			x	prognosis
27	FTTH	ferritin heavy chain 1	Cytoplasm	enzyme		FTTH	0.833	3.78E-03	9.53E-02	x	x	x	x		x	x	x	x	x	x				x	unspecified application
28	GADD45C	growth arrest and DNA damage-inducible 45C	Nucleus	other		GADD45C	1.099	2.60E-03	8.46E-02	x	x	x													efficacy
29	GAST	gastrin	Extracellular	other		GAST	1.47	9.09E-03	1.19E-01	x	x								x		x				efficacy, safety
30	GDF15	growth differentiation factor 15	Extracellular	growth factor	AZD8853	GDF15	0.792	5.23E-03	1.02E-01	x	x	x	x		x	x	x	x	x	x				x	diagnosis, unspecified
31	GMNN	geminin	Nucleus	transcription factor		GMNN	-0.706	7.89E-03	1.12E-01	x	x	x	x		x	x	x	x	x	x				x	unspecified application
32	H2AX	H2A X variant	Nucleus	transcription factor		H2AX	-0.63	3.99E-04	7.04E-02	x	x			x		x	x	x	x	x				x	efficacy

QIAGEN IPA | From Omics Data to Biological Mechanisms

Key functions we will introduce in this session



IPA bridges diverse omics datasets and interprets them as pathways, regulators, functions, and networks—turning lists of molecules into an interpretable biological story.



Better Care with Better Knowledge

若有需要進一步的資訊或在使用軟體上遇到問題歡迎聯繫以下窗口：
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