

## Data Analysis and Pathway Interpretation of Metabolomics and Phosphoproteomics via Qiagen IPA



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Ingenuity  
Pathway  
Analysis



## Install IPA on your computer

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

Click on the button below to download the installer

**IPA for Windows (64-bit)**

(Installer recommended for your computer)

Other options:

[IPA for 32-bit Windows](#)

[IPA for macOS](#)

For more information see this [help page](#).

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

Looking for more information about IPA? Click [here](#).

[IPA Installer Download \(ingenuity.com\)](https://www.ingenuity.com/ipa/installer-download)

## Minimum Software Requirements

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

## Minimum Hardware Requirements

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

Minimum Screen Resolution of 1280 x 800

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

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

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

Notes:

1. We recommend that you install the IPA client on your computer with this installer: <https://analysis.ingenuity.com/pa/installer/select>. The installed IPA client still requires you to have internet access to launch but does *not require* you to install Java (a JRE) or to launch IPA from a web browser.
2. Alternatively, you can launch IPA using Java Web Start, which requires a recent version of Java installed on your computer. Oracle has changed its licensing terms for Java: <https://www.java.com/en/download/>. Therefore, please ensure you are following Oracle's terms and conditions for the Java version on your computer should you choose to launch IPA via Web Start, which is available at this link: <https://analysis.ingenuity.com>. Help on installing and/or launching IPA can be found at the following links:
  - i. Mac: [https://qiagen.my.salesforce-sites.com/KnowledgeBase/articles/Basic\\_Technical\\_Q\\_A/Running-IPA-on-Mac](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](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)

## Introduction to pathway analysis

### What is QIAGEN Ingenuity Pathway Analysis

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

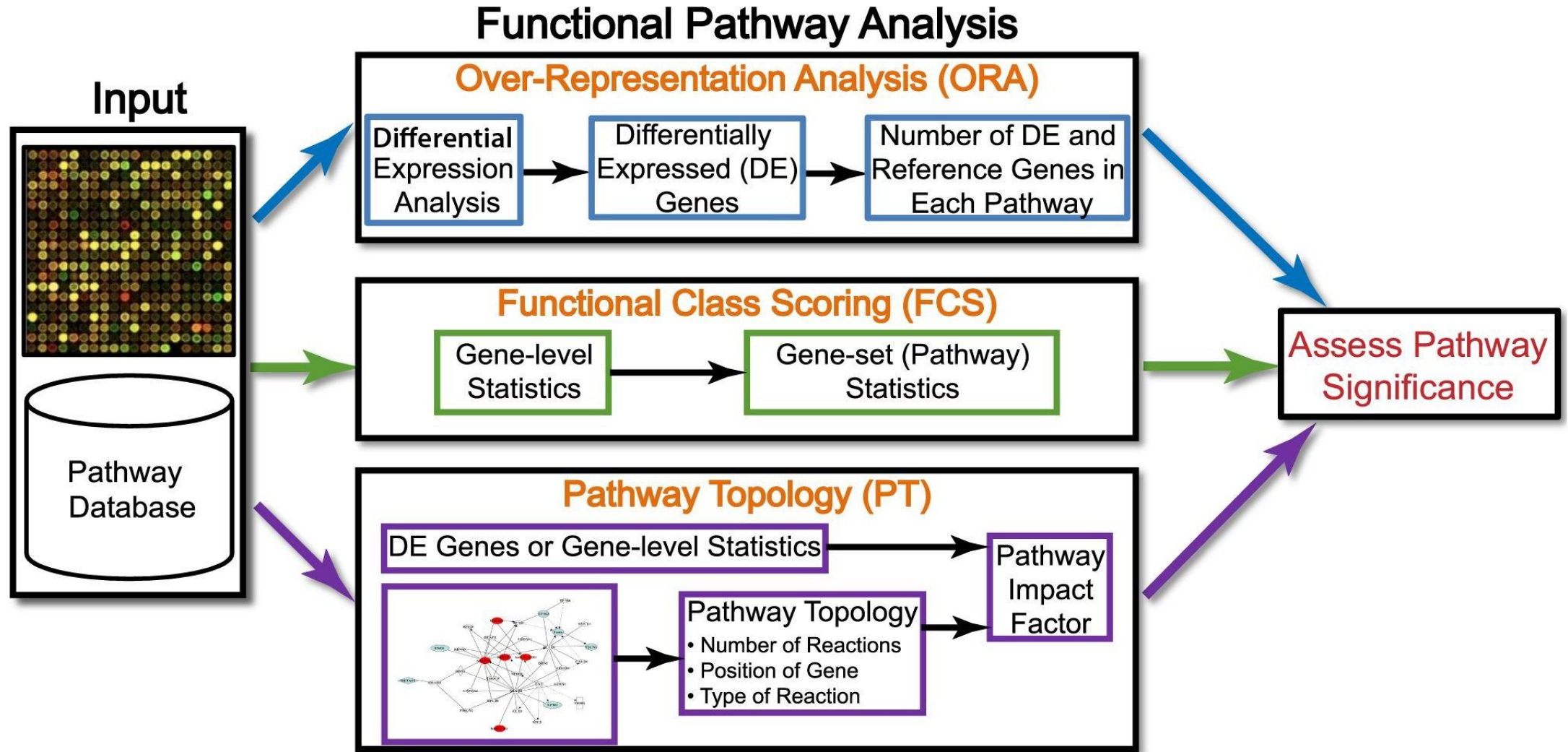
### Machine Learning pathway

### Interpreting your 'omics data using IPA

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

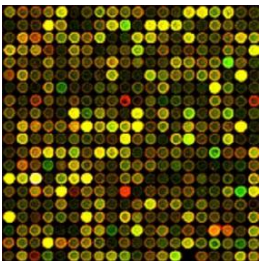
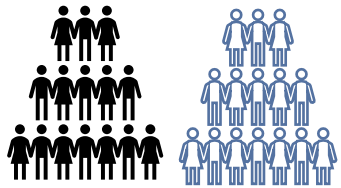
### Create networks from scratch

## Summary



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
- KYNU
- TMEM63C
- S100A11
- PI3
- CDC25B
- CNNM2
- CHRNA1
- LRRN2
- RMDN2
- CNTRF
- CDC14A
- C7orf31
- BACE2
- CXCL1
- SLC36A1
- WDR78
- PKM

Drugs and chemicals

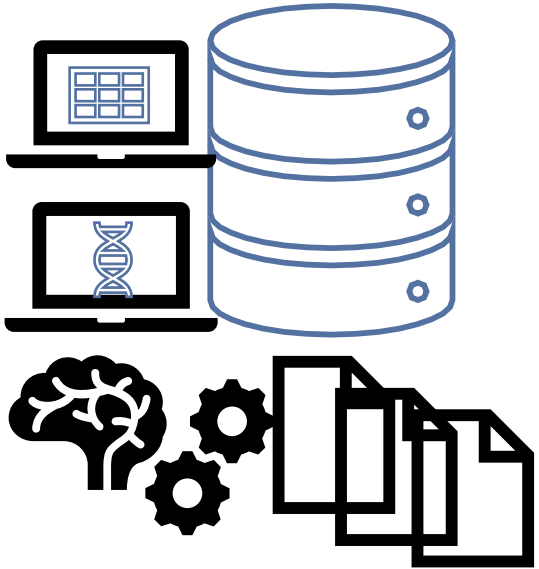
Pathway

Disease

Function

Network

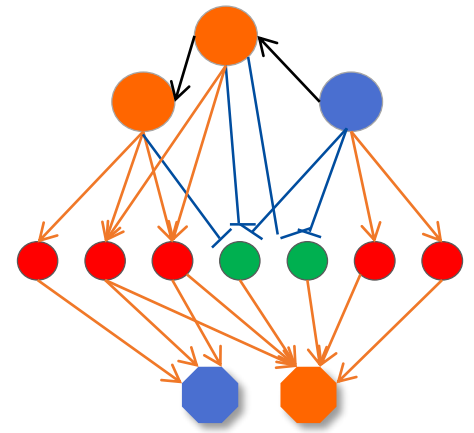
Public /commercial database



ORA/FCS/Topology Pathway Analysis

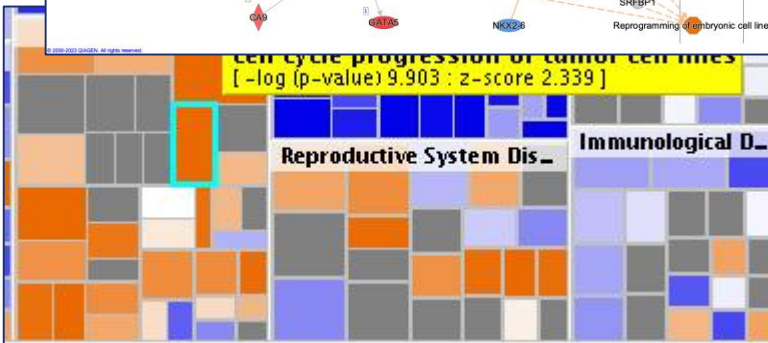
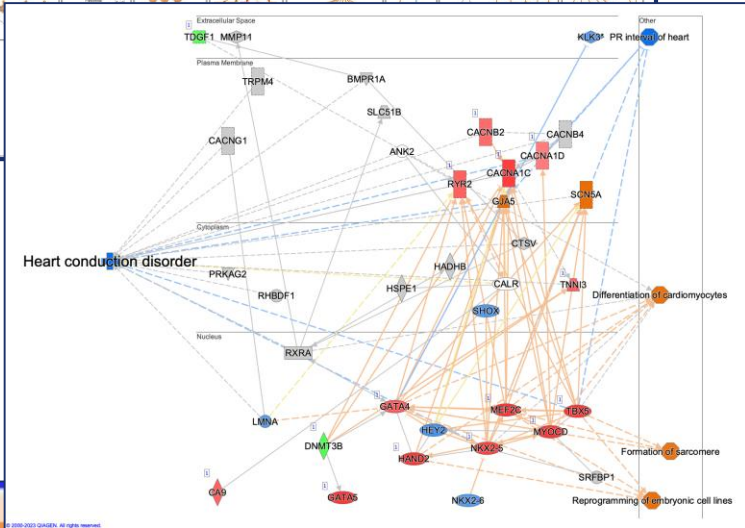
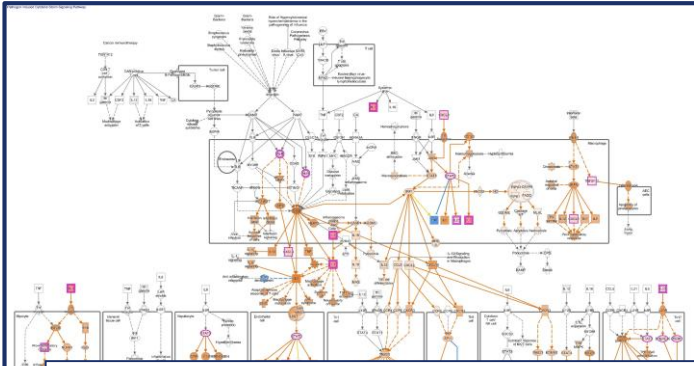
Machine learning

What do they relate to each other?

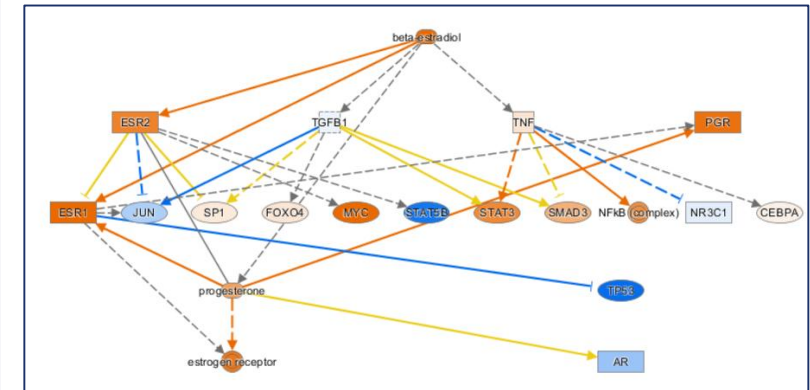
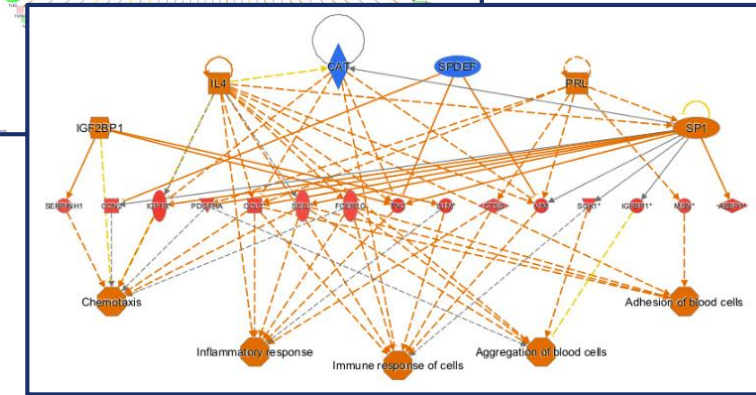
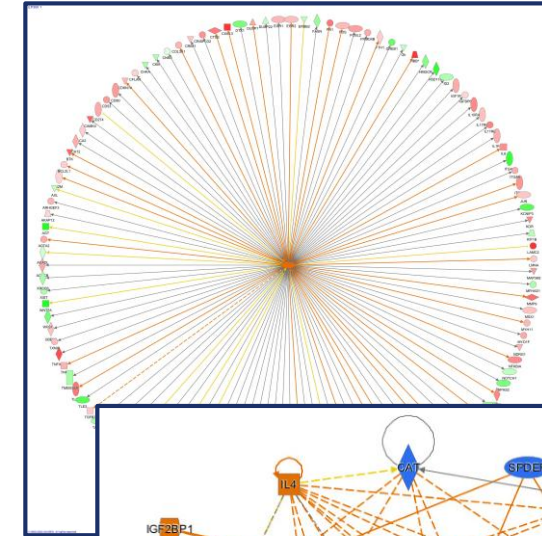
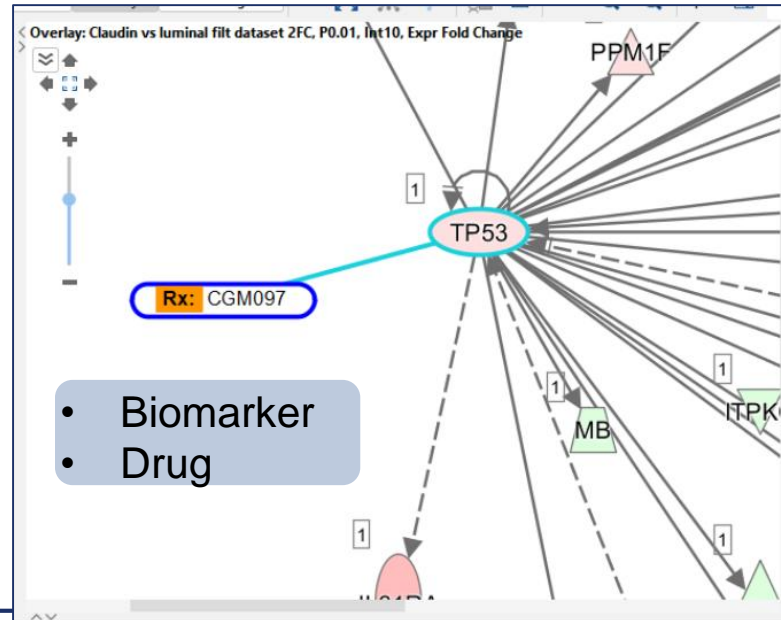


What are the relationship between each molecules?

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



Sample to insight



> *Hepatology 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<sup>+</sup> 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

PubMed® ingenuity pathway analysis

Advanced Create alert Create RSS Search

Save Email Send to Sort by: Best match Display options

1,573 results Page 1 of 158

RESULTS BY YEAR

TEXT AVAILABILITY

- Abstract
- Free full text
- Full text

From 2020-2026  
1,537 literatures

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

**Ingenuity pathway analysis** of alpha-synuclein predicts potential signaling pathways, network molecules, biological functions, and its role in neurological diseases.  
 2  
 Cite Suthar SK, Lee SY.  
*Front Mol Neurosci.* 2022 Nov 29;15:1029682. doi: 10.3389/fnmol.2022.1029682. PMID: 36523604 **Free PMC article.**  
 We have taken the advantage of such a Bioinformatics tool, **ingenuity pathway analysis** to decipher the signaling pathways, interactome, biological functions, and ... Overlapping of the predicted top-five canonical signaling ...

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

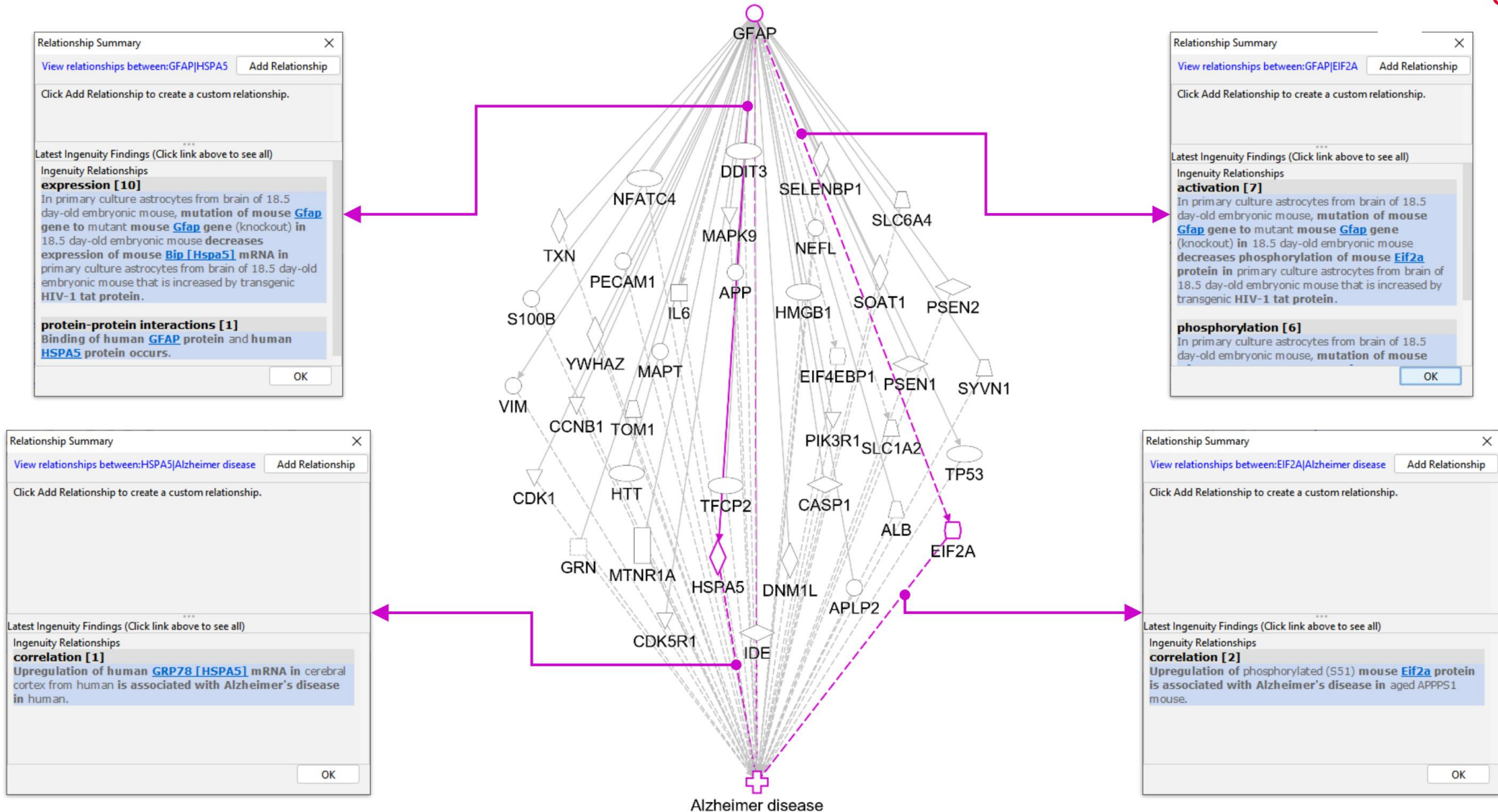
**Histone Trimethylations and HDAC5 Regulate Spheroid Subpopulation and Differentiation Signaling of Human Adipose-Derived Stem Cells**

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:

What species identifiers are accepted for analysis by IPA?



Human

- ✓ 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



Mouse



Rat

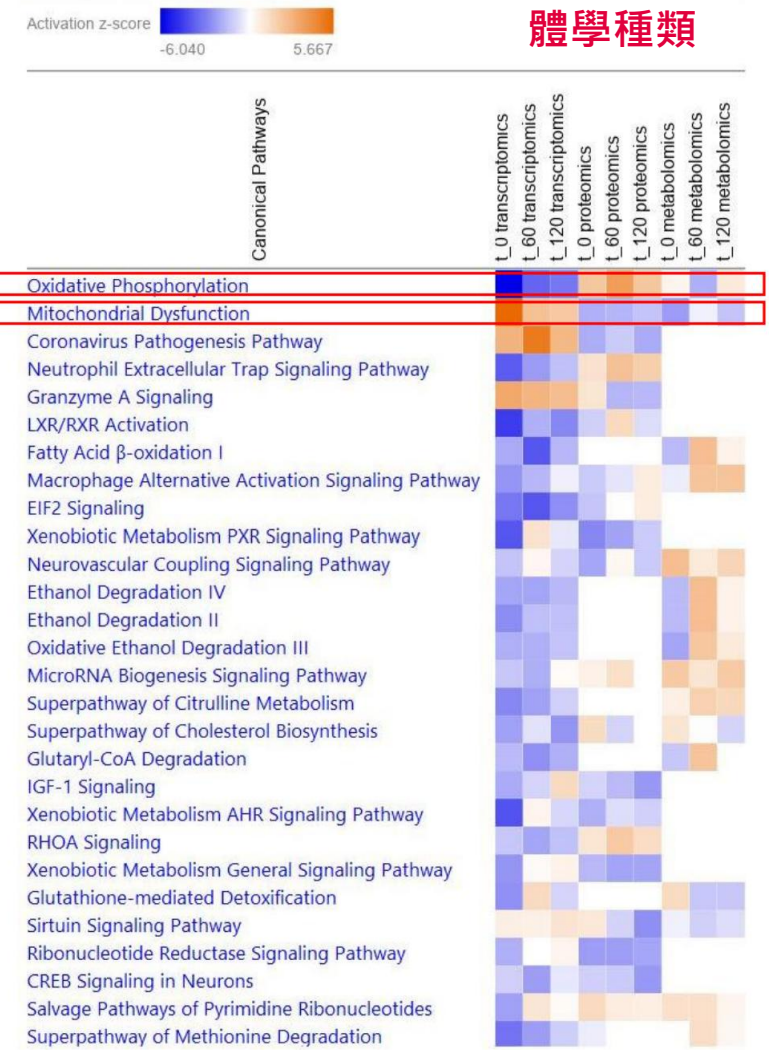
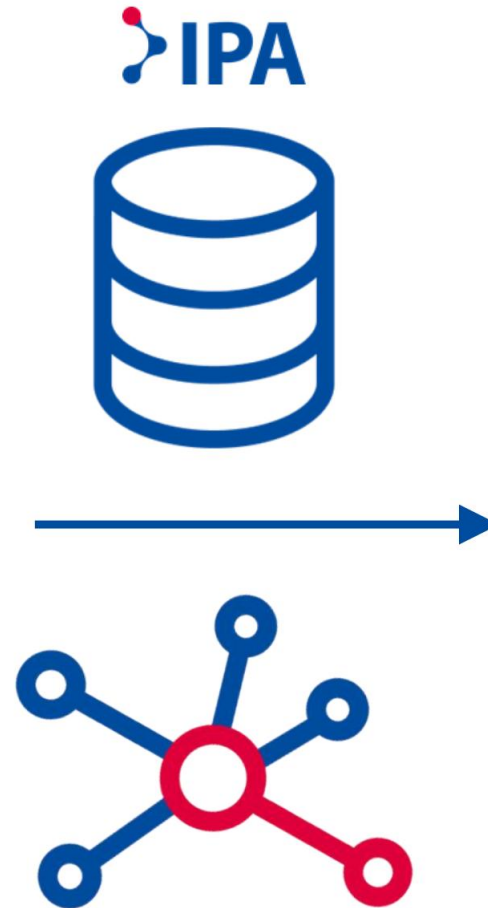
Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

Get more complete mapping during dataset upload!

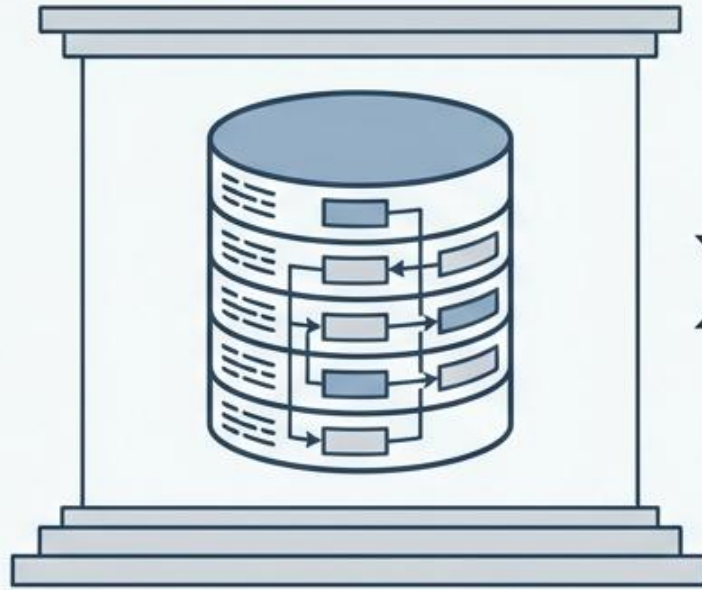
Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2023/8)	GenPept	Ensembl (110)	miRbase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (257)	International Protein Index (IPI)	RefSeq (human, mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human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

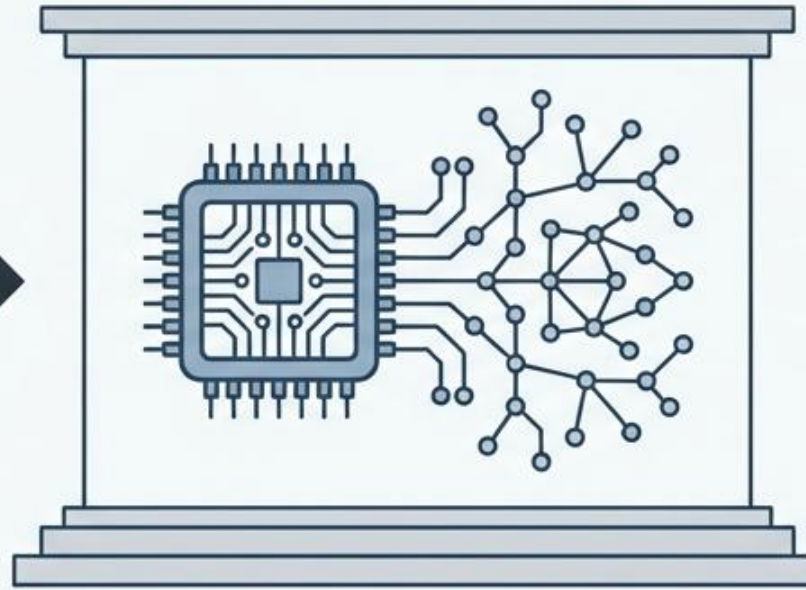






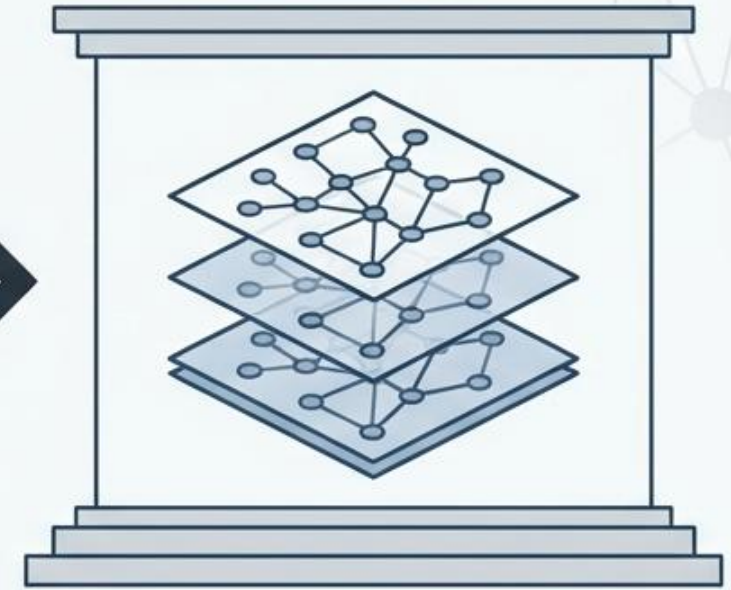
**The Source: QIAGEN Knowledge Base**

Mining decades of **causal findings**.



**The Engine: Machine Learning Generation**

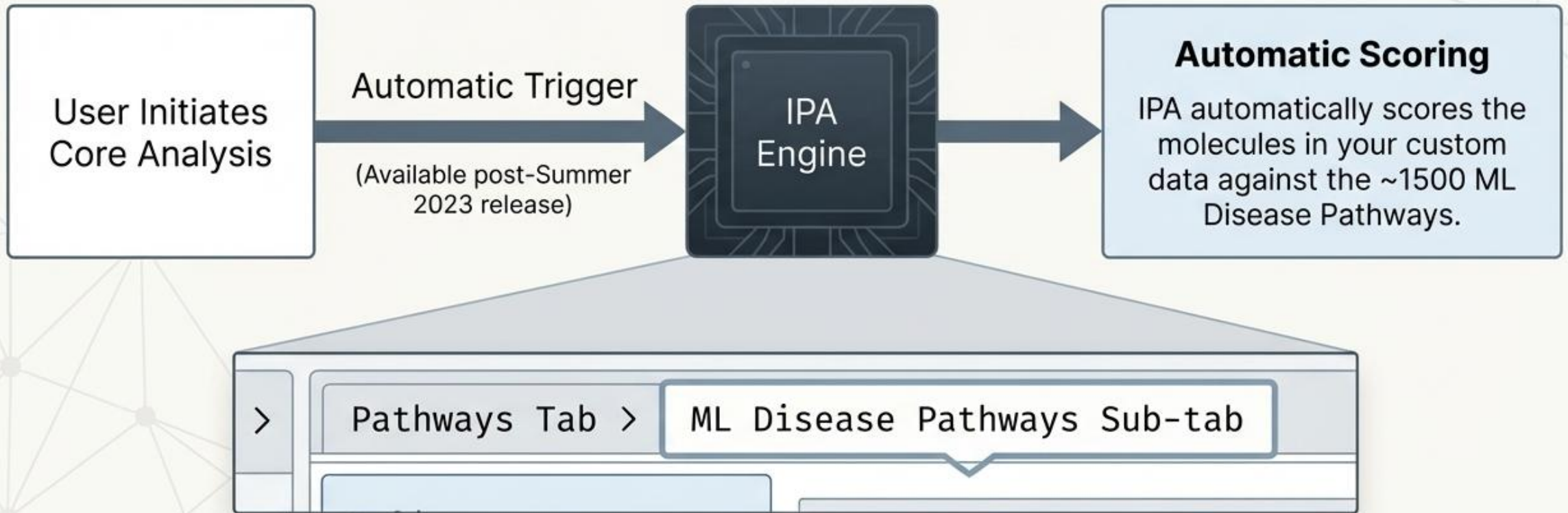
Automated creation of **~1500 disease, phenotype, and function pathways** to prioritize **key causal genes**.

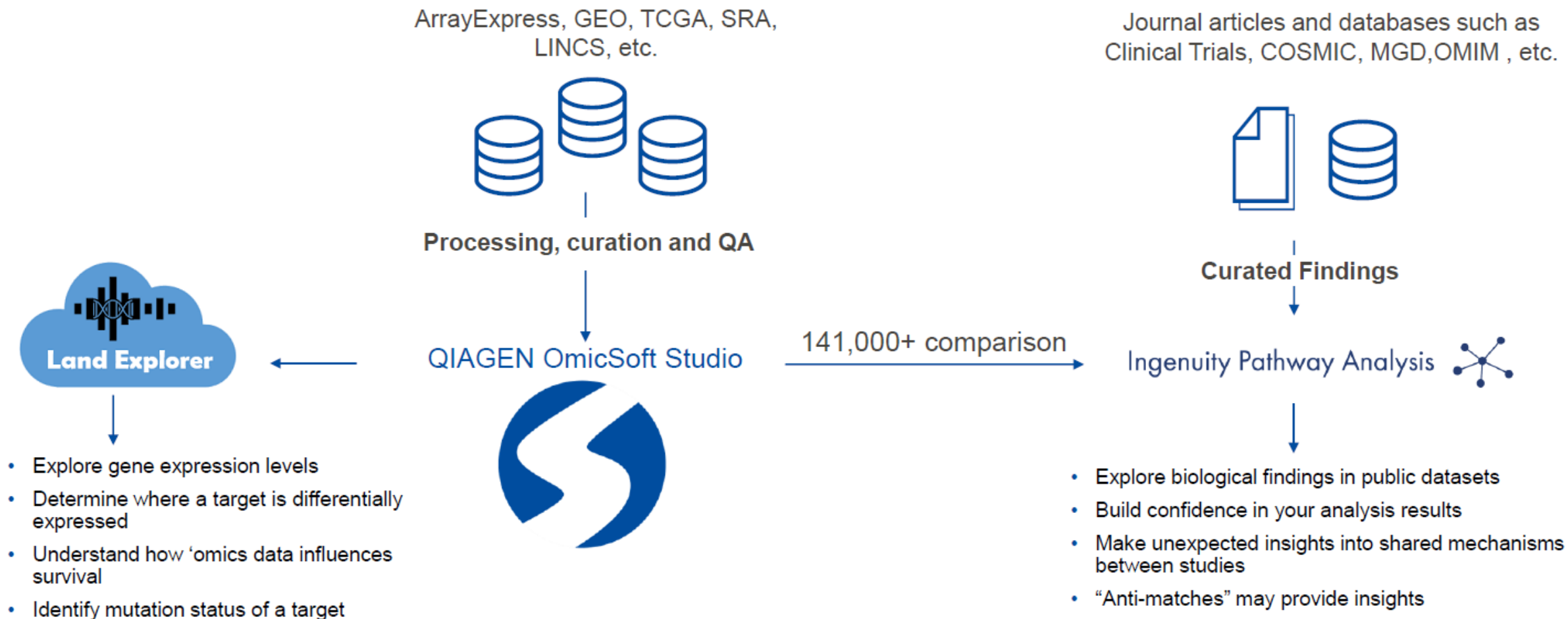


**The Application: Data Overlay**

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**.





IPA

File Edit View Window Help

Provide Feedback | Support Gene Chen Close IPA

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

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

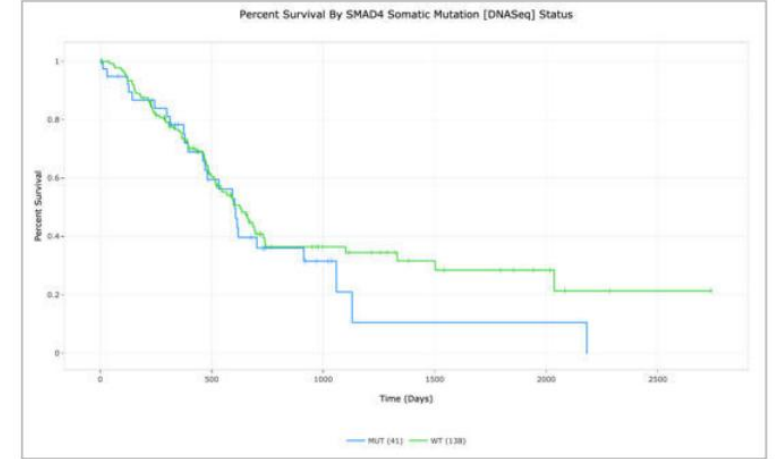
Selected/Total molecules: 0/144



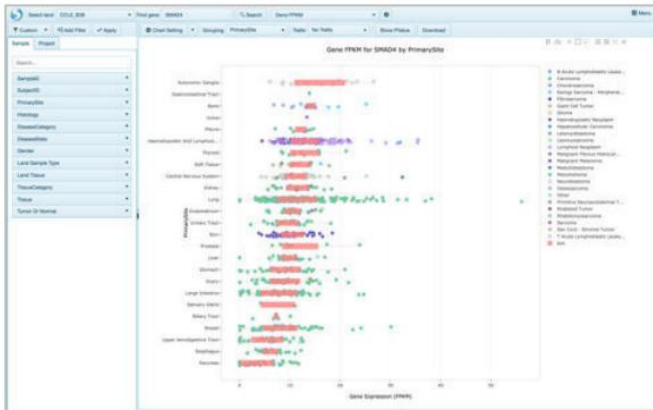
Expression in Rat, Mouse, and Human Disease



Mutation frequency



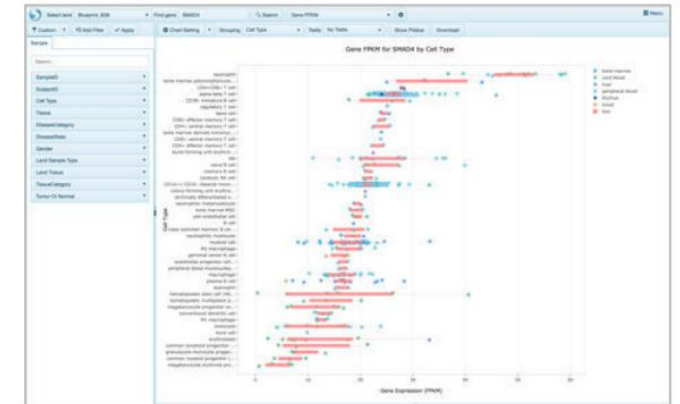
Survival plots



Cell line expression



Tumor expression



Hematopoietic expression (BluePrint)

The screenshot shows the OmicSoft Land Explorer interface. At the top, the search bar contains 'EGFR'. Below it, the search results for EGFR are displayed, showing a table with columns for Symbol, Matched Term, Synonym(s), Entrez Gene Name, and Location. The first result is EGFR, with a blue arrow pointing to it.

Below the search results, a table titled 'OmicSoft Land Explorer: Sample-level experimental data' is shown. A red arrow points to the 'Oncology Consortia' column, with the text 'Choose which you want' next to it.

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

**Land selection**

Select land: TCGA\_B38\_GC33

Custom Add Filter Apply

Sample

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

**Gender**

Check All Check None Invert

- female
- male
- NA

**Metadata filtering**

Race

Tissue category

Tissue

**Search bar**

Find gene: egfr Search

**View selection**

Gene FPKM

Chart Setting Grouping Tumor Type Trellis No Trellis Show PValue Download

Gene FPKM for EGFR by Tumor Type

**Download data for current view**

**View controller**

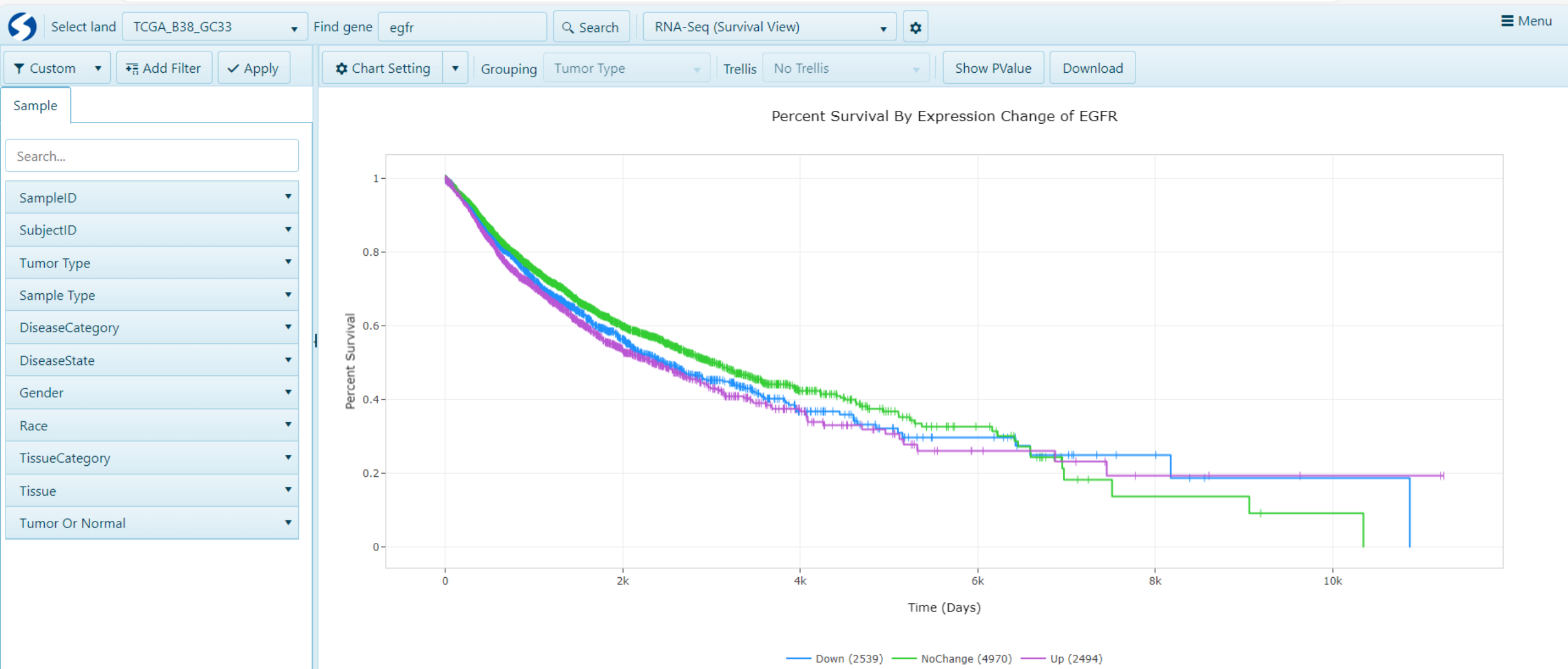
[https://explorer.omicsoft.com/IPA/Home/MainPage?landName=TCGA\\_B38\\_GC33&qeneID=EGFR&viewID=RnaSeq\\_Transcript.GeneVariable&grouping=Tumor.Type&trellis=No.Trellis](https://explorer.omicsoft.com/IPA/Home/MainPage?landName=TCGA_B38_GC33&qeneID=EGFR&viewID=RnaSeq_Transcript.GeneVariable&grouping=Tumor.Type&trellis=No.Trellis)

- 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 navigation bar includes 'Select land' (TCGA\_B38\_GC33), 'Find gene' (egfr), and 'Gene FPKM'. The left sidebar has a 'DiseaseState' filter menu with a red box around it, containing a list of cancer types with checkboxes. The main area displays a scatter plot of EGFR expression (Gene FPKM) for LUAD and BRCA tumor types, with a red box highlighting a specific data point in the BRCA group. Below the plot is a table with columns: SampleID, SubjectID, Tumor Type, Sample Type, CNV Call, GeneID, GeneName, and Expression. A red arrow points from the highlighted data point in the plot to the corresponding row in the table.

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



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 [organoid] 3-D cultu	SingleCellHuman...	normal control	kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GSE110...	https://www...	50.00	52.09	46.38	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:Infer...	GSE20948.GPL1	http://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...	GSE1427...		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...	GSE57816.GPL1	https://www...	55.90	57.45	30.00	45.13	15.11		
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cluster vs Ot...	embryonic st...	GSE1427...		55.90	56.67	31.62	44.96	27.78		
3682- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cell Type vs ...	embryonic st...	GSE1427...		55.90	56.67	31.62	44.96	27.78		
87- disease [airway epithelium] NA 20248	HumanDisease	disease contr...	airway epith...		Treatment1 v...	SamplingTim...	GSE4...		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...	GSE5...		55.90	40.00	31.62	53.59	18.65		
20- normal control [skeletal muscle] NA 8919	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 20248	SingleCellHuman...	osteoarthritis...	synovial mem...		Cluster vs Ot...	synovial fibr...	GSE5...		55.90	53.85	31.62	45.16	16.44		
23- normal control [foreskin] NA 20248	HumanDisease	normal control	foreskin	4-thiouridine	Treatment1 v...	SampleMater...	GSE5...		55.90	53.96	30.00	46.13	15.61		
1- prostate cancer [prostate] NA 20248	MetastaticCancer	prostate can...	prostate		Disease vs. N...	LandSam...	GSE6919.GPL1	https://www...	50.00	57.45	33.17	38.59	34.62		
2- nephrolithiasis [papillary duct] NA 20248	HumanDisease	nephrolithiasis	papillary duct		Cluster vs Ot...	retinal rod ce...	GSE73680...		50.00	53.85	30.00	44.96	24.88		
8878- normal control [colorectal adenocarcinoma] NA 20248	SingleCellHuman...	normal control	colorectal ad...		Cluster vs Ot...	retinal rod ce...	GSE73680...		55.90	58.31	33.17	37.19	33.85		
1388- normal control [embryo] NA 20248	SingleCellHuman...	normal control	embryo		Cluster vs Ot...	retinal rod ce...	GSE73680...		55.90	56.57	22.36	46.13	13.38		
10818- normal control [bladder] NA 20248	SingleCellHuman...	normal control	bladder		Cluster vs Ot...	retinal rod ce...	GSE73680...		55.90	54.77	22.36	46.13	26.44		
216- breast cancer [breast] NA 20248	OncoHuman	breast carcin...	breast	docetaxinib	Treatment vs...	CellLine:Tre...	GSE1...		55.90	41.24	20.00	43.02	8.39		
1- lung adenocarcinoma [lung] NA 20248	MouseDisease	normal control	lung	NA	Treatment vs...	ExperimentG...	GSE1...		55.90	44.91	22.36	48.38	12.46		
161- lung adenocarcinoma [lung] large cell	SingleCellHuman...	lung adenoc...	lung	NA	Cell Type vs ...	unassigned c...	E-M...		55.90	41.46	26.46	42.88	25.93		
5368- normal control [fetal testis] 5367	SingleCellHuman...	normal control	fetal testis		Cluster vs Ot...	unassigned c...	GSE1...		55.90	61.64	47.96	61.89	21.80		
23- normal control [heart] NA 6093	RatDisease	normal control	heart	NA	Treatment vs...	TreatTime:Su...	GSE1...		55.90	42.00	36.06	42.76	12.79		
3- diet induced obesity [lung] NA 20248	MouseDisease	diet induced ...	lung	NA	Disease vs. N...	DiseaseState...	GSE3...		50.00	45.83	33.57	41.26	10.20		
7902- normal control [foreskin] pellet culture; TGF	SingleCellHuman...	normal control	foreskin	pellet culture...	Cell Type vs ...	chondrocyte ...	GSE160625.UN	https://www...	40.82	46.00	30.00	53.59	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 [foreskin] pellet culture; TGF	SingleCellHuman...	normal control	foreskin	pellet culture...	Cluster vs Ot...	chondrocyte ...	GSE1606...		50.00	50.00	26.46	42.53	20.41		
6271- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cell Type vs ...	chondrogeni...	GSE1...		55.90	41.46	30.00	47.27	14.89		
135- normal control [liver] cerivastatin 6363	RatDisease	normal control	liver	cerivastatin	Treatment vs...	TreatTime[da...	GSE57...		55.90	45.83	26.46	46.13	8.52		
7640- idiopathic pulmonary fibrosis [bronchoalve	SingleCellHuman...	idiopathic p...	bronchoalve...		Cluster vs Ot...	epithelial cell...	GSE15...		55.90	56.57	24.49	37.19	27.33		
10- non-small cell lung carcinoma [lung] NA 1141	OncoHuman	non-small cel...	lung	NA	Other Comp...	SmokingStat...	GSE19...		55.90	37.71	20.00	41.52	13.28		
EEC P32 Tumor vs Norm RPKM - 2018-09-28 04:03 AS123									55.90	57.45			42.04		
EEC P32 Tumor vs Norm RPKM - 2020-02-13 11:12 NDMC-0212									55.90	45.39			41.93		
28- colon carcinoma [colon] recombinant hTGF al	OncoHuman	colon carcin...	colon	recombinant ...	Treatment1 v...	CellLine:Trea...	GSE10...		55.90	38.38	31.62	41.82	9.24		
1- normal control [umbilical cord vein] mechanica	HumanDisease	normal control	umbilical cor...	mechanical s...	Treatment vs...	TreatmentTr...	GSE178...		55.90	61.24	43.59	26.46	7.59		
EEC P32 Tumor vs Norm RPKM123 - 2020-02-14 11 NDMC-0212									55.90	86.60	42.43	37.52	41.64		
3- normal control [small airway epithelium] 3132	HumanDisease	normal control	small airway ...		Other Comp...	SmokingStat...	GSE77658.GPL1	http://www...	50.00	48.99	26.46	39.95	41.35		
MetastaticMelanoma mRNA_vs_Normal PMID_204 CT20190116									55.90	61.24	44.72	59.25	41.30		

Selected 0 / 140569

**Your datasets** (left database icon) **compare** (double-headed arrow) **Donor datasets** (right database icon)

**Analysis** (magnifying glass icons over data rows)

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

## Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project

Cell & Tissue

Datasets information

similar

opposite

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

Project

- Select Projects
- Shared Projects
- Libraries
  - OmicSoft
    - OncoLand
    - DiseaseLand
    - SingleCellLand
    - Normal Cells and Tissues
- Or filter using wild card search
 

include: (use \* for wildcard)

[comma-separated list]

exclude:

[comma-separated list]

Apply Cancel

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File Edit View Window Help Provide Feedback | Support Gene Chen Close IPA

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

Create New...  Search [Advanced Search](#)

Search Results - [ ] X

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)

4

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

Libraries > OmicSoft > SingleCellLand > SingleCellHumanUmi > Analyses

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

Case/Control Differences

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

Comparison Context

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

All Experiment Metadata

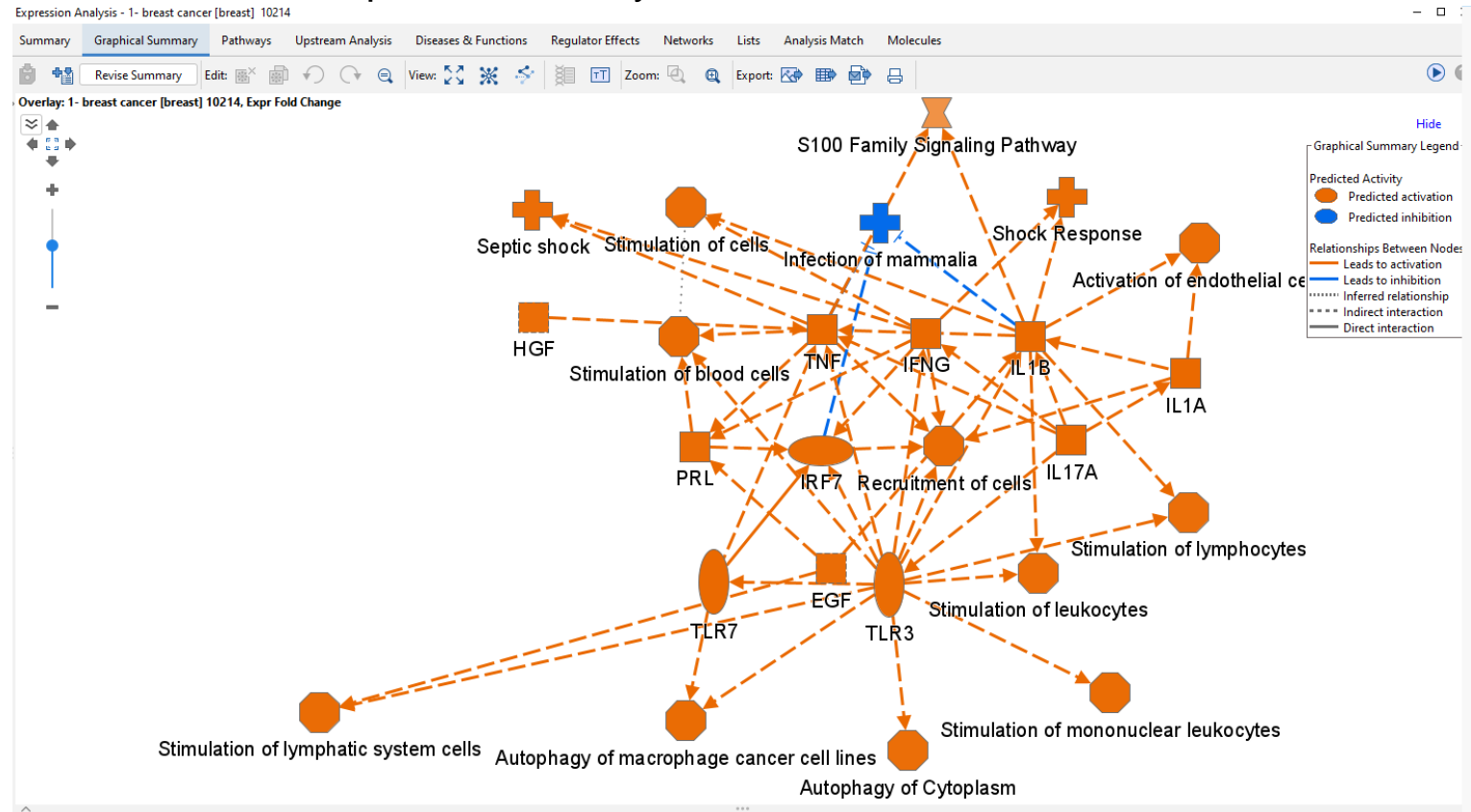
case.cellmarkers CD235A-  
 case.celltype lung cell  
 case.cluster 1  
 case.clustercelltype T cell  
 case.diseasestate lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)  
 case.ethnicity Caucasian  
 case.gender female;male  
 case.samplematerial cryopreserved cells;MACS depleted cells;surgical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

3

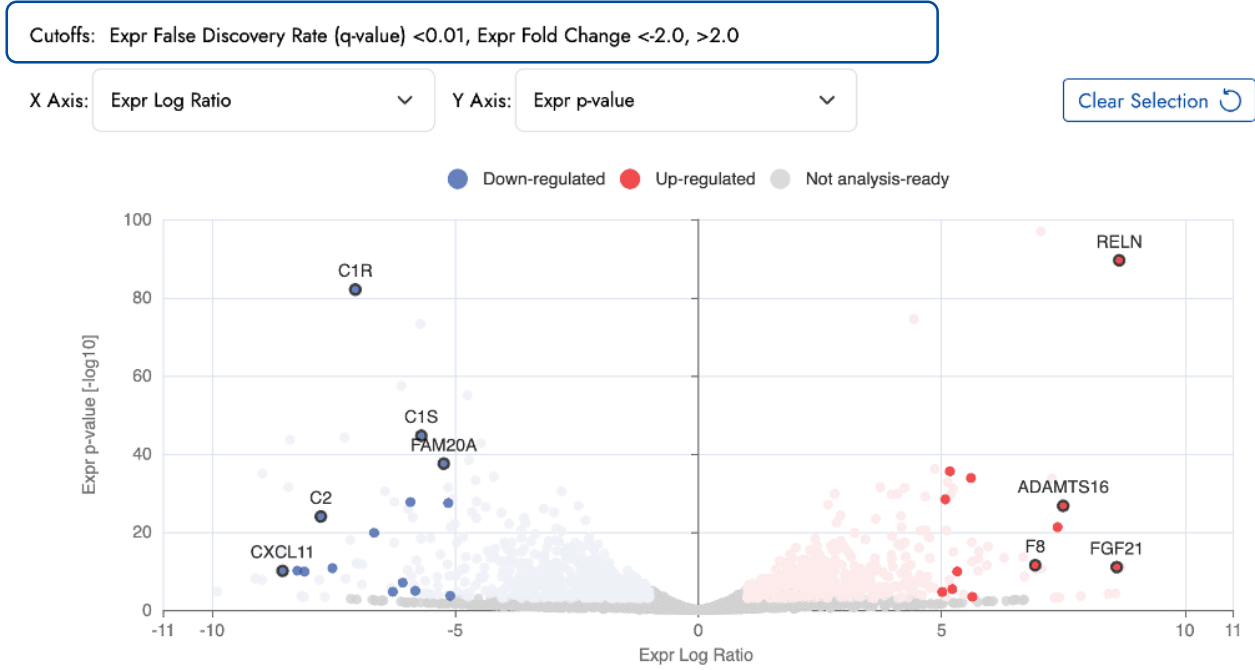
You can also use the repository without your own analysis, just by searching for available analyses of interest.

The Project Manager window displays a hierarchical view of projects and libraries. Under 'My Projects', there is a sub-folder 'Normal Cells and Tissues'. Under 'Libraries', there are folders for 'OmicSoft', 'OncoLand', 'DiseaseLand', 'SingleCellLand', and 'Normal Cells and Tissues'. A search results window is open, showing a list of projects with columns for project name and a numerical value. The project '1- breast cancer [breast] 10214' is highlighted.

## Graphical summary



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

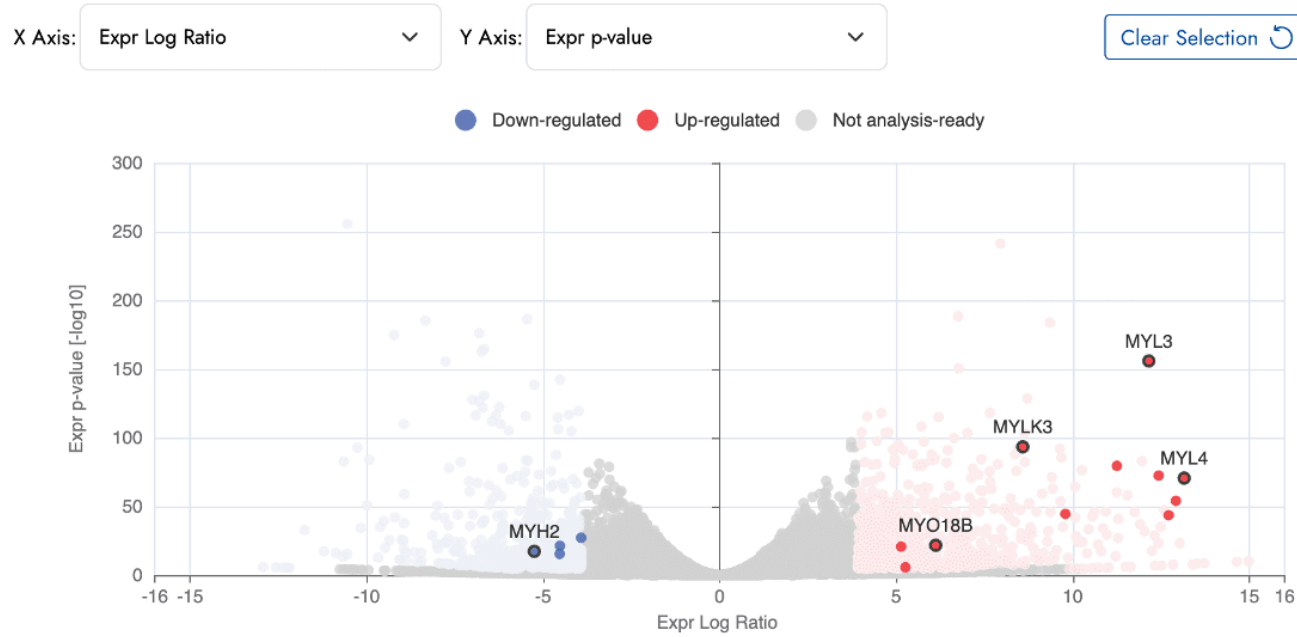
### Dataset molecules

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
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

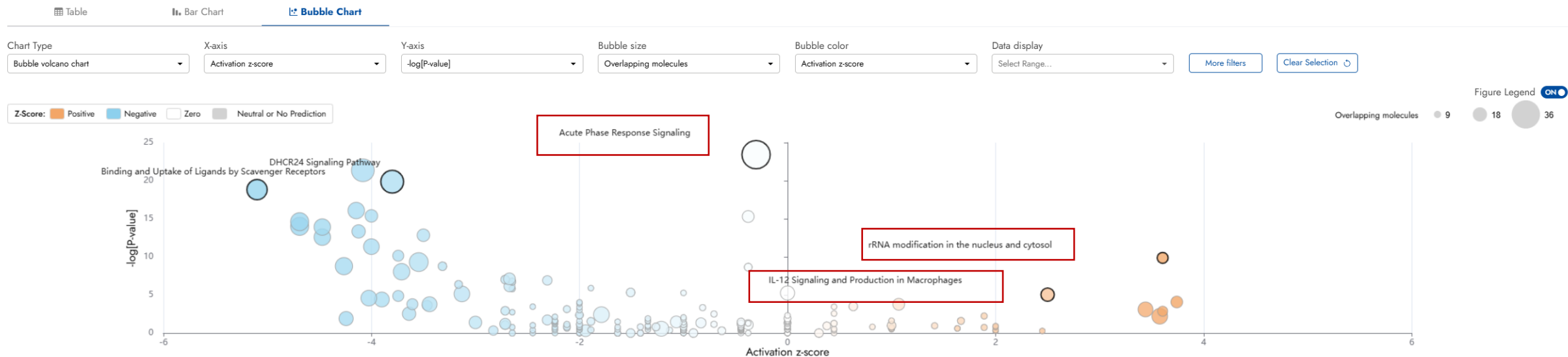
Showing **73** of 27087 molecules

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	<input type="text" value="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 <span style="color:red">■</span>	1 <span style="color:blue">■</span>	other	Cytoplasm	No
MYBPHL	myosin binding protein H like	ENSG00000221986	2.06e-3	1.00	5.69e-3	9.46	3.24 <span style="color:red">■</span>	1 <span style="color:blue">■</span>	other	Cytoplasm	No

M-B / Canonical Pathways / Bubble Chart

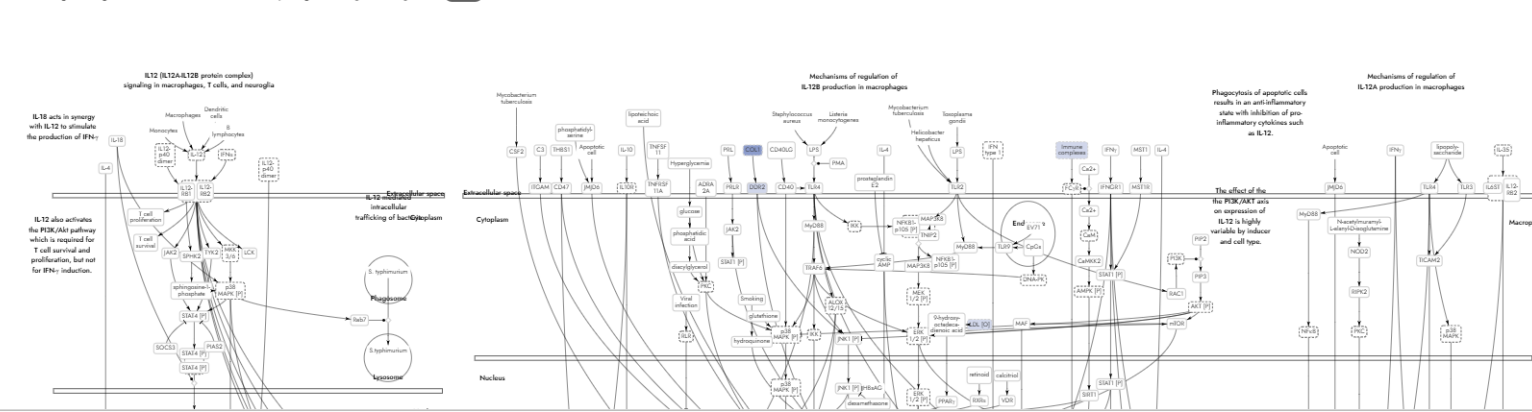
## Canonical Pathways

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  $\gamma$ ), 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  $\gamma$ ) 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  $\gamma$ , both of which are involved in the initiation of cell-mediated immunity. IFN  $\gamma$  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
Intercellular surface interactions	9.22e-17	9.22e-15	4.15	24.71%	21	95

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

	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-1-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

Multi observation

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	-0.182096564999999...	5.067939999999999...	M-D
52	17-hydroxy-11,15-di...	-	-	353.067_3,9	-0.261518497999999...	1.94006E-3	M-D
53	2-(4-Hydroxyphenyl)...	-	-	289.0497_8,8	0.20510102499999999	3.726257999999999...	M-D
54	2-(Methylthiomethyl...	-	-	193.0677_1,5	0.23968714799999999	4.495472999999999...	M-D
55	2-[[hydroxy(1-oxo-1...	-	-	246.0415_9,7	-0.169499689000000...	7.225800000000000...	M-D
56	2-[[hydroxy(5-hydrox...	-	-	233.0564_5,1	-0.775961921000000...	3.961799999999999...	M-D
57	2-Decylfuran	HMDB0032215	-	209.1896_9,7	-4.756241900000000...	2.428599999999999...	M-D
58	2-Deoxy-2-Amino Gl...	HMDB0001504	C06605	260.0533_3,1	-0.193207566	5.902499999999999...	M-D
59	2-Methoxyxanthone	HMDB0032998	-	225.055_7,9	0.29050186300000003	3.906299999999999...	M-D
60	2-oxo-3-(3,4,5-trihy...	-	-	211.0247_8,9	-0.127978258000000...	3.038522000000000...	M-D
61	2-Pyrrolidinone	HMDB0002039	C11118	86.06_1,8	-0.134968731000000...	1.376500000000000...	M-D
62	2,4-Diamino-6-[N-(2...	-	-	340.177_6,6	-0.192521124999999...	2.596532999999999...	M-D
63	2,4,6-Triethyl-1,3,5-...	-	-	207.0877_1,2	-0.130454037999999...	3.546219999999999...	M-D

AI can help parse and map automatically



## OmicSoft datasets

Land	Repository	Datasets Q1 2026
DiseaseLand	HumanDisease	25,069
	LINCS	25,880
	MouseDisease	22,344
	RatDisease	7042
OncoLand	ClinicalProteomicTumor	2747
	ENCODE RNA Binding	460
	NCI Patient-Derived Models	524
	OncoHuman	16,753
	OncoMouse	1043
Single Cell Land	TCGA	2490
	SingleCell CxG*	12,148
	SingleCell Tahoe Perturbagens*	3202
	SingleCellHuman	177
	SingleCellHumanUmi	86,281
	SingleCellMouse	78
	SingleCellMouseUmi	28,852
Normal Cells and Tissues	Human Tissues (GTEx)	1211

\* New in this release.

		Observation 1		Observation 2	
	A	B	C	D	E
1	<b>geneid</b>	<b>UCvsNormal.Log2FoldChange</b>	<b>UCvsNormal.pval</b>	<b>52wksVedolizumabvsBaseline.Log2FoldChange</b>	<b>52wksVedolizumabvsBaseline.pval</b>
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**

IDs (required)

	A	B	C	D
	<b>Proteins</b>	<b>Fold change</b>	<b>P_value</b>	<b>P_value_adjust</b>
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

Ratio, fold change, etc. (recommended)

Significance (optional)

## 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/>

IDs (required)

	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	_AGQTQPNPGLPIQPALT(ph)PR_

Observation 1

Ratio, fold change, etc. (recommended)

Significance (optional)

## 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/>

## 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

## communications biology

ARTICLE

<https://doi.org/10.1038/s42003-022-03942-4> **OPEN**

Check for updates

### Integrated multi-omics analysis of adverse cardiac remodeling and metabolic inflexibility upon ErbB2 and ERR $\alpha$ deficiency

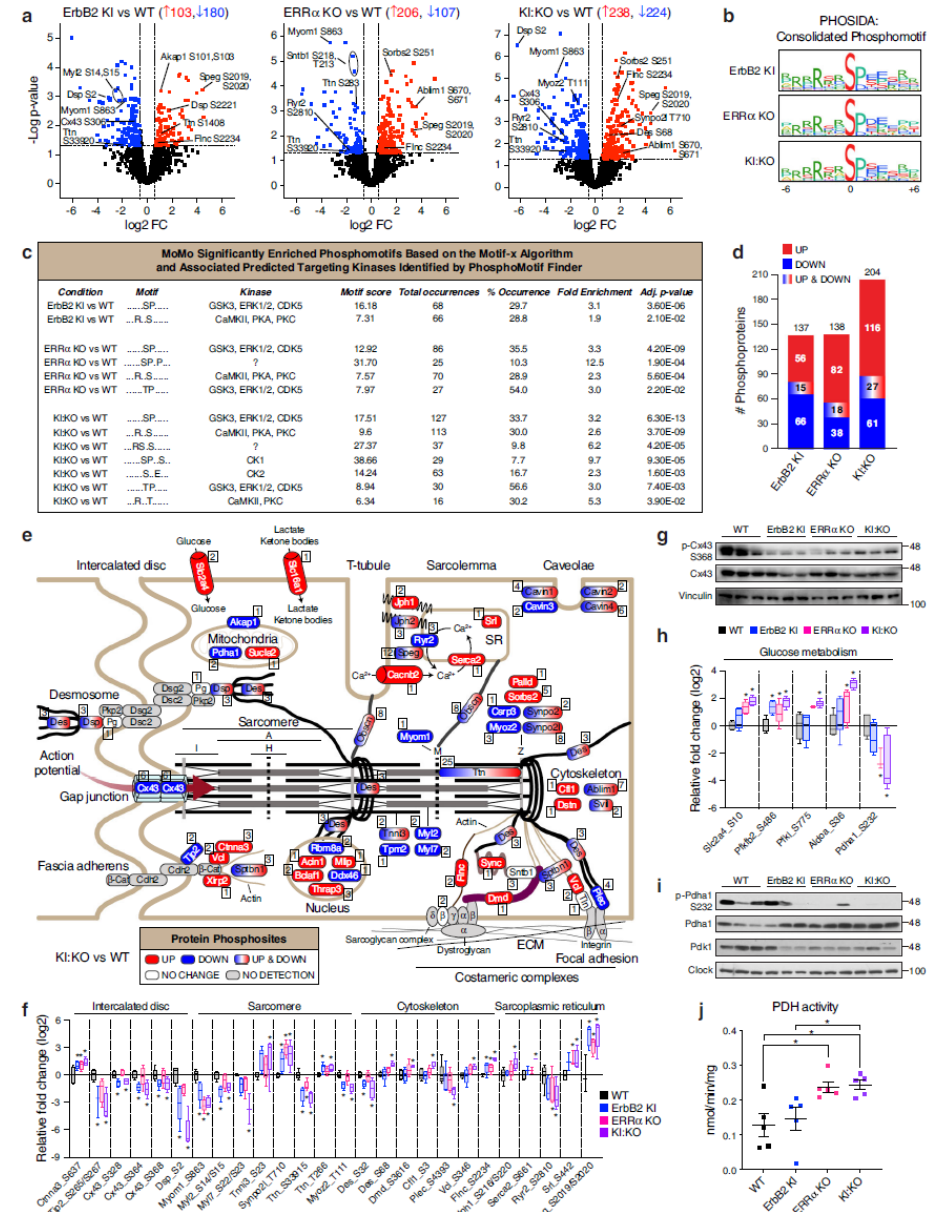
Catherine R. Dufour<sup>1</sup>, Hui Xia<sup>1,2</sup>, Wafa B'chir<sup>1</sup>, Marie-Claude Perry<sup>1,2</sup>, Uros Kuzmanov<sup>3</sup>, Anastasiya Gainullina<sup>4,5</sup>, Kurt Dejaard<sup>2</sup>, Charlotte Scholtes<sup>1</sup>, Carlo Ouellet<sup>1</sup>, Dongmei Zuo<sup>1</sup>, Virginie Sanguin-Gendreau<sup>1</sup>, Christina Guluzian<sup>1,2</sup>, Harvey W. Smith<sup>1</sup>, William J. Muller<sup>1</sup>, Etienne Audet-Walsh<sup>1</sup>, Alexey A. Sergushichev<sup>4</sup>, Andrew Emil<sup>3</sup> & Vincent Giguère<sup>1,2</sup>

Functional oncogenic links between ErbB2 and ERR $\alpha$  in HER2+ breast cancer patients support a therapeutic benefit of co-targeted therapies. However, ErbB2 and ERR $\alpha$  also play key roles in heart physiology, and this approach could pose a potential liability to cardiovascular health. Herein, using integrated phosphoproteomic, transcriptomic and metabolic profiling we uncovered molecular mechanisms associated with the adverse remodeling of cardiac functions in mice with combined attenuation of ErbB2 and ERR $\alpha$  activity. Genetic disruption of both effectors results in profound effects on cardiomyocyte architecture, inflammatory response and metabolism, the latter leading to a decrease in fatty acyl-carnitine species further increasing the reliance on glucose as a metabolic fuel, a hallmark of failing hearts. Furthermore, integrated omics signatures of ERR $\alpha$  loss-of-function and doxorubicin treatment exhibit common features of chemotherapeutic cardiotoxicity. These findings thus reveal potential cardiovascular risks in discrete combination therapies in the treatment of breast and other cancers.

### Education training case | ErbB2 KI, ERR $\alpha$ KO, KI:KO mouse hearts

Source article: Dufour et al., Communications Biology 2022

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# Design: compare each genotype against WT



## Key contrast logic

- ErbB2 KI: attenuated ErbB2 signaling.
- ERR $\alpha$  KO: loss of ERR $\alpha$ -dependent transcriptional/metabolic control.
- KI:KO: combined perturbation, strongest phenotype and largest omics signal.

## Teaching prompt

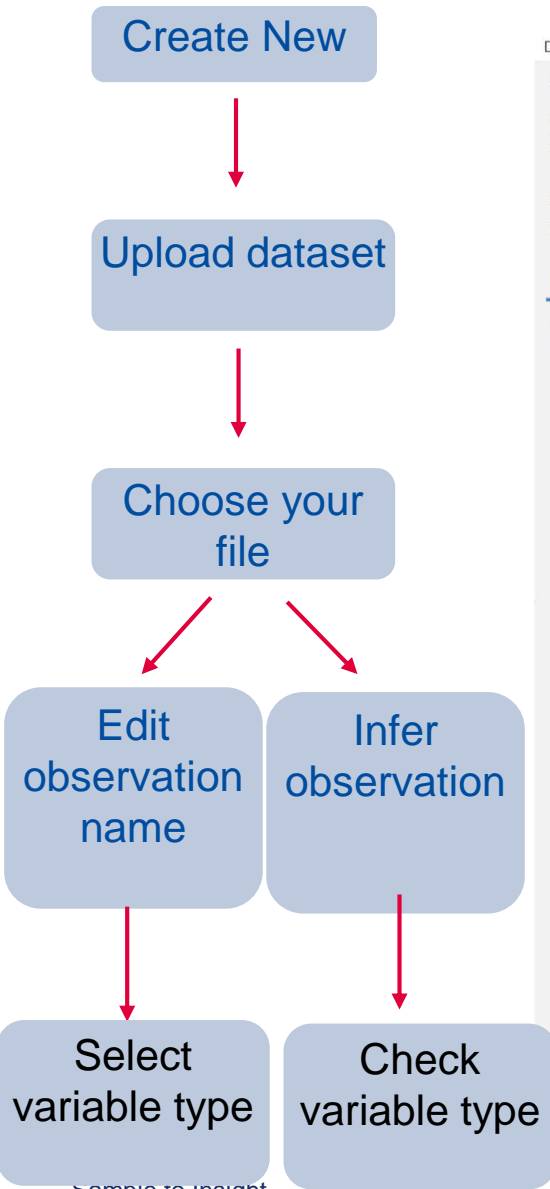
- Which comparison should be uploaded first for IPA demo?
- Which result is useful as a positive-control interpretation?
- How do phosphosites and metabolites provide different evidence types?

# Phosphoprotein upload dataset

## Phosphosite add to observation 1

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Multiplicity	PhosphoSite	Proteins	Protein names	Gene name	Sequence window	ERR $\alpha$ KO vs WT Log2	ERR $\alpha$ KO vs WT	Limma_P.Value_ERR $\alpha$ KO_WT	Limma_adj.P.Val_ERR $\alpha$ KO_WT		Mouse Phosphosite	Human Phosphosite conversion
2	2	T618	Q3UHI0	AP2-associated pt	Aak1	TTPPTIQGQKV	0.761902	1.695725	0.000346	0.021852		Aak1_T618	AAK1_T620
3	2	T671	Q3UHI0	AP2-associated pt	Aak1	AAAAEASLNKS	-3.072715	-8.413552	0.001129	0.038967		Aak1_T671	AAK1_T673
4	2	S670	Q8K4G5	Actin-binding LI	Ablim1	GPPSLAAVGTD	3.553094	11.737829	0.000654	0.028367		Ablim1_S670	ABLIM1_S586
5	2	S671	Q8K4G5	Actin-binding LI	Ablim1	PPSLAAVGTDP	3.553094	11.737829	0.000654	0.028367		Ablim1_S671	ABLIM1_S587
6	1	S838	Q9JIX8	Apoptotic chrom	Acin1	KISVVSATKGV	1.010577	2.014717	0.025629	0.226265		Acin1_S838	ACIN1_S838
7	1	S477	Q9JIX8	Apoptotic chrom	Acin1	AREPLASPHPA	0.712022	1.638099	0.049657	0.285683		Acin1_S477	ACIN1_G476
8	1	S586	Q9QYC0	Alpha-adducin	Add1	ELEEYRREVER	1.083115	2.118606	0.008764	0.120122		Add1_S586	ADD1_S586
9	2	T177	Q8K2K6	Arf-GAP domain	Agfg1	SLLGESAPALHL	1.250643	2.379474	0.019560	0.194976		Agfg1_T177	AGFG1_T177
10	2	S181	Q8K2K6	Arf-GAP domain	Agfg1	ESAPALHLNKG	1.216090	2.323162	0.028935	0.231484		Agfg1_S181	AGFG1_S181
11	1	S314	P29699	Alpha-2-HS-glyc	Ahsg	DLRHAFSPVAS	2.208075	4.620584	0.000680	0.028806		Ahsg_S314	AHSG_S330
12	3	S309	P29699	Alpha-2-HS-glyc	Ahsg	HRTYHDLRHAF	0.942122	1.921352	0.007852	0.112426		Ahsg_S309	AHSG_S325
13	3	S314	P29699	Alpha-2-HS-glyc	Ahsg	DLRHAFSPVAS	0.942122	1.921352	0.007852	0.112426		Ahsg_S314	AHSG_S330
14	3	S312	P29699	Alpha-2-HS-glyc	Ahsg	YHDLRHAFSPV	0.927794	1.902365	0.008368	0.116694		Ahsg_S312	AHSG_S328
15	1	S312	P29699	Alpha-2-HS-glyc	Ahsg	YHDLRHAFSPV	0.735763	1.665278	0.044874	0.281621		Ahsg_S312	AHSG_S328
16	1	S103	O08715	A-kinase anchor	Akap1	PLALPRTRQVR	-2.108487	-4.312388	0.000002	0.001685		Akap1_S103	AKAP1_S107
17	2	S613	Q9WTQ5	A-kinase anchor	Akap12	SFKKMVTPKKR	0.720580	1.647844	0.004303	0.083193		Akap12_S613	AKAP12_S627
18	2	S615	Q9WTQ5	A-kinase anchor	Akap12	KKMVTPKKRVI	0.720580	1.647844	0.004303	0.083193		Akap12_S615	AKAP12_S629
19	1	S36	P05064	Fructose-bisphos	Aldoa	HRIVAPGKGILA	1.488166	2.805321	0.026478	0.227439		Aldoa_S36	ALDOA_S36
20	2	S218	A2A5R2	Brefeldin A-inhib	Arfgef2	QEARELEKPMQ	-1.182960	-2.270421	0.018903	0.192990		Arfgef2_S218	ARFGEF2_S218
21	2	T224	A2A5R2	Brefeldin A-inhib	Arfgef2	EKPMQSKPQSP	-1.182960	-2.270421	0.018903	0.192990		Arfgef2_T224	ARFGEF2_A224
22	2	T740	Q3UIA2	Rho GTPase-acti	Arhgap17	PEPGTPPPQTPT	2.976270	7.869487	0.000352	0.021852		Arhgap17_T740	ARHGAP17_T763
23	2	T736	Q3UIA2	Rho GTPase-acti	Arhgap17	GEQGPEPGTPP	1.288596	2.442903	0.027241	0.229761		Arhgap17_T736	ARHGAP17_T759
24	1	S315	Q8K341	Alpha-tubulin N	Atat1	PHPTARLLLATI	2.499407	5.654528	0.003508	0.073472		Atat1_S315	ATAT1_S315
25	1	S529	P56480	ATP synthase sub	Atp5b	EEAVAKADKLA	0.849422	1.801780	0.043443	0.279235		Atp5b_S529	ATP5B_S529
26	2	S380	Q9JLV1	BAG family mol	Bag3	EKVEVKVSSAP	-1.688048	-3.222203	0.042188	0.273996		Bag3_S380	BAG3_P375
27	1	S285	Q9JLV1	BAG family mol	Bag3	SPFRSPVRGASS	-2.550957	-5.860227	0.007800	0.112426		Bag3_S285	BAG3_S279
28	2	S270	Q9JLV1	BAG family mol	Bag3	KIQGDDWEPRP	-4.833994	-28.521812	0.000525	0.027172		Bag3_S270	BAG3_S264
29	2	S274	Q9JLV1	BAG family mol	Bag3	DDWEPRPLRAA	-4.833994	-28.521812	0.000525	0.027172		Bag3_S274	BAG3_S268
30	3	S130	O88737	Protein bassoon	Bsn	SGQEAESPRRTL	-1.188629	-2.279360	0.025935	0.226265		Bsn_S130	BSN_S133
31	3	T132	O88737	Protein bassoon	Bsn	QEAEPRRTLQV	-1.188629	-2.279360	0.025935	0.226265		Bsn_T132	BSN_T135
32	2	S552	Q8CC27	Voltage-depender	Cacnb2	RSGTGRGLSRQ	0.969649	1.958364	0.033201	0.246561		Cacnb2_S552	CACNB2_S557
33	2	T549	Q8CC27	Voltage-depender	Cacnb2	QNHRSGTGRGL	0.969649	1.958364	0.033201	0.246561		Cacnb2_T549	CACNB2_T554
34	2	S42	Q9CR86	Calcium-regulate	Carhsp1	TRDRSPSPLRGN	4.125630	17.455747	0.002001	0.051809		Carhsp1_S42	CARHSP1_S41
35	3	S31	Q9CR86	Calcium-regulate	Carhsp1	QTSVGLLDTPRT	0.727368	1.655616	0.028304	0.230107		Carhsp1_S31	CARHSP1_S30
36	3	S33	Q9CR86	Calcium-regulate	Carhsp1	SVGLLDTPRTRI	0.727368	1.655616	0.028304	0.230107		Carhsp1_S33	CARHSP1_S32

# Upload dataset from core analysis



Dataset Upload - Erra\_phospho\_KOvsWT.xlsx

- Select File Format: **Flexible Format**
- Contains Column Header:  Yes  No
- Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
- Array platform used for experiments: **Not specified/applicable** Select relevant array platform as a reference set for data analysis.
- Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appropriate measurement value type.

Raw Data (314) Dataset Summary (301) Metadata

**Edit Observation Names** | Infer Observations

ID/Observation Name	ID	ERRα KO vs...	ID	Ignore	Ignore	Ignore	ERRα KO vs...	ERRα KO vs...	ERRα KO vs...	ERRα KO vs...	Ignore	Ignore	Ignore
Measurement/Annotation	0 types sele...	Phospho Site	2 types sele...				Phospho Lo...	Phospho Fol...	Phospho p-...	Expr False ...			
1	Multiplicity	PhosphoSite	Proteins	Protein names	Gene names	Sequence window	ERRα KO vs WT Lo...	ERRα KO vs WT FC	Limma_P.Value_E...	Limma_adj.P.Val_E...	---	Mouse Phosphosite	Human Phosphosit...
2	_2	T618	Q3UHJ0	AP2-associated pr...	Aak1	TTPPTTIQKQKVG...	0.7619020000000...	1.6957247374455...	3.4631902022795...	2.1852431930020...	---	Aak1_T618	AAK1_T620
3	_2	T671	Q3UHJ0	AP2-associated pr...	Aak1	AAAAEASLNKSKSA...	-3.072715000000...	-8.413551997945...	1.1288827442013...	3.8967359910949...	---	Aak1_T671	AAK1_T673
4	_2	S670	Q8K4G5	Actin-binding LIM ...	Ablim1	GPPSLAAVGTDPRR...	3.5530936499999...	11.737828669021...	6.5437810882352...	2.8366530112721...	---	Ablim1_S670	ABLIM1_S586
5	_2	S671	Q8K4G5	Actin-binding LIM ...	Ablim1	PPSLAAVGTDPRR...	3.5530936499999...	11.737828669021...	6.5437810882352...	2.8366530112721...	---	Ablim1_S671	ABLIM1_S587
6	_1	S838	Q9JIX8	Apoptotic chroma...	Acin1	KISVVSATKGVQAG...	1.0105774999999...	2.0147174149860...	2.5628947055743...	0.226265440121525	---	Acin1_S838	ACIN1_S838
7	_1	S477	Q9JIX8	Apoptotic chroma...	Acin1	AREPLASPHPAQLL...	0.7120224999999...	1.6380989430028...	4.9657350503297...	0.2856830288214...	---	Acin1_S477	ACIN1_G476
8	_1	S586	Q9QYCO	Alpha-adducin	Add1	ELEEYRREVERKQK...	1.083115	2.1186055407647...	8.7643011433705...	0.120122480376785	---	Add1_S586	ADD1_S586
9	_2	T177	Q8K2K6	Arf-GAP domain a...	Agfg1	SLLGESAPALHLNK...	1.2506425000000...	2.3794736856938...	1.9560366144173...	0.1949760561109...	---	Agfg1_T177	AGFG1_T177
10	_2	S181	Q8K2K6	Arf-GAP domain a...	Agfg1	ESAPALHLNKGTPS...	1.2160897500000...	2.3231619831689...	2.8935454625973...	0.2314836370077...	---	Agfg1_S181	AGFG1_S181
11	_1	S314	P29699	Alpha-2-HS-glyco...	Ahsg	DLRHAFSPVASVES...	2.2080753333333...	4.6205844053758...	6.7996000474271...	2.8805578382737...	---	Ahsg_S314	AHSG_S330
12	_3	S309	P29699	Alpha-2-HS-glyco...	Ahsg	HRTYHDLRHAFFSP...	0.9421220000000...	1.9213521981800...	7.8520696077168...	0.1124261203834...	---	Ahsg_S309	AHSG_S325
13	_3	S314	P29699	Alpha-2-HS-glyco...	Ahsg	DLRHAFSPVASVES...	0.9421220000000...	1.9213521981800...	7.8520696077168...	0.1124261203834...	---	Ahsg_S314	AHSG_S330
14	_3	S312	P29699	Alpha-2-HS-glyco...	Ahsg	YHDLRHAFFSPVAS...	0.927794000000004	1.9023648977832...	8.3682456589523...	0.1166944567042...	---	Ahsg_S312	AHSG_S328
15	_1	S312	P29699	Alpha-2-HS-glyco...	Ahsg	YHDLRHAFFSPVAS...	0.735762679999999	1.6652775849150...	4.4874096824504...	0.2816206838499...	---	Ahsg_S312	AHSG_S328
16	_1	S103	O08715	A-kinase anchor p...	Akap1	PLALPRTRQVRRRR...	-2.108486899999...	-4.312387736844...	1.7393357770444...	1.6854157236694...	---	Akap1_S103	AKAP1_S107
17	_2	S613	Q9WTQ5	A-kinase anchor p...	Akap12	SFKKMVTPKKRVR...	0.7205795000000...	1.6478438055243...	4.3033093397206...	8.3192912007960...	---	Akap12_S613	AKAP12_S627
18	_2	S615	Q9WTQ5	A-kinase anchor p...	Akap12	KKMVTPKKRVRRR...	0.7205795000000...	1.6478438055243...	4.3033093397206...	8.3192912007960...	---	Akap12_S615	AKAP12_S629
19	_1	S36	P05064	Fructose-bisphosp...	Aldoa	HRIVAPGKGILAAD...	1.4881658599999...	2.8053209975728...	2.6477574617387...	0.227438705469171	---	Aldoa_S36	ALDOA_S36
20	_2	S218	A2A5R2	Brefeldin A-inhib...	Arfgef2	QEARELEKPMQSK...	-1.18296	-2.270421253975...	1.8903165501755...	0.192990369503211	---	Arfgef2_S218	ARFGEF2_S218
21	_2	T224	A2A5R2	Brefeldin A-inhib...	Arfgef2	EKPMQSKPQSPV...	-1.18296	-2.270421253975...	1.8903165501755...	0.192990369503211	---	Arfgef2_T224	ARFGEF2_A224
22	_2	T740	Q3UIA2	Rho GTPase-activ...	Arhgap17	PEPGTPPTPTPTP...	2.9762696666666...	7.8694874090191...	3.5170223063337...	2.1852431930020...	---	Arhgap17_T740	ARHGAP17_T763
23	_2	T736	Q3UIA2	Rho GTPase-activ...	Arhgap17	GEQGPPEGPTTPP...	1.2885963333333...	2.4429025825639...	2.7241027948875...	0.2297614303018...	---	Arhgap17_T736	ARHGAP17_T759
24	_1	S315	Q8K341	Alpha-tubulin N-a...	Atat1	PHPTARLLLATDPG...	2.4994066666666...	5.6545282485020...	3.5080286065093...	7.3471520477904...	---	Atat1_S315	ATAT1_S315
25	_1	S529	P56480	ATP synthase subu...	Atp5b	EAVAKADKLAEEH...	0.8494224999999...	1.8017795420176...	4.3443224942897...	0.2792350734260...	---	Atp5b_S529	ATPSB_S529
26	_2	S380	Q9JLV1	BAG family molec...	Bag3	EKVEVKVSSAIPICP...	-1.688047499999...	-3.222202351850...	4.2187584364850...	0.2739959541813...	---	Bag3_S380	BAG3_P375
27	_1	S285	Q9JLV1	BAG family molec...	Bag3	SPFRSPVRGASSRE...	-2.5509566666666...	-5.860227475795...	7.8000927654122...	0.1124261203834...	---	Bag3_S285	BAG3_S279
28	_2	S270	Q9JLV1	BAG family molec...	Bag3	KIQGDDWEPRPLR...	-4.833993750000...	-28.52181230709...	5.2477716209599...	2.7171795281859...	---	Bag3_S270	BAG3_S264

# Choose which analysis do you want

Analyze filter  
dataset



Core analysis



Choose which  
analysis

Set cut off

Create Core Analysis

Selected Dataset: Erra\_phospho\_KOvsWT

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

Phosphorylation Analysis

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

Phospho Log Ratio

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

Back

Next

# Set Cutoff

Analyze filter dataset



Core analysis



Set cut off

Set Cutoffs    Biological Filters

---

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

Set Cutoffs    Biological Filters

---

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

**Set Cutoffs**

Dataset Column	Measurement Value Type	Range	Cutoff
ERR\ KO vs WT Log2 FC	Phospho Log Ratio	-5.6082 to 5.0888	<input type="text"/> Down <input type="text"/> Up
ERR\ KO vs WT FC	Phospho Fold Change	-48.7788 to 34.0318	<input type="text"/> Down <input type="text"/> Up
Limma_P.Value_ERR\ KO_WT	Phospho p-value	0.0 to 0.0497	<input type="text"/>
Limma_adj.P.Val_ERR\ KO_WT	Expr False Discovery Rate (q-value)	0.0017 to 0.2857	<input type="text"/>

       136 analysis-ready molecules (43 Down and 93 Up)

[Preview Dataset Erra\\_phospho\\_KOvsWT](#)

# Biological Filter in phosphoprotein -omics

Create Phosphorylation Analysis - [analysis : Erra\_phospho\_KOvsWT]

Set Cutoffs **Biological Filters**

> **General Settings**

Population of genes to consider for p-value calculations:

Reference Set **Ingenuity Knowledge Base (Genes Only)**

Relationships to consider:

Affects networks and upstream regulator analysis

Direct and Indirect Relationships

Direct Relationships

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

Create Phosphorylation Analysis - [analysis : Erra\_phospho\_KOvsWT]

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

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

PPARGC1A

Add...

Remove

Save As Default

Advanced

Recalculate

136 analysis-ready molecules (43 Down and 93 Up)

Preview Dataset Erra\_phospho\_KOvsWT

## Pathway or gene activity predicted by IPA



## Actual measurement of gene expression in your dataset



# What do z-scores mean in IPA?

Actual dataset measurement

VS.

What IPA expects if pathway is activated

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

*Pathway inhibited*

**- Z score**

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

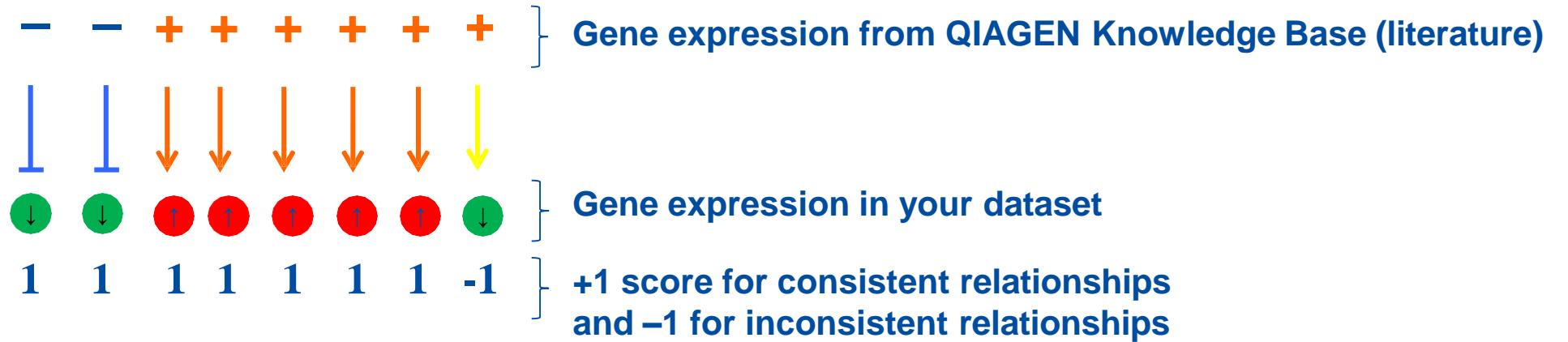
*No clear signal for prediction*  
**Z score = 0**

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

*Pathway activated*

**+ Z score**

*How well do the actual measurements match the expected measurements?*



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

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

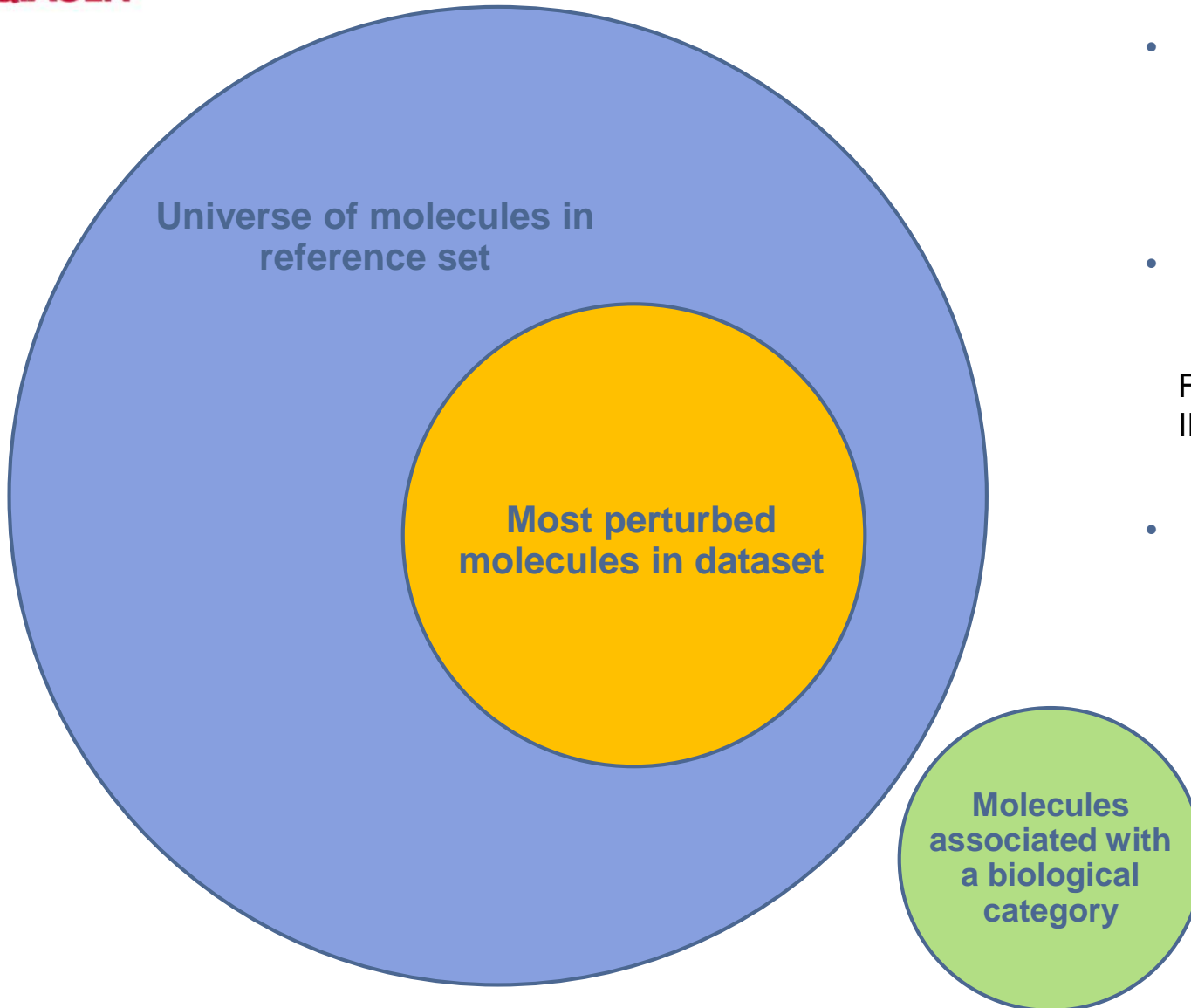
Symbol	Measurement Expr Log Ratio	+ △ ×	Expected
NRSA2	↓ -1.002	↓	Down
ABCB11	↓ -1.056	↓	Down
CYP2B6	↓ -3.063	↓	Down
PPARGC1A	↓ -2.495	↓	Down
ACOX1	↓ -1.727	↓	Down
SLCO1B3	↑ 3.223	↓	Down
TLR4	↑ 1.213	↑	Up
LY96	↑ 1.189	↑	Up
IL1R1	↑ 1.634	↑	Up
IL1RAP	↑ 1.046	↑	Up
IL1B	↑ 3.890	↑	Up
LIPC	↓ -1.375	↑	Up

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

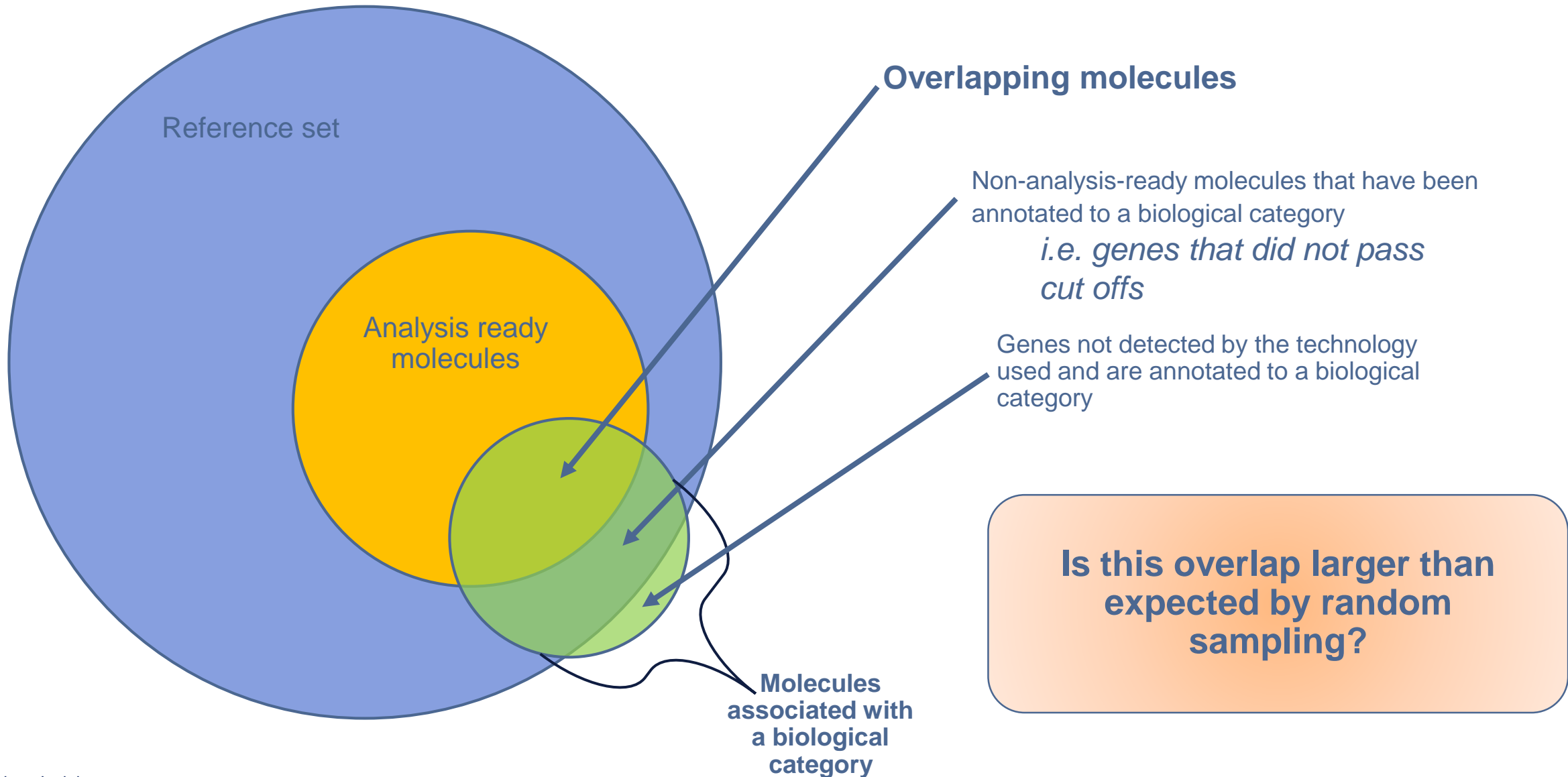
**Z-score = 2.4**  
 10/12 measurements match expected  
 Mostly matching  
 Signal predominantly points to predicted activation

**Z-score = -2.236**  
 4/12 measurements match expected  
 Mostly anti-matching  
 Signal predominantly points to predicted inhibition

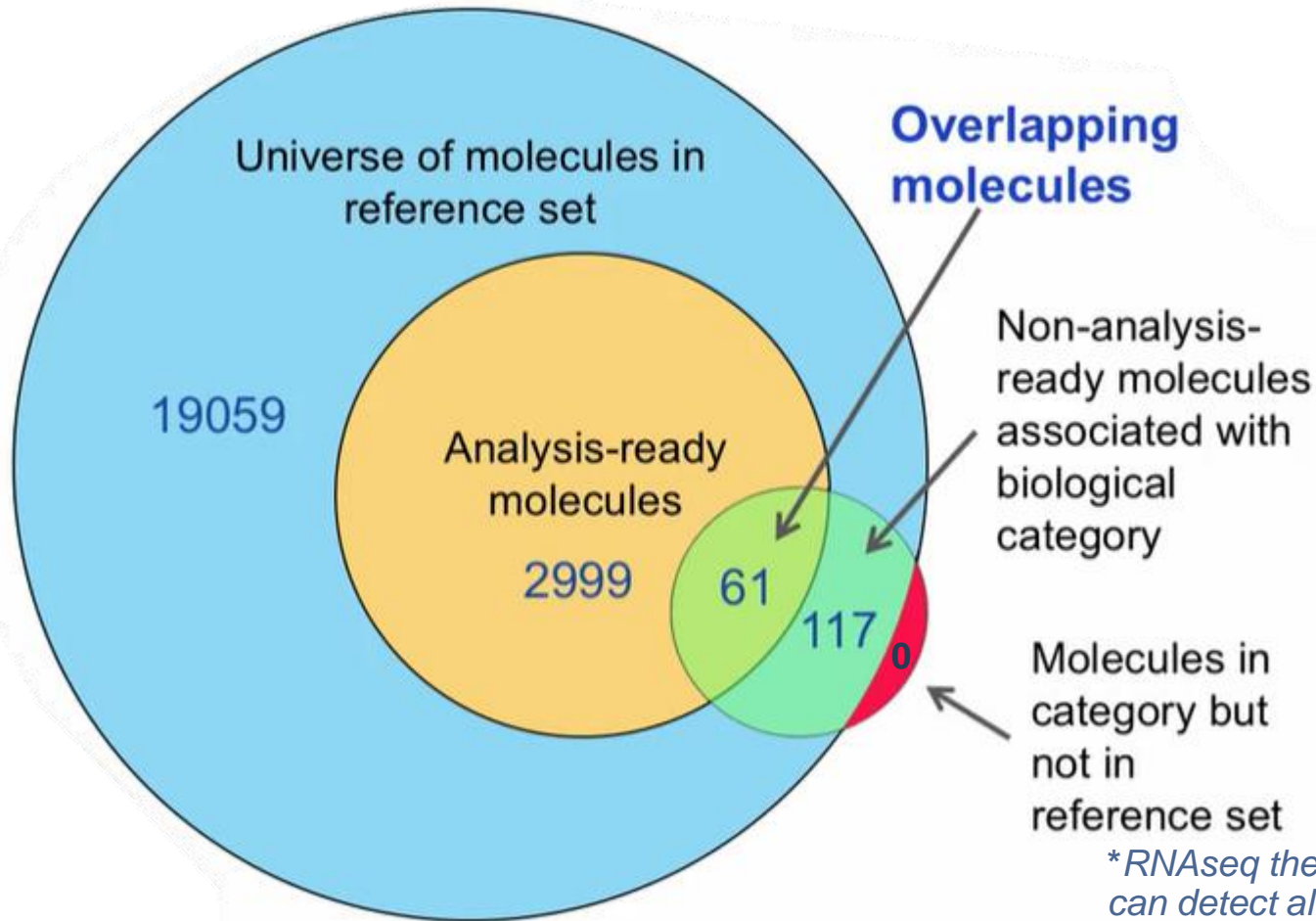
# IPA Analysis Tabs



- Reference set is typically all genes or proteins that can be reliably detected by the ‘omics technology used
- Most perturbed is a subset of measured genes/proteins that were significantly different between experimental groups  
Fold change cut offs and p-value cut offs used  
IPA calls these “Analysis-ready molecules”
- Molecules associated with a biological category are a set of genes/proteins that the IPA knowledgebase has annotated to be important for a biological pathway, function, or disease.



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



$H_0$  = Overlap of molecules for a particular biological category is due to chance

$\alpha$  (significance level) = 0.05

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

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

**P-value =  $2.08 \times 10^{-12}$**

**We can reject the null hypothesis**

Phosphorylation Analysis - KIKO phospho\_WT - 2026-05-19 07:45 下午

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

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

Export:

> Experiment Metadata

> Analysis Settings

∨ Top Canonical Pathways

Name	p-value	Overlap
<a href="#">Protein Kinase A Signaling</a>	1.98E-12	5.2 % 21/400
<a href="#">Dilated Cardiomyopathy Signaling Pathway</a>	6.03E-12	9.3 % 14/151
<a href="#">Apoptotic execution phase</a>	1.33E-10	17.3 % 9/52
<a href="#">Striated Muscle Contraction</a>	6.76E-09	19.4 % 7/36
<a href="#">ILK Signaling</a>	2.46E-08	6.1 % 12/197

∨ Top Upstream Regulators

∨ Upstream Regulators

Name	p-value	Predicted Activation
<a href="#">GH1</a>	6.96E-10	
<a href="#">CSNK2A1</a>	2.89E-06	
<a href="#">NPY</a>	1.29E-05	
<a href="#">BSG</a>	5.65E-05	
<a href="#">CACNA1C</a>	1.06E-04	

∨ Causal Network

Name	p-value	Predicted Activation
<a href="#">GH1</a>	6.96E-10	
<a href="#">CSNK2A1</a>	2.68E-06	
<a href="#">NPY</a>	9.56E-06	
<a href="#">BSG</a>	4.26E-05	
<a href="#">isoproterenol</a>	6.48E-05	

∨ Top Diseases and Bio Functions

∨ Diseases and Disorders

## Cluster 6 vs Cluster2

QIAGEN IPA Interpret | Analysis

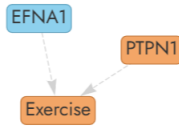
Home Help Gene Chen

KIKO phospho\_WT - 2026-05-19 07:45 下午 / Graphical Summary

**KIKO phospho\_WT - 2026-05-19 07:45 下午**

Created on May 19, 2026, from dataset "KIKO phospho\_WT"

KIKO phospho\_WT - 2026-05-19 07:45 下午 Figure Legend  OFF



### Exercise-Modulated Ephrin and PTP1B Signaling in Metabolic Regulation AI-Suggested

#### Exercise-Driven Remodeling of Metabolic Signaling Networks

The network's core output is "increase of Exercise," influenced by changes in EFNA1 and PTPN1. This implies that these genes either regulate the propensity for physical activity or are embedded in pathways whose activity correlates with exercise behavior or capacity. The directional edges ("decrease of EFNA1 → increase of Exercise" and "increase of PTPN1 → increase of Exercise") suggest that specific molecular states (low EFNA1, high PTPN1) favor exercise-associated phenotypes, pointing to a regulatory axis where signaling and phosphatase activity tune metabolic and neuromuscular readiness for physical activity.

#### Ephrin-A1 (EFNA1) in Vascular and Tissue Remodeling Linked to Exercise

EFNA1 encodes ephrin-A1, a ligand for Eph receptors involved in vascular patterning, endothelial cell behavior, and tissue organization. The edge "decrease of EFNA1 → increase of Exercise" suggests that reduced ephrin-A1 signaling may facilitate conditions conducive to exercise, such as altered vascular tone, angiogenic responsiveness, or tissue remodeling that improves oxygen delivery and muscle perfusion. In some contexts, high EFNA1 is associated with endothelial activation and inflammatory or maladaptive vascular states; its reduction here may reflect a shift toward a vascular/organ microenvironment that better supports sustained physical activity and metabolic flexibility.

#### PTPN1 (PTP1B) as a Modulator of Insulin and Leptin Signaling in Exercise Adaptation

PTPN1 encodes protein-tyrosine phosphatase 1B (PTP1B), a key negative regulator of insulin and leptin receptor signaling and a central node in metabolic homeostasis. The relationship "increase of PTPN1 → increase of Exercise" indicates that elevated PTP1B is associated with higher exercise levels, which at first seems counter to its classical role as a promoter of insulin resistance. This directionality suggests a context where increased exercise either induces PTP1B expression as a feedback brake on growth factor/insulin signaling or where individuals/conditions with robust exercise capacity engage compensatory upregulation of PTP1B to fine-tune energy signaling. Thus, PTPN1 here may represent a feedback regulator in the adaptive metabolic signaling circuitry engaged by repeated or intense exercise.

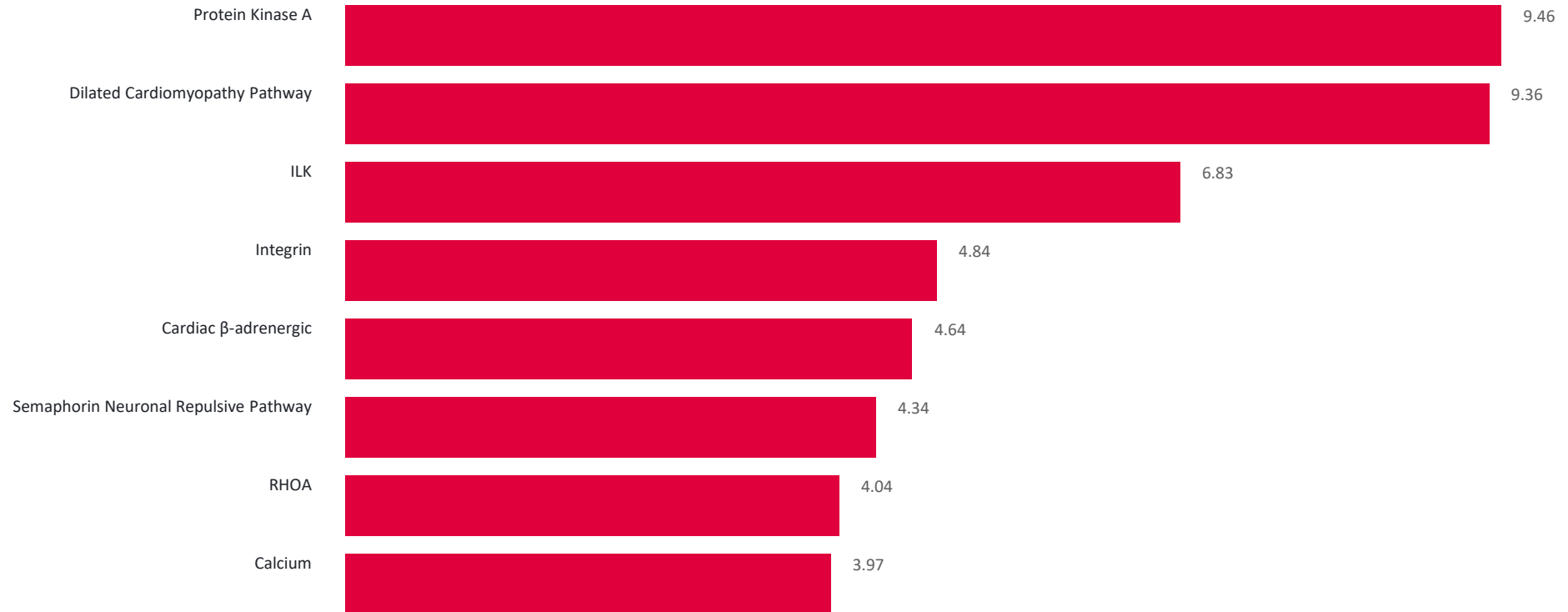
#### Integration of Vascular (EFNA1) and Metabolic (PTPN1) Signals in Exercise Capacity

The convergence of EFNA1 (vascular and tissue patterning) and PTPN1 (metabolic and hormonal signaling) on the "Exercise" node points to an integrated theme: exercise capacity is shaped by both vascular architecture and nutrient/hormone signaling. Reduced EFNA1 activity may favor more flexible or less inflamed vascular and

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



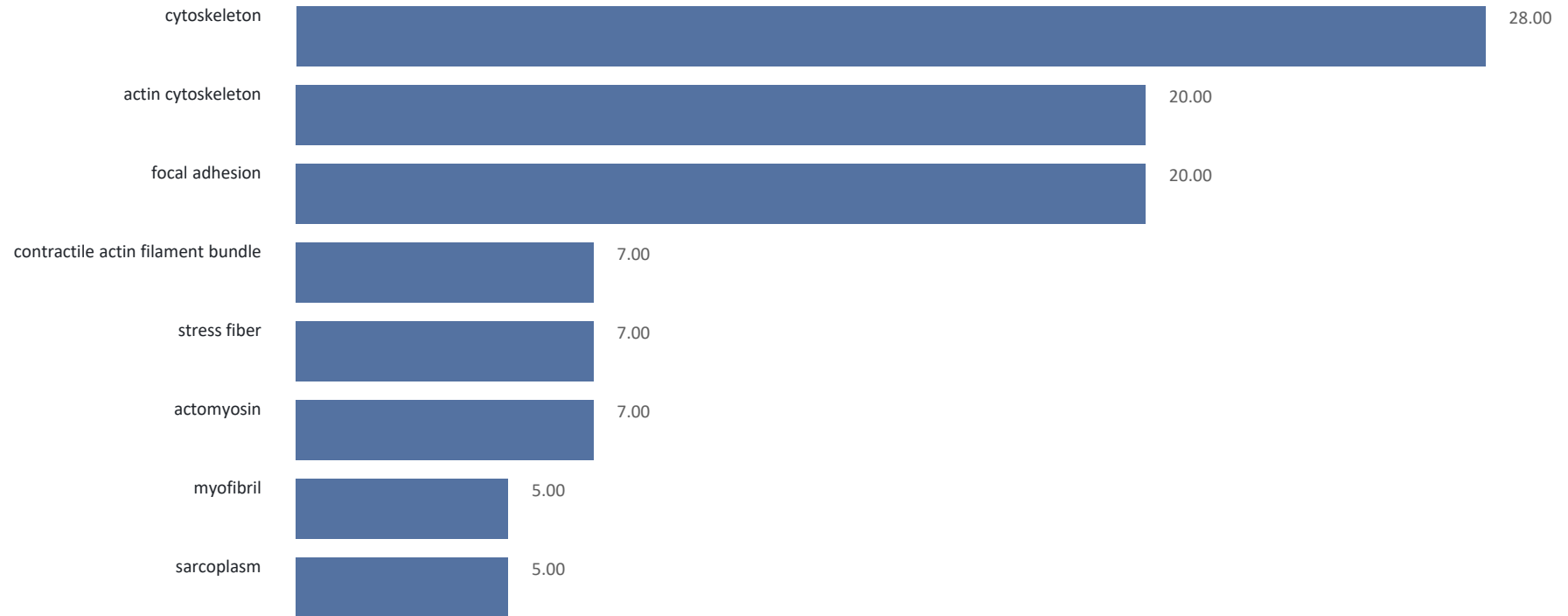
### KI:KO phosphoproteomics IPA canonical pathways (-log p-value)



**Protein Kinase A (PKA) signaling** and **Dilated Cardiomyopathy signaling** are closely linked because cardiac remodeling involves both functional and structural adaptations of cardiomyocytes.

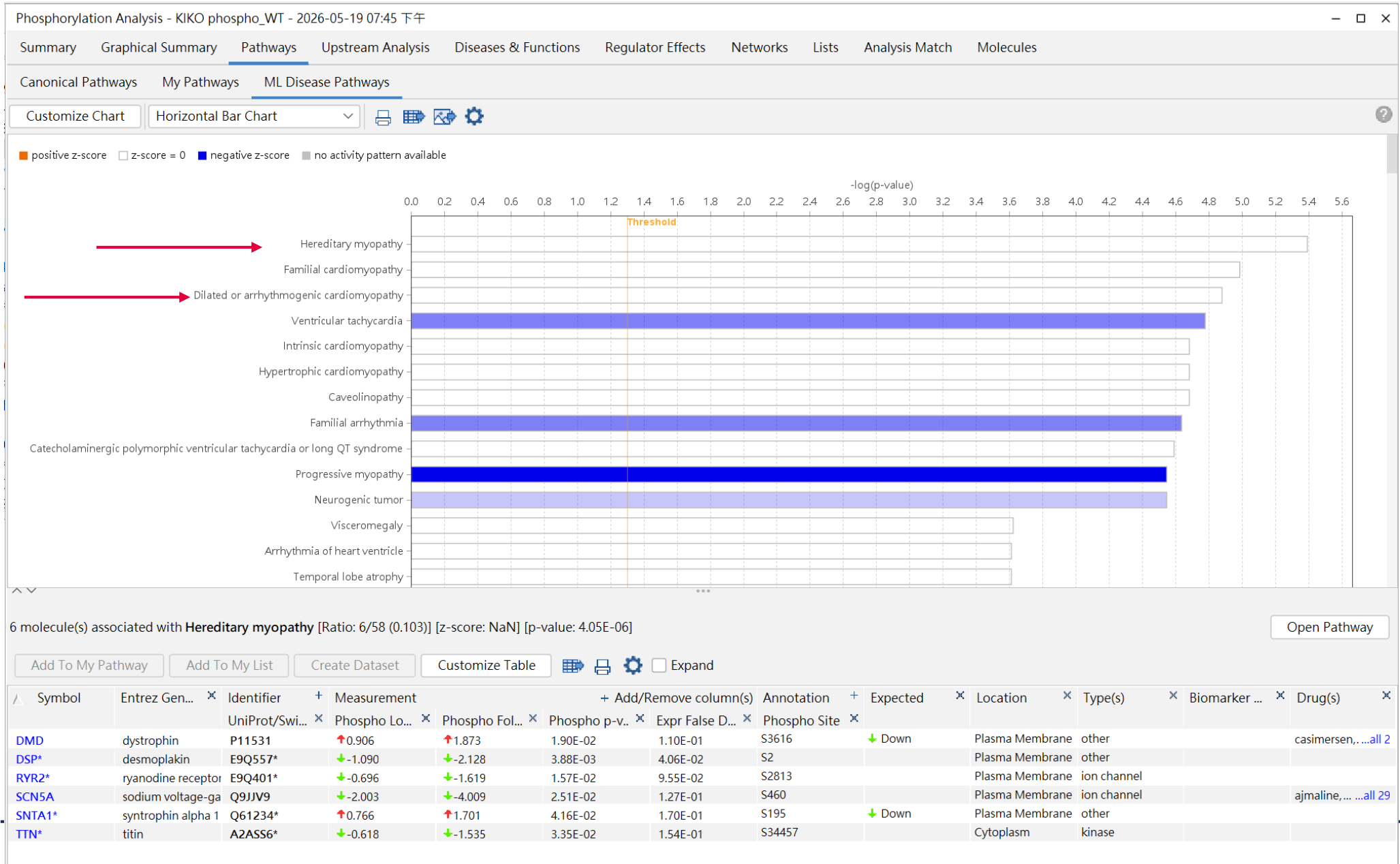
# Cellular component enrichment localizes the signal

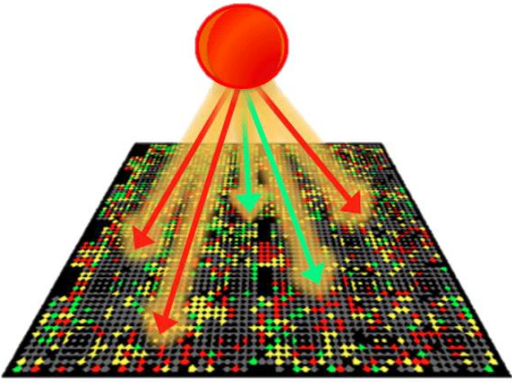
## KI:KO enriched GO cellular components (# genes)



Teaching move: after IPA reports pathways, use localization terms to make the story concrete: cytoskeleton, actin cytoskeleton, sarcomere, intercalated disc, and contractile apparatus.







- Use experimentally observed relationships (vs. Predicted event) between Upstream Regulators and genes to predict potential regulator and activation
- Predict activation or inhibition of regulator to explain the changes in gene expression in your dataset
- Calculates two complementary statistical measures:
  - Activation z-score
  - Overlap p-value

Upstream Reg...	Phospho Fold ...	Phospho Log R...	Phospho p-val...	Molecule Type	Predicted Acti...	Activation z-sc...	p-value of...	Target Molecu...	Mechanistic N...
GH1				growth factor		0.651	6.96E-10	↑ACIN1, ↑ACLY, ...all 19	
CSNK2A1				kinase		1.243	2.89E-06	↑ACIN1, ↑BCL2, ...all 20	
NPY				other		1.265	1.29E-05	↑ACIN1, ↑FCHO2, ...all 10	
BSG				transmembrane receptor		-0.213	5.65E-05	↑ACIN1, ↑CFL1, ...all 9	
CACNA1C				ion channel			1.06E-04	↑PLN, ↑RYR2, ...all 3	
isoproterenol				chemical drug			1.23E-04	↑ACLY, ↑GJA1, ...all 9	
EFNA1				other	Inhibited	-2.590	2.19E-04	↑ACLY, ↑EHBP, ...all 11	
PDE4 (family)				group			2.59E-04	↑PLN, ↑RYR2, ...all 3	
PKD2				ion channel			2.59E-04	↑H1-5, ↑PLN, ...all 3	
wortmannin				chemical drug		0.336	3.08E-04	↑ACLY, ↑EIF4G1, ...all 11	
RPS6KA2				kinase		-1.387	4.09E-04	↓BSN, ↓GSK3A, ...all 5	
EPM2A				phosphatase			5.06E-04	↓GSK3A, ↓MAPT, ...all 3	
CAMK (complex)				complex		0.000	8.43E-04	↑ATP2A2, ↑PLN, ...all 4	
SLC18A3				transporter			9.08E-04	↑PLN, ↓TNNI3, ...all 2	
AKAP10				other			9.08E-04	↑PLN, ↓TNNI3, ...all 2	
ACADVL				enzyme			9.08E-04	↑PLN, ↑RYR2, ...all 2	
opioid				chemical drug			9.08E-04	↓MAPT, ↑RPS6, ...all 2	
GSK1904529A				chemical drug			9.08E-04	↓PDHA1, ↑PFKFB2, ...all 2	
ABL2				kinase		0.555	9.26E-04	↓MAPT, ↑MYL2, ...all 5	
INSULIN (family)				group		0.452	1.45E-03	↑ACLY, ↑EIF4B, ...all 16	
CAMP-DEPENDENT PRO				complex		0.606	1.48E-03	↑ACLY, ↑DMD, ...all 7	
IL13				cytokine			2.06E-03	↑BCIAP1, ↑CCNY, ...all 8	
CAMK2D				kinase		-1.686	2.18E-03	↓EIF4B, ↑PLN, ...all 4	
WNT1				cytokine			2.66E-03	↓GSK3A, ↓MAPT, ...all 4	
MYBPC3				other			2.67E-03	↑PLN, ↓TNNI3, ...all 2	
LIMK2				kinase			2.67E-03	↑CFL1, ↑DSTN, ...all 2	
TCL1A				transcription regulator			2.67E-03	↓GSK3A, ↓RPS6, ...all 2	
ATP2B4				transporter			2.67E-03	↑PLN, ↓TNNI3, ...all 2	
cardiolipin				chemical - endogenou...			2.67E-03	↑PAK2, ↓RPS6, ...all 2	
PICTP				other			2.21E-03	↑ACLY, ↓GSK3A, ...all 4	

Immediately upstream of dataset genes regulators

One additional level upstream of regulatory networks

Measurement from your dataset for this regulator

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

Highlight row and click to display at network map

Export

Filter icons

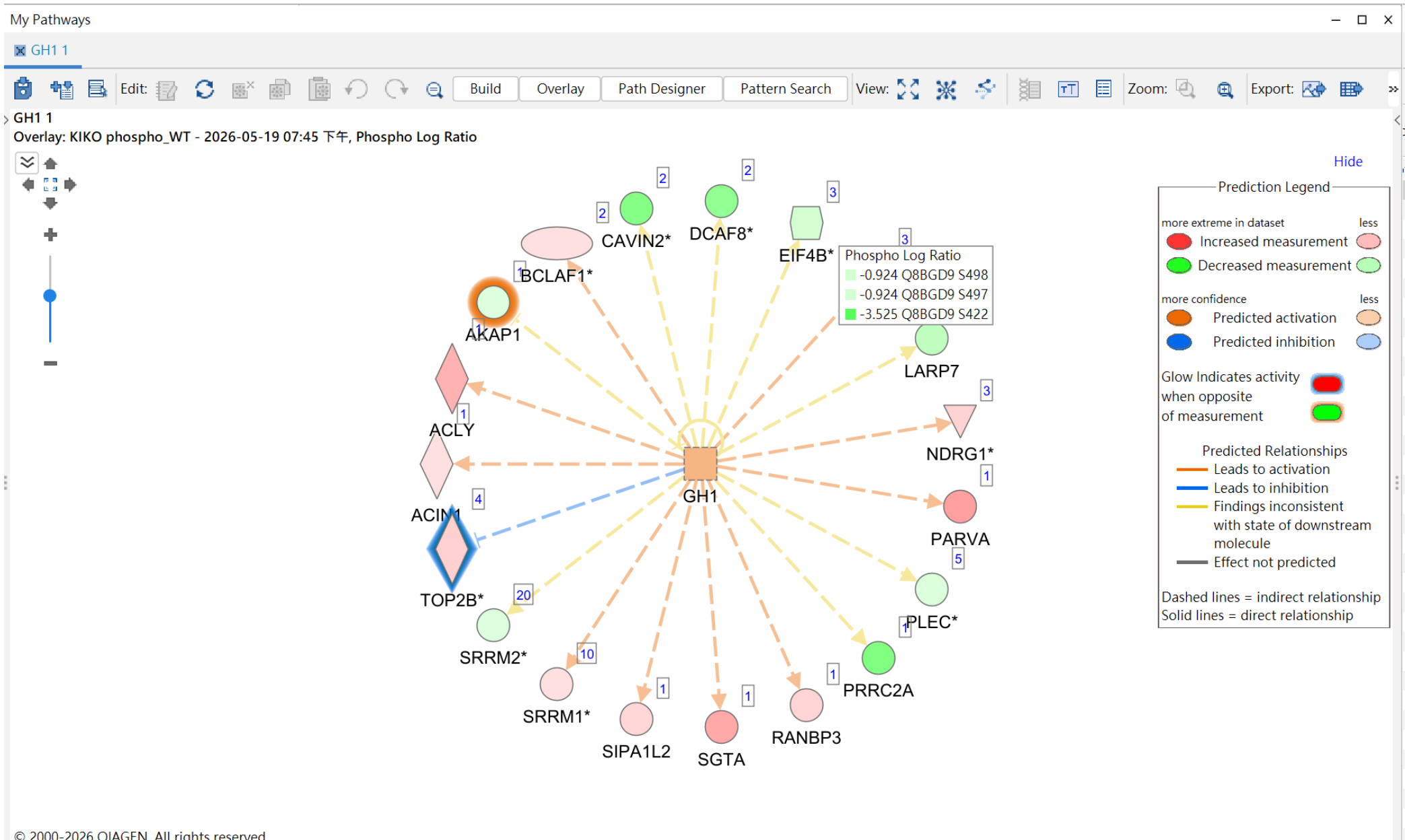
Activity prediction

Genes that this regulator targets present in your filtered dataset

P-value of significance

Regulators that may be contributing to the signal observed in your data. Some have been measured in your dataset and some have been predicted by IPA

**\*\* ALL COLUMNS ARE FILTERABLE \*\***



Phosphorylation Analysis - Erra\_phospho\_KOVsWT - 2026-05-19 07:42 下午

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

Upstream Regulators **Causal Networks**

Add To My Pathway Add To My List Display as Network Activity Plot Customize Table

Depth 3 - 1 (1/3)

**Interesting gene/chemical**

Mast...	Ph...	Ph...	Ph...	M...	Pa...	T ×	Pr...	N...	Ac...	p...	N...	Ta...	Ca...	Ta...	PP...	PP...	Inc...	D...
TPTE2				phosphat...	AD.....all 21	3	Inhibited		-2.646	3.15E-03	4.26E-02	↑A.....all 28	28 (21)	18	2   1	AB(1)		
MTMR2				phosphat...	AKT .....all 7	3			-1.265	1.78E-02	4.56E-02	↑A.....all 10	10 (7)	4	2   13	AB(12),		
CASQ2				other	CAL.....all 3	3			-1.414	9.11E-03	7.00E-03	↓M.....all 2	2 (3)	2	2   20	AB(8),		
FIG4				enzyme	AD.....all 21	3	Inhibited		-2.646	3.40E-03	4.55E-02	↑A.....all 28	28 (21)	18	2   7	AB(5),		
N-omega-p cypermethri				chemical r...	CAL.....all 3	3			-1.414	9.11E-03	7.00E-03	↓M.....all 2	2 (3)	2	2   4	DB(1),		
PTPRQ				chemical t...	AC.....all 20	3			-1.414	1.79E-03	1.84E-02	↑A.....all 32	32 (20)	15	2   17	AB(2),		
9,13-di-cis-r lomonitinib				chemical ...	9,13.....all 6	3			-0.905	1.37E-02	4.12E-02	↑A.....all 11	11 (6)	3	2   2	DB(1),		
N(6)-(3-iodc HH30134				chemical ...	FLT3.....all 3	2	biased		-0.577	2.63E-02	2.47E-02	↓M.....all 3	3 (3)	2	3   105	AB(56),		
phospholipi docosahexa				chemical ...	AXL.....all 3	2			0.577	1.99E-02	1.96E-02	↓M.....all 3	3 (3)	2	3   160	AB(74),		
PRKAB1				chemical ...	AK.....all 10	2			1.569	5.83E-03	4.84E-02	↑A.....all 26	26 (10)	10	2   80	AB(41),	S-a.....all 1	cycl.....all 2
EXOCYST (c SESN1				chemical ...	AK.....all 17	2			-0.730	5.16E-03	4.78E-02	↑A.....all 30	30 (17)	16	2   179	AB(28),		A-7.....all 1
IRS2				kinase	AM.....all 5	2			-0.707	6.49E-03	1.27E-02	↓CL.....all 8	8 (5)	5	2   102	AB(60),		
valproic acic PHB2				complex	EXO.....all 3	2			1.414	3.11E-02	1.59E-02	↓M.....all 2	2 (3)	2	2   2	AB(2)		
A-769662				other	AM.....all 3	2			-0.816	2.26E-02	3.53E-02	↓CL.....all 6	6 (3)	2	2   22	AB(6),		
Uox				enzyme	AK.....all 12	2			-1.177	3.34E-03	4.55E-02	↑A.....all 26	26 (12)	11	1   1	AB(1)	cycl.....all 8	KL .....all 1
TT-00973				chemical ...	AK.....all 11	2			-0.816	6.43E-03	4.66E-02	↑A.....all 24	24 (11)	10	2   136	AB(35),		
PAK1/2/3 (f GRB14				transcripti...	AKT .....all 4	2			0.632	1.89E-02	4.29E-02	↑A.....all 10	10 (4)	3	2   118	AB(92),		
PP2C (famil KC1036				chemical r...	A-7.....all 8	2			0.707	1.43E-02	3.37E-02	↓CL.....all 8	8 (8)	8	1   1	IU(1)		
RPS6KA6				enzyme	LATS1 .....all 4	2			0.577	3.38E-02	3.29E-02	↓AK.....all 3	3 (4)	3	1   1	DU(1)		
methylene t reproterol				chemical ...	AXL.....all 3	2			0.577	1.13E-02	9.80E-03	↓M.....all 3	3 (3)	2	3   154	AB(71),		
EI24				group	AKT .....all 4	2			0.302	1.18E-02	3.65E-02	↑A.....all 11	11 (4)	3	2   3	DB(1),		
DAPK (famil LDN192960				other	AKT .....all 3	2			-1.941	6.34E-03	2.28E-02	↑A.....all 13	13 (3)	2	2   23	AB(8),		
CIDEA				group	AM.....all 5	2	Inhibited		-2.530	1.40E-02	4.32E-02	↓C.....all 10	10 (5)	5	2   10	AB(1),		
				chemical ...	AXL.....all 3	2		biased	0.577	3.38E-02	3.41E-02	↓M.....all 3	3 (3)	2	3   297	AB(144),		
				kinase	CHE.....all 2	2	Inhibited		-2.000	1.95E-02	3.42E-02	↓BSN .....all 4	4 (2)	2	2   15	AB(12),		
				chemical ...	AM.....all 3	2			0.378	4.00E-03	6.80E-03	↓CL.....all 7	7 (3)	2	1   1	AU(1)		
				chemical ...	ADR.....all 3	2			1.414	3.58E-02	3.13E-02	↑PLN .....all 2	2 (3)	2	2   1	IB(1)		
				other	AM.....all 3	2			-0.816	2.07E-02	3.20E-02	↓CL.....all 6	6 (3)	2	2   28	AB(16),		
				group	CDC.....all 4	2			-1.633	1.42E-02	2.01E-02	↓M.....all 6	6 (4)	3	2   20	AB(7),		
				chemical ...	DYR.....all 3	2			-0.577	1.44E-02	1.19E-02	↑D.....all 3	3 (3)	2	2   1	IB(1)		
				transporter	AM.....all 3	2			0.000	1.10E-02	2.23E-02	↓CL.....all 6	6 (3)	2	1   1	ID(1)	CAY.....all 3	

Sample to

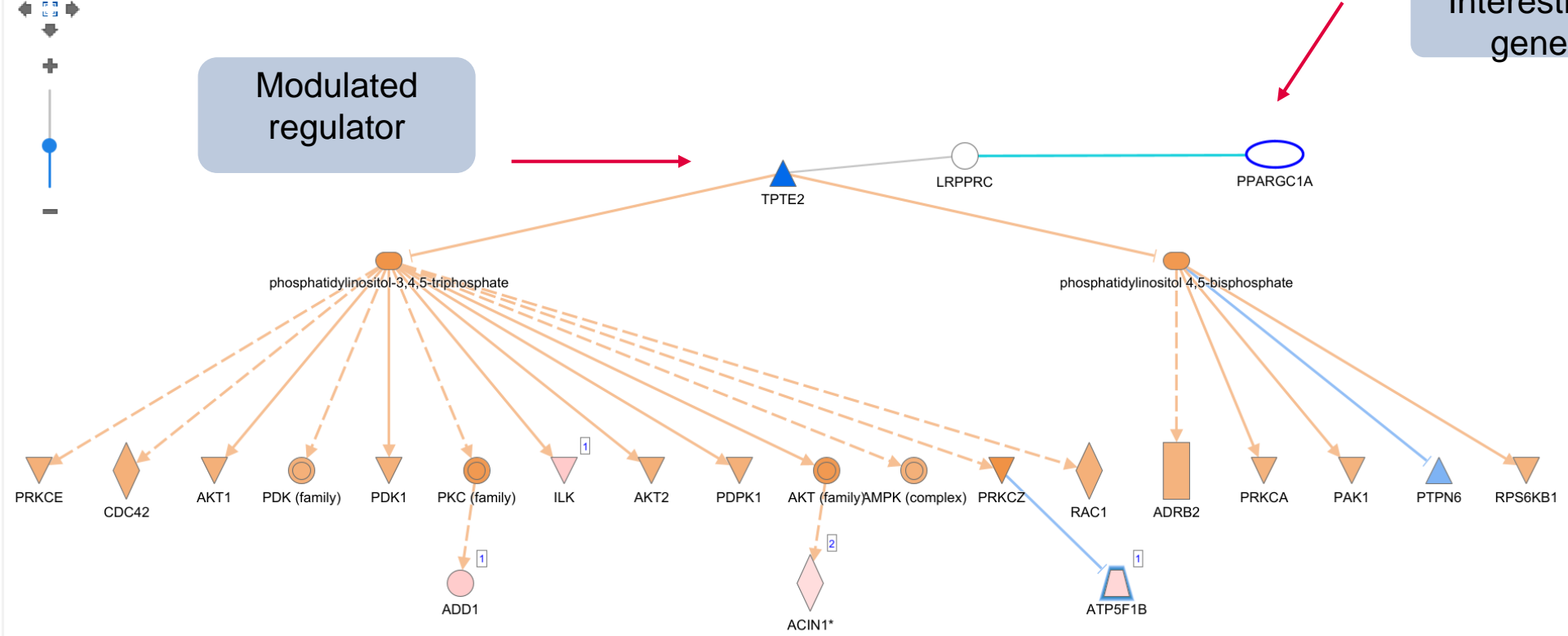
TPTE2 4

Overlay: Erra\_phospho\_KOvsWT - 2026-05-19 07:42 下午, Phospho Log Ratio

Navigation icons: Home, Zoom, Pan, Add, Slider

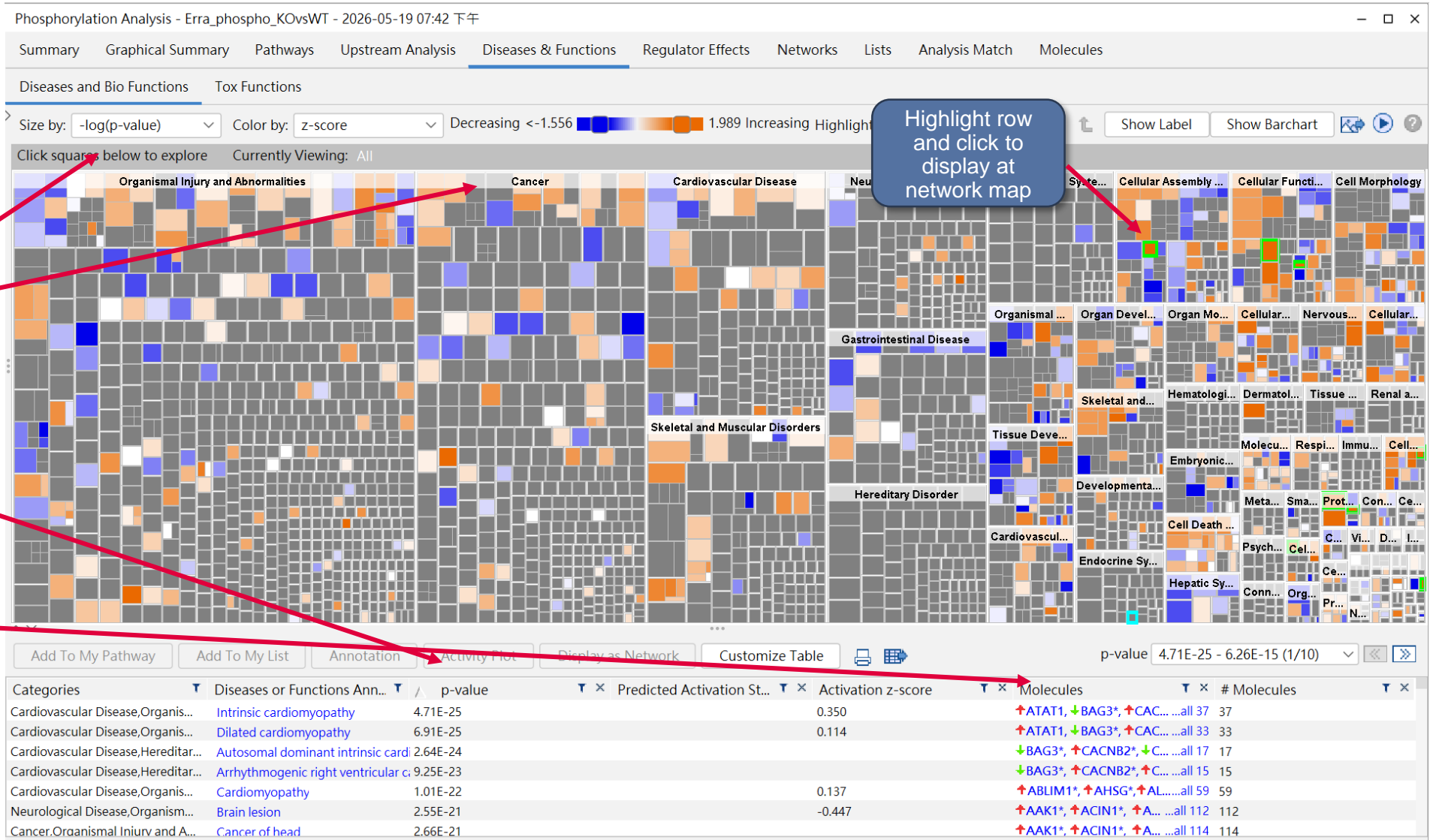
Modulated regulator

Interesting gene



Prediction Legend

- more extreme in dataset
  - Increased measurement (Red circle)
  - Decreased measurement (Green circle)
- more confidence
  - Predicted activation (Orange circle)
  - Predicted inhibition (Blue circle)
- Glow Indicates activity when opposite of measurement (Red/Green glow)
- Predicted Relationships
  - Leads to activation (Orange line)
  - Leads to inhibition (Blue line)
  - Findings inconsistent with state of downstream molecule (Yellow line)
  - Effect not predicted (Grey line)
- Dashed lines = indirect relationships
- Solid lines = direct relationship



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

Organized by biological themes

Significance of enrichment

Genes from dataset involved in disease or function

Highlight row and click to display at network map

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

Phosphorylation Analysis - KIKO phospho\_WT - 2026-05-19 07:45 下午

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

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

Regulators involved in network

Genes from dataset involved in disease or function

Disease or function

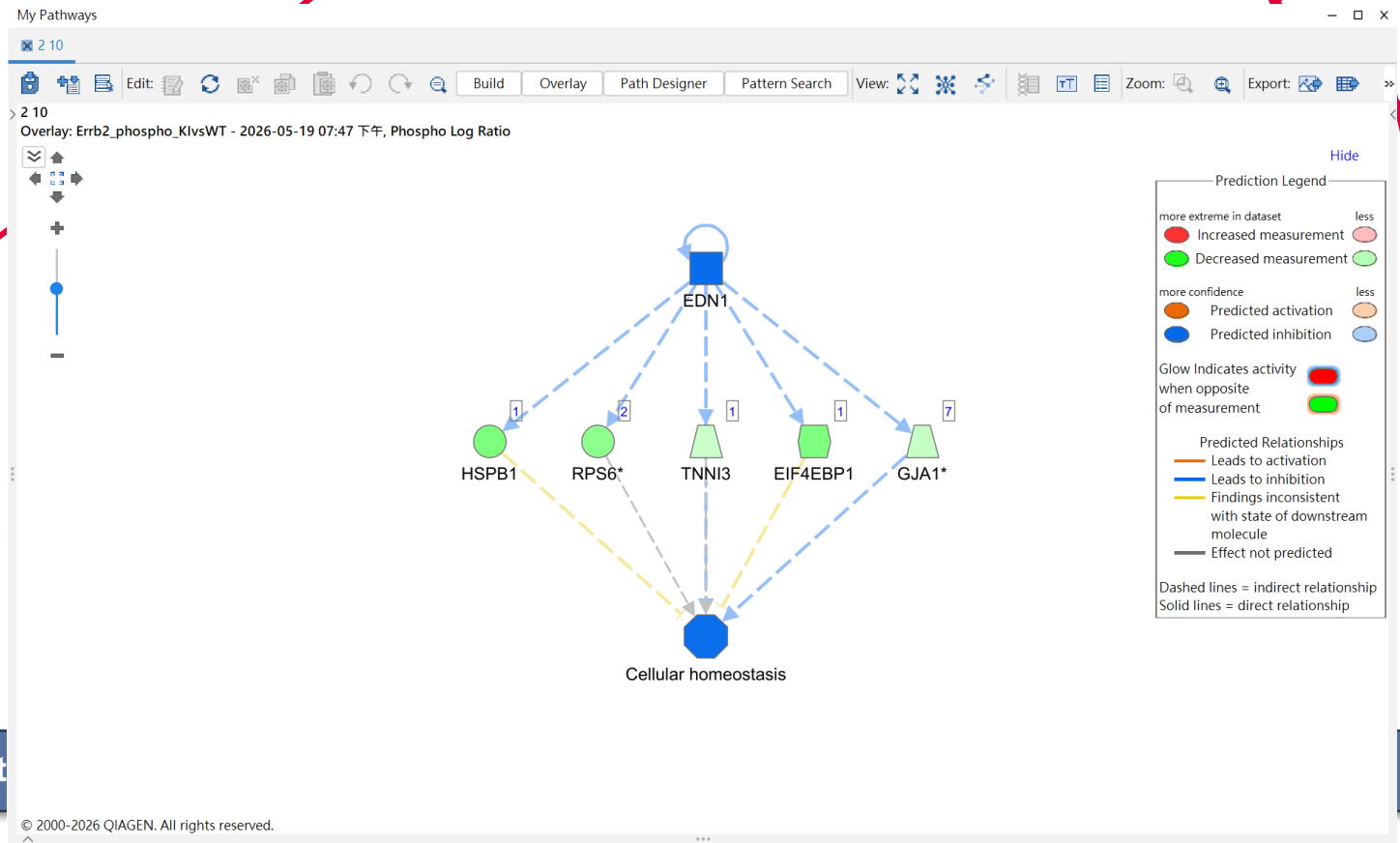
Known connections in IPA between regulator and disease & function-discover novel relationships

Ties dataset

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

Generate Networks Add To My Pathway Add To My List Display as Network Customize Table

Consisten...	Node Total	Regulator To...	Regulators	Target Total	Target Molec...	Disease & Fu...	Diseases & Fu...	Know
2.000	6	1	PTPN1	4	↑BCLAF1, ↑CCNY...	1	Size of body	100%
-17.555	8	1	EFNA1	6	↑ACLY, ↑FLNC, ↑...	1	Cell movement ...	100%



Network of highly connected molecules, click to open network map

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

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

Networks Overlapping Networks

View Networks Add To My Pathway Add To My List Merge Networks Functions Annotation Customize Table Expand

The analysis is composed of 14 networks. To view a network, select the appropriate network(s) and click View Networks. To merge selected networks, click Merge Networks. Total selected molecules: 0

ID	Molecules in Network	Score	Focus...	Top Diseases and Functions
1	ADP:Calcium Bound Myosin Actin, alpha actinin, ATP:Calcium Bound Myosin Actin, <b>↓BAG3</b> , beta tubulin, Calcium Bound Myosin Actin, ...all 35	49	24	Cardiac Dilation, Cardiac Enlargement, Cardiovascular Dis...all 3
2	<b>↓AKAP1</b> , <b>↑ATP2A2</b> , C1Q (family), calmodulin, calpain, <b>↑CLASP2</b> , <b>↑COBLL1</b> , <b>↑DYNC112</b> , ERK, <b>↓GJA1</b> ...all 35	47	23	Cardiovascular Disease, Cellular Assembly and Organization...all 3
3	<b>↓ABLIM1</b> , <b>↑ACIN1</b> , <b>↑ACLY</b> , <b>↑ATAT1</b> , <b>↑BCLAF1</b> , Calcineurin (complex), <b>↑CANX</b> , <b>↑CARHSP1</b> , caspase, <b>↑CTNND1</b> ...all 35	44	22	Cellular Assembly and Organization, Cellular Function an...all 3
4	Actin alpha/Ca2 /Myosin/Tropomyosin/TroponinC/Troponin I/Troponin T, Actomyosin, ADP:Calcium Bound Sarcomere Protein, <b>AKT</b> , ...all 35	34	18	Cardiovascular Disease, Hereditary Disorder, Organismal I...all 3
5	ALP, apyrase, calcineurin A, <b>↑CFL1</b> , CK2, cofilin, <b>↑CTNNA3</b> , <b>↑DSTN</b> , <b>↑EHD4</b> , F Actin ...all 35	34	18	Cardiovascular Disease, Cardiovascular System Developm...all 3
6	actin, <b>↑AHSG</b> , <b>↑ALDOA</b> , alpha catenin, <b>↑ARHGAP17</b> , CG, Collagen type I (complex), CREB, Ficolin-rich granule lumen proteins, FSH ...all 35	31	17	Cardiovascular Disease, Cellular Movement, Hair and Skin...all 3
7	40S ribosome/eIF3/mRNA/eIF4A/eIF4B/eIF4E/eIF4G, 43S: Ceruloplasmin mRNA:eIF4F:eIF4B:eIF4H:PABP, 43S:mRNA:eIF4F:eIF4B:eIF4H...all 35	29	16	Cell Cycle, Neurological Disease, Organismal Injury and A...all 3
8	3' end cleaved, ligated exon containing, ABL1/2, <b>↑ALKBH3</b> , Alternative Splicing Factors, capped, methylated pre-mRNA:CBC, <b>↑CHC...</b> all 35	27	15	Cancer, Dermatological Diseases an...all 3
9	26S proteasome, <b>↓AAK1</b> , alpha tubulin, CDC42 effectors, CDC42:GTP:CDC42 effectors, DFF40 associated with chromatin, <b>↓FCHO2</b> , ...all 35	20	12	Cell Cycle, Cellular Assembly and Or...all 3
10	ARMC10, ATAD2, Atad3a, BCL6, <b>↓CFAP161</b> , CRACR2B, DDIAS, DDX39A, E2F4, <b>↓EFTAKMT1</b> ...all 35	18	11	Cell Cycle, Cell Death and Survival, C...all 3
11	ADRB, Camk, CaMKII, cAMP-dependent protein kinase, <b>↓CAVIN1</b> , <b>↑CCNY</b> , EIF4G, ERK1/2, filamin, glycogen synthase ...all 35	16	10	Cardiac Dilation, Cardiac Enlargeme...all 3
12	14-3-3, AMPK, Ap1, <b>↓BSN</b> , <b>↑CACNB2</b> , CD3 (complex), <b>↑COQ9</b> , estrogen receptor, <b>↑ETV6</b> , focal adhesion kinase ...all 35	10	7	Cardiovascular Disease, Developme...all 3
13	BCL9L, <b>↑CCDC110</b> , CDR2L, CUL5, DLG4, <b>↑EHBP1L1</b> , ELFN2, <b>↓EPN3</b> , GRIK1, HEMK1 ...all 35	10	7	Cancer, Cellular Development, Organismal Injury and Abn...all 3
14	MCHR1, SSTR3, <b>↑Wdr20t</b> ...all 3	2	1	Nutritional Disease, Organismal Injury and Abnormalities,...all 3

Disease or function predicted to be an outcome

Networks constructed from your dataset with level of connectivity prioritized

Analysis Name	Project	ca...	ca...	ca...	co...	co...	co...	la...	pr...	w...	C...	U...	C...	D...	17.03	15.67
18- eye disease;normal control [fetal neu	SingleCellMo...	eye disea...	fetal neur...	NA	Cell Type ...	retinal co...	CMP:cbj5C	MouseU...	GSE149040	https://w...				68.14	17.03	18.71
45- control [breast] CMP_d4ee5194e33e	SingleCell CxG	control	breast		CellType v...	vascular e...	CMP:d4ee5	HumanCE...	CxG000075	https://ce...				68.14	17.03	3.02
58- control [ileum] CMP_d71c2bed48b5	SingleCell CxG	control	ileum		CellType v...	fibroblast...	CMP:d71c2	HumanCE...	CxG000109	https://ce...				68.14	17.03	11.82
579- normal control [embryo] differentia	SingleCellHu...	normal c...	embryo	differenti...	Cell Type ...	muscle pr...	CMP:sOGm	HumanU...	GSE164092	https://w...				65.47	16.37	9.05
502- normal control [embryo] differentia	SingleCellHu...	normal c...	embryo	differenti...	Cell Type ...	retinal pr...	CMP:a6CZv	HumanU...	GSE164092	https://w...				65.47	16.37	
4915- normal control [brain] NA CMP_Cz	SingleCellMo...	normal c...	brain	NA	Cell Type ...	medulla ...	CMP:CzPnF	MouseU...	GSE246717	https://w...				65.47	16.37	13.33
523- normal control [embryo] differentia	SingleCellHu...	normal c...	embryo	differenti...	Cell Type ...	retinal pr...	CMP:inBmC	HumanU...	GSE164092	https://w...				65.47	16.37	1.54
50- normal control [fetal kidney] NA CMF	SingleCellMo...	normal c...	fetal kidney	NA	Cell Type ...	renal epit...	CMP:2oGQ	MouseU...	GSE108291	https://w...				65.47	16.37	1.83
3137- normal control [fetal hindbrain;fet	SingleCellMo...	normal c...	fetal hind...	NA	Cluster vs...	neurobla...	CMP:AXNEI	MouseU...	SRP266379	https://tr...				65.47	16.37	8.94
173- genetic disease;normal control [hea	SingleCellMo...	genetic di...	heart	NA	Cell Type ...	cardiac st...	CMP:I10qz	MouseU...	GSE131181	https://w...				65.47	16.37	16.00
2054- acute myeloid leukemia (LAML) [bc	SingleCellHu...	acute my...	bone mar...	NA	Cluster vs...	precursor...	CMP:YRqPx	HumanU...	GSE235063	https://w...				65.47	16.37	3.16
16- hepatocellular carcinoma (LIHC) [live	OncoHuman	hepatocel...	liver	NA	Tissue1 vs...	RelapseFr...	CMP:IMuZk	OncoHu...	GSE76427	https://w...				65.47	16.37	2.13
14- hepatocellular carcinoma (LIHC) [live	OncoHuman	hepatocel...	liver	NA	Tissue1 vs...	RelapseFr...	CMP:pm2ln	OncoHu...	GSE76427	https://w...				65.47	16.37	4.08
1- urinary tract transitional cell carcinom	OncoHuman	urinary tr...	urinary sy...	NA	Disease v...	Etiology:T...	CMP:gTpR2	OncoHu...	GSE166716	https://w...				65.47	16.37	-5.14
1- hepatocellular carcinoma (LIHC) [liver]	OncoHuman	hepatocel...	liver	NA	Tissue1 vs...	TissueDes...	CMP:3zaEP	OncoHu...	GSE76427	https://w...				65.47	16.37	4.08
9- acute lymphocytic leukemia (ALL) [bor	TARGET	acute lym...	bone mar...	NA	Tissue1 vs...	PairingSt...	CMP:Oxykt	TARGET_...	TARGET	https://o...				65.47	16.37	-5.00
88- disease control [epidermis] NA CMP_	SingleCellHu...	disease c...	epidermis	NA	Cell Type ...	basal epi...	CMP:W3vjp	HumanU...	GSE147482	https://w...				65.47	16.37	6.32
6- normal control [peripheral blood] anti	HumanDisease	normal c...	periphera...	anti-CD2...	Treatmen...	Treatmen...	CMP:gfcAo	HumanDi...	GSE89133	https://w...				65.47	16.37	-4.08
5- normal control [retinal pigment epith	HumanDisease	normal c...	retinal pi...	NA	Other	GeneticM...	CMP:0k2MI	HumanDi...	GSE154684	https://w...				65.47	16.37	
4- normal control [peripheral blood] anti	HumanDisease	normal c...	periphera...	anti-CD2...	Treatmen...	Treatmen...	CMP:ozyWj	HumanDi...	GSE89133	https://w...				65.47	16.37	-1.96
13- lung adenocarcinoma (LUAD) [bronc	HumanDisease	lung ade...	bronchial...	NA	Treatmen...	Infection...	CMP:1vG5E	HumanDi...	GSE17400	https://w...				65.47	16.37	-4.08
7- disease control [brain] NA CMP_OP5M	MouseDisease	disease c...	brain	NA	Treatmen...	SampleD...	CMP:OP5M	MouseDis...	GSE131869	https://w...				65.47	16.37	-3.16
5- disease control [hindlimb muscle] NA	MouseDisease	disease c...	hindlimb ...	NA	CellType1...	Genotype...	CMP:Yodgz	MouseDis...	GSE47177	https://w...				65.47	16.37	-5.88
1- systemic JIA [peripheral blood] NA CM	HumanDisease	systemic J...	periphera...	NA	Disease v...	DiseaseSt...	CMP:0X04C	HumanDi...	GSE29536	http://ww...				65.47	16.37	15.00
1442- normal control [liver] NA CMP_A8f	RatDisease	normal c...	liver	NA	Treatmen...	Experime...	CMP:A8pSz	RatDiseas...	GSE57815	https://w...				65.47	16.37	
66- control [trachea] CMP_08c7e467187	SingleCell CxG	control	trachea		CellType v...	vein endo...	CMP:08c7e	HumanCE...	CxG000198	https://ce...				65.47	16.37	8.32
45836- hepatocellular carcinoma (LIHC) [	SingleCell Ta...	hepatocel...	liver	digitoxin	Treatmen...	CellLine:E...	CMP:c7f85c	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	-10.00
32359- non-small cell lung carcinoma [lu	SingleCell Ta...	non-smal...	lung	oxaliplatin	Treatmen...	CellLine:E...	CMP:44a63	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	3.16
4218- lung adenocarcinoma (LUAD) [lun	SingleCell Ta...	lung ade...	lung	anethole ...	Treatmen...	CellLine:E...	CMP:f1e30f	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	7.07
29- nonpapillary renal cell carcinoma [kic	SingleCell CxG	nonpapill...	kidney		CellType v...	CD4+ nai...	CMP:6b498	HumanCE...	CxG000252	https://ce...				65.47	16.37	6.35
3180- renal cell carcinoma (RCC) [kidney]	SingleCell Ta...	renal cell ...	kidney	drosipren...	Treatmen...	CellLine:E...	CMP:7c9bb	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	-11.55
30- myocardial infarction [heart left vent	SingleCell CxG	myocardi...	heart left ...		CellType v...	cardiac e...	CMP:01f771	HumanCE...	CxG000142	https://ce...				65.47	16.37	11.86
37195- lung large cell carcinoma [lung] g	SingleCell Ta...	lung larg...	lung	gefitinib	Treatmen...	CellLine:E...	CMP:c59a1i	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	
23677- normal control [pancreatic duct]	SingleCell Ta...	normal c...	pancreati...	ouabain ...	Treatmen...	CellLine:E...	CMP:bbf45i	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	-1.83
36511- lung large cell carcinoma [lung] g	SingleCell Ta...	lung larg...	lung	ouabain	Treatmen...	CellLine:E...	CMP:Safe0i	Tahoe_B3...	Tahoe100V	https://h...				65.47	16.37	-8.57



Create Core Analysis ×

Selected Dataset: KI vs WT metabolomic ?

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

Metabolomics Analysis ▼

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

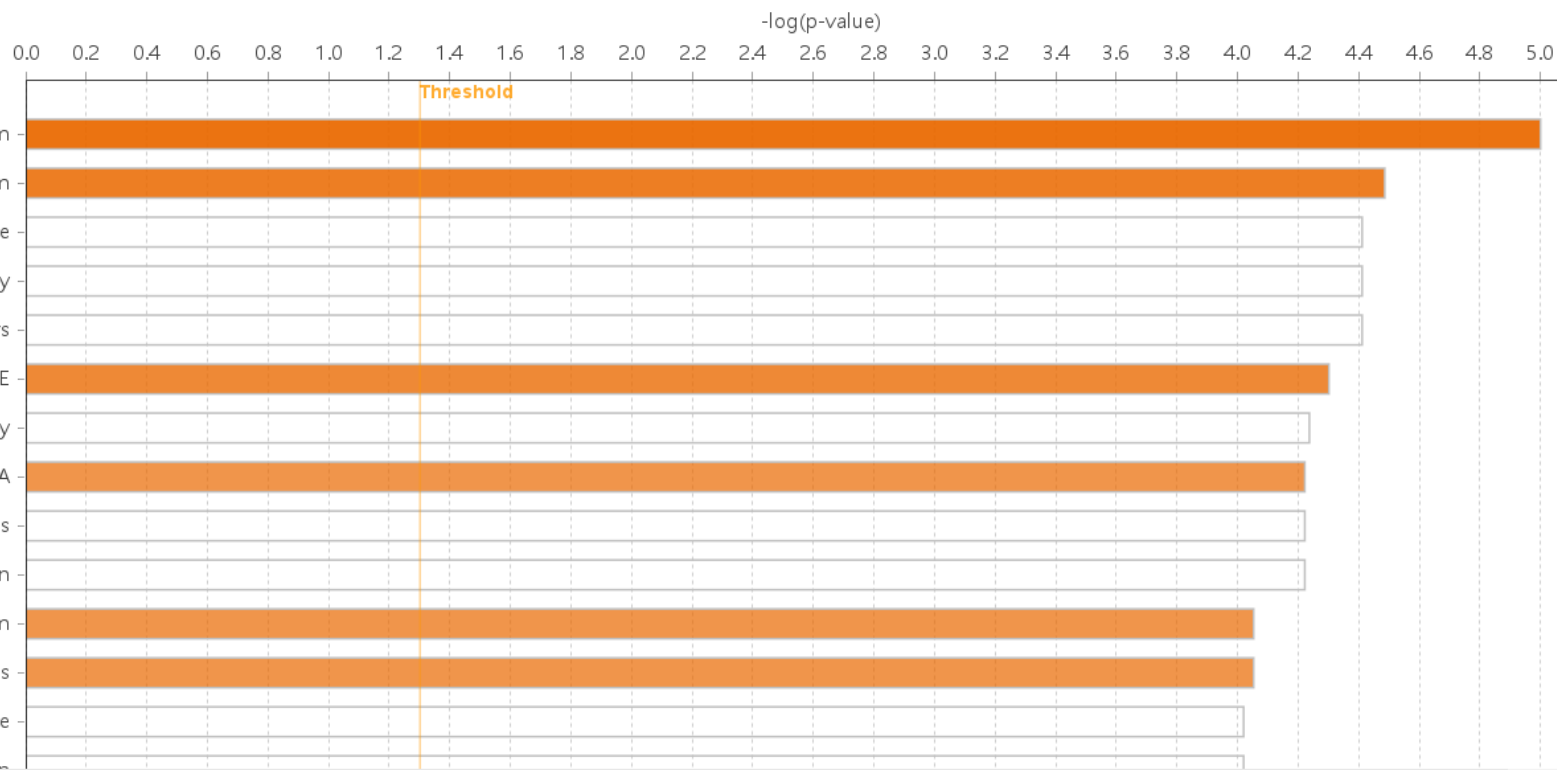
Expr Fold Change ▼ This measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

Back Next

heart energy  
substrate  
reprogramming

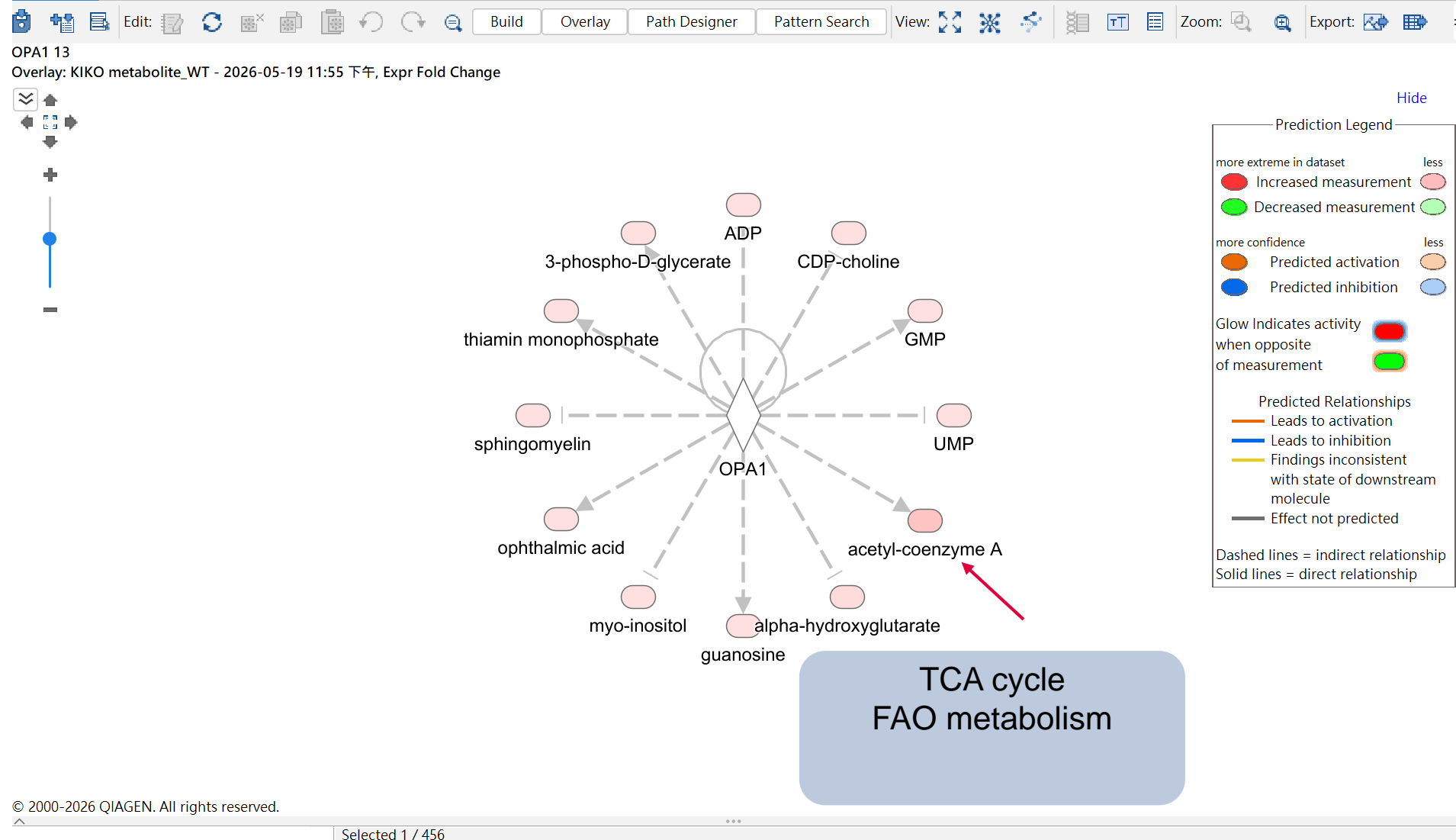


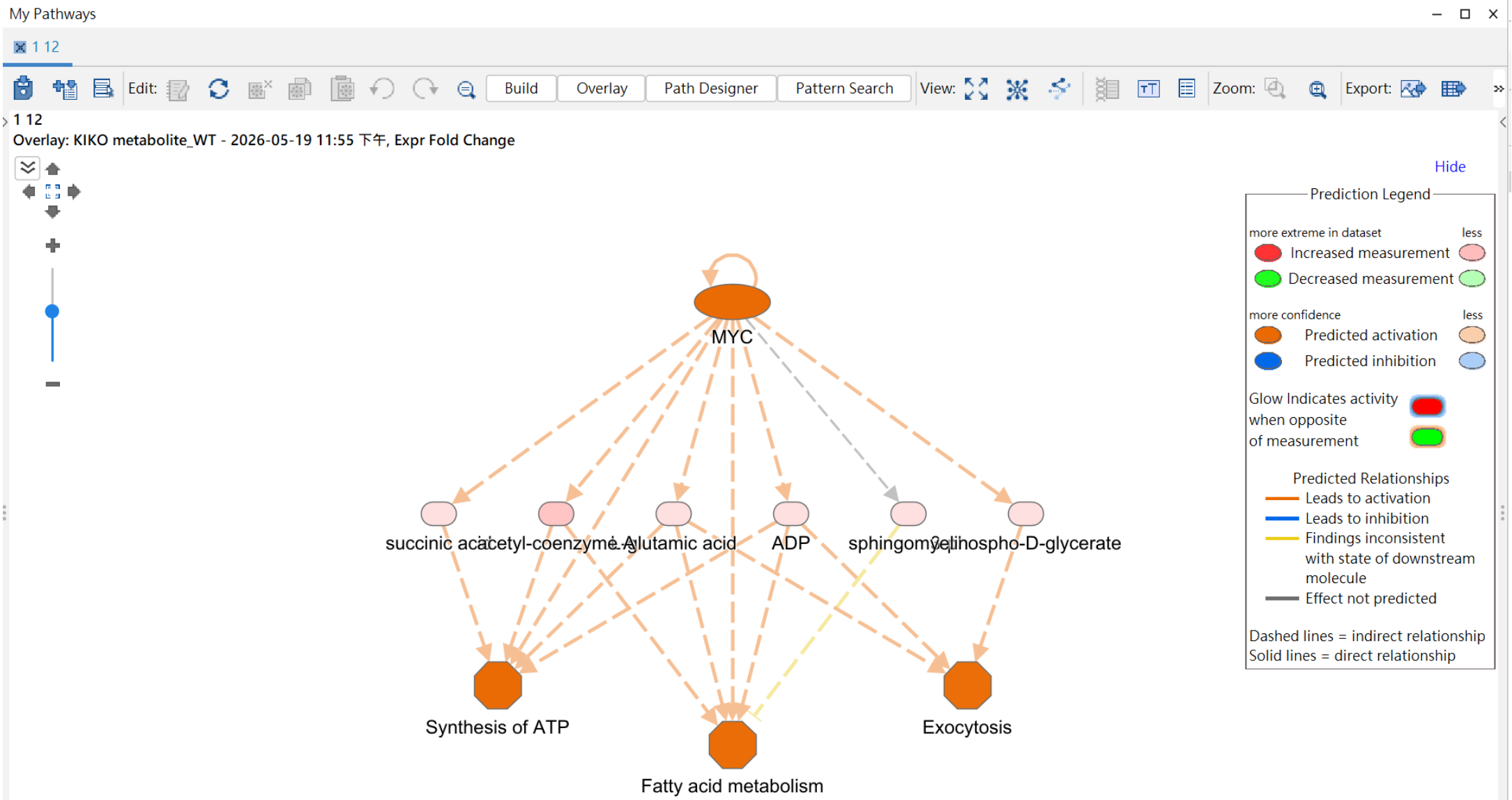
failing heart phenotype



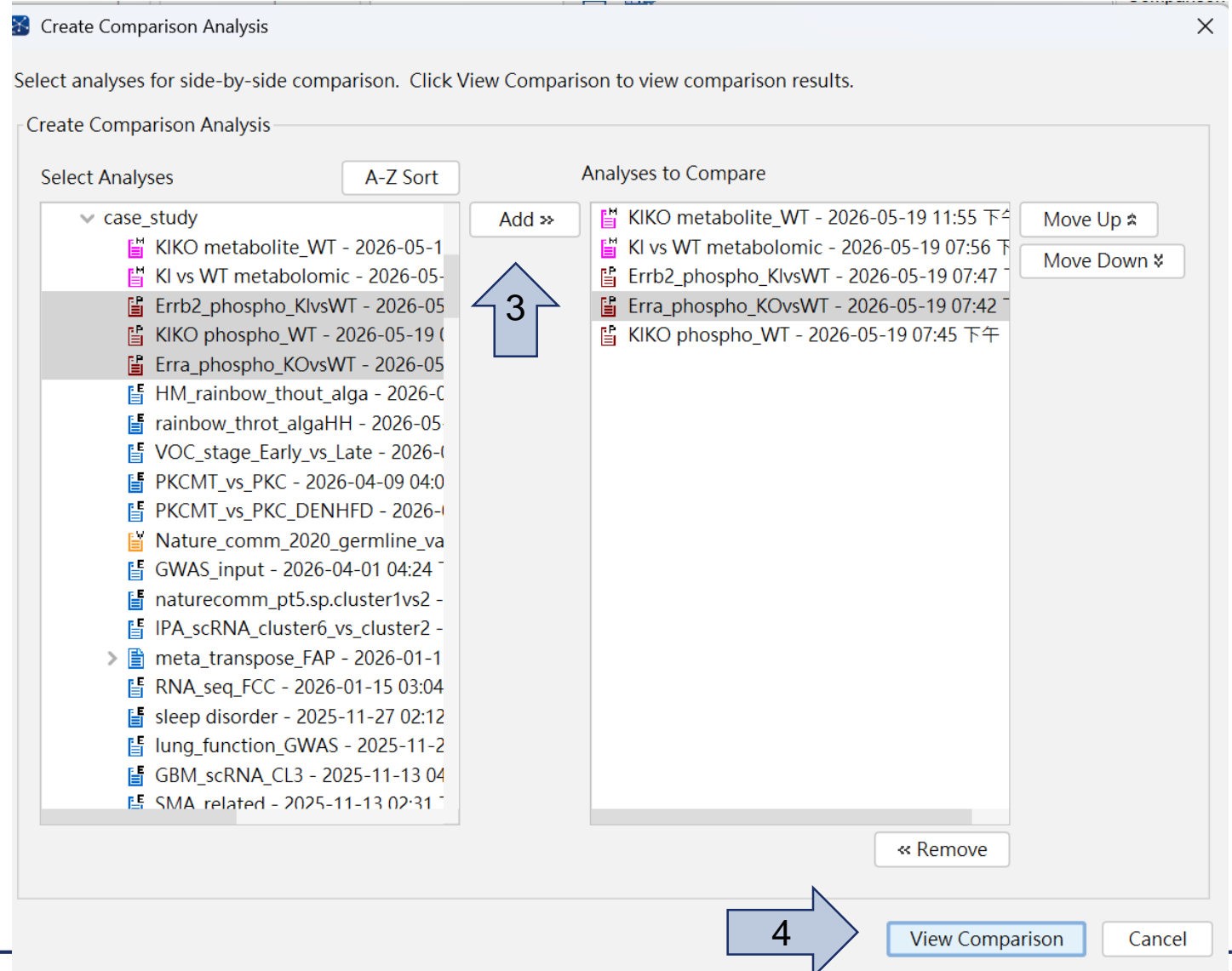
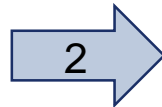
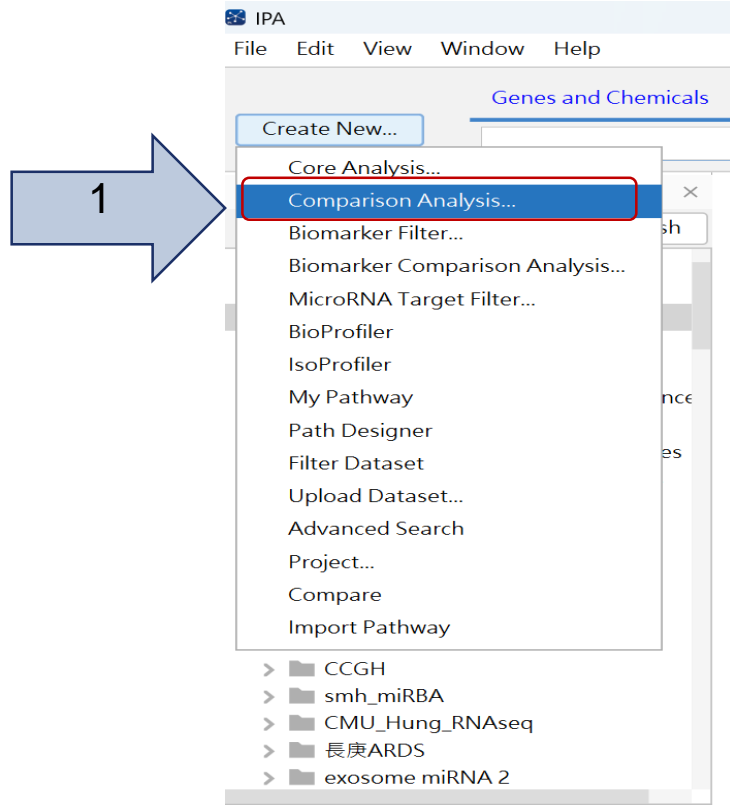
Upstream Regul...	Expr Fold Change	Molecule Type	Predicted Activ...	Activation z-sco...	Flags	p-value of o...	Target Molecul...	Mechanistic Ne...
ibrutinib		chemical drug		0.632	bias	4.09E-14	↑3-phospho-D-g... all 16	
BCR (complex)		complex				1.19E-09	↑3-phospho-D-g... all 12	
CD40		transmembrane receptor	Activated	3.162	bias	2.06E-09	↑3-phospho-D-g... all 10	
digoxin		chemical drug		0.333	bias	7.44E-08	↑5'-CMP, ↑ADP, ↑... all 9	
gemcitabine		chemical drug	Activated	2.872	bias	9.12E-08	↑3-phospho-D-gl... all 9	
lipopolysaccharide		chemical drug	Activated	3.222	bias	3.17E-07	↑3-phospho-D-g... all 16	17 (5)
OPA1		enzyme		0.000		7.53E-07	↑3-phospho-D-g... all 12	
HTT		transcription regulator		0.772		3.01E-06	↑corticosterone, ↑... all 8	
CD274		transmembrane receptor		1.342		3.82E-06	↑ADP, ↑creatine, ↑... all 9	
empagliflozin		chemical drug				9.21E-06	↑1,5-anhydroglu... all 11	
CPT1B		enzyme	Inhibited	-2.630	bias	1.03E-05	↑5'-CMP, ↑acetyl-... all 7	
CHKA		kinase		0.000		1.10E-05	↑ADP, ↑creatine, ↑... all 6	
IDH1		enzyme		0.246	bias	2.37E-05	↑5'-CMP, ↑acetyl-... all 5	
liraglutide		biologic drug		-0.537		4.06E-05	↑acetyl-coenzyme A ... all 9	
GAPDH		enzyme				4.07E-05	↑ADP, ↑coenzyme... all 6	
n-nitrosomethylbenzylamii		chemical toxicant				6.13E-05	↑1,5-anhydrogluci... all 7	
GSKJ4		chemical reagent		-1.134		6.13E-05	↑3-phospho-D-gl... all 7	
CNTF		cytokine				6.53E-05	↑3-phospho-D-gl... all 6	
ERG		transcription regulator				1.19E-04	↑CDP-choline, ↑L-... all 3	
PGAM2		phosphatase				1.19E-04	↑3-phospho-D-gl... all 3	
metyrapone		chemical drug				1.19E-04	↑corticosterone, ↑... all 3	
INHA		growth factor	Inhibited	-2.121	bias	1.39E-04	↑ADP, ↑biopterin, ↑... all 8	
MYC		transcription regulator	Activated	2.412	bias	1.46E-04	↑3-phospho-D-gl... all 7	
ZNF395		transcription regulator	Activated	2.219	bias	1.59E-04	↑5'-CMP, ↑alpha-... all 5	
FASN		enzyme		1.131		1.69E-04	↑3-phospho-D-gl... all 6	
pilocarpine		chemical drug		0.577		2.16E-04	↑ADP, ↑L-glutami... all 4	
deoxycholate		chemical - endogenous ...	Inhibited	-2.401	bias	2.42E-04	↑5'-CMP, ↑ADP, ↑... all 6	
D-glucose		chemical - endogenous ...		1.400	bias	2.83E-04	↑3-phospho-D-gl... all 8	10 (2)
curcumin		chemical drug	Inhibited	-2.219	bias	3.01E-04	↑corticosterone, ↑... all 5	
GLS		enzyme				3.23E-04	↑alpha-hydroxygl... all 3	
GAMT		enzyme				3.43E-04	↑creatine, ↑creati... all 2	
UQCRFS1		enzyme				3.43E-04	↑alpha-hydroxygl... all 2	
cyanamide		chemical - endogenous ...				3.43E-04	↑acetyl-coenzyme A ... all 2	

OPA1 is a key regulator of mitochondrial fusion and mitochondrial integrity. IPA upstream regulator analysis suggests that the observed metabolite profile is associated with OPA1-related mitochondrial remodeling and altered energy metabolism.





## Step for You to do your compared analysis



## Welcome to IPA Interpret

Transform complex omics data into meaningful biological insights

### Available Analyses

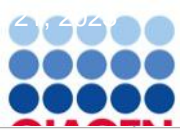
Analyses

2. Press Create Comparison

× 2 analyses selected **Create Comparison**

	Analysis Name	Type	Analyzed Genes	Reference Set	Owner	Last Activity	
<input type="checkbox"/>	case	Filter	+1 ▾	Filter ≥	Select ▾	Filter	Select ▾
<input type="checkbox"/>	case_study	PKCMT_vs_PKC_DENHFD - 2026-04-09 04:07 下午	Expression	1431	Ingenity Knowledge Base (Genes Only)	Me	Thu Apr 09 16:33:01 GMT+8 2026
<input type="checkbox"/>	case_study	PKCMT_vs_PKC - 2026-04-09 04:09 下午	Expression	110	Ingenity Knowledge Base (Genes Only)	Me	Thu Apr 09 16:31:27 GMT+8 2026
<input type="checkbox"/>	case_study	GWAS_input - 2026-04-01 04:24 下午	Expression	179	Ingenity Knowledge Base (Genes Only)	Me	Wed Apr 01 16:30:41 GMT+8 2026
<input checked="" type="checkbox"/>	case_study	naturecomm_pt5.sp.cluster1vs2 - 2026-03-23 04:12 下午	Expression	113	Ingenity Knowledge Base (Genes Only)	Me	Mon Mar 23 17:01:48 GMT+8 2026
<input checked="" type="checkbox"/>	case_study	IPA_scRNA_cluster6_vs_cluster2 - 2026-03-23 03:48 下午	Expression	2017	Ingenity Knowledge Base (Genes Only)	Me	Mon Mar 23 16:12:35 GMT+8 2026
<input type="checkbox"/>	case_study	RNA_seq_FCC - 2026-01-15 03:04 下午	Expression	1960	Ingenity Knowledge Base (Genes Only)	Me	Thu Jan 15 16:34:12 GMT+8 2026
<input type="checkbox"/>	case_study	sleep disorder - 2025-11-27 02:12 下午	Expression	192	Ingenity Knowledge Base (Genes + Endogenous Chemicals)	Me	Thu Nov 27 14:31:52 GMT+8 2025

1. Choose which analyses you want to comparison



# Compare Analysis Result

Comparison Analysis - Analysis Comparison 1

## Canonical pathway

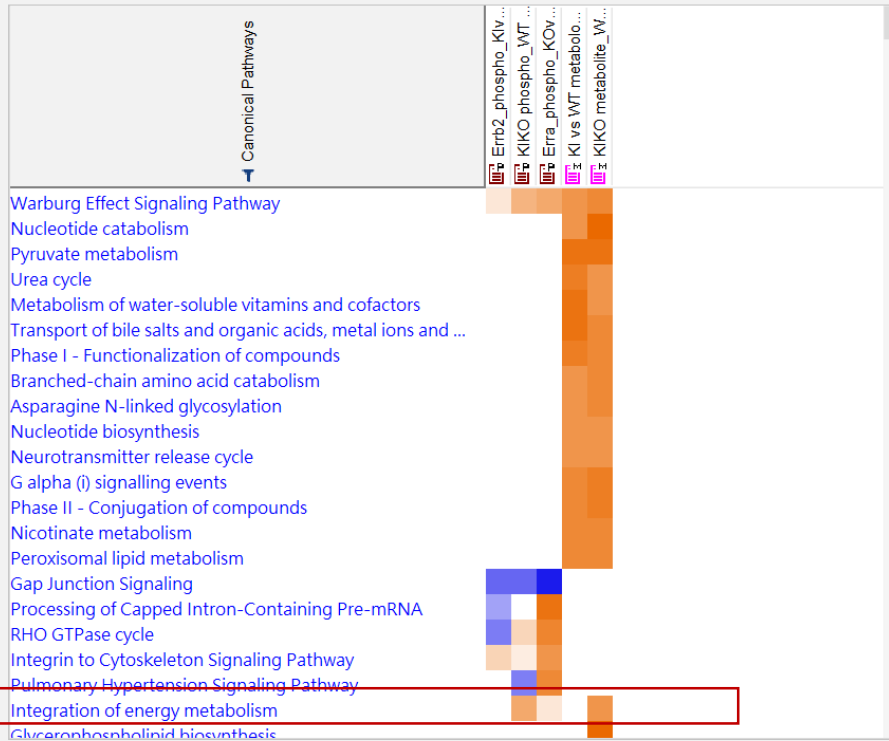
Filter

Measurement: Activation z-score -2.236 2.828

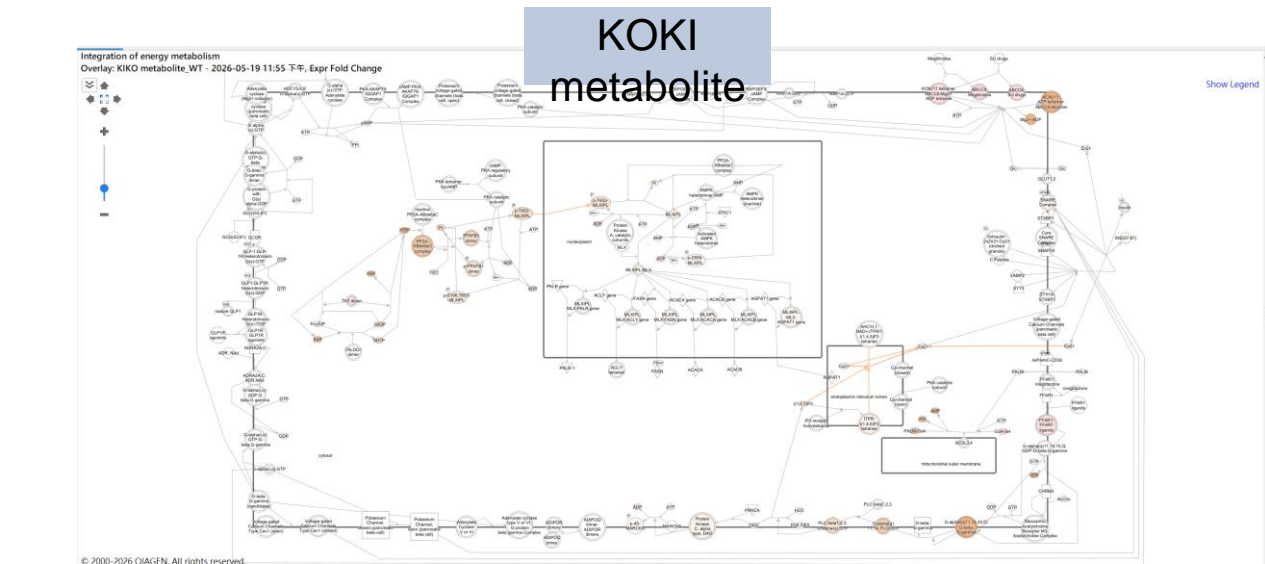
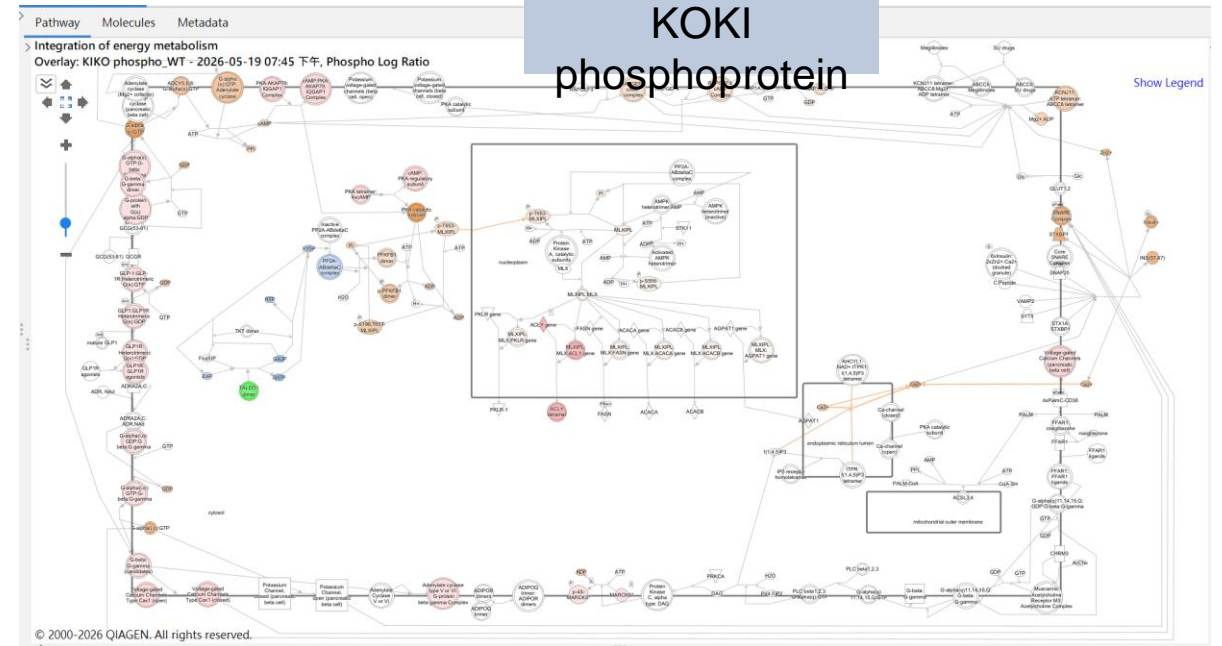
Sort Method: Hierarchical Clustering Visualize: z-score

Insignificance Threshold:  (absolute value)

Expand Header  Cluster Columns



Sample to Insight



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## 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



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## <sup>1</sup>H NMR serum metabolomics and its endogenous network pharmacological analysis of Gushudan on kidney-yang-deficiency-syndrome rats

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### ARTICLE INFO

**Keywords:**  
Kidney-yang-deficiency-syndrome  
Gushudan  
Pharmacodynamics  
<sup>1</sup>H NMR metabolomics  
Endogenous network pharmacology strategy

### ABSTRACT

The pharmacodynamics, <sup>1</sup>H NMR metabolomics and endogenous network pharmacology strategy approaches were integrated to investigate the preventive mechanism of Gushudan (GSD) on kidney-yang-deficiency-syndrome (KYDS) rats in this study. Firstly, the KYDS rat model was achieved by hydrocortisone induction, and the efficacy of GSD on KYDS model rats was assessed by the pharmacodynamic indicators. Next, the comprehensive untargeted serum metabolic profile of rats was obtained in <sup>1</sup>H NMR metabolomics study, 29 potential biomarkers closely associated with KYDS were identified, which were mainly involved in carbohydrate metabolism, amino acid metabolism and intestinal flora metabolism. In addition, the potential biomarkers-targets-pathways-disease metabolic network was further investigated for deeper understanding the preventive effects of GSD on KYDS rats and its mechanism, which was further obtained for the important targets related to biomarkers and diseases such as NOS3, PTGS2 and CXCL6, and important metabolic pathways such as glyoxylate and dicarboxylate metabolism, arginine and proline metabolism, and microbial metabolism in diverse environments. Finally, compared with our previous anti-osteoporosis study of GSD, it suggested that some similar metabolic pathways, which would provide some scientific reference of the existence of the kidney-bone axis under the traditional Chinese medicine (TCM) theory of “kidney dominates bone”.

### 1. Introduction

Gushudan (GSD) was a traditional Chinese compound prescription based on the “kidney dominates bone” theory in traditional Chinese medicine (TCM) and clinical practices, which was carefully formulated by the technical platform of the “A basic concept of establishing platforms for operational techniques in systems of elaborately selecting small prescriptions of traditional Chinese medicine” [1]. It consists of *Epimedium brevicornu* Maxim, *Drynaria fortunei* (Kunze) J. Sm, *Cnidium monnieri* (L.) Cuss and *Salvia miltiorrhiza* Bge, which had the effect of strengthening tendons and bones and benefiting kidneys. In the Pharmacopoeia of the People’s Republic of China (2020 edition), these four Chinese herbs of GSD were included. The preclinical pharmacodynamic research showed that GSD could prevent and treat osteoporosis by increasing bone mineral density, serum calcium and bone gla protein levels, etc [2,3]. The high performance liquid chromatography (HPLC) chemical fingerprints of GSD had been studied in our previous research [4,5]. Subsequently, the main active ingredients of GSD include icariin, osthole, naringin and tanshinone, and pharmacokinetic studies of the

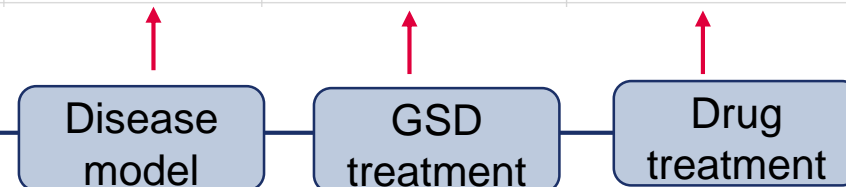
related active ingredients were performed based on ultra performance liquid chromatography-mass spectrometry (UPLC-MS) [6,7]. In addition, metabolomics studies had been further conducted from the perspective of the bone strengthening effects of GSD, and it was found to have a preventive effect on glucocorticoid osteoporosis (GIOP) by call-backing metabolite levels and adjusting metabolic pathways [8,9]. According to the “kidney dominates bone” theory of TCM, it proved that the kidney-bone axis existed [10]. However, the effects of GSD in tonifying the kidney are still unclear, and how does GSD play the roles in tonifying the kidney and strengthening the bones? Further researcher on the effects of GSD as a whole on “kidney deficiency syndrome” in TCM theory are of great significance, which would help to reveal the comprehensive mechanism of GSD *in vivo* and provide a scientific basis of its clinical application.

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

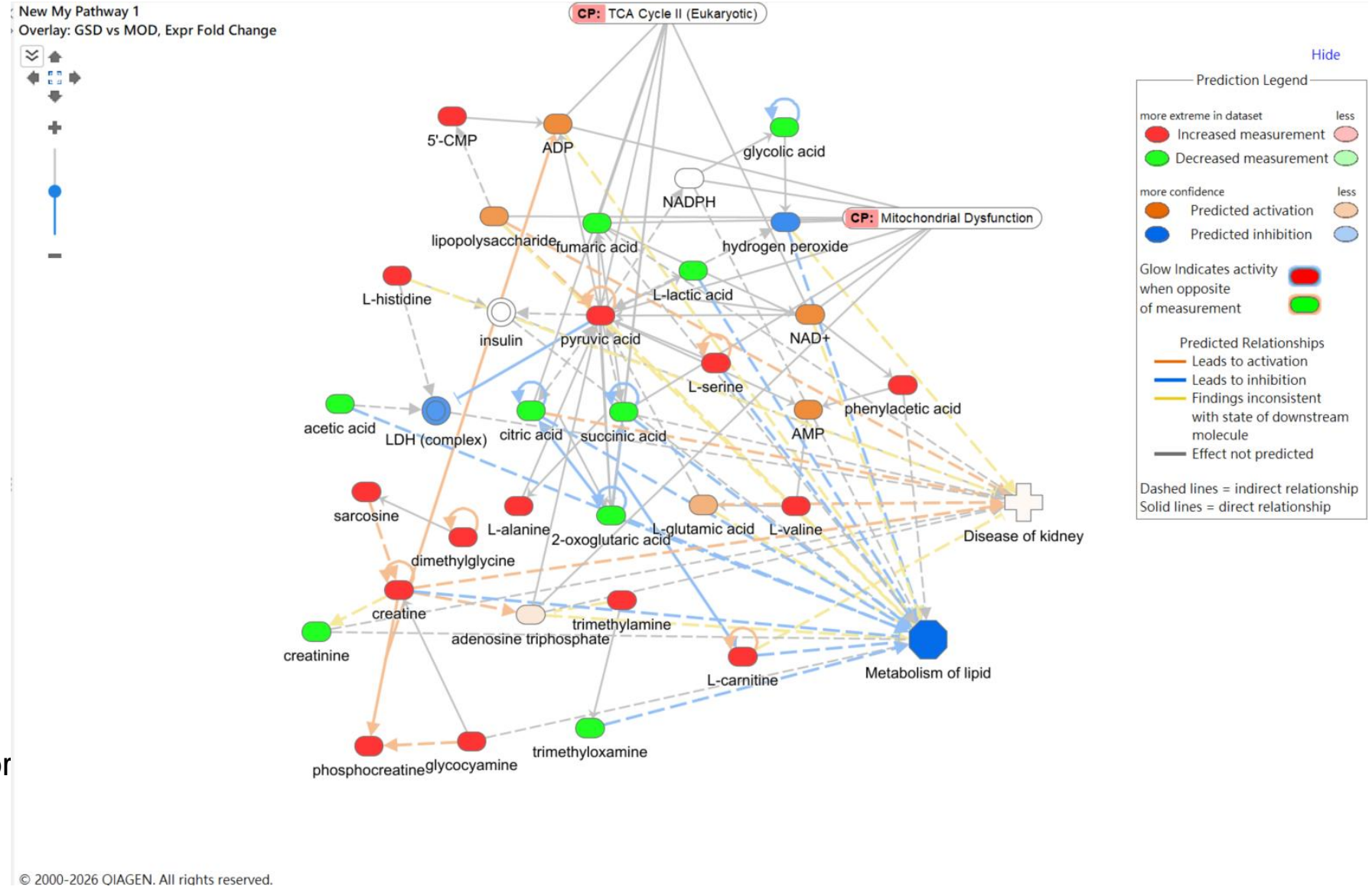
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E-mail address: [beary200@126.com](mailto:beary200@126.com) (Z. Xiong).

	A	B	C	D
1	HMDB ID	MOD vs CON	GSD vs MOD	POS vs MOD
2	HMDB0000172	0.8	1.5	1.5
3	HMDB0000883	0.8	1.5	1.5
4	HMDB0000190	1.5	0.8	0.8
5	HMDB0000161	0.8	1.5	1.5
6	HMDB0000042	1.5	0.8	0.8
7	HMDB0000243	0.8	1.5	1.5
8	HMDB0000254	1.5	0.8	0.8
9	HMDB0000208	1.5	0.8	0.8
10	HMDB0000094	1.5	0.8	0.8
11	HMDB0000095	0.8	1.5	1.5
12	HMDB0000906	0.8	1.5	1.5
13	HMDB00001511	0.8	1.5	1.5
14	HMDB0000062	0.8	1.5	1.5
15	HMDB0000925	1.5	0.8	0.8
16	HMDB0000209	0.8	1.5	1.5
17	HMDB0000167	0.8	1.5	1.5
18	HMDB0000271	0.8	1.5	1.5
19	HMDB0000711	0.8	1.5	1.5
20	HMDB0000092	0.8	1.5	1.5
21	HMDB0000714	0.8	1.5	1.5
22	HMDB0000128	0.8	1.5	1.5
23	HMDB0000187	0.8	1.5	1.5
24	HMDB0000064	0.8	1.5	1.5
25	HMDB0000115	1.5	0.8	0.8
26	HMDB0000562	1.5	0.8	0.8
27	HMDB0000462	0.8	1.5	1.5
28	HMDB0000134	1.5	0.8	0.8
29	HMDB0000177	0.8	1.5	1.5
30	HMDB0000142	0.8	1.5	1.5



**New feature:**  
**Cells and Tissues overlay**  
*Predict cell types associated with the genes on your network or pathway using data from The Human Protein Atlas*

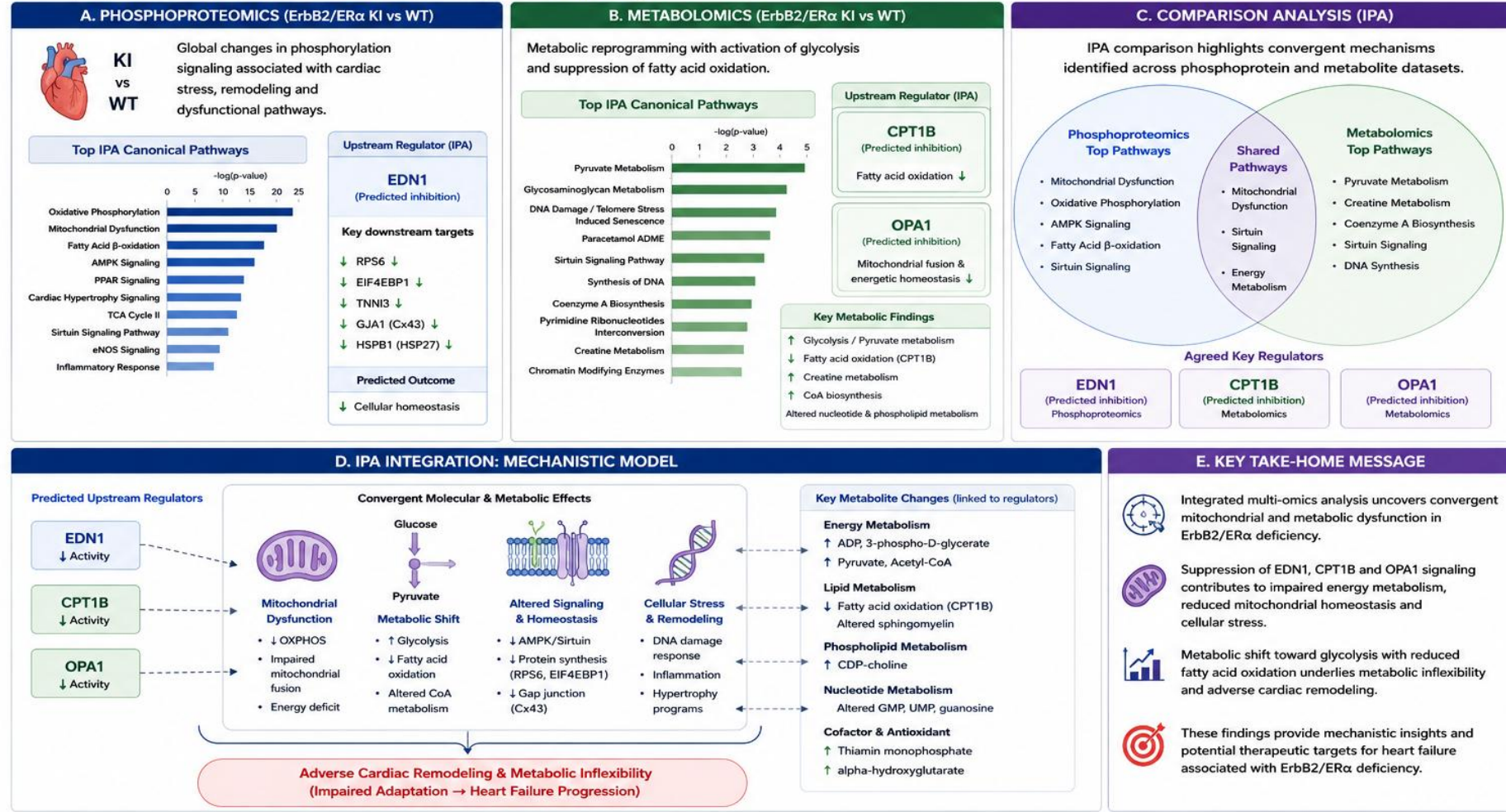


- Upload list
- Build: grow/network/ path-explore (molecular or disease a function)
- Search for disease
- Path explore
- Overlay: Molecule activity predictor datasets, Drug, Cells & Tissues
- Drug: IPA Chem View

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## Integrated Multi-Omics Analysis Reveals Mechanisms of Metabolic Inflexibility and Adverse Cardiac Remodeling in ErbB2/ERα Deficient Heart

Phosphoproteomics, Metabolomics and IPA Integration Summary



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



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