

Multi-omics analysis and knowledge base queries using 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)

Operating systems

- ◆ Windows operating systems:
 - Windows 11, 10, 8
- ◆ Mac operating systems:
 - macOS Sonoma, Ventura, Monterey
- ◆ Internet browsers:
 - Firefox 91 or later*
 - Safari 16 or later*
 - Chrome 110 or later*
 - Microsoft Edge 94 or later*
- ◆ Java runtime environment ([JRE](#); not needed if you [install](#) the IPA client):
 - JRE 8 to 10

Hardware

- Core™ i5 processor or equivalent running at 2 GHz or higher with 64-bit OS and Java
- Minimum at least 3 GB RAM free for Java

Introduction to pathway analysis

What is QIAGEN Ingenuity Pathway Analysis

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

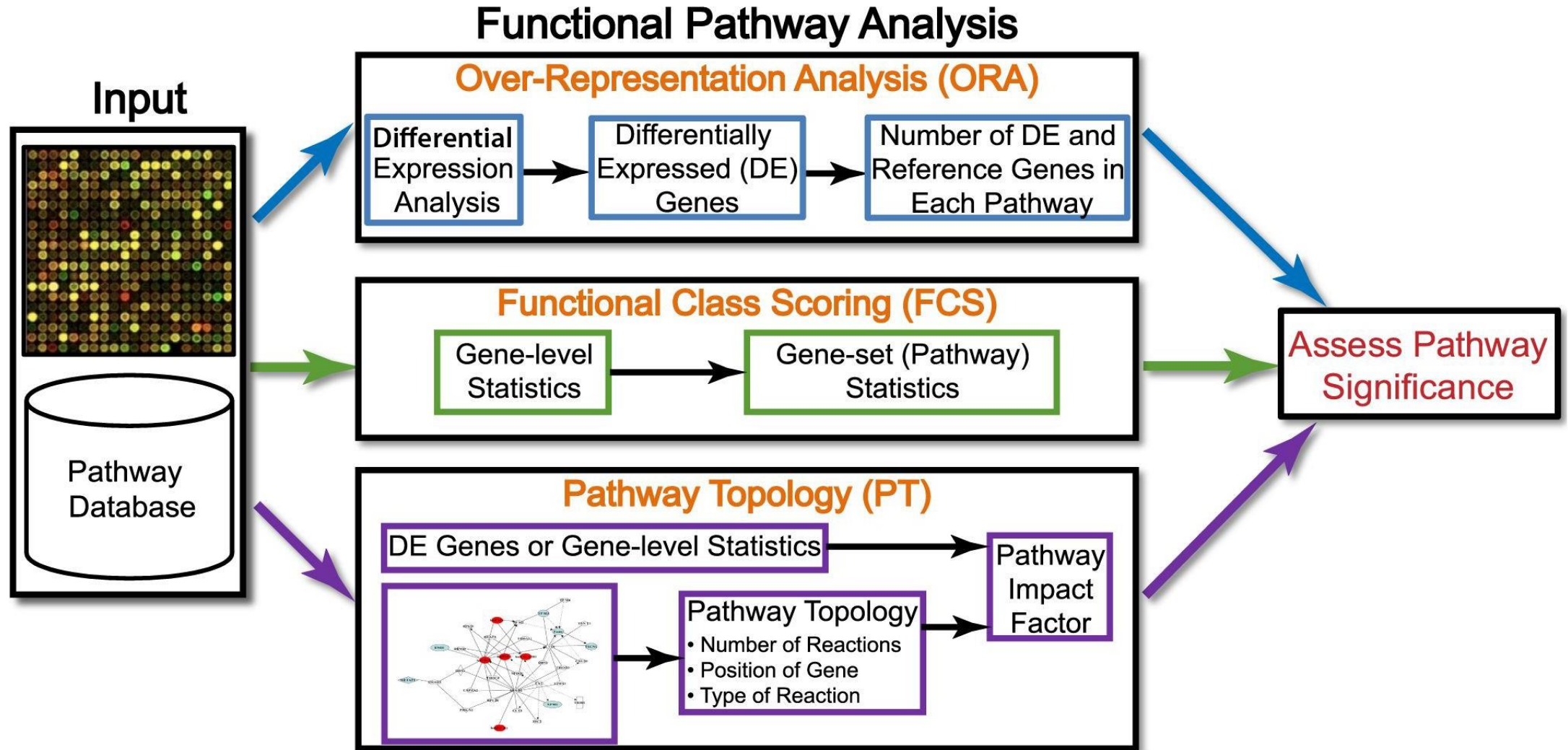
Test hypothesis in silico

Interpreting your 'omics data using IPA

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

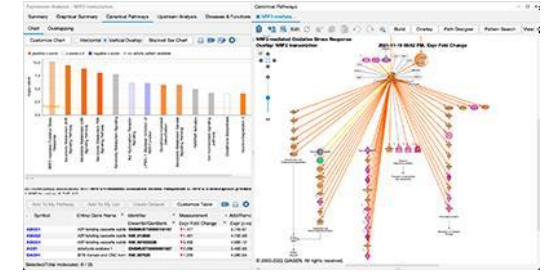
Creating networks from compare molecules

Summary



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

An example: Analyzing variant data from Sample to Insight



Sample to data

NGS library prep
Sequencing

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

Data to information

Normalization and quality control
Read mapping
Variant calling

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

BaseSpace and Amazon Web Service integration

Information to knowledge

Data integration
Metadata exploration
Differential expression

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

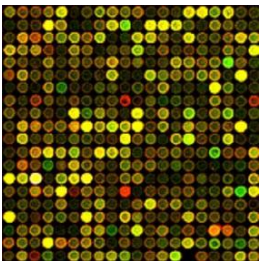
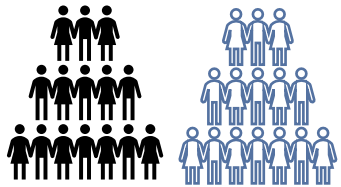
Knowledge to insight

Interpretation
Pathway analysis

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

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

Your dataset



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

Drugs and chemicals

Pathway

Disease

Function

Network

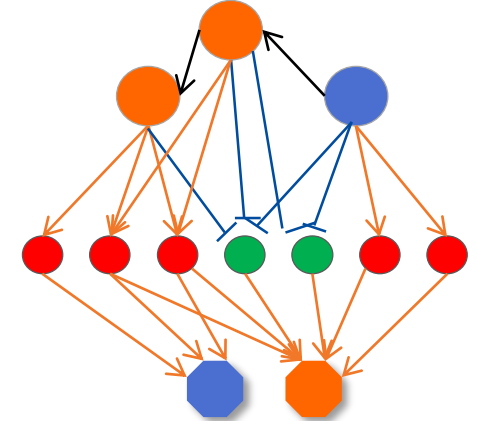
ORA/FCS/Topology
Pathway Analysis

Public
/commercial
database



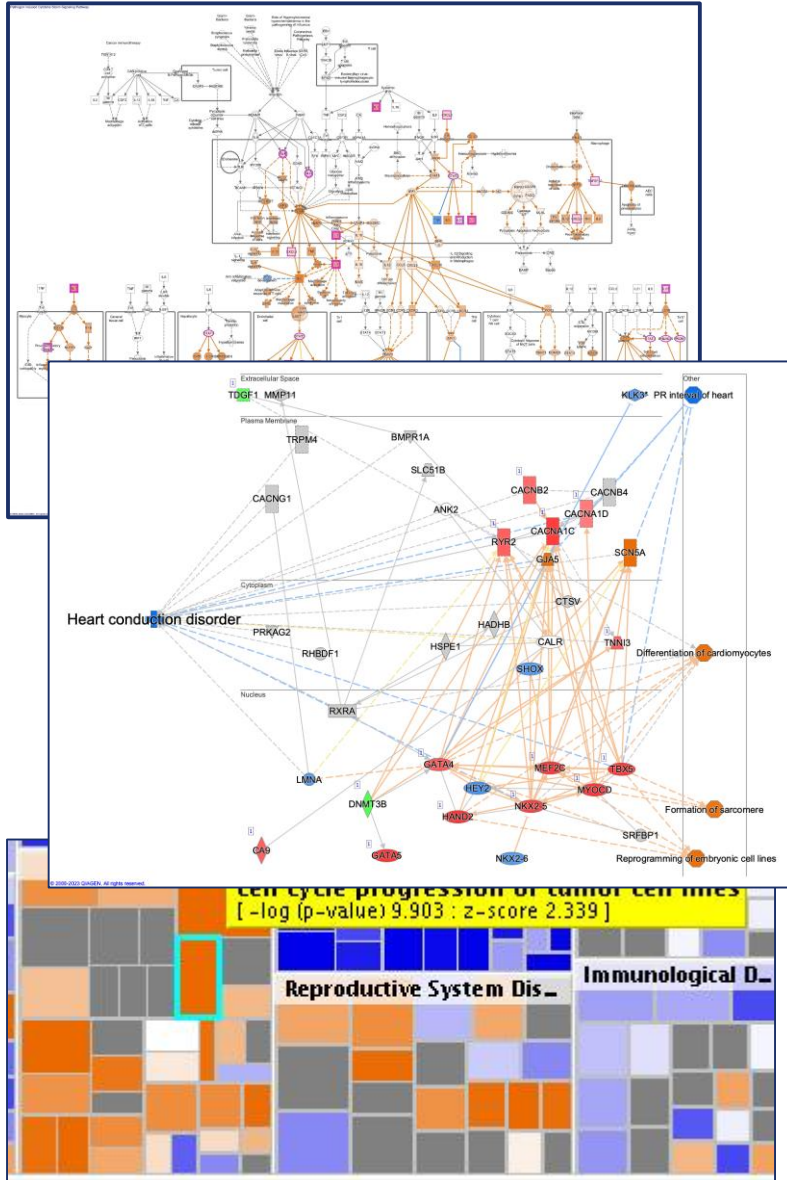
Machine
learning

What do they
relate to each
other?

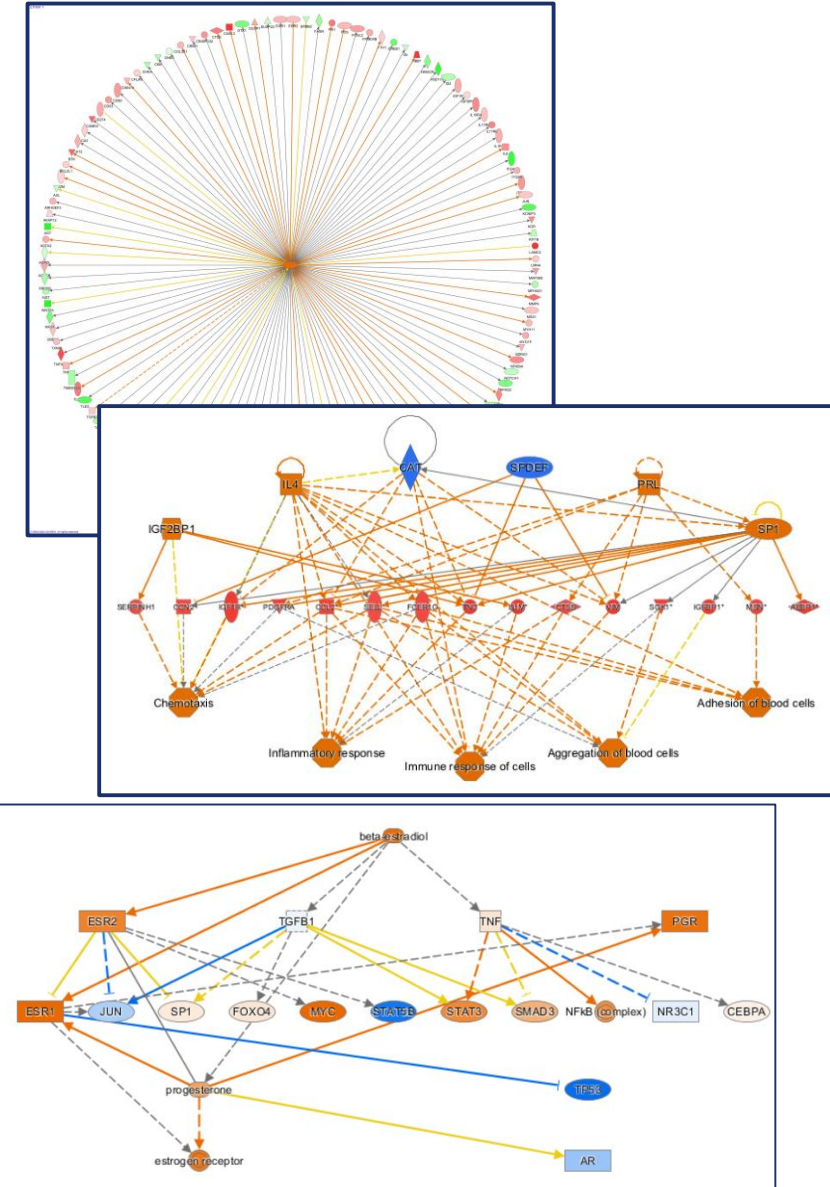
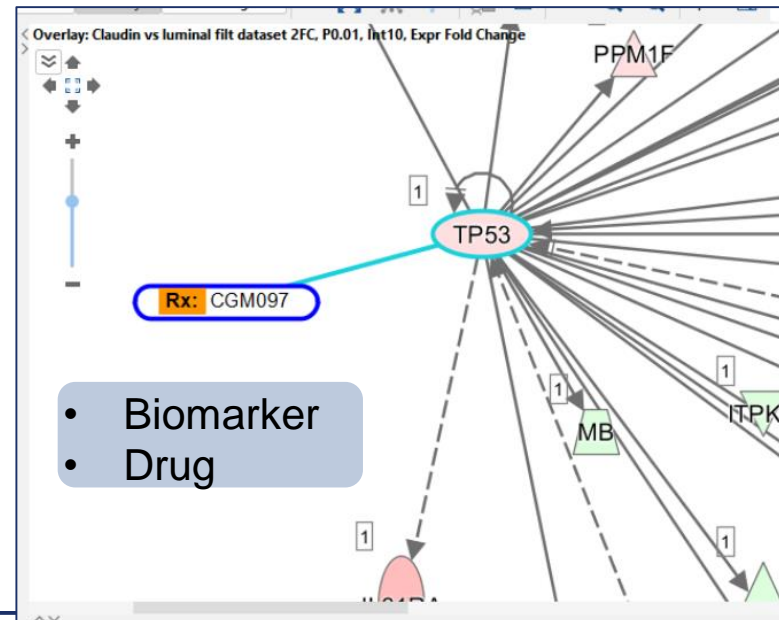


What are the
relationship
between each
molecules?

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



Sample to insight



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

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

GWAS

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

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

transcriptomic

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

Galectin-10 in serum extracellular vesicles reflects asthma pathophysiology

proteomics

> [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

From 2019-2025
1,738 literatures



The screenshot shows the NIH Medline search interface. The search term "ingenuity pathway analysis" is entered in the search bar. The results page shows 1,738 results. The first result is titled "Ingenuity pathway analysis of alpha-synuclein predicts potential signaling pathways, network molecules, biological functions, and its role in neurological diseases." by Suthar SK, Lee SY. The second result is titled "Gene set enrichment analysis and ingenuity pathway analysis to verify the impact of Wnt signaling in psoriasis treated with Taodan granules." by Chen Y, Zhang Z, Zhang Y, Jiang J, Luo Y, Fei X, Ru Y, Li B, Zhang H, Liu T, Yang Y, Kuai L, Song J, Luo Y. The third result is titled "Gene set enrichment analysis and ingenuity pathway analysis to identify biomarkers in Sheng-ji Hua-yu formula treated diabetic ulcers." by Ru Y, Zhang Y, Xiang YW, Luo Y, Luo Y, Jiang JS, Song JK, Fei XY, Yang D, Zhang Z, Z...

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

Single-cell RNA-seq



Ingenuity Literature Findings

Ingenuity Expert Findings – manually curated Findings from the full-text with contextual details from top journals

Ingenuity ExpertAssist Findings – automated text Findings that are manually reviewed from abstracts covering a broader range of publications – comprise a small percentage of IPA's findings



Ingenuity Modeled Knowledge

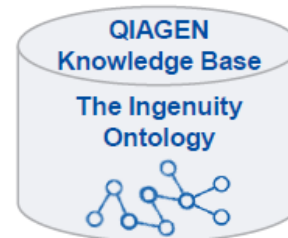
Ingenuity Expert Knowledge – content we model such as canonical pathways, toxicity lists, etc.

Ingenuity-Supported Third-Party Information – content areas include protein-protein, miRNA, biomarker, clinical trial information and others

Databases such as COSMIC, Clinical Trials, OMIM, TargetScan, BioGRID, MGD and HumanCyc



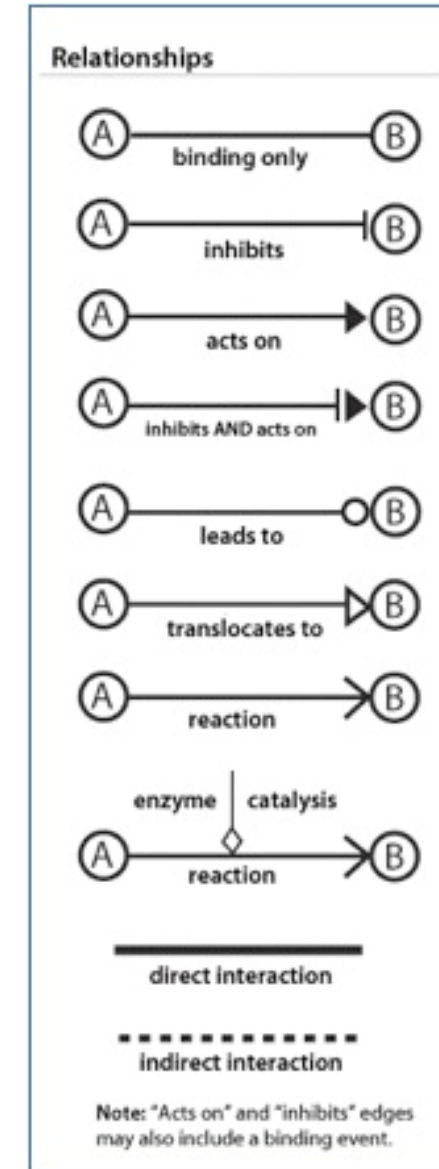
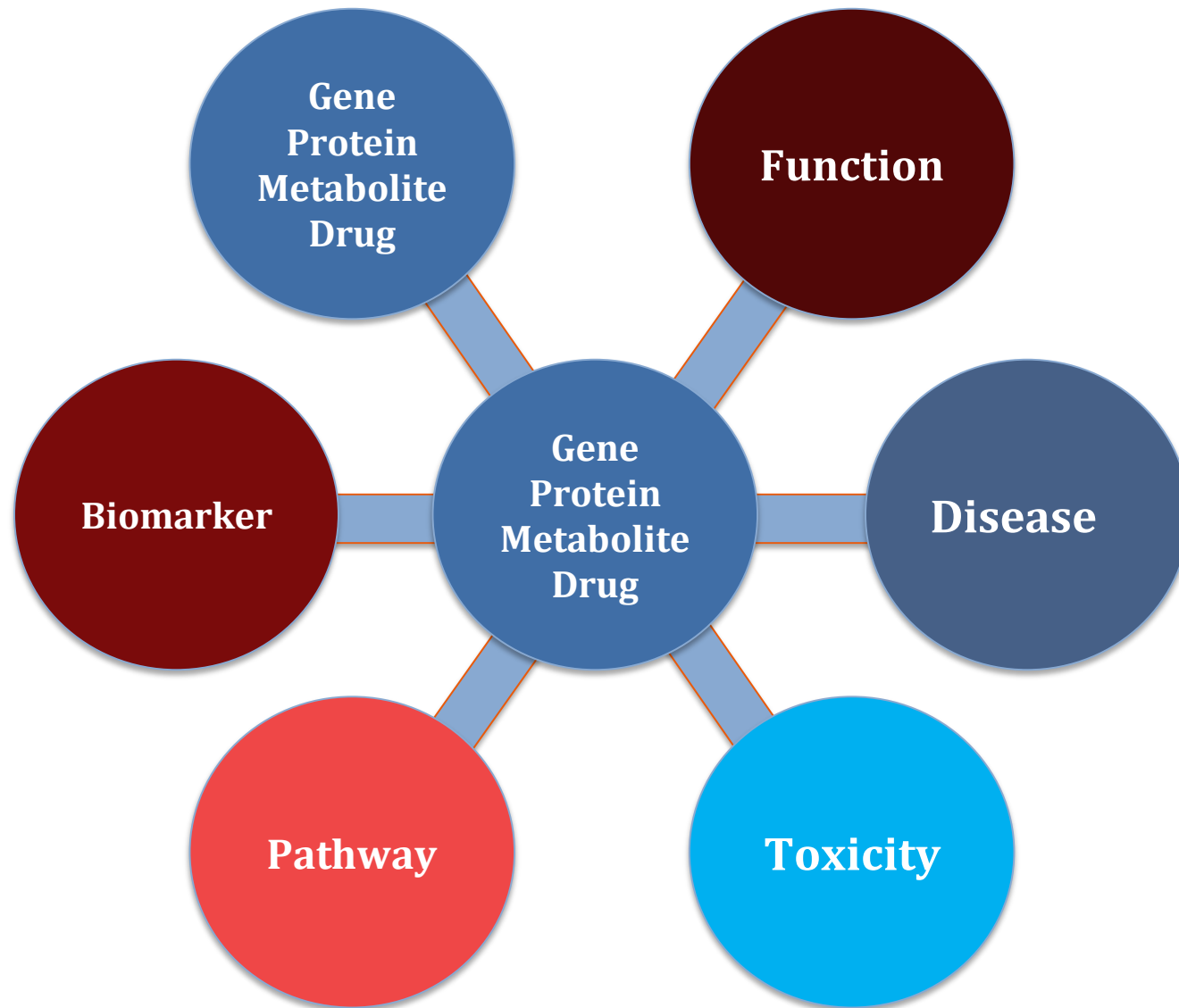
A massive, manually curated Knowledge Base updated weekly for the last ~20 years

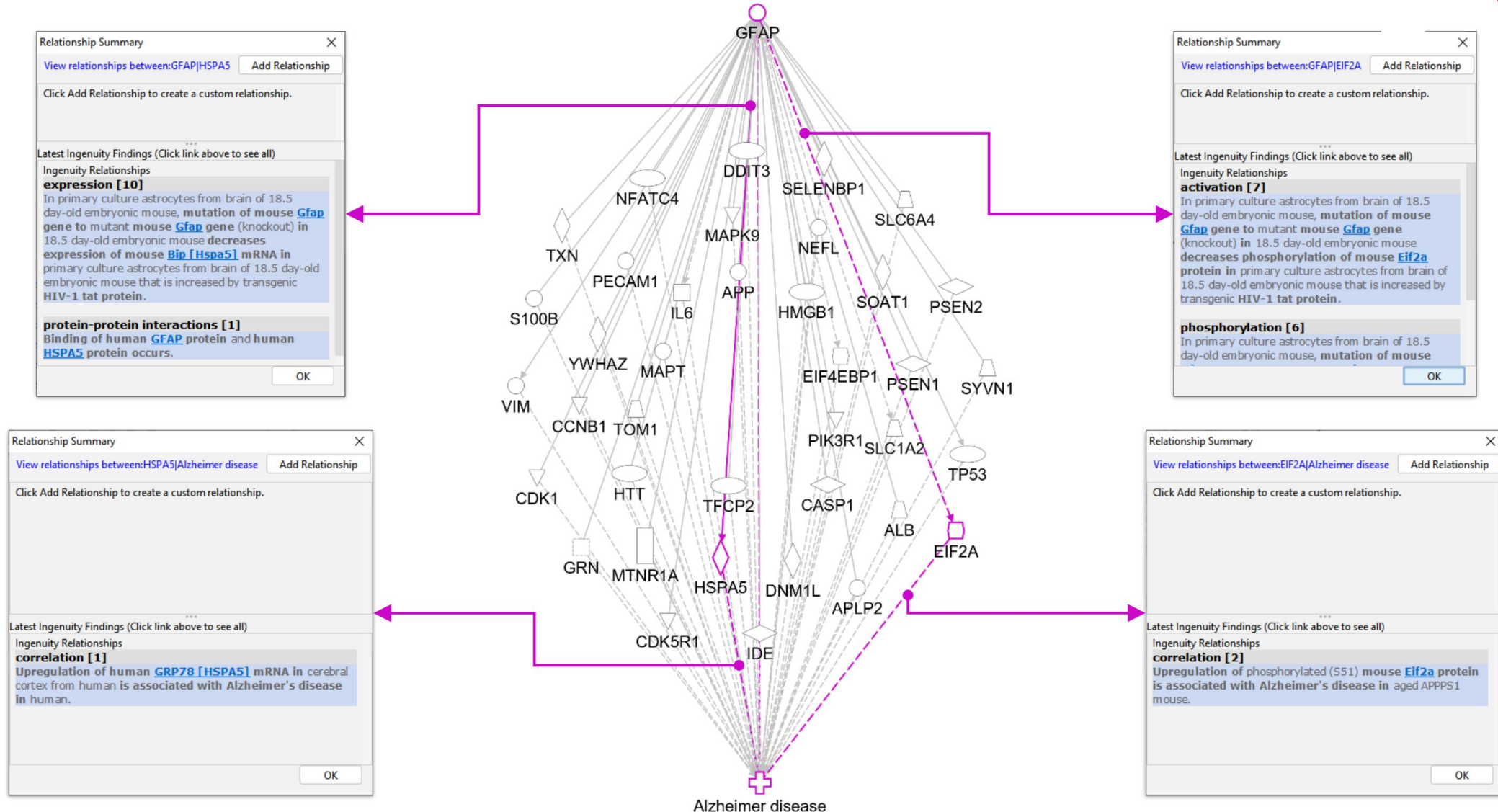


>12.6 million findings

Ingenuity Pathway Analysis







Fully supported:



Human



Mouse



Rat

What species identifiers are accepted for analysis by IPA?

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

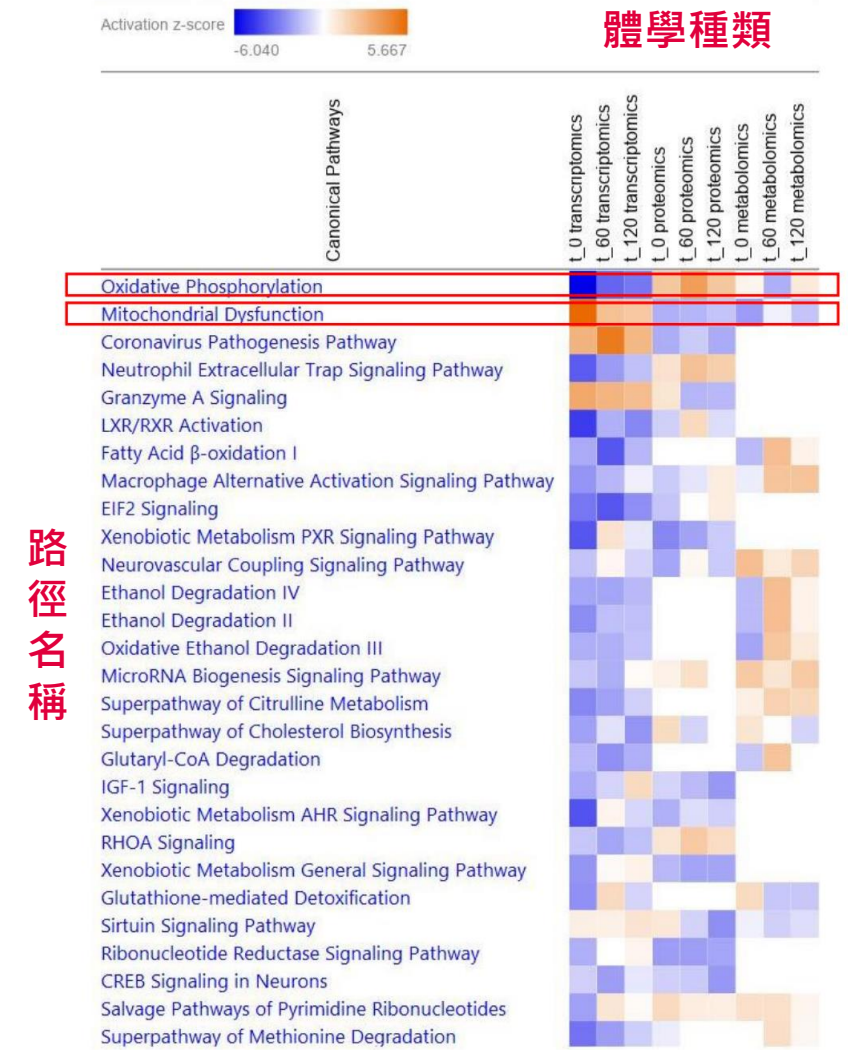
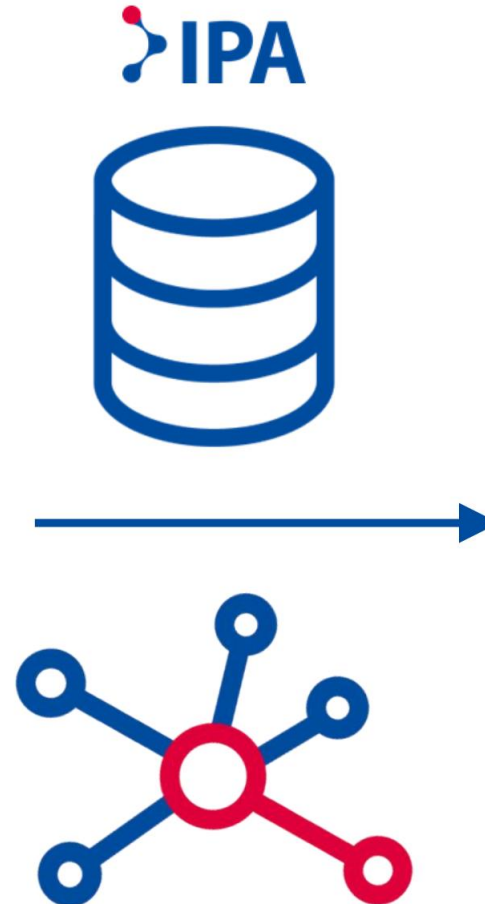
Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

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.

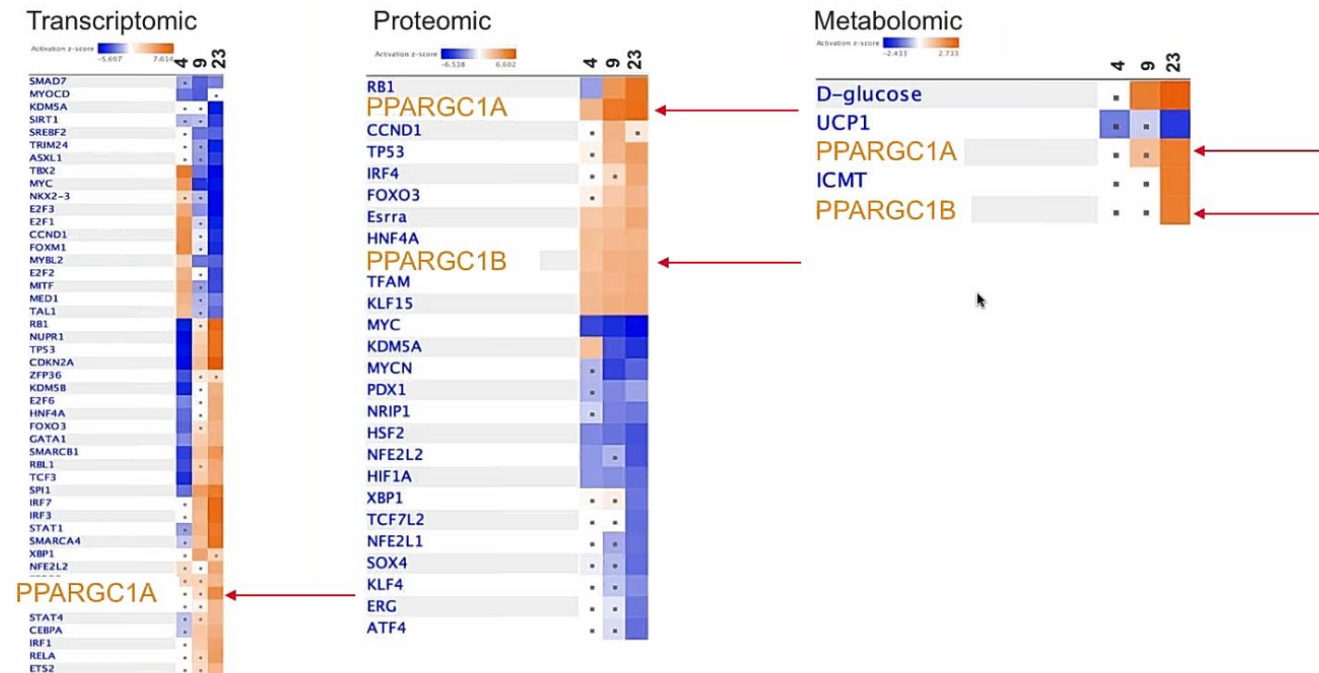


Integrate and compare genomics, transcriptomics, proteomics and metabolomics data to see the big picture on your focus research

Transcriptomics, proteomics and metabolic changes in the postnatal mouse heart identified by QIAGEN IPA and OmicSoft

Multi-omics analysis indicate similar transcriptional drivers

Upstream Analysis of transcriptomic, proteomic, and metabolomic data show induction of fatty oxidation regulation by PPARG coactivators.



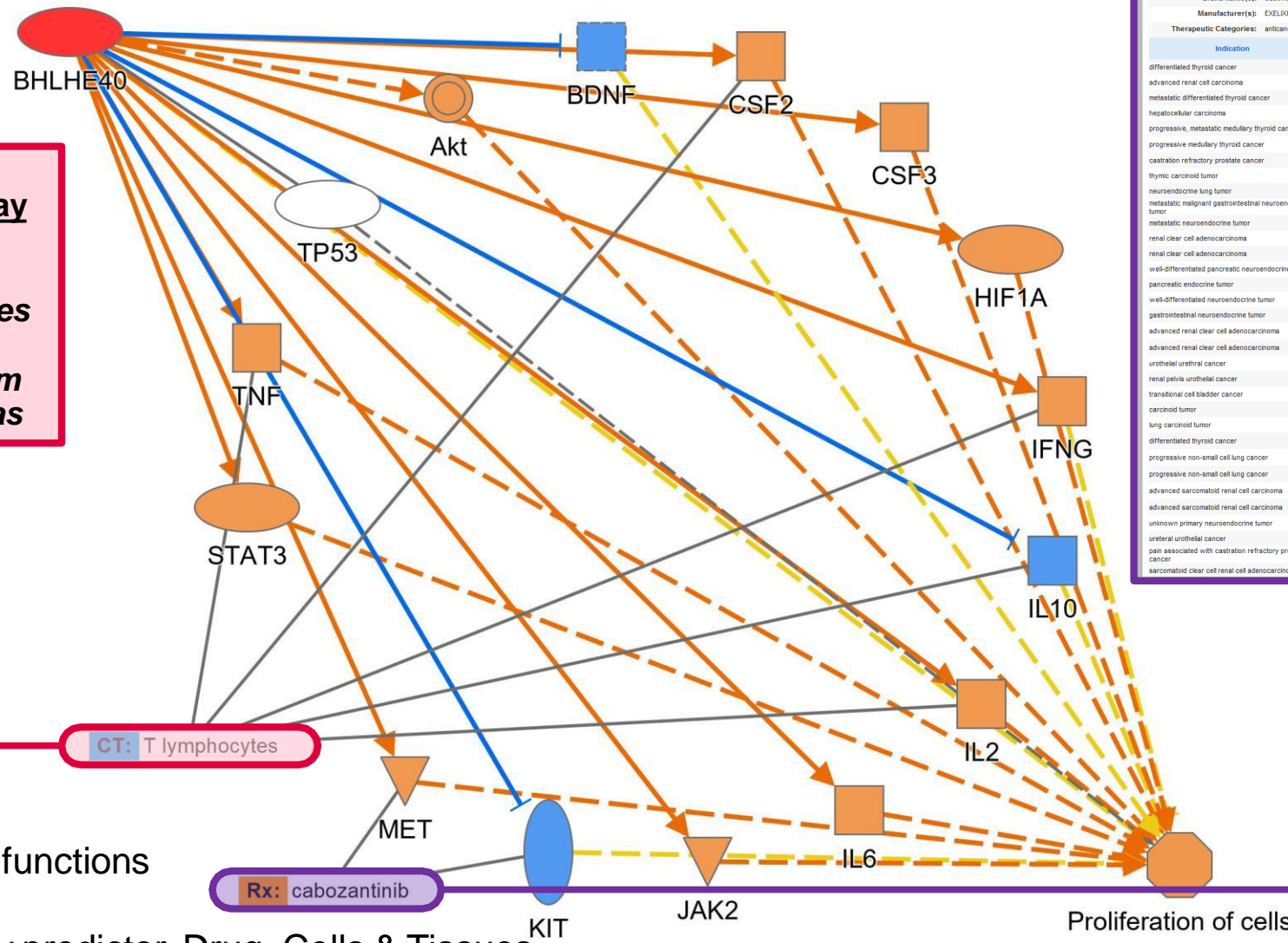
<https://go.qiagen.com/IPA-multi-omics-analysis-webinar>

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



Drug Information					
Brand Name(s): Cabometyx, Cometriq					
Manufacturer(s): EXELUNX, EXELUNX INC, PSEN PHARMA					
Therapeutic Categories: anticancer agent					
Indication	FDA Approval Status	Trial Status	Clinical Trial Sponsor(s)	NCT#	Last Updated
differentiated thyroid cancer	Approved	—	—	—	—
advanced renal cell carcinoma	Approved	—	—	—	—
metastatic differentiated thyroid cancer	Approved	—	—	—	—
hepatocellular carcinoma	Approved	—	—	—	—
progressive, metastatic medullary thyroid cancer	Approved	—	—	—	—
progressive medullary thyroid cancer	Phase 4	Active, not recruiting	Exelunx	NCT018864702022-09-28	—
castration refractory prostate cancer	Phase 3	Completed	Exelunx	NCT016652272018-02-14	—
thyroid carcinoma	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
neuroendocrine lung tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
metastatic malignant gastrointestinal neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
metastatic neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
renal clear cell adenocarcinoma	Phase 3	Recruiting	Merck Sharp & Dohme LLC	NCT045862312023-01-09	—
renal clear cell adenocarcinoma	Phase 3	Recruiting	Merck Sharp & Dohme LLC	NCT045862312023-01-09	—
well-differentiated pancreatic neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
pancreatic endocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
well-differentiated neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
gastrointestinal neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
advanced renal clear cell adenocarcinoma	Phase 3	Active, not recruiting	Bristol-Myers Squibb	NCT031411772022-12-19	—
advanced renal clear cell adenocarcinoma	Phase 3	Active, not recruiting	Bristol-Myers Squibb	NCT031411772022-12-19	—
urothelial urethral cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050829502023-01-07	—
renal pelvis urothelial cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050829502023-01-07	—
transitional cell bladder cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050829502023-01-07	—
carcinoid tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
lung carcinoid tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
differentiated thyroid cancer	Phase 3	Active, not recruiting	Exelunx	NCT036903802021-07-13	—
progressive non-small cell lung cancer	Phase 3	Active, not recruiting	Hoffmann-La Roche	NCT044714202022-12-09	—
progressive non-small cell lung cancer	Phase 3	Active, not recruiting	Hoffmann-La Roche	NCT044714202022-12-09	—
advanced sarcomatoid renal cell carcinoma	Phase 3	Active, not recruiting	Bristol-Myers Squibb	NCT031411772022-12-19	—
advanced sarcomatoid renal cell carcinoma	Phase 3	Active, not recruiting	Bristol-Myers Squibb	NCT031411772022-12-19	—
unknown primary neuroendocrine tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
urethral urothelial cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050829502023-01-07	—
pain associated with castration refractory prostate cancer	Phase 3	Terminated	Exelunx	NCT015224432018-04-23	—
sarcomatoid clear cell renal cell adenocarcinoma	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT037931662023-01-10	—

Step by Step slide 57-63

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



Processing, curation and QA

QIAGEN OmicSoft Studio



141,000+ comparison

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



Curated Findings

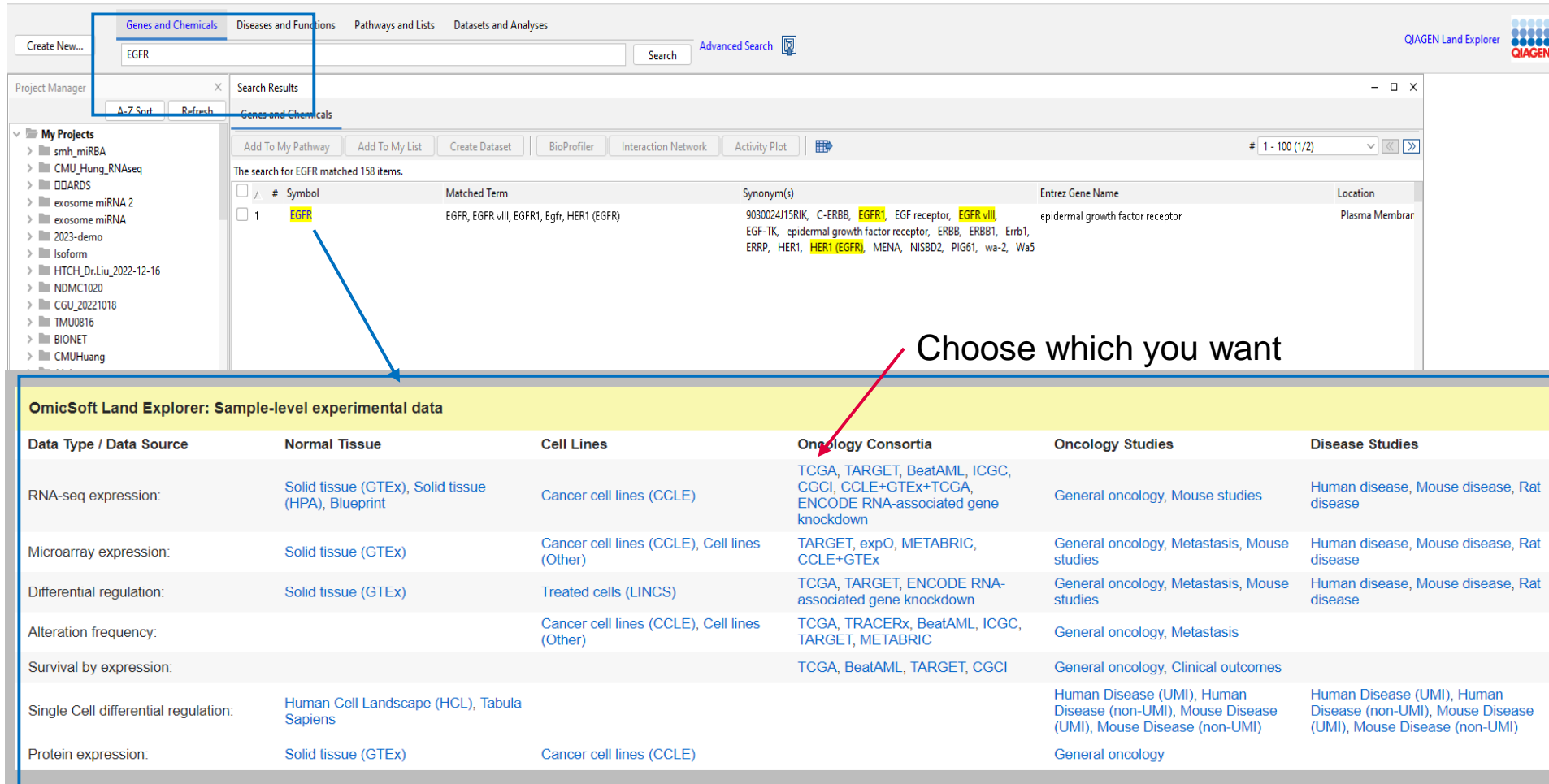
Ingenuity Pathway Analysis



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

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

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

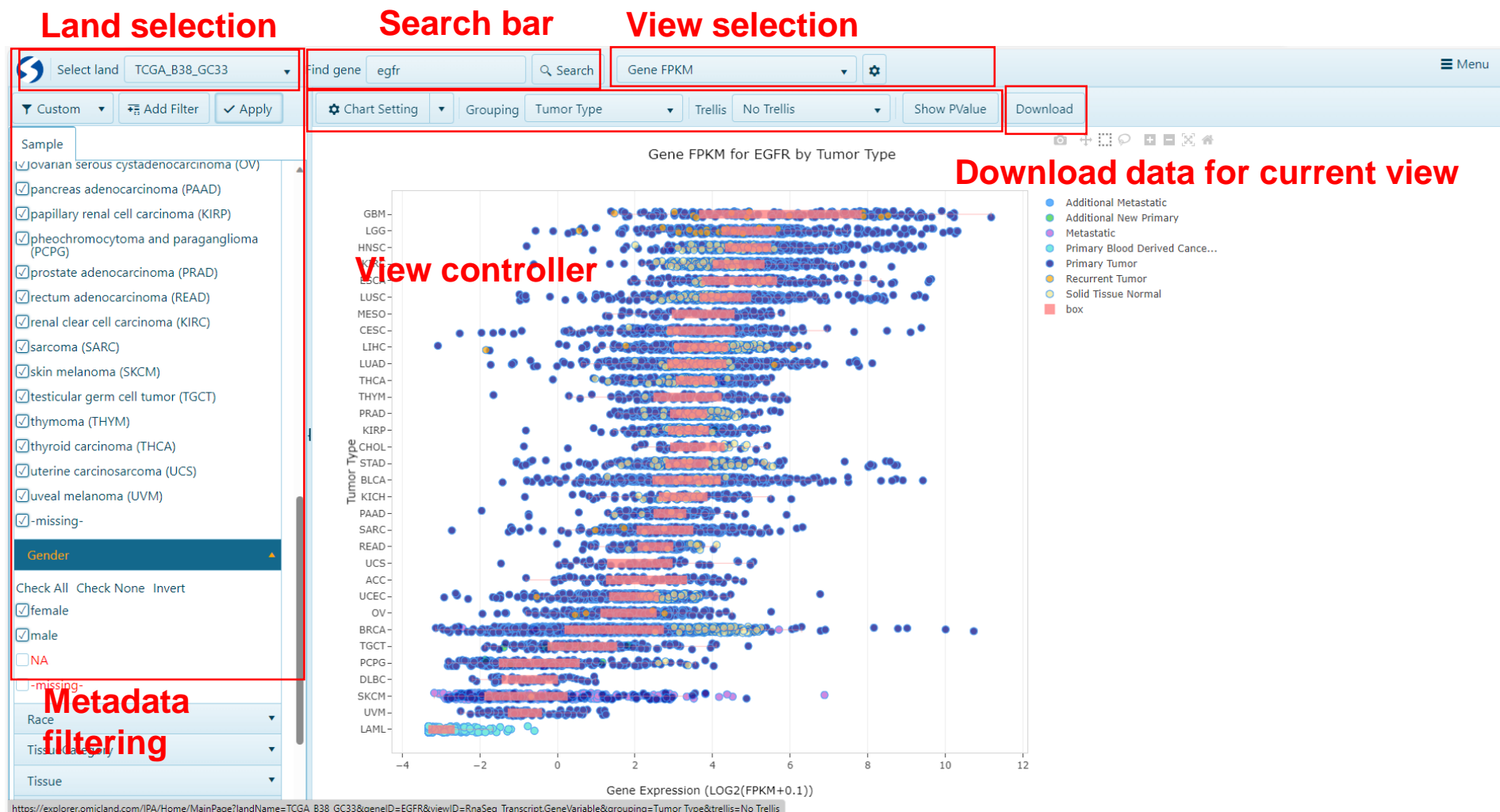


The screenshot shows the OmicSoft Land Explorer interface. The top navigation bar includes tabs for Genes and Chemicals, Diseases and Functions, Pathways and Lists, and Datasets and Analyses. The search bar contains "EGFR" and the search results show 158 items. A blue arrow points from the "EGFR" search result in the top panel to the "OmicSoft Land Explorer: Sample-level experimental data" table below. A red arrow points from the text "Choose which you want" to the "Oncology Consortia" column in the table.

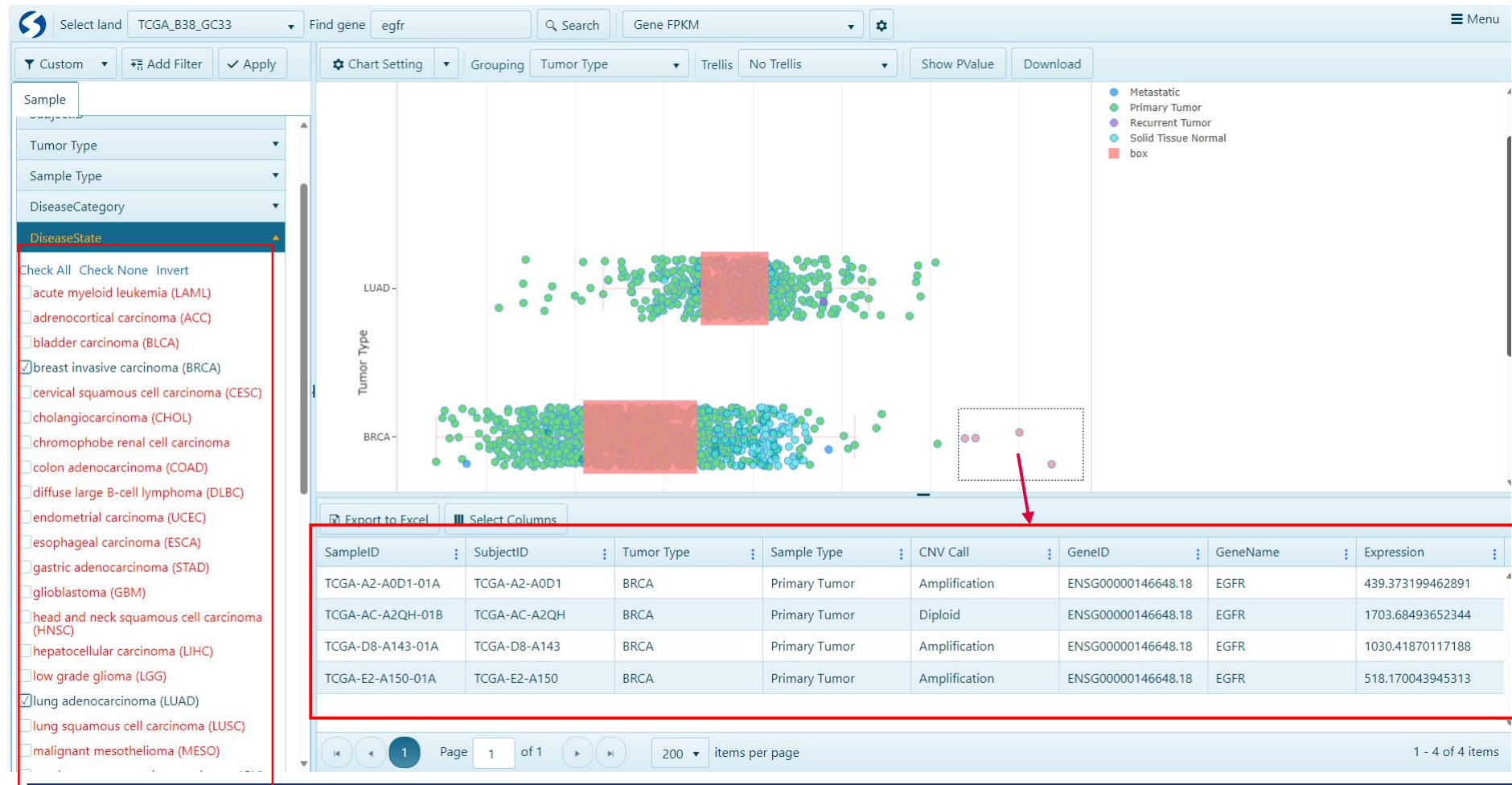
Data Type / Data Source	Normal Tissue	Cell Lines	Oncology Consortia	Oncology Studies	Disease Studies
RNA-seq expression:	Solid tissue (GTEx), Solid tissue (HPA), Blueprint	Cancer cell lines (CCLE)	TCGA, TARGET, BeatAML, ICGC, CGCI, CCLE+GTEx+TCGA, ENCODE RNA-associated gene knockdown	General oncology,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

IPA Gene View :OmicSoft Land Explorer

- TCGA-B38-G33



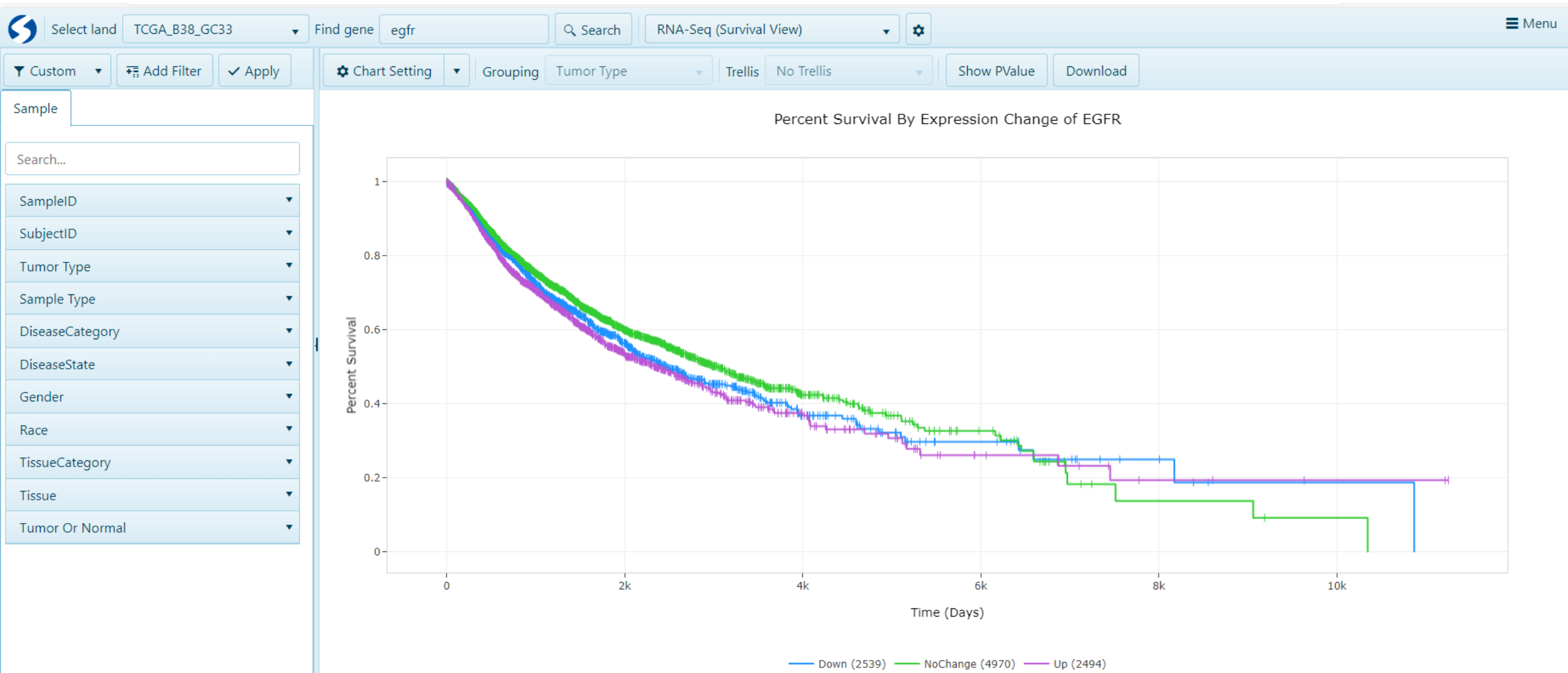
- Through DiseaseState filter, to observe the expression difference of EGFR gene in cancer type in TCGA
- Select a specific experimental group to view more detailed information.



The screenshot shows the OmicSoft Land Explorer interface. The top navigation bar includes a search bar for 'egfr' and a dropdown for 'Gene FPKM'. The left sidebar shows a list of filters, with 'DiseaseState' selected. The main plot area displays a scatter plot of EGFR expression (log2 FPKM) across different cancer types (LUAD, BRCA). The plot is grouped by 'Tumor Type' and 'Trellis'. A red box highlights the BRCA group, and a red arrow points to a detailed view of BRCA samples.

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



Create New...

Genes and Chemicals

Diseases and Functions

Pathways and Lists

Datasets and Analyses

Sleep Disorders [abnormal sleep pattern,sleep difficulties,...]

Search

Advanced Search

Project Manager

A-Z So

QCIT_mod

selected_skin_re

selected_miRNA

myList

colon cancer-a

Ulcerative Colit

hsa_miRNA filte

hsa_miRNA

cataract

cataract.sig

HCC_CD8

HCC_relapse

HCC_relapse_d

Analyses

Nature_comm

Nature_comm

QCIT_mod - 20

selected_skin_re

selected_miRNA

colon cancer-a

Ulcerative Colit

hsa_miRNA - 20

cataract - 2024-0

Summary

Experiment M

Analysis Set

Top Canonic

Top Upstream

Top Diseases

Search Results

Diseases and Functions

Add To My Pathway

Add To My List

Annotations

Show Findings

Effect on Function

BioProfiler

Activity Plot

Show Functions

Expand Functions

The search for Sleep Disorders matched 1 diseases and functions.

Matching Diseases & Functions

Organismal Injury and Abnormalities

sleep disorder

Sleep Disorders

Neurological Disease

sleep disorder

Sleep Disorders

Psychological Disorders

sleep disorder

Sleep Disorders

Associated Molecule

312

312

312

312

312

312

312

312

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

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

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

Evaluate Metadata View As Heatmap View Comparison Customize Table

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

Analysis Name	Project	case...	case.t...	case.t...	case.t...	comp...	comp...	comp...	webli...	CP (z...	UR (z...	CN (z...	DE (z...	z...	DM (z...
1358- normal control [hepatocellular carcinoma] 3-D culture	SingleCellHuman...	normal control	kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GSE110...	50.00	52.09	46.93	47.23	25.79			
19- normal control [skeletal muscle] NA 8925	RatDisease	normal control	skeletal muscle	NA	Treatment vs...	TreatTime[da...	GSE57816.GPL1	https://www...	55.90	45.83	38.73	46.93	15.79		
671- normal control [bronchial epithelium] air liq	SingleCellHuman...	normal control	bronchial epi...	air liquid int...	Cell Type vs ...	pulmonary io...	GSE102580.UN	https://www...	55.90	48.99	30.00	51.57	13.41		
654- normal control [bronchial epithelium] air liq	SingleCellHuman...	normal control	bronchial epi...	air liquid int...	Cluster vs Ot...	pulmonary io...	GSE102580.UN	https://www...	55.90	48.99	30.00	51.57	13.41		
25- hepatocellular carcinoma (LIHC) [liver] NA 116	OncoHuman	hepatocellul...	liver	NA	Treatment1 v...	CellLine:Infec...	GSE20948.GPL1	https://www...	55.90	52.92	26.46	50.53	16.87		
5349- intrahepatic cholangiocarcinoma [liver] 53	SingleCellHuman...	intrahepatic ...	liver		Cell Type vs ...	cytotoxic T ce...	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...	GSE1427...		55.90	57.45	30.00	45.13	15.11		
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cluster vs Ot...	embryonic st...	GSE1427...		55.90	56.67	31.62	44.96	27.78		
3682- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cell Type vs ...	embryonic st...	GSE1427...		55.90	56.67	31.62	44.96	27.78		
87- disease [airway epithelium] NA 6093	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...	GSE1427...		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...	GSE1427...		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...	GSE1427...		55.90	53.85	31.62	45.16	16.44		
23- normal control [fore skin] 4-thiouridine	HumanDisease	normal control	fore skin	4-thiouridine	Treatment1 v...	SampleMat...	GSE59...		55.90	53.96	30.00	46.13	15.61		
1- prostate cancer [prostate] NA 116	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 116	HumanDisease	nephrolithiasis	papillary duct				GSE73680...		50.00	53.85	30.00	44.96	24.88		
8878- normal control [colorectal cancer] NA 116	SingleCellHuman...	colorectal can...	colon rectu...				GSE1427...		55.90	58.31	33.17	37.19	33.85		
1388- normal control [embryo] NA 116	SingleCellMouse...	normal control	embryo				GSE1427...		55.90	56.57	22.36	46.13	13.38		
10818- normal control [bladder] NA 116	SingleCellHuman...	normal control	bladder				GSE1427...		55.90	54.77	22.36	46.13	26.44		
216- breast cancer [breast] NA 116	OncoHuman	breast carcin...	breast				GSE1427...		55.90	41.24	20.00	43.02	8.39		
1- normal control [lung] NA 116	MouseDisease	normal control	lung	NA	Treatment vs...	ExperimentG...	GSE1427...		55.90	44.91	22.36	48.38	12.46		
161- lung adenocarcinoma [lung] NA 116	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...	GSE1427...		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...	GSE1427...		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...	GSE36...		55.90	45.83	33.57	41.26	10.20		
7902- normal control [fore skin] pellet culture; TGF	SingleCellHuman...	normal control	fore skin	pellet culture...	Cell Type vs ...	chondrocyte ...	GSE160625.UN	https://www...	40.82	46.00	30.00	53.59	14.20		
105- normal control [heart] NA 2522	RatDisease	normal control	heart	NA	Other Comp...	Tissue:Gend...	GSE53960.GPL1	https://www...	50.00	48.11	28.28	43.76	10.05		
7781- normal control [fore skin] pellet culture; TGF	SingleCellHuman...	normal control	fore skin	pellet culture...	Cluster vs Ot...	chondrocyte ...	GSE160625.UN	https://www...	50.00	50.00	26.46	42.53	20.41		
6271- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiation...	Cell Type vs ...	chondrogeni...	GSE1427...		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...	GSE1427...		55.90	45.83	26.46	42.10	8.52		
7640- idiopathic pulmonary fibrosis [bronchoalve	SingleCellHuman...	idiopathic p...	bronchoalve...		Cluster vs Ot...	epithelial cell...	GSE15...		55.90	56.57	24.49	42.06	27.33		
10- non-small cell lung carcinoma [lung] NA 1141	OncoHuman	non-small cel...	lung	NA	Other Comp...	SmokingStat...	GSE15...		55.90	37.71	20.00	42.05	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...	Treatment:Tr...	GSE1781...		55.90	61.24	43.59	35.73	7.59		
EEC P32 Tumor vs Norm RPKM123 - 2020-02-14 11 NDMC-0212									55.90	86.60		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	8.66	
MetastaticMelanoma mRNA_vs_Normal PMID_204 CT20190116									55.90	61.24	44.72	59.25	41.30		

Selected 0 / 140569

Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project

Cell & Tissue

Datasets
information

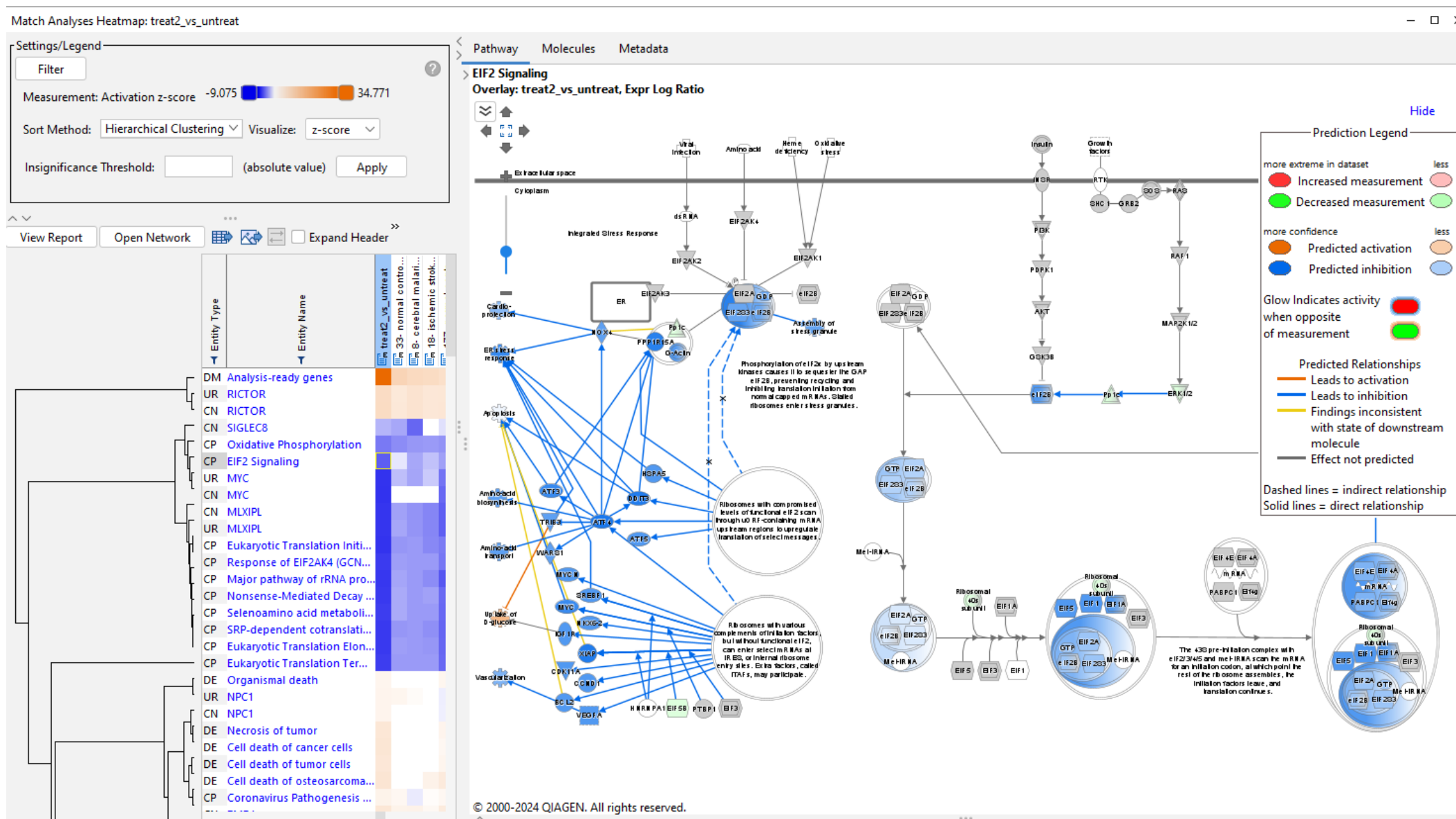
similar

opposite

The screenshot displays the OmicSoft IPA Analysis Match interface. On the left, a 'Project' selection panel shows a tree view with 'OmicSoft' expanded, containing 'OncoLand', 'DiseaseLand', 'SingleCellLand', and 'Normal Cells and Tissues'. The main window is divided into two panes. The left pane lists analysis results with columns for 'Analysis Name', 'Project', 'Case', 'Tissue', 'Treatment', 'CellLine', 'SamplingTime', and 'GSE'. The right pane shows a table of z-scores for various datasets, with columns for 'CP (z-s...', 'UR (z-s...', 'CN (z-s...', 'DE (z-s...', 'z-score...', and 'D...'. The table contains numerical values for each dataset, with some cells highlighted in pink and others in blue, indicating different levels of similarity or opposition.

atasets
ta

z-scores



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...

lung cancer

Search

Advanced Search

QIAGEN Land Explorer



Search Results

Diseases and Functions **Datasets and Analyses**

Search Results

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

Folder Types

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

Open

Add to Comparison

Customize Table

Cre... 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 adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)
2446- normal control;pulmonary fibrosis [lung] 2445	analysis	2024/01/12 09:16:59	normal control;pulmonary fibrosis
6615- hepatocellular carcinoma (LIHC);intrahepatic cholangiocar...	analysis	2024/01/12 09:16:30	hepatocellular carcinoma (LIHC);intrahepatic cholangiocarcinoma (ICC)
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 obstructive pulmonary disease (COPD);disease co...
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 leukemia (LAML) [bone marrow] NA 168
1- acute myeloid leukemia (LAML) [bone marrow] NA 213	analysis	2024/01/09 02:16:46	acute myeloid leukemia (LAML) [bone marrow] NA 213
1- breast cancer [breast;lymph node;peripheral blood] 0	analysis	2024/01/09 02:13:03	breast cancer
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 [breast] estradiol;ethanol 0
1- breast carcinoma [breast] estradiol;ethanol 4	analysis	2024/01/09 02:12:05	breast carcinoma [breast] estradiol;ethanol 4
1- germ cell cancer [ovary] NA 4	analysis	2024/01/09 02:09:17	germ cell cancer
1- kidney clear cell sarcoma (CCSK) [kidney] NA 14	analysis	2024/01/09 02:07:58	kidney clear cell sarcoma (CCSK) [kidney] NA 14
1- kidney rhabdoid cancer [kidney] Transfection_BAF47 442	analysis	2024/01/09 02:07:40	kidney rhabdoid cancer [kidney] Transfection_BAF47 442
1- childhood acute lymphocytic leukemia [hematopoietic tissue]...	analysis	2024/01/09 02:02:21	childhood acute lymphocytic leukemia [hematopoietic tissue]...
1- endometrial cancer;endometrial squamous cell carcinoma;ova...	analysis	2024/01/09 02:01:04	endometrial cancer;endometrial squamous cell carcinoma;ova...

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

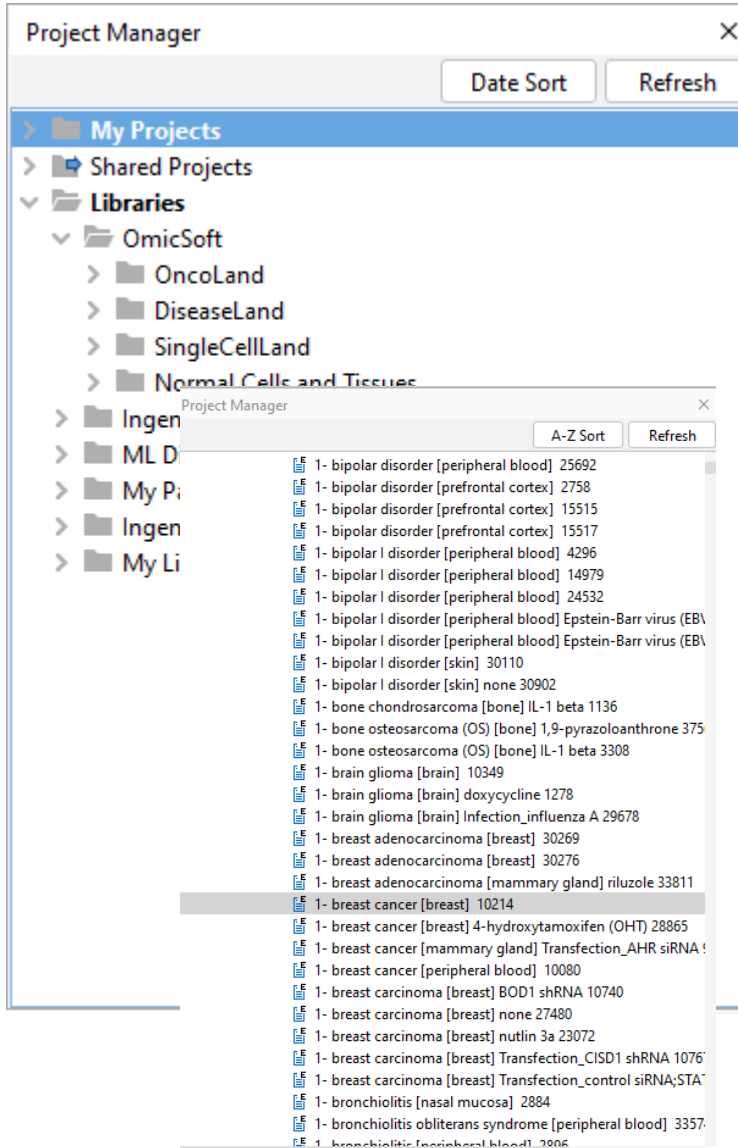
cellmarkers	CD235A-
celltype	lung cell
comparisoncategory	Cluster vs Others
comparisoncontrast	T cell (cluster) vs others
diseasestate	lung adenocarcinoma (LUAD);lung squamous cell carcinoma (LUSC)
ethnicity	Caucasian
gender	female;male
organism	human
platformname	NGS.Illumina.NextSeq500
smokingstatus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

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

Graphical summary



Project Manager

My Projects

Shared Projects

Libraries

OmicSoft

OncoLand

DiseaseLand

SingleCellLand

Normal Cells and Tissues

Ingen

ML D

My P

Ingen

My Li

Project Manager

A-Z Sort

Refresh

1- bipolar disorder [peripheral blood] 25692

1- bipolar disorder [prefrontal cortex] 2758

1- bipolar disorder [prefrontal cortex] 15515

1- bipolar disorder [prefrontal cortex] 15517

1- bipolar I disorder [peripheral blood] 4296

1- bipolar I disorder [peripheral blood] 14979

1- bipolar I disorder [peripheral blood] 24532

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

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

1- bipolar I disorder [skin] 30110

1- bipolar I disorder [skin] none 30902

1- bone chondrosarcoma [bone] IL-1 beta 1136

1- bone osteosarcoma (OS) [bone] 1,9-pyrazoloanthrone 375

1- bone osteosarcoma (OS) [bone] IL-1 beta 3308

1- brain glioma [brain] 10349

1- brain glioma [brain] doxycycline 1278

1- brain glioma [brain] Infection_influenza A 29678

1- breast adenocarcinoma [breast] 30269

1- breast adenocarcinoma [breast] 30276

1- breast adenocarcinoma [mammary gland] riluzole 33811

1- breast cancer [breast] 10214

1- breast cancer [breast] 4-hydroxytamoxifen (OHT) 28865

1- breast cancer [mammary gland] Transfection_AHR siRNA

1- breast cancer [peripheral blood] 10080

1- breast carcinoma [breast] BOD1 shRNA 10740

1- breast carcinoma [breast] none 27480

1- breast carcinoma [breast] nutlin 3a 23072

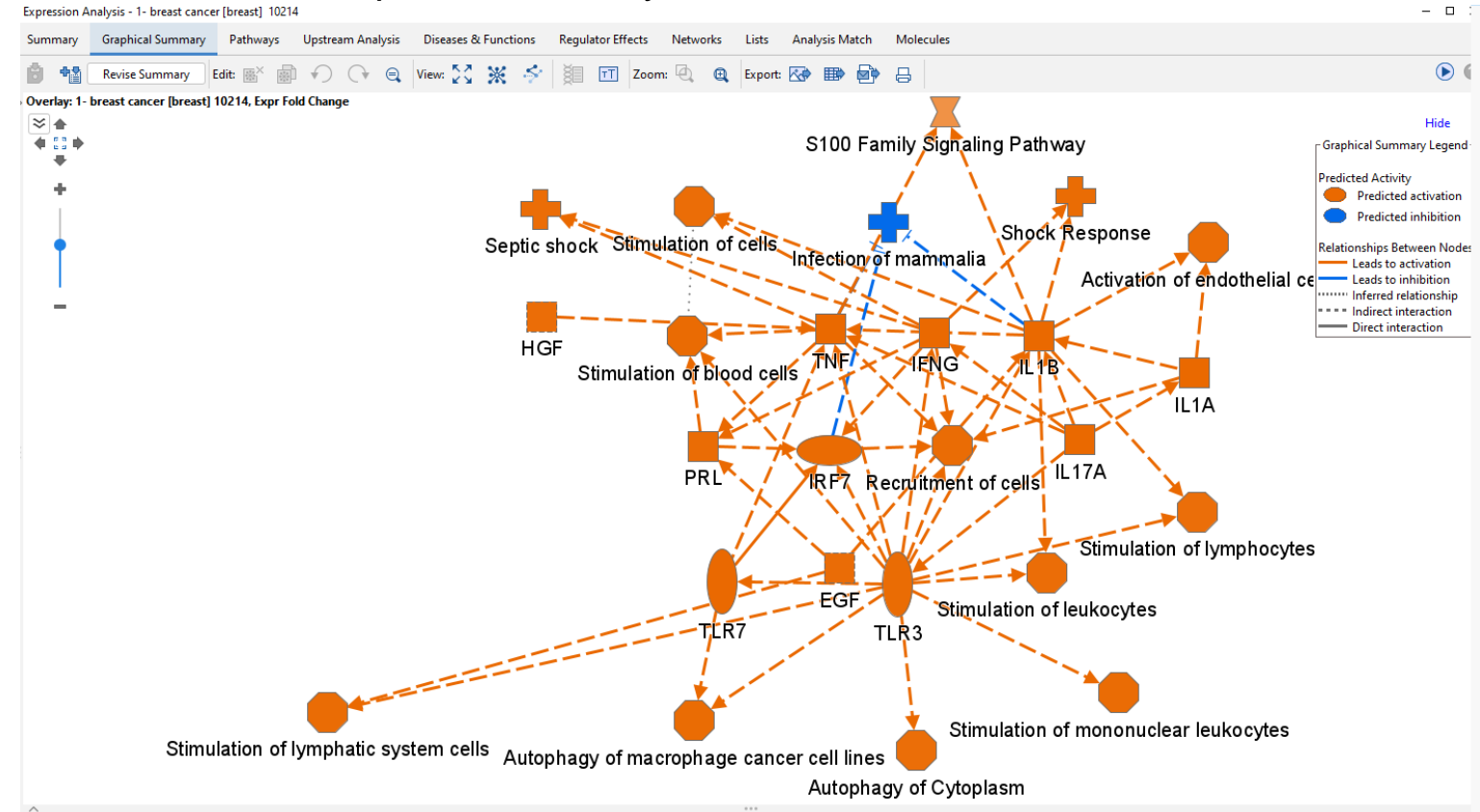
1- breast carcinoma [breast] Transfection_CISD1 shRNA 1076

1- breast carcinoma [breast] Transfection_control siRNA;STA

1- bronchiolitis [nasal mucosa] 2884

1- bronchiolitis obliterans syndrome [peripheral blood] 3357

1- bronchiolitis [peripheral blood] 2806



RNA-seq analysis portal

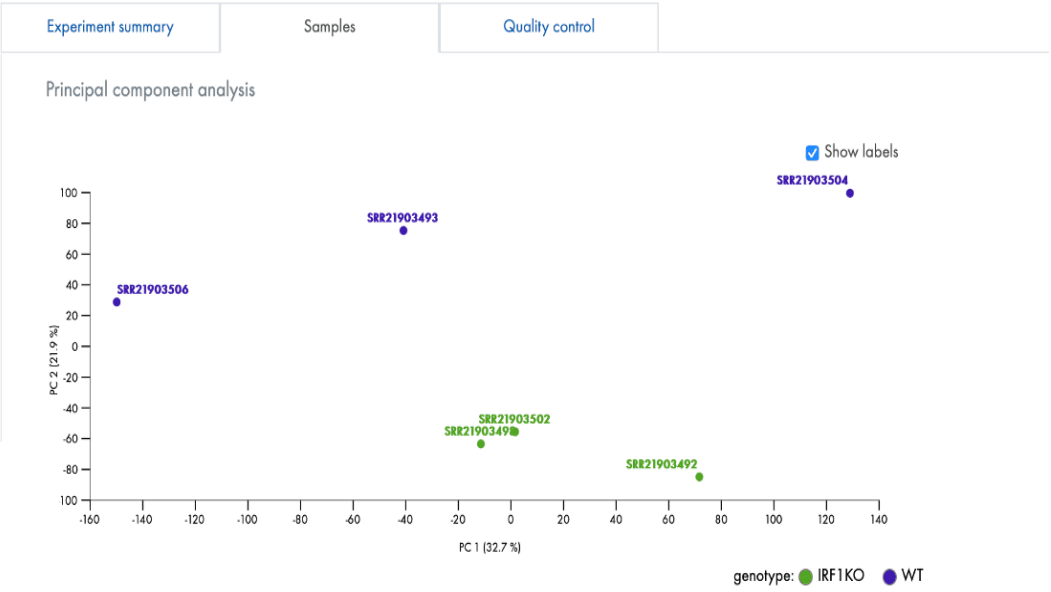


For the easy three step
You can analyze your RNA-seq
via IPA

1. Upload your data
From SRA or your files
2. Align and count
Align to genome (more than 20 species)
Normalization counts
3. Create experiment
Evaluate Differential gene expression

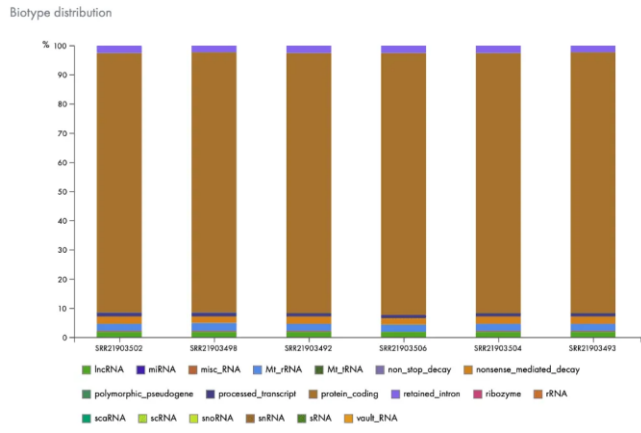
RNA-seq analysis portal QC plot

Experiment summary and QC
Summary of experiment setup, samples and attributes, and sample quality control [Print view](#)



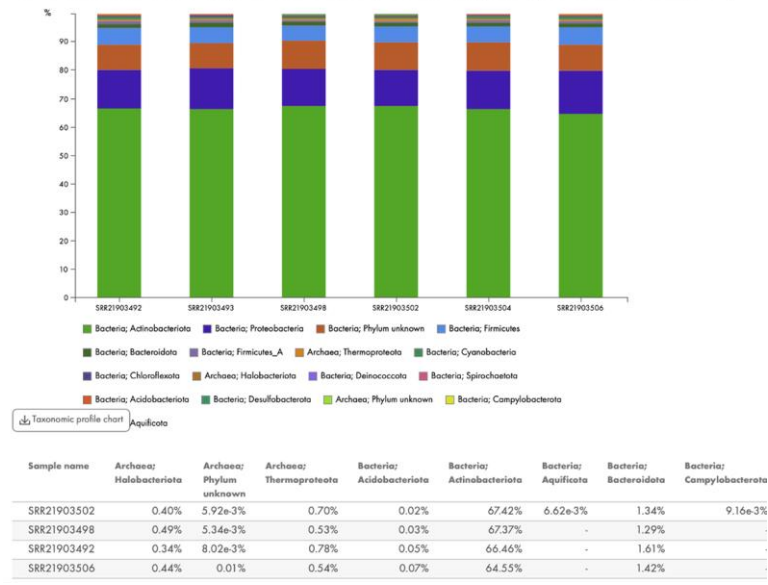
Mapped by type

Sample name	Mapped to gene (intron + exon)	Mapped to intron	Mapped to exon	Mapped to intergenic region
SRR21903502	93.76%	11.29%	82.47%	6.24%
SRR21903498	93.59%	11.70%	81.89%	6.41%
SRR21903492	94.13%	10.79%	83.35%	5.87%
SRR21903506	94.12%	10.89%	83.23%	5.88%
SRR21903504	93.71%	11.65%	82.06%	6.29%
SRR21903493	94.05%	10.57%	83.47%	5.95%

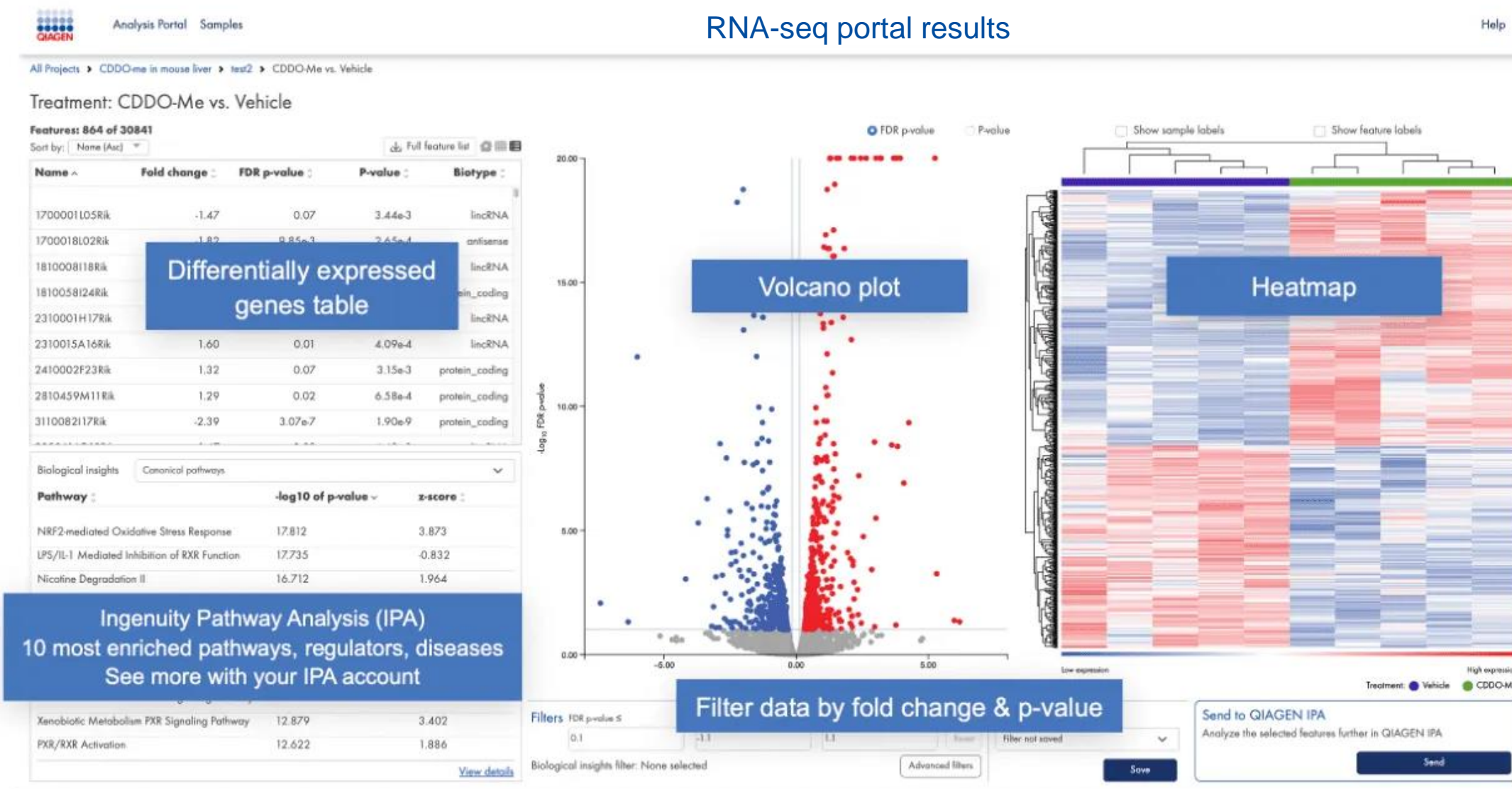


Taxonomic profile of unmapped reads

Taxonomic profiling is performed for samples with a high level of unmapped reads as this can indicate sample contamination. If all samples have low levels of unmapped reads, the taxonomic profile is not shown. Plot and table show the relative abundance at phylum level. Reads that map equally well to two or more phyla are assigned to the common ancestor (kingdom level).



RNA-seq portal results



IPA interpret

early vs norm

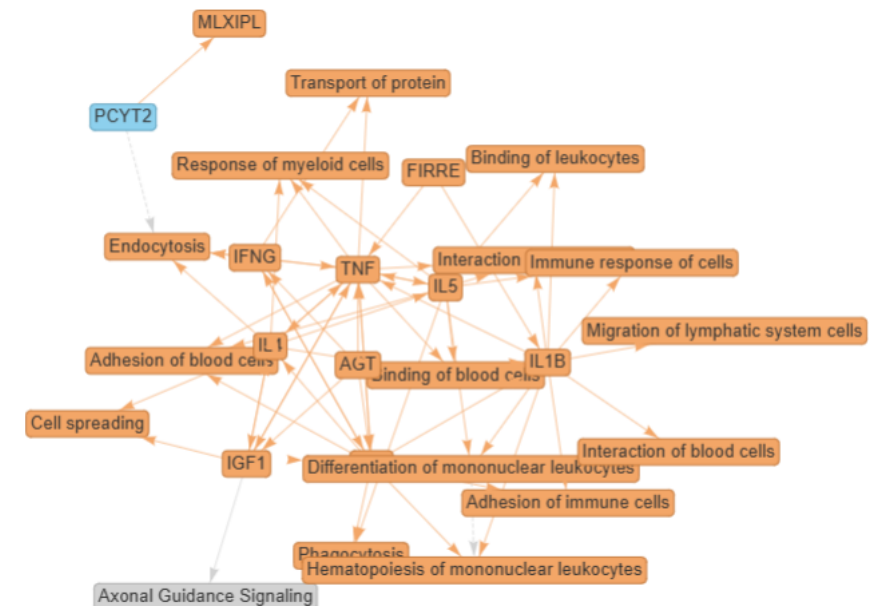
Created on September 30, 2024, from observation "early vs norm" in dataset "All MSG Levels"



Dataset molecules

Name	P-value ▲	Fold Change	Molecule Type
Filter	Filter <	Filter abs. >	Select items ▼
RP11-49K24.6	5.55e-12	181.31	other
AL671762.1	1.49e-10	168.56	other
COMMD3-BMI1	3.64e-10	27.84	transcription regulator
LOC124909373	6.85e-10	249.29	other
PLEC	1.05e-9	5.13	other

Graphical Summary



Top Biological Themes

1. Immune Response and Inflammation

This network extensively depicts relationships between various inflammatory cytokines and immune cells. Genes such as IL1B, IL4, IL5, IL13, and TNF are generally associated with immune responses and inflammatory processes. The interactions suggest a complex network regulating immune responses, cell signaling, and inflammatory phenomena.








2. Cell Adhesion and Interaction

The network shows significant activity in genes involved in the adhesion of blood and immune cells, and in binding functions. IL13, IL1B, IL4, IL5, and TNF all contribute to the adhesion and interaction of cells, which is crucial for immune surveillance and response to infection or injury.

Canonical Pathways





















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

Pathway	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter <	Filter abs. >	Filter >
Collagen biosynthesis and modifying enzymes	4.94e-8 	4.36 	28.36 
Axonal Guidance Signaling	8.64e-8 	--	13.13 
Elastic fibre formation	6.00e-7 	3.21 	31.82 
Sirtuin Signaling Pathway	1.72e-6 	0.18 	14.43 
Assembly of collagen fibrils and other multimeric structures	1.76e-6 	3.50 	26.23 
Neutrophil Extracellular Trap Signaling Pathway	2.03e-6 	2.26 	13.08 

Upstream Regulators

















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

Regulator	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter <	Filter abs. >	Filter >
TP73	1.91e-8 	4.88 	13.29 
NTRK1	6.59e-8 	5.98 	15.21 
COLQ	3.26e-7 	-1.80 	26.09 
levodopa	1.77e-6 	-0.73 	11.39 
PGR	2.22e-6 	-3.31 	12.30 
CRX	3.39e-6 	2.40 	34.38 

Diseases and Functions





















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

Disease or Function	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter <	Filter abs. >	Filter >
Thyroid carcinoma	4.22e-153 	--	10.34 
Thyroid gland tumor	1.79e-152 	--	10.30 
Neck neoplasm	1.51e-151 	--	10.24 
Nonpituitary endocrine tumor	4.35e-151 	1.00 	10.18 
Head and neck carcinoma	3.60e-148 	0.00	9.99 
Head and neck cancer	9.45e-147 	-0.37 	9.47 

Tox Functions



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

Tox Function	P-value ▲	Activation z-score	Percentage overlap
Filter	Filter <	Filter abs. >	Filter >
Liver tumor	1.68e-14 	-1.50 	8.33 
Liver cancer	1.45e-13 	-0.71 	8.43 
Liver carcinoma	7.41e-13 	-0.84 	8.41 
Congenital heart disease	2.98e-5 	-3.81 	11.42 
Failure of heart	3.01e-5 	-3.02 	11.31 
Ventricular dysfunction	8.93e-5 	-0.48 	10.73 

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

A hub-and-spoke diagram illustrating the central role of FIRRE in regulating various genes. FIRRE is positioned at the center, with arrows pointing outwards to 30 target genes arranged in a circle. The genes include CROCC, CSF1, CSK, EDF1, EEF1D, FBXL15, FOXF4, GNB2, HMGA1, INTS1, LYPLA2, MAP2K4, MBD3, MRPL4, NAALADL1, NOS2, PALM, PCNX3, PGLS, PPR37, PPR12, PPR5, RBM10, RPS15, TFEB, THEM8, TRABD, TSC22D4, ACADS, ADCK5, ARHGAP45, CAPN1, CARMIL2, CC2D1A, CCDC88B, and CHTF18.

AI suggests the following synopsis of this network:

Gene Regulation and Expression

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

Metabolic Pathways

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

Signal Transduction

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

Immune Response

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

Label gene names of interest in the volcano plot

Dataset

882 genes passed cutoffs (491 down and 391 up)

Cutoffs:

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

X Axis:

Expr Log Ratio

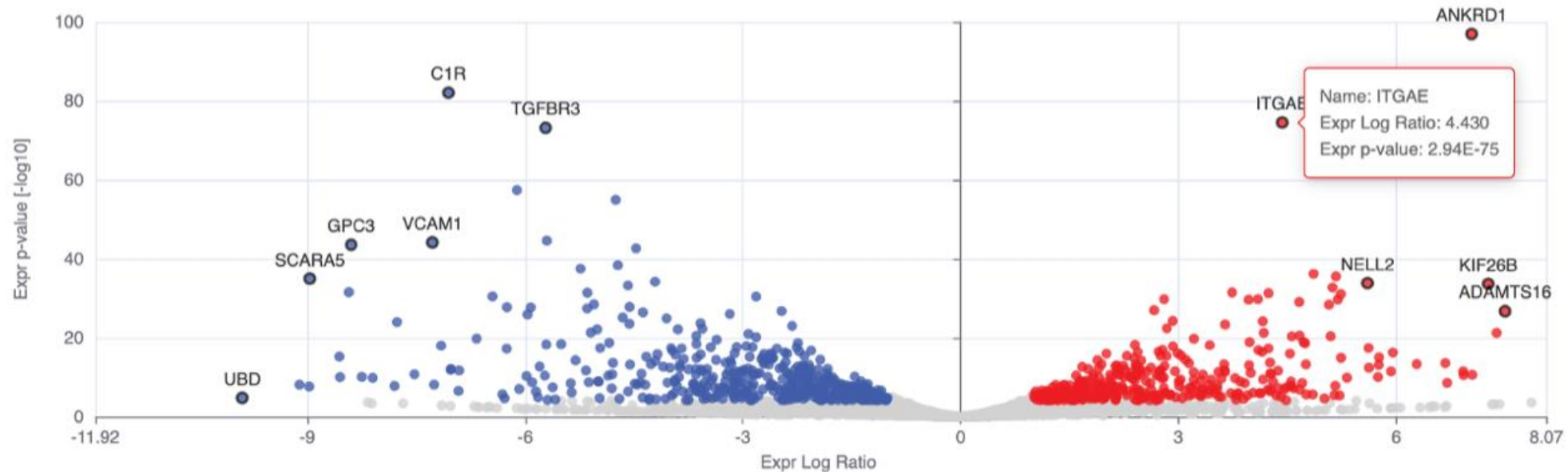


Y Axis:

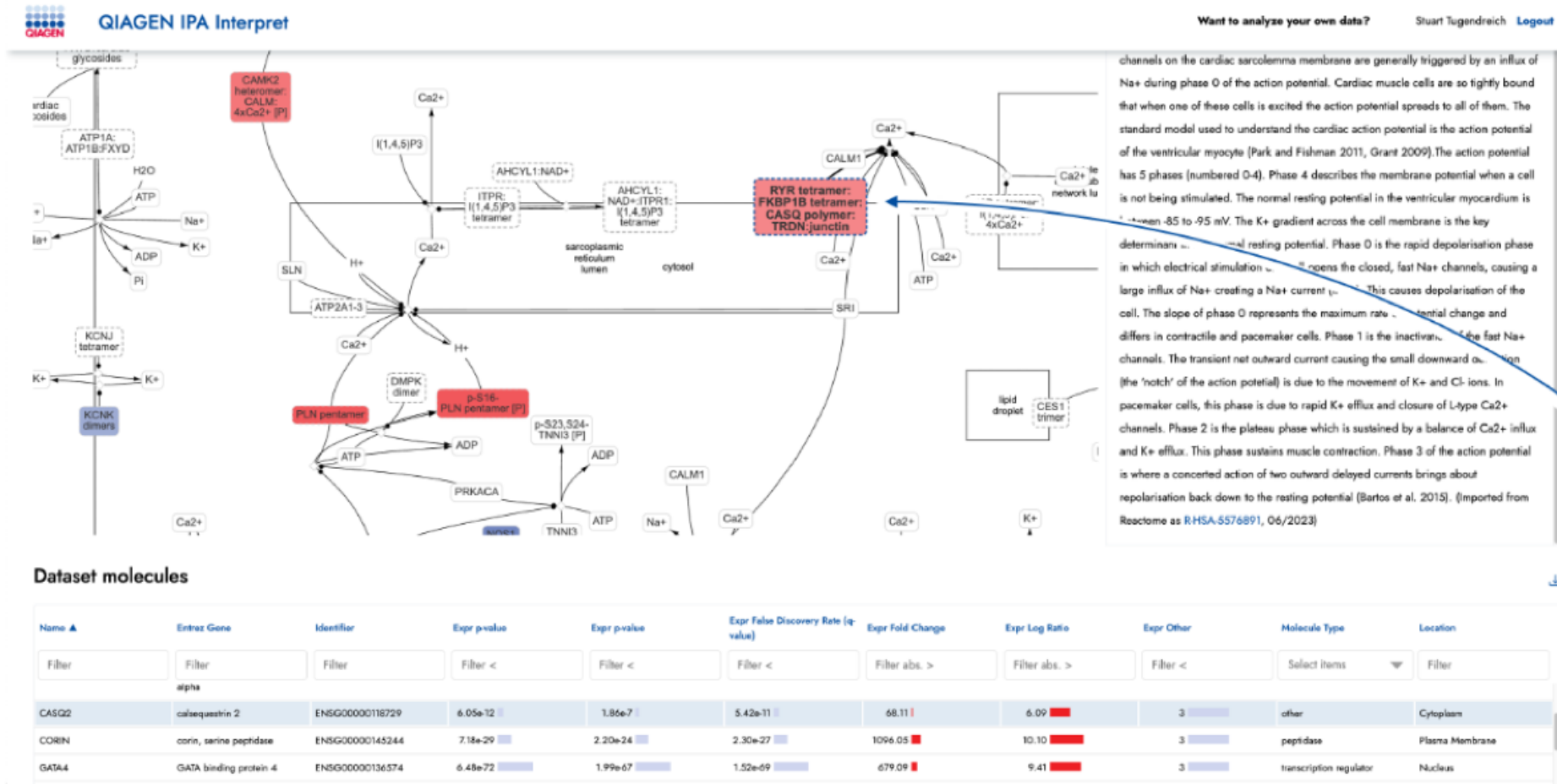
Expr p-value



● Down-regulated ● Up-regulated ● Not analysis-ready



Highlight nodes of interest in a canonical pathway or network



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

1) Clicking row(s) here

Observation 1		Observation 2		
A	B	C	D	E
geneid	UCvsNormal.Log2FoldChange	UCvsNormal.pval	52wksVedolizumabvsBaseline.Log2FoldChange	52wksVedolizumabvsBaseline.pval
DDX11L1	-0.1067	0.2878	0.1183	0.1624
WASH7P	-0.1883	0.0097	0.3063	0.0006
FAM138F	-0.0761	0.4699	0.2466	0.0191
OR4F5	0.1474	0.5311	0.1713	0.2913
LOC729737	0.4789	0.0017	0.029	0.8331
LOC100133331	0.4789	0.0017	0.029	0.8331
LOC100132062	0.4789	0.0017	0.029	0.8331
OR4F29	0.2495	0.2389	0.2181	0.1887
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)

Ratio, fold change, etc. (recommended)

Significance (optional)

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

Common protein IDs

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

UniProt ID conversion tool:

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

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)

	A	B	C	D	E
1	ID	Symbol	Phospho Fold Change	Phospho p-value	Phospho Site
2	IPI00137139	1700003H04Rik	-1.271	0.221	M(ox)ET(ph)LGEK_
3	IPI00224491	2900026A02Rik	-1.244	0.25	RQS(ph)LYENQA_
4	IPI00224491	2900026A02Rik	-1.404	0.156	SEECs(ph)PQWLK_
5	IPI00652957	4930594M22Rik	-5.729	5.47E-09	MFKSS(ph)PR_
6	IPI00137111	4933402E13Rik	2.196	0.000423	AWALNDS(ph)ANT(ph)SPNAWFVER_
7	IPI00137111	4933402E13Rik	2.196	0.000423	AWALNDS(ph)ANT(ph)SPNAWFVER_
8	IPI00137111	4933402E13Rik	2.196	0.000423	AWALNDS(ph)ANT(ph)SPNAWFVER_
9	IPI00654190	4933431E20Rik	-1.184	0.304	VGGLS(ph)PR_
10	IPI00654176	4933439C10Rik	-1.097	0.431	SPHLSGS(ph)LPR_
11	IPI00225598	A430057M04Rik	1.079	0.299	ALPT(ph)EPR_
12	IPI00227449	A730008H23Rik	-1.448	0.133	GM(ox)TLQWLIS(ph)PVK_
13	IPI00311509	AAAS	-1.085	0.37	ITHIPLYFVNAQFPRFS(ph)PVLGR_
14	IPI00458612	AAK1	1.07	0.311	VGSLT(ph)PPSS(ph)PKTQR_
15	IPI00458612	AAK1	1.07	0.311	VGSLT(ph)PPSS(ph)PKTQR_
16	IPI00458612	AAK1	1.057	0.332	AGQTQPNPILPIQPALT(ph)PR

Observation 1

Common protein IDs

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

UniProt ID conversion tool:

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

Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

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

Observation 1

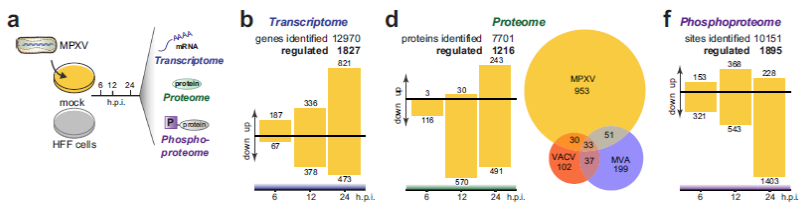
Common metabolite IDs

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

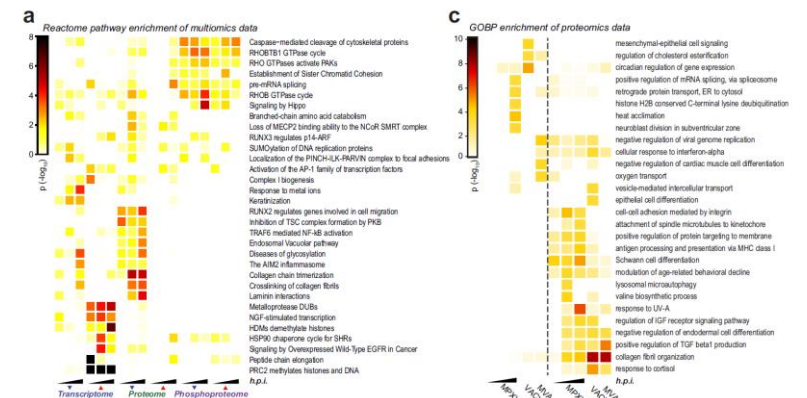
Metabolite ID conversion tools:

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

Multi-omics Case Study



DEG, DEP,
DEphospho



Pathway
analysis

nature communications

Article <https://doi.org/10.1038/s41467-024-S1074-6>

Multi-omics characterization of the monkeypox virus infection

Received: 19 December 2023
Accepted: 26 July 2024
Published online: 08 August 2024
Check for updates

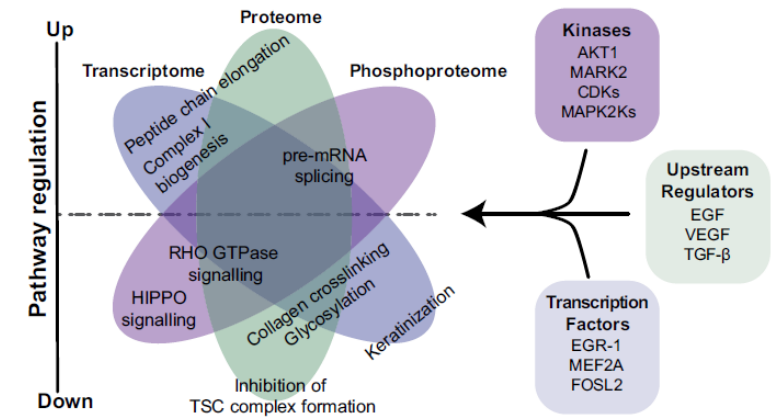
Yiqi Huang^{1,13}, Valter Bergant^{2,3}, Vincent Grass^{1,13}, Quirin Emslander^{1,13}, M. Sabri Hamad¹, Philipp Huber^{2,3}, Julia Mergner⁴, Antonio Piras¹, Karsten Krey⁵, Alexander Henrich⁶, Rupert Öllinger⁶, Yonas M. Tesfamariam⁶, Ilaria Dalla Rosa⁷, Till Bunse⁸, Gerd Sutter^{8,9}, Gregor Ebert¹⁰, Florian I. Schmidt⁶, Michael Way^{7,11}, Roland Rad⁶, Andrew G. Bowie¹², Ulrike Protzer^{9,10} & Andreas Pichlmair¹³✉

Multiple omics analyses of Vaccinia virus (VACV) infection have defined molecular characteristics of poxvirus biology. However, little is known about the monkeypox (mpox) virus (MPXV) in humans, which has a different disease manifestation despite its high sequence similarity to VACV. Here, we perform an in-depth multi-omics analysis of the transcriptome, proteome, and phosphoproteome signatures of MPXV-infected primary human fibroblasts to gain insights into the virus-host interplay. In addition to expected perturbations of immune-related pathways, we uncover regulation of the HIPPO and TGF- β pathways. We identify dynamic phosphorylation of both host and viral proteins, which suggests that MAPKs are key regulators of differential phosphorylation in MPXV-infected cells. Among the viral proteins, we find dynamic phosphorylation of H5 that influenced the binding of H5 to dsDNA. Our extensive dataset highlights signaling events and hotspots perturbed by MPXV, extending the current knowledge on poxviruses. We use integrated pathway analysis and drug-target prediction approaches to identify potential drug targets that affect virus growth. Functionally, we exemplify the utility of this approach by identifying inhibitors of MTOR, CHUK/I κ BKB, and splicing factor kinases with potent antiviral efficacy against MPXV and VACV.

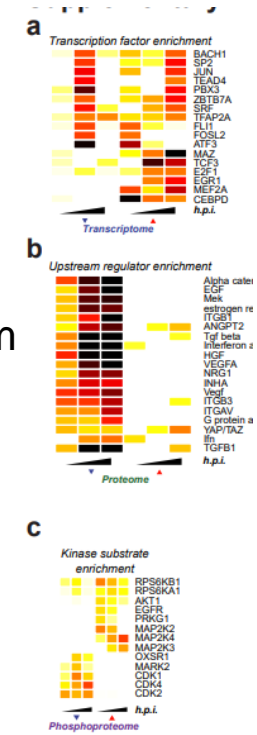
Monkeypox (mpox) virus (MPXV) is a pathogenic orthopoxvirus and etiological agent of the zoonosis mpox, first identified in 1970¹. The virus species is separated into clade I (Central African, Congo basin) and clade II (West African), the latter of which includes the 2022 mpox outbreak strain that caused the first widespread community transmission of MPXV outside Africa²⁻⁴. Its rapid spread in 2022 resulted in the WHO's declaration of a Public Health Emergency of International Concern (PHEIC) and has so far caused over 88,000 cases in 110 countries

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b



Upstream
regulator



Upload dataset protein

gene_names	majority_protein_acs	protein_descriptions	fold_change_log2.6h	p_value.6h	sd_log2.6h	fold_change_log2.12h	p_value.12h	sd_log2.12h	fold_change_log2.24h	p_value.24h	sd_log2.24h
ECI1	P42126;P4	Enoyl-CoA	0.020782	0.625849	0.088114	-0.27308	0.00637	0.094351	-0.2675	0.007543	0.092892
ZNF655	Q8N720;C	Isoform 3	-0.00513	0.868699	0.275334	-0.29187	0.498631	1.136184	-0.4941	0.45764	1.208837
REXO4	Q9GZR2;C	Isoform 2	-5.40E-04	0.974864	0.249492	4.36E-03	0.972872	0.348411	#####	0.972059	0.452495
TRPC4;TR	Q9UBN4;C	Isoform Be	0.010651	0.806988	0.294768	0.20156	0.422214	0.327123	0.27075	0.380342	0.356281
H2BC12;H	O60814;P	Histone H2	-0.00568	0.825376	0.089293	-0.17613	0.177472	0.146675	0.48612	0.014394	0.167852
SLC25A13	Q9UJS0;Q	Calcium-b	8.10E-04	0.955019	0.134052	-1.24E-01	0.5102	0.311733	#####	0.053837	1.883655
MTF2	Q9Y483;C	Isoform 2	-5.30E-04	0.983102	0.312366	-3.45E-03	0.9801	0.416438	#####	0.987752	0.517113
HMCN1	Q96RW7;C	Hemicenti	-0.06077	0.661838	0.8515	-0.18828	0.618256	0.990568	-0.3461	0.57236	1.644312
UBA2	Q9UBT2;C	Isoform 2	-0.07779	0.203745	0.062755	-0.13952	0.018426	0.0665	-0.0462	0.581246	0.078769
SIK3	Q9Y2K2;C	Isoform 2	0.00759	0.865679	0.246627	-0.0021	0.957318	0.341034	0.0428	0.860514	0.433613
C18L	URK2047	EEV matu	0.015445	0.756648	0.57927	7.308955	0.018775	1.180561	8.63038	2E-30	0.458489
TP53BP1	Q12888;Q	Isoform 2	-0.48227	1.82E-15	0.090086	-0.41636	1.41E-04	0.0791	0.11047	6.34E-01	0.199222
MED20	Q9H944;C	Isoform 2	-7.55113	0.156617	3.100783	-7.77114	0.130145	2.97066	-7.8503	0.129947	2.985137
C14orf119	Q9NWWQ9	Uncharacte	-1.80E-04	0.995055	0.283443	3.30E-04	0.997761	0.390233	#####	0.996969	0.499867
IGSF8	Q969P0;Q	Immunogl	1.45E-04	0.992257	0.278244	3.00E-02	0.857931	0.610434	#####	0.984178	0.686134
DBI	P07108;P	Acyl-CoA	-0.27533	0.117023	0.120542	-0.22712	0.288257	0.14373	0.14014	0.105436	0.401042
SERPINC1	P05155;P	Isoform 2	-3.00E-05	0.989995	0.278616	-1.22E-03	0.990086	0.388089	#####	0.991549	0.503044
ERCC3	P19447	General tra	-0.06495	0.536297	0.226869	-0.09165	0.637654	0.592063	-0.7241	0.362523	1.875634
GIGYF2	Q6Y7W6;C	GRB10-int	-0.128	0.187357	0.110387	-0.00655	0.935944	0.096195	0.28259	0.048404	0.147293
MED18	Q9BUE0	Mediator c	-0.05308	0.556803	0.20512	-0.69637	0.016849	0.298775	-3.6638	0.015897	1.829028
SLC30A1	Q9Y6M5	Zinc transp	0.002905	0.892267	0.103152	0.010003	0.907859	0.160528	1.15156	0.003427	0.259957
UBR2	Q8IWW8;C	E3 ubiquit	-0.00292	0.902407	0.226661	-0.02245	0.863112	0.300279	-0.0382	0.866697	0.379871
STEAP2	Q8NFT2;C	Isoform 2	-0.32202	0.272952	0.347788	-0.11895	0.696604	0.43266	-0.2276	0.508265	0.40804
TAX1BP3	Q14907	Tax1-bind	-0.03272	0.597803	0.136065	-0.09365	0.467287	0.168453	-0.0954	0.527945	0.176823

Create New

Upload dataset

Choose your file

Edit observation name

Infer observation

Dataset Upload - MOESEM_protein.xlsx

1. Select File Format:

Flexible Format

2. Contains Column Header:

☒ Yes ☐ No

3. Select Identifier Type:

Please assign at least one column below as "ID", and assign the identifier type(s).
Assign additional columns as ID to improve mapping coverage if desired.

4. Array platform used for experiments:

Not specified/applicable

Select relevant array platform as a reference set for data analysis.

5. Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appropriate measurement value type.

Raw Data (7702)

Dataset Summary (0)

Metadata

Edit Observation Names

Infer Observations

ID/Observation Name	Ignore	Ignore
Measurement/Annotation		
1	gene_names	majority_protein_acs
2	EC11	P42126;P42126-2
3	ZNF655	Q8N720;Q8N720-3
4	REXO4	Q9GZR2;Q9GZR2-2
5	TRPC4;TRPC5	Q9UBN4;Q9UL62;Q...
6	H2BC12;H2BC13;H2...	O60814;P57053;P588...
7	SLC25A13	Q9UIS0;Q9UIS0-2
8	MTF2	Q9Y483;Q9Y483-2;Q...
9	HMCN1	Q96RW7;Q96RW7-2...
10	UBA2	Q9UBT2;Q9UBT2-2
11	SIK3	Q9Y2K2;Q9Y2K2-6;Q...
12	C18L	URK20479.1
13	TP53BP1	Q12888;Q12888-2;Q...
14	MED20	Q9B944;Q9B944-2
15	C14orf119	Q9NWQ9
16	IGSF8	Q969P0;Q969P0-2;Q...
17	DBI	P07108;P07108-2;P0...
18	SERPING1	P05155;P05155-2;P0...
19	ERCC3	P19447
20	GIGYF2	Q6Y7W6;Q6Y7W6-3...
21	MED18	Q9BUE0
22	SLC30A1	Q9Y6M5
23	UBR2	Q8IWW8;Q8IWW8-2...
24	TEAP2	Q8NFT2;Q8NFT2-2...
25	STX1BP3	O14907
26	SRSF7	Q16629;Q16629-2;Q...
27	SFSWAP	Q12872;Q12872-2
28	ANXA13	P27216;P27216-2
29	TERF1	P54274;P54274-2

Edit Observation Names

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

Edit Observation Names

Observation Name

1. Observation 1

2. Observation 2

3. Observation 3

4. Observation 4

5. Observation 5

6. Observation 6

7. Observation 7

OK Cancel

Ignore	Ignore	Ignore
fold_change_log2.2...	p_value.24h	sd_log2.24h
-0.267495550000000...	7.5430876500756699...	9.28915038320519E-2
-0.494064999999999...	0.4576397276695309...	1.2088366425480801
-9.5749999999999889...	0.9720591511091649...	0.4524954842321570...
0.270749999999999...	0.380341728316895	0.3562806529816229...
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0.110474999999999...	0.634492908667461	0.1992221002607250...
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-0.724079999999999...	0.362523190756112	1.8756340543427601
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1.1515560499999999	3.4266735339520999...	0.2599574173142100...
-3.821999999999989...	0.8666968915045030...	0.3798707638404609...
-0.227585000000000...	0.5082650323241549...	0.4080403041260199...
-9.536050000000000...	0.5279445437520450...	0.1768228456816919...
0.610759999999999...	7.4747780841027302...	0.117401839885863
0.8632089953956040...	1.25799626205648	
0.95104999999999704...	0.6605636001239140...	0.3202115717559749...
7.9237015992669496...	0.352280272453129...	

Core analysis

Analyze filter
dataset

Core analysis

Set cut off

Annotated Dataset: MOESEM_protein
Preview Dataset MOESEM_protein Observation: protein.6 (7063)

Mapped IDs (7186) Unmapped IDs (515) All IDs (7701) Metadata

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

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
0.071	1.95E-01	A1BG		A1BG	alpha-1-B glycoprotein	Extracellular Space	other	
-0.246	1.47E-01	AAAS		AAAS	aladin WD repeat nucleoporin	Nucleus	other	
-0.007	8.22E-01	AACS		AACS	acetoacetyl-CoA synthetase	Cytoplasm	enzyme	
-0.074	4.83E-01	AAGAB		AAGAB	alpha and gamma adaptin binding protein	Cytoplasm	other	
-0.161	1.91E-01	AAK1		AAK1	AP2 associated kinase 1	Cytoplasm	kinase	LP-935509, SM1-71
-0.003	8.89E-01	AAMDC		AAMDC	adipogenesis associated Mth938 domain containing	Cytoplasm	other	
-0.318	2.74E-01	AAMP		AAMP	angio associated migratory cell protein	Plasma Membrane	other	
-5.732	4.79E-02	AAR2		AAR2	AAR2 splicing factor	Other	other	
-0.277	1.06E-19	AARS1		AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme	
0.011	7.89E-01	AARS2		AARS2	alanyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme	
-0.403	4.41E-04	AARSD1		AARSD1	alanyl-tRNA synthetase domain containing 1	Nucleus	enzyme	
-0.195	1.01E-01	AASDHPT		AASDHPT	aminoadipate-semialdehyde dehydrogenase-phos...	Cytoplasm	enzyme	
0.000	9.84E-01	AASS		AASS	aminoadipate-semialdehyde synthase	Cytoplasm	enzyme	
-0.447	2.21E-01	AATF		AATF	apoptosis antagonizing transcription factor	Nucleus	transcription regulator	
-0.001	9.61E-01	ABCA2		ABCA2	ATP binding cassette subfamily A member 2	Plasma Membrane	transporter	
-0.007	8.78E-01	ABCB10		ABCB10	ATP binding cassette subfamily B member 10	Cytoplasm	transporter	
-0.043	7.01E-01	ABCB7		ABCB7	ATP binding cassette subfamily B member 7	Cytoplasm	transporter	
-0.001	9.67E-01	ABCB8		ABCB8	ATP binding cassette subfamily B member 8	Cytoplasm	transporter	
-0.479	4.42E-02	ABCC1		ABCC1	ATP binding cassette subfamily C member 1 (ABCC1)	Plasma Membrane	transporter	sulfinpyrazone
0.001	9.68E-01	ABCC10		ABCC10	ATP binding cassette subfamily C member 10	Plasma Membrane	transporter	
-0.001	9.67E-01	ABCC3		ABCC3	ATP binding cassette subfamily C member 3	Plasma Membrane	transporter	
-0.331	4.00E-02	ABCC4		ABCC4	ATP binding cassette subfamily C member 4 (PEL bL...	Plasma Membrane	transporter	
-0.047	4.02E-01	ABCD3		ABCD3	ATP binding cassette subfamily D member 3	Cytoplasm	transporter	
0.001	9.73E-01	ABCD4		ABCD4	ATP binding cassette subfamily D member 4	Cytoplasm	transporter	
-0.133	8.76E-02	ABCE1		ABCE1	ATP binding cassette subfamily E member 1	Cytoplasm	transporter	
-0.294	6.93E-03	ABCF1		ABCF1	ATP binding cassette subfamily F member 1	Cytoplasm	transporter	
-0.247	1.35E-01	ABCF2		ABCF2	ATP binding cassette subfamily F member 2	Cytoplasm	transporter	
-0.039	4.84E-01	ABCF3		ABCF3	ATP binding cassette subfamily F member 3	Other	transporter	
0.021	6.85E-01	ABHD10		ABHD10	abhydrolase domain containing 10, depalmitoylase	Cytoplasm	enzyme	
-0.007	8.67E-01	ABHD11		ABHD11	abhydrolase domain containing 11	Cytoplasm	enzyme	
-0.198	3.86E-02	ABHD12		ABHD12	abhydrolase domain containing 12, lysophospholip...	Plasma Membrane	enzyme	
-0.081	2.59E-01	ABHD14B		ABHD14B	abhydrolase domain containing 14B	Cytoplasm	enzyme	
-0.024	6.77E-01	ABHD16A		ABHD16A	abhydrolase domain containing 16A, phospholipase	Other	enzyme	
-0.044	6.31E-01	ABHD5		ABHD5	abhydrolase domain containing 5, lysophosphatidi...	Cytoplasm	enzyme	
-0.000	9.92E-01	ABHD6		ABHD6	abhydrolase domain containing 6, acylglycerol lipase	Cytoplasm	enzyme	
-0.434	4.35E-03	ABI1		ABI1	abi interactor 1	Cytoplasm	other	
-0.246	2.33E-01	ABI2		ABI2	abi interactor 2	Cytoplasm	other	
0.000	9.86E-01	ABL1		ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	Nucleus	kinase	olverembatinib, temozolomide, filgrastim/imatinib, ...
0.001	9.60E-01	ABL2		ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase	Cytoplasm	kinase	nilotinib, dasatinib
0.074	6.36E-01	ABLUM1		ABLUM1	actin binding LIM protein 1	Cytoplasm	other	
-0.253	1.36E-01	ABLUM3		ABLUM3	actin binding LIM protein family member 3	Cytoplasm	other	
-0.062	4.70E-01	ABR		ABR	ABR activator of RhoGTP and GTPase	Cytoplasm	other	
-0.032	5.27E-01	ABRACL		ABRACL	ABRA C-terminal like	Nucleus	other	
-0.031	6.01E-01	ABRAXAS2		ABRAXAS2	abraxas 2, BRISC complex subunit	Nucleus	other	
-0.000	9.82E-01	ABT1		ABT1	activator of basal transcription 1	Nucleus	transcription regulator	
-0.088	2.97E-01	ACAA1		ACAA1	acetyl-CoA acyltransferase 1	Cytoplasm	enzyme	trimetazide
0.001	9.45E-01	ACAA2		ACAA2	acetyl-CoA acyltransferase 2	Cytoplasm	enzyme	

0 / 7186

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

Core Analysis
Biomarker Filter
Filter Dataset
microRNA Target Filter
BioProfiler
IsoProfiler

Edit Dataset Settings Analyze/Filter Dataset Close

Analyze filter dataset

Core analysis

Set cut off

Recalculate

Create Expression Analysis - [analysis : Naturecomm_protein]

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	
fold_change_log2.6h	Expr Log Ratio	-12.4565 to 17.5536	-0.58	0.58
p_value.6h	Expr p-value	0.0 to 1.0	0.05	

Advanced

Recalculate

1110 analysis-ready molecules across observations

Preview Dataset Naturecomm_protein Observation: protein.6 (189)

Analysis-Ready (189) Mapped IDs (7186) Unmapped IDs (515) All IDs (7701) Metadata

Add To My Pathway

Add To My List

Create Dataset

Customize Table

Expr Log Ratio ☒ Expr p-value ☒ ID ☒ Flags ☒ Symbol ☒ Entrez Gene Name ☒ Location ☒ Type(s) ☒ Drug(s) ☒

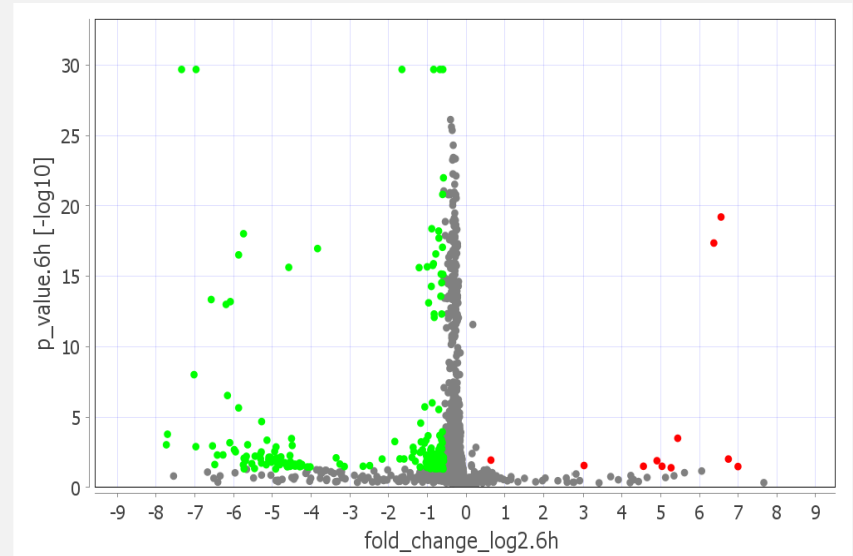
Symbol AAR2 - LUC7L2 (1/2)

Run Analysis

Cancel

Volcano plot

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



fold_change_log2.6h p_value.6h [-log10] Update Axes Clear Molecule Names

General Settings

Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species Human

Tissues & Cell Lines

Mutation All

Save As Default

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)

Analysis Filter Summary

Consider only molecules and/or relationships here

Species = Human) AND

Confidence = Experimentally Observed) AND

Mol. types = biologic drug OR canonical pathway OR chemical - endogenous mammalian OR chemical - endogenous non-mammalian OR chemical - kinase inhibitor OR chemical - other OR chemical - protease inhibitor OR chemical reagent OR chemical toxicant OR complex OR cytokine OR disease OR enzyme OR function OR G-protein coupled receptor OR group OR growth factor OR ion channel OR kinase OR ligand-dependent nuclear receptor OR mature microRNA OR microRNA OR other OR peptidase OR phosphatase OR related pathway node OR transcription regulator OR translation

Advanced Recalculate 1110 analysis-ready molecules across observations

Preview Dataset Naturecomm_protein Observation: protein.6 (189)

Analysis-Ready (189) Mapped IDs (7186) Unmapped IDs (515) All IDs (7701) Metadata

Set Cutoffs Biological Filters

General Settings

> Networks Interaction & Ca...

Node Types biologic drug...

Data Sources All

miRNA Confidence Experi...

Species Human

Tissues & Cell Lines

Mutation All

Save As Default

Generate the following Networks (increases analysis time)

☒ Interaction networks☒ Include endogenous chemicals

Molecules per network

Networks per analysis

Genes are always included

35

25

☒ Causal networks

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

☐ Score using causal paths only

Add...

Remove

Analysis Filter Summary

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

Advanced

Recalculate

1110 analysis-ready molecules across observations

Preview Dataset Naturecomm_protein Observation: protein.6 (189)

Analysis-Ready (189)

Mapped IDs (7186)

Unmapped IDs (515)

All IDs (7701)

Metadata

Add To Mv Pathway

Add To Mv List

Create Dataset

Customize Table



Symbol AAR2 - LUC7L2 (1/2)



Set Cutoffs Biological Filters



General Settings ?

Networks Interaction & Ca... ?

Node Types biologic drug... ?

Data Sources All ?

miRNA Confidence Experi... ?

Species Human ?

> Tissues & Cell Lines ?

Mutation All ?

Save As Default

☐ Select all

☒ Tissues and Primary Cells

☐ Tissues and Primary Cells not otherwise specified

☐ Cells
 ☐ Nervous System
 ☐ Organ Systems
 ☐ Other Tissues and Primary Cells

☒ Cell Line

☐ Cell Line not otherwise specified

☐ Breast Cancer Cell Lines
 ☐ Cervical cancer cell line
 ☐ CNS Cell Lines
 ☐ Colon Cancer Cell Lines
 ☐ Fibroblast cell lines

☒ Stringent filter (filter molecules and relationships) ?
☐ Relaxed filter (filter molecules) ?

Analysis Filter Summary

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

Advanced Recalculate **1110** analysis-ready molecules across observations

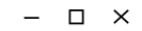
Preview Dataset Naturecomm_protein Observation: protein.6 (189) ▼

Analysis-Ready (189) Mapped IDs (7186) Unmapped IDs (515) All IDs (7701) Metadata

Add To My Pathway Add To My List Create Dataset Customize Table Symbol AAR2 - LUC7L2 (1/2) ◀ ▶

Summary

Expression Analysis - protein.6

[Summary](#) [Graphical Summary](#) [Pathways](#) [Upstream Analysis](#) [Diseases & Functions](#) [Regulator Effects](#) [Networks](#) [Lists](#) [Analysis Match](#) [Molecules](#)

QIAGEN IPA Interpret

Enhanced web view






Export:



> Experiment Metadata

> Analysis Settings






v Top Canonical Pathways

Name		p-value	Overlap	
TNF signaling		6.13E-06	10.5 %	6/57
Coronavirus Pathogenesis Pathway		1.65E-04	4.1 %	8/193
Necroptosis Signaling Pathway		2.24E-04	4.6 %	7/152
Apelin Liver Signaling Pathway		4.40E-04	15.8 %	3/19
IL-12 Signaling and Production in Macrophages		4.78E-04	3.5 %	8/226

1 2 3 4 5 6 7 8 9 >




v Top Upstream Regulators

v Upstream Regulators

Name		p-value	Predicted Activation
IFNG		1.14E-05	Inhibited
IFNA2		1.22E-05	
RETRG3		6.94E-05	
TSIX		6.94E-05	
PARP2		6.94E-05	

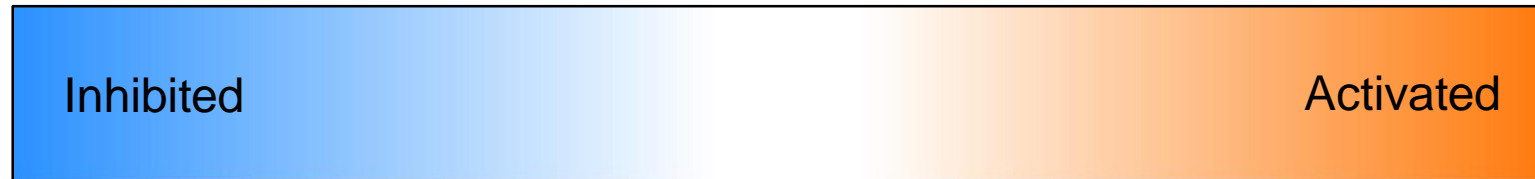
1 2 3 4 5 6 7 8 9 >

v Causal Network

Name		p-value	Predicted Activation
NTRK1		1.14E-07	
AKT1		3.72E-07	
PKA (complex)		4.47E-07	Activated

What do colors mean in IPA?

Pathway or gene activity predicted by IPA



Actual measurement of gene expression in your dataset



What do z-scores mean in IPA?

Actual dataset
measurement

VS.

What IPA expects if pathway
is activated

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

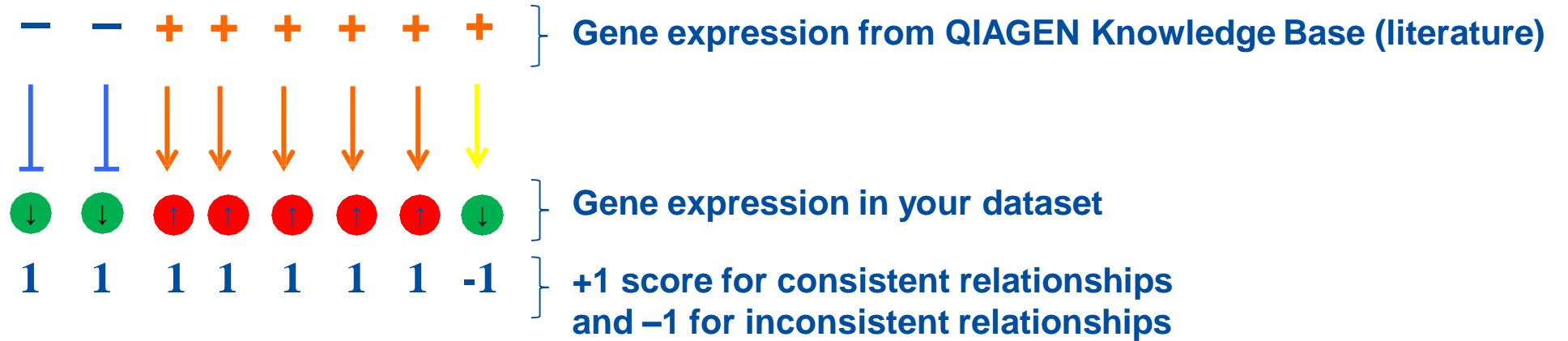
*Pathway inhibited**- Z score*

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

*No clear signal
for prediction
Z score = 0*

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

*Pathway activated**+ Z score**How well do the actual measurements match the expected measurements?*



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

- 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

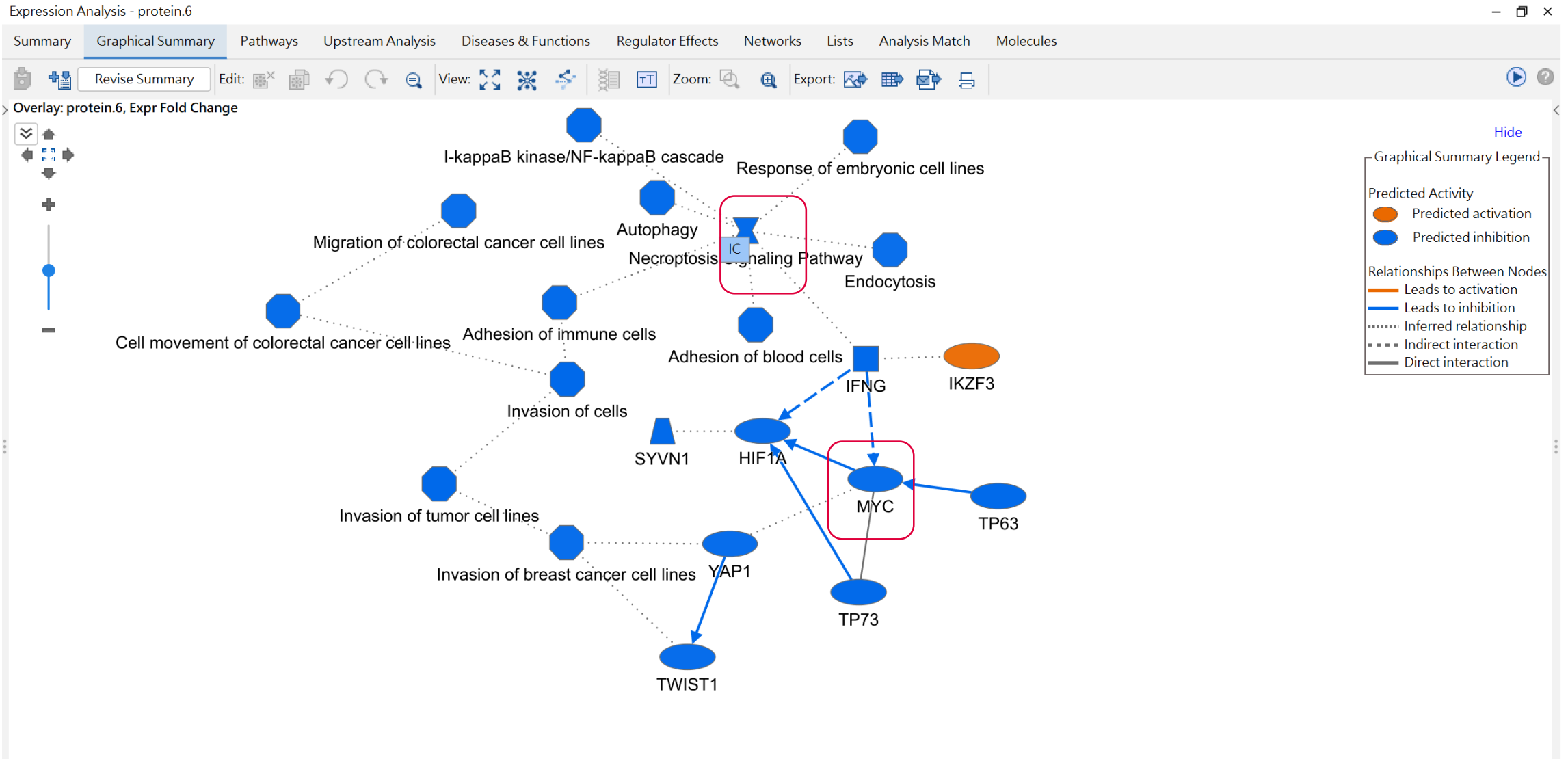
Symbol	Measurement Expr Log Ratio	+ ×	Expected
NR5A2	↓ -1.002	↓	Down
ABCB11	↓ -1.056	↓	Down
CYP2B6	↓ -3.063	↓	Down
PPARGC1A	↓ -2.495	↓	Down
ACOX1	↓ -1.727	↓	Down
SLCO1B3	↑ 3.223	↓	Down
TLR4	↑ 1.213	↑	Up
LY96	↑ 1.189	↑	Up
IL1R1	↑ 1.634	↑	Up
IL1RAP	↑ 1.046	↑	Up
IL1B	↑ 3.890	↑	Up
LIPC	↓ -1.375	↑	Up

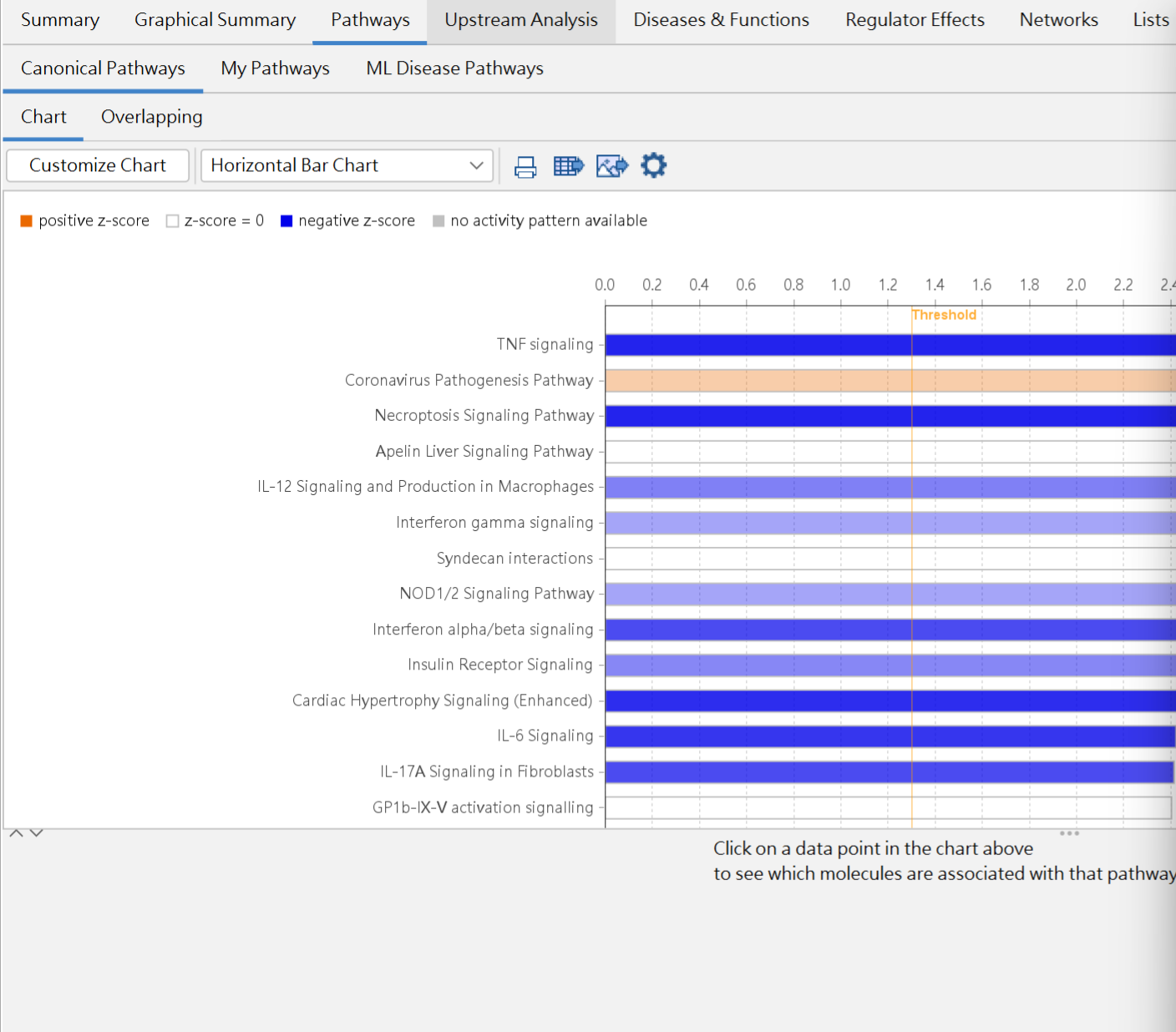
Z-score = 2.4**10/12 measurements match expected****Mostly matching****Signal predominantly points to predicted activation**

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

Graphical summary





Customize Chart

Select Canonical Pathways to Display

☒ Tree View☐ List View

Start typing to find Canonical Pathways that scored in your analysis

- ☒ Ingenuity Canonical Pathways
 - ☒ Metabolic Pathways
 - ☒ Biosynthesis
 - ☒ Amines and Polyamines Biosynthesis
 - ☒ Urate Biosynthesis/Inosine 5'-phosphate Degradation
 - ☒ Amino Acids Biosynthesis
 - ☒ Individual Amino Acids Biosynthesis
 - ☒ Cysteine Biosynthesis
 - ☒ Cysteine Biosynthesis III (mammalia)
 - ☒ Carbohydrates Biosynthesis
 - ☒ Polysaccharides Biosynthesis
 - ☒ Glycosaminoglycans Biosynthesis

Filter by Gene(s)

Include:

(use * for wildcard)

Exclude:

[comma-separated list]

P-Value Type to Determine Bar Length

Fisher's Exact Test p-value

Score Cutoff

Display only entities that have

a $-\log(p\text{-value})$ greater than:

1.3

(between 0 and 5.21)

an absolute value z-score greater than:

(between 0 and 2.83)

Select Sort Order

☒ $-\log(p\text{-value})$ ☐ z-score☐ alphabetical

Expression Analysis - protein.6

— □ ×

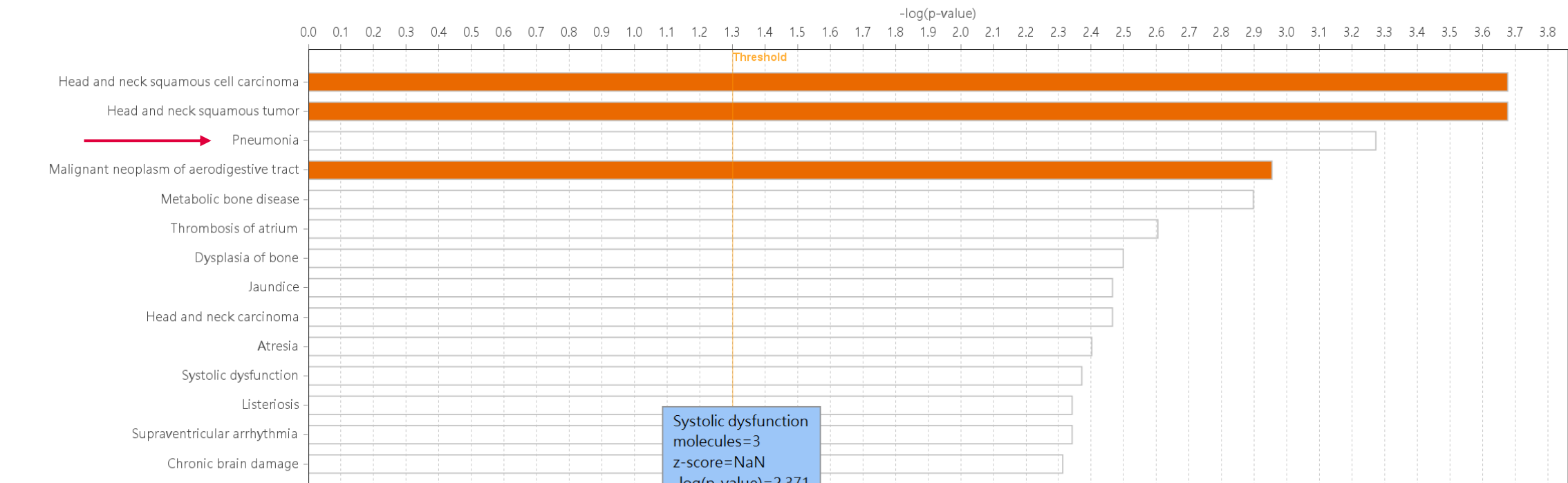
Summary Graphical Summary **Pathways** Upstream Analysis Diseases & Functions Regulator Effects Networks Lists Analysis Match Molecules

Canonical Pathways My Pathways **ML Disease Pathways**

Customize Chart Horizontal Bar Chart

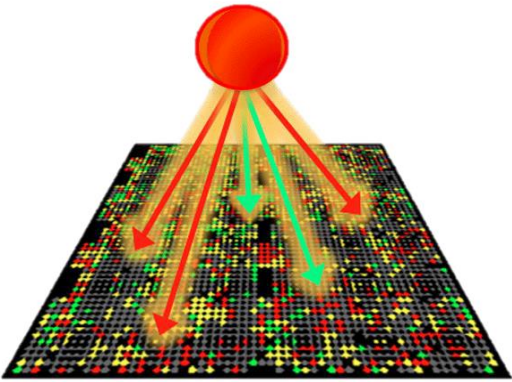


■ positive z-score □ z-score = 0 ■ negative z-score ■ no activity pattern available



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

Click on a disease to see which molecules are associated with that pathway



- 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 regulator

Expression Analysis - protein.6

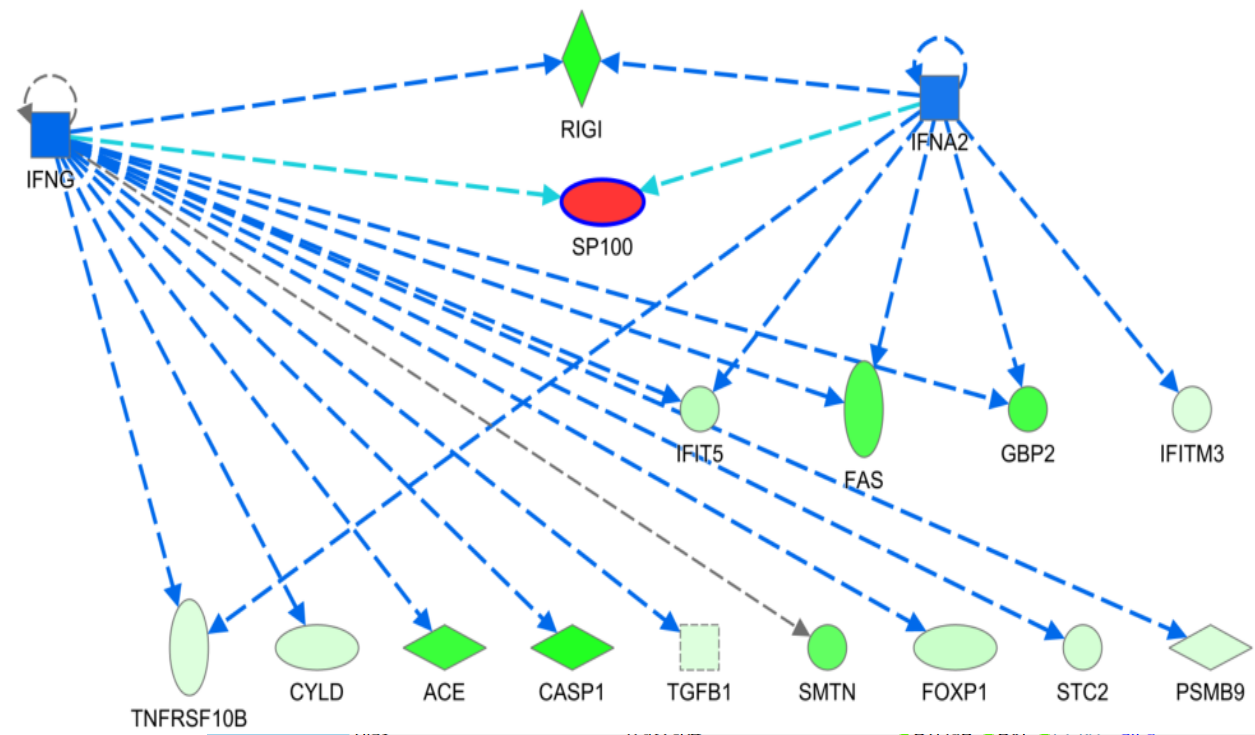
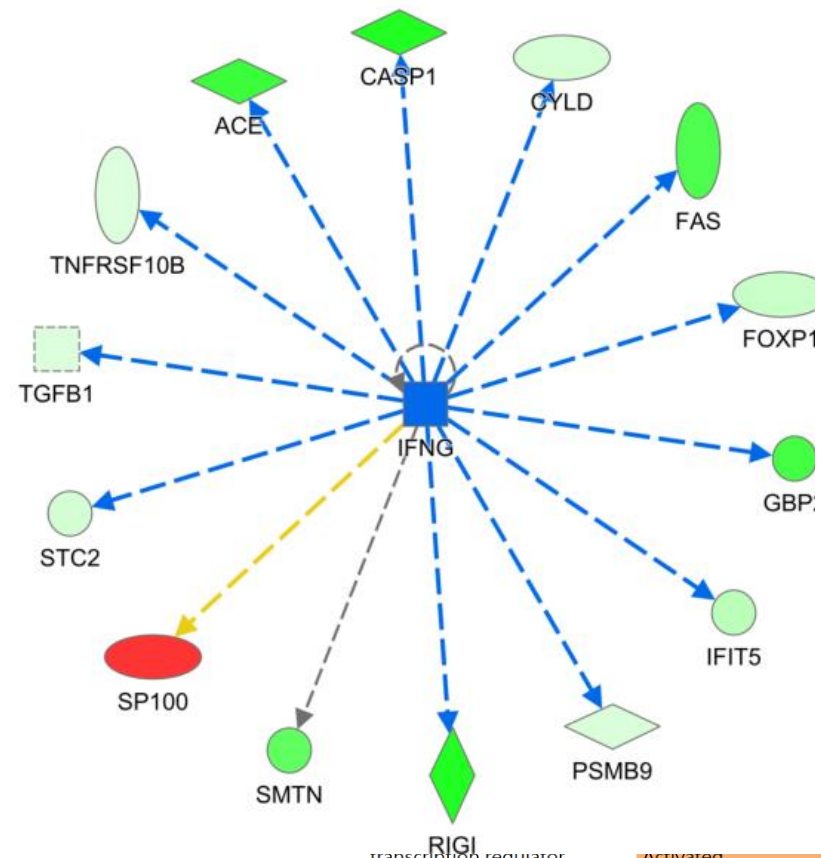
Summary Graphical Summary Pathways Upstream Analysis Diseases & Functions Regulator Effects Networks Lists Analysis Match Molecules

Upstream Regulators Causal Networks

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

p-val... 1.14E-05 - 3.63E-03 (1/6)

- Upstream Re
- IFNG
- IFNA2
- RETRG3
- TSIX
- PARP2
- SYVN1
- IKZF1
- TP73
- MAPK1
- ENTPD5
- NAA30
- EN1
- USP8
- ITGAV
- IFNL1
- EPRS1
- ZNF750
- ISG15
- RC3H1
- TWIST1
- TP53COR1
- ERBB2
- LINC02159
- SHMT2
- NTRK1
- HIF1A
- ETV3
- PDGF-BB (complex)
- ZBTB7B



transcription regulator	Activated	2.000	bias	0.92E-04	↓ RIGI, ↓ ACE, ↓ CCN1, ...all 5
complex				9.33E-04	↓ IFIT5, ↓ PSMB9, ↓ RIGI, ...all 4
transcription regulator				1.00E-03	↓ AKT2, ↓ CCN1, ↓ COL1A1, ...all 5
				1.02E-03	↓ COL1A1, ↓ COL1A2, ...all 2

Expression Analysis - protein.6

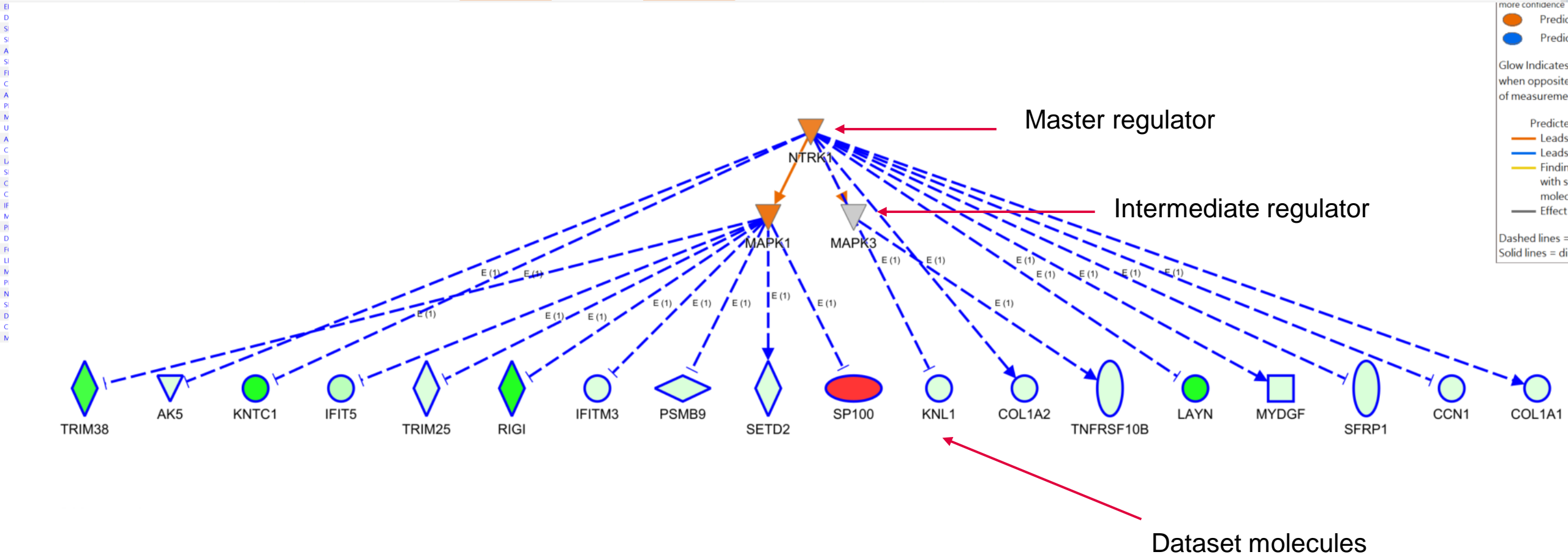
Summary Graphical Summary Pathways Upstream Analysis Diseases & Functions Regulator Effects Networks Lists Analysis Match Molecules

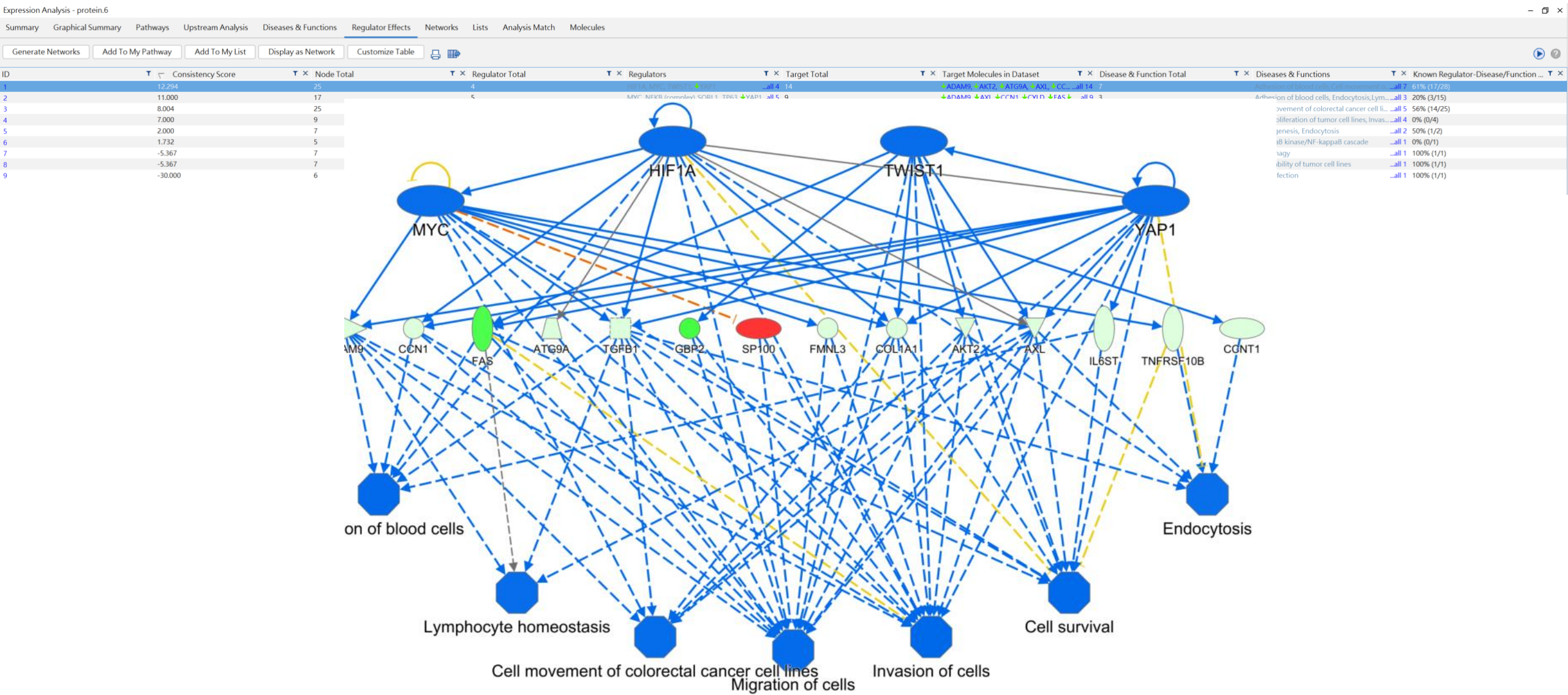
Upstream Regulators Causal Networks

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

p-val... 1.14E-07 - 6.93E-05 (1/3)

Master Regulator	Expr Log Ratio	Molecule Type	Participating reg...	Depth	Predicted Activat...	Notes	Activation z-score	p-value of ov...	Network bias-cor...	Target Molecule...	Causal network	Target-connecte...	Viral Infection (Le...	Viral Infection (P...	Increases/Downs...	Decreases/Down...
NTRK1		kinase	MAPK1, MAPK3, ...all 3	2			1.414	1.14E-07	1.00E-04	AK5, CCN1, ...all 18	18 (3)	3				
AKT1	+0.022	kinase	26S PROTEASOME (...all 29	3			0.309	3.72E-07	1.20E-03	ADAM9, AKT2, ...all 42	42 (29)	24			CD40, CD44, CD...all 14	
PKA (complex)		complex	26S PROTEASOME (...all 36	3	Activated		2.598	4.47E-07	1.60E-03	ADAM9, AKT2, ...all 48	48 (36)	32			CG (complex), MYOC ...all 2	





How signatures are created and compared

➤ Data source from Omicsoft datalands

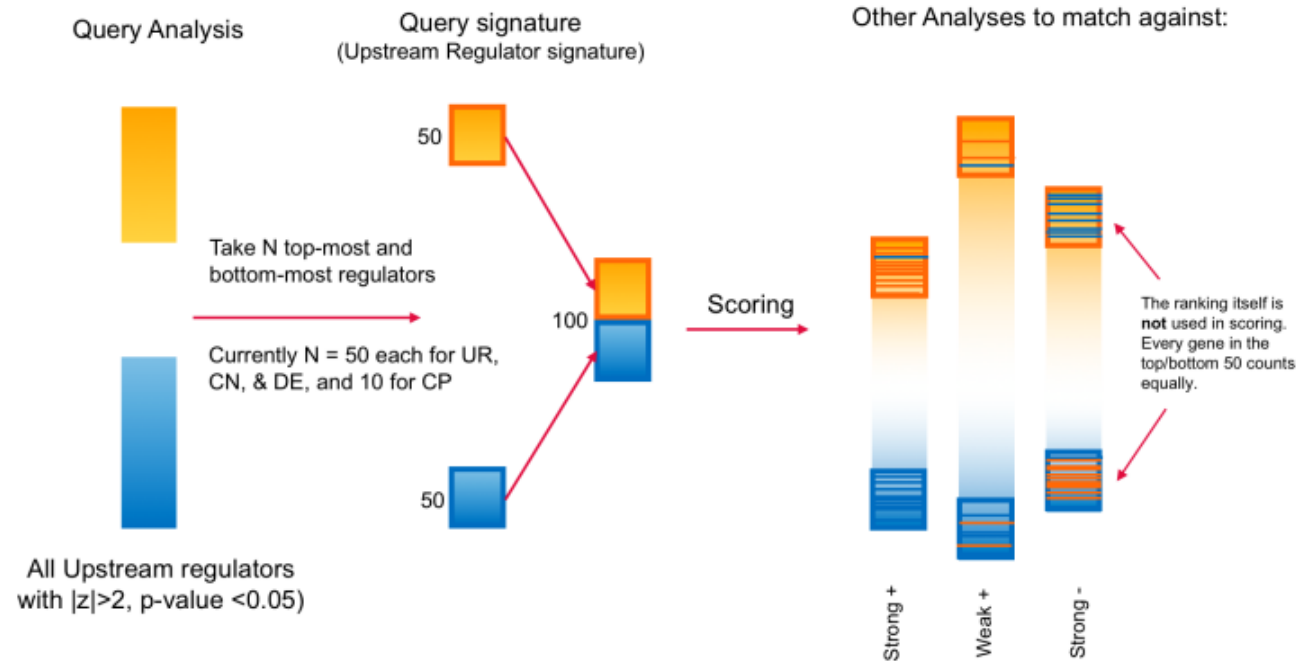
Canonical Pathways (up to 20 pathways)

Upstream Regulators (up to 100 regulators)

Causal Networks (up to 100 master regulators)

Diseases & Functions (up to 100 diseases or functions)

Example



Analysis match

Expression Analysis - protein.6

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... 52.76 - 35.53 (1/954)									
Analysis Name	Project	case.disea...	case.tissue	case.treat...	compariso...	compariso...	compariso...	compariso...	weblink
Naturecomm_mpxo...protein - 2025-03-09 11:30 上午, p...case_study									
28- colon carcinoma [colon] recombinant hTGF alpha C	OncoHuman	colon carcinoma	colon	recombinant hTGF ...	Treatment1 vs. Trea...	CellLine:TreatTime...	GSE105094.GPL1115...	CMP:jni3MUC2RL1	https://www.ncbi.n...
12527- normal control [eye] CMP_0sU52dkyhxp	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	erythroid cell vs ker...	TabulaSapiens_UMI...	CMP:0sU52dkyhxp	https://tabula-sapi...
4- glioblastoma (GBM) [brain] sphere forming culture C	OncoHuman	glioblastoma (GBM)	brain	sphere forming cult...	CellType1 vs. CellTy...	ExperimentGroup =...	GSE153746.GPL1679	CMP:E3INF5pvh0ZH	https://www.ncbi.n...
Naturecomm_mpxo...protein - 2025-03-09 11:30 上午, p...case_study									
25- normal control [pancreatic islets] CMP_Wb52NUYN	SingleCellMouseUmi	normal control	pancreatic islets		Cell Type vs Cell Ty...	pancreatic alpha cel...	GSE84133_UMI.GPL1	CMP:Wb52NUYNyDb	https://www.ncbi.n...
161- exudative age-related macular degeneration/norr	SingleCellHumanUmi	normal control	macula lutea:periph...		Cell Type vs Cell Ty...	melanocyte vs peric...	GSE135922_UMI.GPL	CMP:hs3RTQLJyCxt	https://www.ncbi.n...
2701- normal control [pancreas] CMP_g3ISCVYQqOW	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:g3ISCVYQqOW	https://tabula-sapi...
3- normal control [artificial human skin tissue] UV CMP	HumanDisease	normal control	artificial human ski...	UV	Treatment vs. Contr...	Treatment => UV v...	GSE48586.GPL13938	CMP:UweFkVmjM6p	http://www.ncbi.n...
13135- normal control [large intestine;small intestine]	SingleCellHumanUmi	normal control	large intestine;smal...		Cell Type vs Cell Ty...	goblet cell vs radial...	TabulaSapiens_UMI...	CMP:RBjvRDeo5pn3	https://tabula-sapi...
17642- normal control [pancreas] CMP_kqOXsVGNAlte	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:kqOXsVGNAlte	https://tabula-sapi...
18318- normal control [lung] CMP_wUCWD82OJVP	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	pulmonary ionocyt...	TabulaSapiens_UMI...	CMP:wUCWD82OJVP	https://tabula-sapi...
18283- normal control [prostate] CMP_d4TIQW8hEeh	SingleCellHumanUmi	normal control	prostate		Cell Type vs Cell Ty...	prostate gland lumi...	TabulaSapiens_UMI...	CMP:d4TIQW8hEeh	https://tabula-sapi...
12558- normal control [eye] CMP_ugmbzb1oZ1IC	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	erythroid cell vs my...	TabulaSapiens_UMI...	CMP:ugmbzb1oZ1IC	https://tabula-sapi...
14147- normal control [large intestine] CMP_lLoD3VIf7	SingleCellHumanUmi	normal control	large intestine		Cell Type vs Cell Ty...	intestinal crypt ste...	TabulaSapiens_UMI...	CMP:lLoD3VIf7A4c	https://tabula-sapi...
18604- normal control [eye] CMP_kkBY6IZsYVIf	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	retinal pigment epi...	TabulaSapiens_UMI...	CMP:kkBY6IZsYVIf	https://tabula-sapi...
38- normal control [skin] CMP_HQo0mNgvYfIU	SingleCellHumanUmi	normal control	skin		Cell Type vs Cell Ty...	glandular epithelia...	GSE130973_UMI.GPL	CMP:HQo0mNgvYfIU	https://www.ncbi.n...
14317- normal control [large intestine;small intestine]	SingleCellHumanUmi	normal control	large intestine;smal...		Cell Type vs Cell Ty...	intestinal enteroen...	TabulaSapiens_UMI...	CMP:pulP3qEsKD3D	https://tabula-sapi...
5674- normal control [salivary gland] CMP_hooysBn5k	SingleCellHumanUmi	normal control	salivary gland		Cell Type vs Cell Ty...	acinar cell of salivar...	TabulaSapiens_UMI...	CMP:hooysBn5kEr	https://tabula-sapi...
2507- normal control [eye] CMP_VpazsBTH6rKb	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	melanocyte vs radi...	TabulaSapiens_UMI...	CMP:VpazsBTH6rKb	https://tabula-sapi...
2351- normal control [eye] CMP_BeBCmsjZGgoM	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	erythroid cell vs ker...	TabulaSapiens_UMI...	CMP:BeBCmsjZGgoM	https://tabula-sapi...
18606- normal control [eye] CMP_oKWneUXPozKx	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	retinal pigment epi...	TabulaSapiens_UMI...	CMP:oKWneUXPozKx	https://tabula-sapi...
17671- normal control [pancreas] CMP_7rstuja07Si	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:7rstuja07Si	https://tabula-sapi...
94- skin melanoma (SKCM) [skin] culture medium CMP	OncoHuman	skin melanoma (SK...	skin	culture medium	Other Comparisons	GeneticSubtype =>...	GSE151825.GPL1857	CMP:j7ubhnP3YggC	https://www.ncbi.n...
1466- normal control [skin] CMP_VsM4rDaErGCO	SingleCellHumanUmi	normal control	skin		Cell Type vs Cell Ty...	mast cell vs smooth...	TabulaSapiens_UMI...	CMP:VsM4rDaErGCO	https://tabula-sapi...
87- skin melanoma (SKCM) [skin] culture medium CMP	OncoHuman	skin melanoma (SK...	skin	culture medium	Other Comparisons	GeneticSubtype =>...	GSE151825.GPL1857	CMP:DokiFys2bTEL	https://www.ncbi.n...
240- normal control [peripheral blood] S_ aureus (heat	HumanDisease	normal control	peripheral blood	S. aureus (heat killed)	Other Comparisons	TreatmentAgeCate...	GSE103500.GPL10551	CMP:ZBP7u51YRqo	https://www.ncbi.n...
15579- normal control [lung] CMP_UesQfKuI2d5Y	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	lung ciliated cell vs ...	TabulaSapiens_UMI...	CMP:UesQfKuI2d5Y	https://tabula-sapi...
12000- normal control [small intestine] CMP_3d7qjb0B	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	enterocyte of epith...	TabulaSapiens_UMI...	CMP:3d7qjb0B67cV	https://tabula-sapi...
18776- normal control [small intestine] CMP_ieTZeeRzjBb	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	small intestine gobl...	TabulaSapiens_UMI...	CMP:ieTZeeRzjBb	https://tabula-sapi...
17983- normal control [small intestine] CMP_3yZeCBYI	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	paneth cell of epith...	TabulaSapiens_UMI...	CMP:3yZeCBYTZdNN	https://tabula-sapi...
17625- normal control [pancreas] CMP_nmhmZ2E6S9CsJ	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:nmhmZ2E6S9CsJ	https://tabula-sapi...
83- disease control [secondary auditory cortex] NA CMF	HumanDisease	disease control	secondary auditory...	NA	Tissue1 vs. Tissue2	ExperimentGroup =...	GSE127898.GPL2030	CMP:6CcyPd5jJ78	https://www.ncbi.n...
14- normal control [peripheral blood] CL097 CMP_PXQ	HumanDisease	normal control	peripheral blood	CL097	Treatment vs. Contr...	AgeCategory:CellSu...	GSE94496.GPL10558	CMP:PXQY00ot3Nrv	https://www.ncbi.n...
84- coronavirus disease 2019 (COVID-19);disease contr	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	airway mucous cell ...	GSE171524_UMI.GPL	CMP:ewr1soiktI7j	https://www.ncbi.n...
16361- normal control [eye;skin] CMP_5bN4EomZj0yg	SingleCellHumanUmi	normal control	eyes;skin		Cell Type vs Cell Ty...	melanocyte vs retin...	TabulaSapiens_UMI...	CMP:5bN4EomZj0yg	https://tabula-sapi...
11374- normal control [small intestine] CMP_aFtLq34j	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	duodenum glandul...	TabulaSapiens_UMI...	CMP:aFtLq34jpej3	https://tabula-sapi...
6- ovarian cancer [ovary] NA CMP_LVelpNWagJOO	OncoHuman	ovarian cancer	ovary	NA	Treatment1 vs. Trea...	SubjectTreatment =...	GSE112798.GPL570...	CMP:LVElpNWagJOO	https://www.ncbi.n...
44- normal control [skin] CMP_h311BPTWjk12	SingleCellHumanUmi	normal control	skin		Cell Type vs Cell Ty...	lymphatic endothe...	GSE147424_UMI.GPL	CMP:h311BPTWjk12	https://www.ncbi.n...
10125- normal control [lung] CMP_ILl8jGEMajk1	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	club cell vs pericyte...	TabulaSapiens_UMI...	CMP:ILl8jGEMajk1	https://tabula-sapi...
16- breast cancer [breast] CMP_RLS4ZqwmHMSX	SingleCellHumanUmi	breast cancer	breast		Cluster vs Others	B cell (cluster) vs ot...	GSE135710_UMI.GPL	CMP:RLS4ZqwmHMS	https://www.ncbi.n...
5- normal control [peripheral blood] IL-2 CMP_p4wF08j	HumanDisease	normal control	peripheral blood	IL-2	CellType1 vs. CellTy...	CellDescription => ...	GSE118165.GPL2030	CMP:p4wF08jP3dfa	https://www.ncbi.n...
97- diffuse scleroderma;normal control [skin] CMP_sTG	SingleCellHumanUmi	diffuse scleroderma...	skin		Cluster vs Others	epidermal keratino...	GSE138669_UMI.GPL	CMP:sTG5dj80wyVE	https://www.ncbi.n...
7- diffuse scleroderma;normal control [skin] CMP_BTfI	SingleCellHumanUmi	diffuse scleroderma...	skin		Cell Type vs Others	epidermal keratino...	GSE138669_UMI.GPL	CMP:8TFHlU4LZGGO	https://www.ncbi.n...
62- NA [peripheral blood] NA CMP_HBEKic46qHzv	HumanDisease	NA	peripheral blood	NA	Other Comparisons	ExperimentGroup =...	GSE198449.GPL24671	CMP:HBEKic46qHzv	https://www.ncbi.n...
230- normal control [peripheral blood] S_ aureus (heat	HumanDisease	normal control	peripheral blood	S. aureus (heat killed)	Other Comparisons	TreatmentAgeCate...	GSE103500.GPL10551	CMP:rls6SdEk7MZxZ	https://www.ncbi.n...
104- keloid [skin] CMP_F29ddQGON25E	SingleCellHumanUmi	keloid	skin		Cluster vs Others	epidermal keratino...	HRA000425_UMI.GPL	CMP:F29ddQGON25E	https://ngdc.cncb.a...
45- normal control [skin] CMP_ELzKV91RyZ91	SingleCellHumanUmi	normal control	skin		Cell Type vs Cell Ty...	lymphatic endothe...	GSE147424_UMI.GPL	CMP:ELzKV91RyZ91	https://www.ncbi.n...
15- normal control [peripheral blood] lipopolysaccharid	HumanDisease	normal control	peripheral blood	lipopolysaccharide ...	Treatment vs. Contr...	AgeCategory:CellSu...	GSE94496.GPL10558	CMP:05I3iJ2MTUly	https://www.ncbi.n...
60- pulmonary tuberculosis [peripheral blood] NA CMP	HumanDisease	pulmonary tubercu...	lung	NA	Other Comparisons	DiseaseStateExper...	GSE42832.GPL10558	CMP:ciCVOLxkfbko	https://www.ncbi.n...
439- triple-receptor negative breast cancer (TNBC) [bre	SingleCellHumanUmi	triple-receptor neg...	breast;peripheral bl...		Cell Type vs Cell Ty...	gamma-delta T cell ...	GSE169246_UMI.GPL	CMP:bQvIBN7HZy2t	https://www.ncbi.n...
48- acute myeloid leukemia (LAM1) [peripheral blood] r	HumanDisease	acute myeloid leuk...	peripheral blood	none	Treatment1 vs. Trea...	ExperimentGroup =...	GSE133317.GPL1679	CMP:XLwa70GLKjot	https://www.ncbi.n...
17- type 1 diabetes mellitus [peripheral blood] NA CMP	HumanDisease	type 1 diabetes mel...	peripheral blood	NA	Treatment vs. Contr...	ExperimentGroup:S...	GSE124284.GPL1679	CMP:fuRm15MNd4h	https://www.ncbi.n...
67- cervical squamous cell carcinoma (CESC) [cervix] NA	TCGA	cervical squamous ...	cervix	NA	Other Comparisons	DNASeqSomaticMu...	TCGA_CESC.GPLnaD	CMP:l0o4Q6BTGve2	https://www.cancer...
5- bladder transitional cell carcinoma [bladder] PD1730	OncoHuman	bladder transitiona...	bladder	PD173074	Treatment vs. Contr...	CellDescription:Trea...	GSE201395.GPL17581	CMP:OXBan1oM9bsX	https://www.ncbi.n...

Biomarker Application

Drug

Expression Analysis - protein.6

Application									
Add To My Pathway				Add To My List		Create Dataset		Customize Table	
Symbol A1BG - ACYP2 (1/71)									
Symbol	Entrez Gene Name	Identifier	Measurement	Location	Type(s)	Biomarker Application(s)	Drug(s)		
		Gene Symbol - human (HUGO ...	Expr Log Ratio						
A1BG	alpha-1-B glycoprotein	A1BG	↑0.071	Extracellular Space	other	unspecified application			
AAAS	aladin WD repeat nucleoporin	AAAS	↓-0.246	Nucleus	other				
AACS	acetoacetyl-CoA synthetase	AACS	↓-0.007	Cytoplasm	enzyme				
AAGAB	alpha and gamma adaptin binding protein	AAGAB	↓-0.074	Cytoplasm	other				
AAK1	AP2 associated kinase 1	AAK1	↓-0.161	Cytoplasm	kinase		LP-935509, SM1-71		
AAMDC	adipogenesis associated Mth938 domain...	AAMDC	↓-0.003	Cytoplasm	other				
AAMP	angio associated migratory cell protein	AAMP	↓-0.318	Plasma Membrane	other				
AAR2	AAR2 splicing factor	AAR2	↓-5.732	Other	other				
AARS1	alanyl-tRNA synthetase 1	AARS1	↓-0.277	Cytoplasm	enzyme				
AARS2	alanyl-tRNA synthetase 2, mitochondrial	AARS2	↑0.011	Cytoplasm	enzyme				
AARSD1	alanyl-tRNA synthetase domain containi...	AARSD1	↓-0.403	Nucleus	enzyme				
AASDHPPT	aminoadipate-semialdehyde dehydroge...	AASDHPPT	↓-0.195	Cytoplasm	enzyme				
AASS	aminoadipate-semialdehyde synthase	AASS	↑0.000	Cytoplasm	enzyme				
AATF	apoptosis antagonizing transcription fact...	AATF	↓-0.447	Nucleus	transcription regulator				
ABCA2	ATP binding cassette subfamily A membe...	ABCA2	↓-0.001	Plasma Membrane	transporter				
ABCB10	ATP binding cassette subfamily B membe...	ABCB10	↓-0.007	Cytoplasm	transporter				
ABCB7	ATP binding cassette subfamily B membe...	ABCB7	↓-0.043	Cytoplasm	transporter	unspecified application			
ABCB8	ATP binding cassette subfamily B membe...	ABCB8	↓-0.001	Cytoplasm	transporter				
ABCC1	ATP binding cassette subfamily C membe...	ABCC1	↓-0.479	Plasma Membrane	transporter	prognosis	sulfinpyrazone		
ABCC10	ATP binding cassette subfamily C membe...	ABCC10	↑0.001	Plasma Membrane	transporter				
ABCC3	ATP binding cassette subfamily C membe...	ABCC3	↓-0.001	Plasma Membrane	transporter	diagnosis, prognosis, prognosis			
ABCC4	ATP binding cassette subfamily C membe...	ABCC4	↓-0.331	Plasma Membrane	transporter				
ABCD3	ATP binding cassette subfamily D membe...	ABCD3	↓-0.047	Cytoplasm	transporter				
ABCD4	ATP binding cassette subfamily D membe...	ABCD4	↑0.001	Cytoplasm	transporter				
ABCE1	ATP binding cassette subfamily E membe...	ABCE1	↓-0.133	Cytoplasm	transporter				
ABCF1	ATP binding cassette subfamily F membe...	ABCF1	↓-0.294	Cytoplasm	transporter				
ABCF2	ATP binding cassette subfamily F membe...	ABCF2	↓-0.247	Cytoplasm	transporter				
ABCF3	ATP binding cassette subfamily F membe...	ABCF3	↓-0.039	Other	transporter				
ABHD10	abhydrolase domain containing 10, depa...	ABHD10	↑0.021	Cytoplasm	enzyme				
ABHD11	abhydrolase domain containing 11	ABHD11	↓-0.007	Cytoplasm	enzyme				
ABHD12	abhydrolase domain containing 12, lyso...	ABHD12	↓-0.198	Plasma Membrane	enzyme				
ABHD14B	abhydrolase domain containing 14B	ABHD14B	↓-0.081	Cytoplasm	enzyme				
ABHD16A	abhydrolase domain containing 16A, ph...	ABHD16A	↓-0.024	Other	enzyme				
ABHD5	abhydrolase domain containing 5, lysop...	ABHD5	↓-0.044	Cytoplasm	enzyme				
ABHD6	abhydrolase domain containing 6, acylgl...	ABHD6	↓-0.000	Cytoplasm	enzyme				
ABI1	abl interactor 1	ABI1	↓-0.434	Cytoplasm	other				
ABI2	abl interactor 2	ABI2	↓-0.246	Cytoplasm	other				
ABL1	ABL proto-oncogene 1, non-receptor tyr...	ABL1	↑0.000	Nucleus	kinase	efficacy, response to therapy,	ABL1 inhibitor, GNF-5, HG-7-85-01,		
ABL2	ABL proto-oncogene 2, non-receptor tyr...	ABL2	↑0.001	Cytoplasm	kinase		dasatinib, nilotinib		
ABLIM1	actin binding LIM protein 1	ABLIM1	↑0.074	Cytoplasm	other				
ABLIM3	actin binding LIM protein family member 3	ABLIM3	↓-0.253	Cytoplasm	other				
ABR	ABR activator of RhoGEF and GTPase	ABR	↓-0.062	Cytoplasm	other				
ABRACL	ABRA C-terminal like	ABRACL	↓-0.032	Nucleus	other				
ABRAXAS2	abraxas 2, BRISC complex subunit	ABRAXAS2	↓-0.031	Nucleus	other				
ABT1	activator of basal transcription 1	ABT1	↓-0.000	Nucleus	transcription regulator				
ACAA1	acetyl-CoA acyltransferase 1	ACAA1	↓-0.088	Cytoplasm	enzyme		trimetazidine		
ACAA2	acetyl-CoA acyltransferase 2	ACAA2	↑0.001	Cytoplasm	enzyme	unspecified application			
ACACA	acetyl-CoA carboxylase alpha	ACACA	↓-0.013	Cytoplasm	enzyme				
ACACB	acetyl-CoA carboxylase beta	ACACB	↓-0.021	Cytoplasm	enzyme				
ACAD10	acyl-CoA dehydrogenase family member ...	ACAD10	↑0.002	Cytoplasm	enzyme				
ACAD11	acyl-CoA dehydrogenase family member ...	ACAD11	↑0.004	Cytoplasm	enzyme				
ACAD8	acyl-CoA dehydrogenase family member 8	ACAD8	↑0.007	Cytoplasm	enzyme				
ACAD9	acyl-CoA dehydrogenase family member 9	ACAD9	↓-0.534	Cytoplasm	enzyme				
ACADM	acyl-CoA dehydrogenase medium chain	ACADM	↓-0.072	Cytoplasm	enzyme	unspecified application			

Upload dataset phosphoprotein

ptmgroup_id	ptmgroup_label	ptm_site	gene_name	protein_ac	protein_description	fold_change_log2.6h	protein_fold_change_log2.6h	p_value.6h	protein_p_value.6h	sd_log2.6h	fold_change_log2.12h	protein_fold_change_log2.12h	p_value.12h	protein_p_value.12h	sd_log2.12h	fold_change_log2.24h	protein_fold_change_log2.24h	p_value.24h	protein_p_value.24h	sd_log2.24h
1402	Phospho_	S14	AAK1	Q2M2I8	AP2-assoc	0.016175	-0.161099	0.7996454	0.1908782	1.0728027	0.415605	-0.223489	0.4397424	0.0846668	1.2347047	0.512405	-0.178266	0.4121578	0.3769807	1.248460
1403	Phospho_	S18	AAK1	Q2M2I8	AP2-assoc	-0.00392	-0.161099	0.9157634	0.1908782	0.444943	-0.01761	-0.223489	0.9075284	0.0846668	0.525266	-0.02205	-0.178266	0.9392419	0.3769807	0.599767
1404	Phospho_	S20	AAK1	Q2M2I8	AP2-assoc	0.001115	-0.161099	0.955101	0.1908782	0.1323393	0.01692	-0.223489	0.8628406	0.0846668	0.172894	0.028365	-0.178266	0.8747586	0.3769807	0.306159
1405	Phospho_	S21	AAK1	Q2M2I8	AP2-assoc	-0.01303	-0.161099	0.7495535	0.1908782	0.1302761	-0.09286	-0.223489	0.5009719	0.0846668	0.1820468	-0.38518	-0.178266	0.0730571	0.3769807	0.267719
1406	Phospho_	S637	AAK1	Q2M2I8	AP2-assoc	9.60E-04	-0.161099	0.9776073	0.1908782	0.2863605	0.06182	-0.223489	0.711682	0.0846668	0.480873	0.00985	-0.178266	0.9787208	0.3769807	0.638505
1407	Phospho_	S846	AAK1	Q2M2I8	AP2-assoc	0.04384	-0.161099	0.5944792	0.1908782	0.2093386	0.044875	-0.223489	0.826919	0.0846668	1.2032438	0.16985	-0.178266	0.6922961	0.3769807	1.314624
1409	Phospho_	S652	AAK1	Q2M2I8	AP2-assoc	-0.001225	-0.161099	0.9398131	0.1908782	0.1107301	-0.16419	-0.223489	0.3335143	0.0846668	0.211761	-0.29161	-0.178266	0.1876435	0.3769807	0.252798
1411	Phospho_	T606	AAK1	Q2M2I8	AP2-assoc	-0.002095	-0.161099	0.9302625	0.1908782	0.1913935	0.005795	-0.223489	0.9560054	0.0846668	0.2804999	-0.07337	-0.178266	0.7968987	0.3769807	0.743179
1412	Phospho_	S203	AATF	Q9NY61	Protein A	-0.03955	-0.44736	0.6604824	0.2211426	0.7119437	-0.11218	-0.475305	0.6237351	0.2188032	0.8113718	-0.193465	0.7504477	0.6069083	0.3735299	0.888031
1413	Phospho_	S930	ABCC1	P33527	Multidrug	0.194585	-0.479257	0.4983829	0.0442408	0.5701773	0.39033	-0.196155	0.4688539	0.2016444	0.6811833	0.17477	-0.133812	0.7839488	0.4769558	1.02442
1415	Phospho_	S638	ABCC4	O15439	ATP-bindi	0.001625	-0.330803	0.9582258	0.0399986	0.3041878	0.020665	-0.48169	0.9000945	1.86E-04	0.4671723	0.05732	0.214965	0.851822	0.2677113	0.65970
1416	Phospho_	T646	ABCC4	O15439	ATP-bindi	0.00151	-0.330803	0.9278971	0.0399986	0.0954347	0.03269	-0.48169	0.7297084	1.86E-04	0.135285	-0.876605	0.214965	0.0425582	0.2677113	0.377520
1417	Phospho_	S228	ABCF1	Q8NE71	ATP-bindi	-0.492011	-0.293674	0.091018	0.0069282	0.2182538	-0.102733	-0.317664	0.4490637	1.34E-11	0.1807272	-0.99007	0.273173	0.1095249	0.0022072	0.385484
1418	Phospho_	S140	ABCF1	Q8NE71	ATP-bindi	-5.60E-04	-0.293674	0.9788018	0.0069282	0.6188695	0.77145	-0.317664	0.1570357	1.34E-11	0.771127	0.53757	0.273173	0.5728005	0.0022072	0.864295
1419	Phospho_	S109	ABCF1	Q8NE71	ATP-bindi	0.012275	-0.293674	0.7316444	0.0069282	0.1062173	0.061295	-0.317664	0.5756118	1.34E-11	0.1464715	-0.55149	0.273173	0.0181205	0.0022072	0.236043
1420	Phospho_	S595	ABCF1	Q8NE71	ATP-bindi	0.287295	-0.293674	0.4998504	0.0069282	1.7691229	4.536555	-0.317664	0.0010871	1.34E-11	1.1360847	4.493625	0.273173	0.0011688	0.0022072	1.139043
1421	Phospho_	S323	ABI1	Q8IZP0	Abl interac	-0.235135	-0.434244	0.3000211	0.0043545	0.2636538	-0.25567	-0.108867	0.3583243	0.6146324	0.3362974	-0.39159	0.3368868	0.336206	0.0959762	0.739996
1422	Phospho_	S183	ABI1	Q8IZP0	Abl interac	-0.13769	-0.434244	0.2847223	0.0043545	0.1688397	-0.12909	-0.108867	0.3342269	0.6146324	0.1433546	-0.388565	0.3368868	0.0284942	0.0959762	0.195017
1423	Phospho_	S224	ABI2	Q9NYB9	Abl interac	-0.007785	-0.246494	0.870845	0.2330501	0.4275876	-0.02535	-0.161979	0.8877086	0.3937105	0.5833276	0.04887	-0.131951	0.8738884	0.5402341	0.865836
1424	Phospho_	S227	ABI2	Q9NYB9	Abl interac	-0.01118	-0.246494	0.7644881	0.2330501	0.1170305	0.034615	-0.161979	0.7802558	0.3937105	0.2151022	-0.1775	-0.131951	0.3772164	0.5402341	0.228836
1425	Phospho_	S183	ABI2	Q9NYB9	Abl interac	-0.001675	-0.246494	0.9259217	0.2330501	0.1128329	0.03025	-0.161979	0.7799462	0.3937105	0.1834037	-0.1064	-0.131951	0.6278211	0.5402341	0.322243
1426	Phospho_	S631	ABL2	P42684	Tyrosine-p	-0.0066	9.65E-04	0.8265216	0.9597367	0.1065753	-0.057655	0.005105	0.5935272	0.9676906	0.1422786	-0.23217	0.00877	0.1996556	0.9693272	0.222124
1427	Phospho_	S618	ABL2	P42684	Tyrosine-p	-0.0022	9.65E-04	0.9312214	0.9597367	0.3250531	-0.012815	0.005105	0.9267229	0.9676906	0.4589765	-0.024155	0.00877	0.9323583	0.9693272	0.558834
1428	Phospho_	S620	ABL2	P42684	Tyrosine-p	-0.0022	9.65E-04	0.9170780	0.9597367	0.2700707	-0.0024	0.005105	0.90906	0.9676906	0.4174601	-0.03658	0.00877	0.907123	0.9693272	0.638054

Create New

Upload dataset

Choose your file

Edit observation name

Infer observation

Dataset Upload - MOESEM_protein.xlsx

1. Select File Format: Flexible Format
2. Contains Column Header: Yes
3. Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
4. Array platform used for experiments: Not specified/applicable
5. Use the dropdown menus to specify the column n

Edit Observation Names

Raw Data (7702) Dataset Summary (0) Met

Edit Observation Names Infer Observation

ID/Observation Name Ignore
Measurement/Annotation

1 gene_names
2 EC1
3 ZNF655
4 REXO4
5 TRPC4,TRPC5
6 H2BC12,H2BC13,H2...
7 SLC25A13
8 MTF2
9 HMCN1
10 UBA2
11 SIK3
12 C18L
13 TP53BP1
14 MED20
15 C14orf119
16 IGSF8
17 DBI
18 SERPING1
19 ERCC3
20 GIGYF2
21 MED18
22 SLC30A1
23 UBR2
24 STEAP2
25 TAX1BP3
26 SRSF7
27 SFSWAP
28 ANXA13
29 TERF1

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

Edit Observation Names

Observation Name

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

OK Cancel

sd_log2.12h fold_change_log2.2... p_value.24h sd_log2.24h
11696_ 9.4350989242599007... -0.2674955500000000... 7.5430876500756699... 9.28915038320519E-2
12559_ 1.1361835636320601... -0.4940649999999999... 0.4576397276695309... 1.2088366425480801
17779_ 0.3484108559920199... -9.574999999999999... 0.9720591511091649... 0.4524954842321570...
15570_ 0.3271231223601029... 0.2707499999999999... 0.380341728316895... 0.3562806529816229...
16929_ 0.1466748253231280... 0.4861150000000000... 1.4394252647286301... 0.1678519601499839...
11580_ 0.311732699096334... -4.234709999999999... 5.3837009198685302... 1.8836548463955201...
14069_ 0.4164384761217920... -3.9050000000000039... 0.9877520642211119... 0.5171131399459959...
8150_ 0.9905678668802709... -0.3460749999999999... 0.5723601284551610... 1.64431208954147...
171E_ 6.6499914238070307... -4.6177500000000000... 0.5812464974222110... 7.8768809979468196...
16610_ 0.3410343244147229... 4.279999999999999... 0.8605141383867239... 0.4336125290605820...
0501_ 1.18056131579177... 8.630378499999999... 1.999999999999999... 0.458489081433477...
14401_ 7.90995978953207E... 0.1104749999999999... 0.634492908667461... 0.1992221002607250...
10360_ 2.9706599189906102... -7.8502855... 0.1299470877263939... 2.9851368758577999...
17890_ 0.390233150485919... 1.5000000000320301... 0.9969694623128220... 0.4998669027721590...
15220_ 0.6104338992602830... 5.799999999999999... 0.984178090094929... 0.6861339143223850...
8229_ 0.1437304679631019... 0.1401350000000000... 0.1054355947707039... 0.401042192027527...
12349_ 0.388088850210287... 3.2350000000000089... 0.9915485814740040... 0.5030443827824170...
12670_ 0.5920631663241769... -0.7240799999999999... 0.362523190756112... 1.8756340543427601...
Q6Y7W6;Q6Y7W6-3; GRB10-interacting ... -0.128 0.1873572106644660... 0.110386826989713 -6.554999999999860... 0.9359435765987800... 9.6195135493622394... 0.2825934999999999... 4.8404147917430397... 0.1472934103667830...
Q9BUE0 Mediator of RNA po... -5.3080000000000000... 0.5568033435216249... 0.205120468961248 -0.6963699999999999... 1.6849045377717899... 0.298775425212705 -3.6637749999999999... 1.58972622239568E... 1.8290275854350899...
Q9Y6M5 Zinc transporter 1 2.9050000000000039... 0.8922665977373059... 0.1031524145485519... 1.0002499999999999... 0.9078591089505180... 0.1605284274894699... 1.1515560499999999... 3.4266735339520999... 0.2599574173142100...
Q8IWW8;Q8IWW8-2; E3 ubiquitin-protei... -2.920000000000047E... 0.902407005749428 0.2266605614155509... -2.2445000000000020... 0.8631123965920339... 0.3002789334246849... -3.8219999999999899... 0.8666968915045030... 0.3798707638404609...
Q8NFT2;Q8NFT2-2; Isoform 2 of Metallo... -0.3220199999999999... 0.2729524983550289... 0.3477879328360050... -0.11895 0.6966039104794290... 0.4326601529452039... -0.2275850000000000... 0.5082650323241549... 0.4080403041260199...
O14907 Tax1-binding protei... -3.2718814999999990... 0.5978026480978380... 0.1360646491398740... -9.3651349999999999... 0.4672874170461809... 0.1684528518085519... -9.5360500000000000... 0.5279445437520450... 0.1768228456816919...
Q16629;Q16629-2;Q... Isoform 2 of Serine/... -0.1444449999999999... 9.0269716765870603... 8.3621732674460297... -0.164715 5.8345456322383402... 8.8685647088321995... 0.6107599999999999... 7.4747780841027302... 0.117401839985863...
Q12872;Q12872-2 Isoform 2 of Splicin... 0.4294999999999999... 0.4675380842290319... 1.1502532543994499... 0.113165 0.7662513975447250... 1.2762468159726701... 8.7379999999999999... 0.8632089953956040... 1.25799626205648...
P27216;P27216-2 Annexin A13;Isofor... 3.1759999999998401... 0.5972789340081039... 0.1645485591511489... 5.4969999999999901... 0.6844190240611239... 0.2036497339085920... 9.51049999999999704... 0.6605636001239140... 0.3202115717559749...
P54274;P54274-2 Isoform 2 of Telome... 0.2908350000000000... 0.3479381862434209... 0.3599952997251399... 0.6164999999999990... 0.1151406608574680... 0.4005604545699140... 0.6288799999999999... 7.9237015992669496... 0.3522820272453129...

Analyze filter dataset

Core analysis

Set cut off

Annotated Dataset: MOESEM_protein

Preview Dataset MOESEM_protein Observation: protein.6 (7063)

Mapped IDs (7186) Unmapped IDs (515) All IDs (7701) Metadata

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

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
0.071	1.95E-01	A1BG		A1BG	alpha-1-B glycoprotein	Extracellular Space	other	
-0.246	1.47E-01	AAAS		AAAS	aladin WD repeat nucleoporin	Nucleus	other	
-0.007	8.22E-01	AACS		AACS	acetoacetyl-CoA synthetase	Cytoplasm	enzyme	
-0.074	4.83E-01	AGAB		AGAB	alpha and gamma adaptin binding protein	Cytoplasm	other	
-0.161	1.91E-01	AAK1		AAK1	AP2 associated kinase 1	Cytoplasm	kinase	LP-935509, SM1-71
-0.003	8.89E-01	AAMDC		AAMDC	adipogenesis associated Mth938 domain containing	Cytoplasm	other	
-0.318	2.74E-01	AAMP		AAMP	angio associated migratory cell protein	Plasma Membrane	other	
-5.732	4.79E-02	AAR2		AAR2	AAR2 splicing factor	Other	other	
-0.277	1.06E-19	AARS1		AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme	
0.011	7.89E-01	AARS2		AARS2	alanyl-tRNA synthetase 2, mitochondrial	Cytoplasm	enzyme	
-0.403	4.41E-04	AARSD1		AARSD1	alanyl-tRNA synthetase domain containing 1	Nucleus	enzyme	
-0.195	1.01E-01	AASDHPT		AASDHPT	aminoadipate-semialdehyde dehydrogenase-phos...	Cytoplasm	enzyme	
0.000	9.84E-01	AASS		AASS	aminoadipate-semialdehyde synthase	Cytoplasm	enzyme	
-0.447	2.21E-01	AATF		AATF	apoptosis antagonizing transcription factor	Nucleus	transcription regulator	
-0.001	9.61E-01	ABCA2		ABCA2	ATP binding cassette subfamily A member 2	Plasma Membrane	transporter	
-0.007	8.78E-01	ABCB10		ABCB10	ATP binding cassette subfamily B member 10	Cytoplasm	transporter	
-0.043	7.01E-01	ABCB7		ABCB7	ATP binding cassette subfamily B member 7	Cytoplasm	transporter	
-0.001	9.67E-01	ABCB8		ABCB8	ATP binding cassette subfamily B member 8	Cytoplasm	transporter	
-0.479	4.42E-02	ABCC1		ABCC1	ATP binding cassette subfamily C member 1 (ABCC1 ...	Plasma Membrane	transporter	sulfinpyrazone
0.001	9.68E-01	ABCC10		ABCC10	ATP binding cassette subfamily C member 10	Plasma Membrane	transporter	
-0.001	9.67E-01	ABCC3		ABCC3	ATP binding cassette subfamily C member 3	Plasma Membrane	transporter	
-0.331	4.00E-02	ABCC4		ABCC4	ATP binding cassette subfamily C member 4 (PEL bL...	Plasma Membrane	transporter	
-0.047	4.02E-01	ABCD3		ABCD3	ATP binding cassette subfamily D member 3	Cytoplasm	transporter	
0.001	9.73E-01	ABCD4		ABCD4	ATP binding cassette subfamily D member 4	Cytoplasm	transporter	
-0.133	8.76E-02	ABCE1		ABCE1	ATP binding cassette subfamily E member 1	Cytoplasm	transporter	
-0.294	6.93E-03	ABCF1		ABCF1	ATP binding cassette subfamily F member 1	Cytoplasm	transporter	
-0.247	1.35E-01	ABCF2		ABCF2	ATP binding cassette subfamily F member 2	Cytoplasm	transporter	
-0.039	4.84E-01	ABCF3		ABCF3	ATP binding cassette subfamily F member 3	Other	transporter	
0.021	6.85E-01	ABHD10		ABHD10	abhydrolase domain containing 10, depalmitoylase	Cytoplasm	enzyme	
-0.007	8.67E-01	ABHD11		ABHD11	abhydrolase domain containing 11	Cytoplasm	enzyme	
-0.198	3.86E-02	ABHD12		ABHD12	abhydrolase domain containing 12, lysophospholip...	Plasma Membrane	enzyme	
-0.081	2.59E-01	ABHD148		ABHD148	abhydrolase domain containing 148	Cytoplasm	enzyme	
-0.024	6.77E-01	ABHD16A		ABHD16A	abhydrolase domain containing 16A, phospholipase	Other	enzyme	
-0.044	6.31E-01	ABHD5		ABHD5	abhydrolase domain containing 5, lysophosphatidi...	Cytoplasm	enzyme	
-0.000	9.92E-01	ABHD6		ABHD6	abhydrolase domain containing 6, acylglycerol lipase	Cytoplasm	enzyme	
-0.434	4.35E-03	ABI1		ABI1	abl interactor 1	Cytoplasm	other	
-0.246	2.33E-01	ABI2		ABI2	abl interactor 2	Cytoplasm	other	
0.000	9.86E-01	ABL1		ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	Nucleus	kinase	olverembatinib, temozolomide, filgrastim/matatinib, ...
0.001	9.60E-01	ABL2		ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase	Cytoplasm	kinase	nilotinib, dasatinib
0.074	6.36E-01	ABLUM1		ABLUM1	actin binding LIM protein 1	Cytoplasm	other	
-0.253	1.36E-01	ABLUM3		ABLUM3	actin binding LIM protein family member 3	Cytoplasm	other	
-0.062	4.70E-01	ABR		ABR	ABR activator of RhoGEF and GTPase	Cytoplasm	other	
-0.032	5.27E-01	ABRACL		ABRACL	ABRA C-terminal like	Nucleus	other	
-0.031	6.01E-01	ABRAXAS2		ABRAXAS2	abraxas 2, BRISC complex subunit	Nucleus	other	
-0.000	9.82E-01	ABT1		ABT1	activator of basal transcription 1	Nucleus	transcription regulator	
-0.088	2.97E-01	ACAA1		ACAA1	acetyl-CoA acyltransferase 1	Cytoplasm	enzyme	trimetazid...
0.001	9.45E-01	ACAA2		ACAA2	acetyl-CoA acyltransferase 2	Cytoplasm	enzyme	

0 / 7186

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

Edit Dataset Settings Analyze/Filter Dataset Close

Load Volcano plot

Analyze filter dataset

Core analysis

Set cut off

Create Phosphorylation Analysis - [analysis : Naturecomm_phosphoprotein]

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
fold_change_log2.6h	Phospho Log Ratio	-10.4236 to 13.7086	<input type="text" value="-0.58"/> Down <input type="text" value="0.58"/> Up
p_value.6h	Phospho p-value	0.0 to 1.0	<input type="text" value="0.05"/>

recalculate

Advanced

Recalculate

2216 analysis-ready molecules across observations

Preview Dataset Naturecomm_phosphoprotein

Observation: phospho.6 (676)

Analysis-Ready (676)

Mapped IDs (10115)

Unmapped IDs (36)

All IDs (10151)

Metadata

Add To My Pathway

Add To My List

Create Dataset

Customize Table

Phospho Log Ratio

Phospho p-value

Phospho Site

ID

Flags

Symbol

Entrez Gene Name

Location

Type(s)

Drug(s)

Run Analysis

Cancel

Load volcano plot

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

fold_change_log2.6h

p_value.6h [-log10]

Update Axes

Clear Molecule Names

Sample to Insight

Analyze filter
dataset

Core analysis

Set cut off

Biological
Filter

Create Phosphorylation Analysis - [analysis : Naturecomm_phosphprotein]

Set Cutoffs Biological Filters

General Settings

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

Save As Default

Population of genes to consider for p-value calculations: **Use dataset**

Reference Set: **User Dataset**

Relationships to Affects networks:
☒ Direct and Indirect
☐ Direct Relationships

Optional Analyses:
☒ My Project
☒ My Pathways
☒ My Lists

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

Advanced Recalculate **2216** analysis-ready molecules across observations

Preview Dataset Naturecomm_phosphprotein Observation: phsopho.6 (676)

Analysis-Ready (676) Mapped IDs (10115) Unmapped IDs (36) All IDs (10151) Metadata

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

Symbol: AAMP - CD19 (1/7)

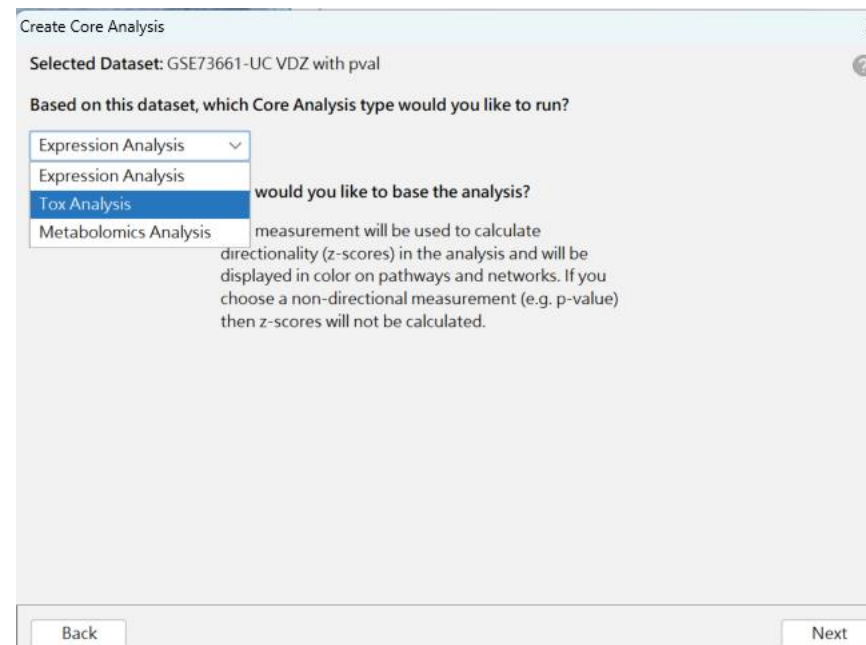
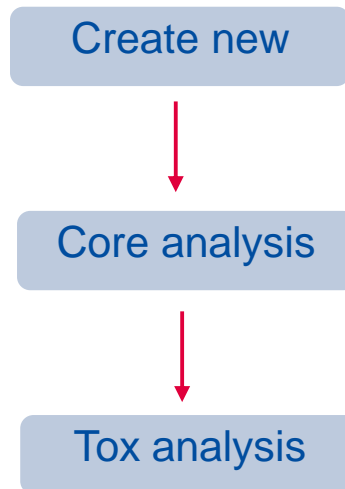
Phospho Log Ratio	Phospho p-value	Phospho Site	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-1.336	5.14E-04	S679	11297		AAMP	angio associated migrat...	Plasma Membrane	other	
-1.294	3.45E-02	T18	8647	D	ABCB11*	ATP binding cassette su...	Plasma Membrane	transporter	
-1.340	6.03E-03	S443	8308	D	ACOX1*	acyl-CoA oxidase 1	Cytoplasm	enzyme	
-3.531	1.78E-02	T70	2181		ACSL3	acyl-CoA synthetase lon...	Cytoplasm	enzyme	
-4.739	2.37E-03	S311	9178		ACTL6A	actin like 6A	Nucleus	other	
-6.301	1.59E-16	S676	8423		ACTR1B	actin related protein 1B	Cytoplasm	other	

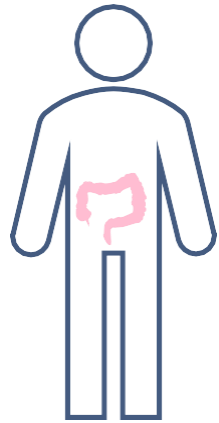
Run Analysis Cancel

- Tox Analysis in IPA helps identify potential toxicological effects of gene expression changes.
- It links molecular data to toxicity biomarkers, organ-specific toxicity, and known toxic pathways
- Useful for drug safety assessment, environmental toxicology, and disease mechanism studies

Use Cases of Tox Analysis

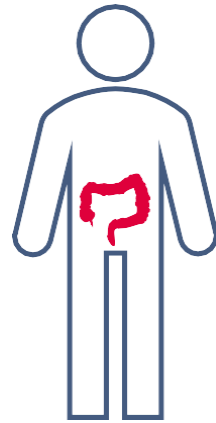
- Drug Development:** Evaluating potential toxicity of drug candidates.
- Environmental Toxicology:** Assessing gene expression changes in response to pollutants.
- Disease Research:** Understanding toxicity-related pathways in various diseases



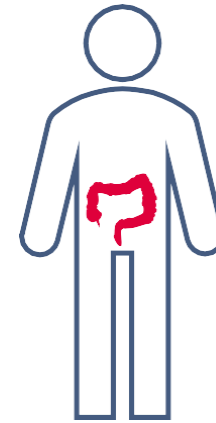


Control

vs

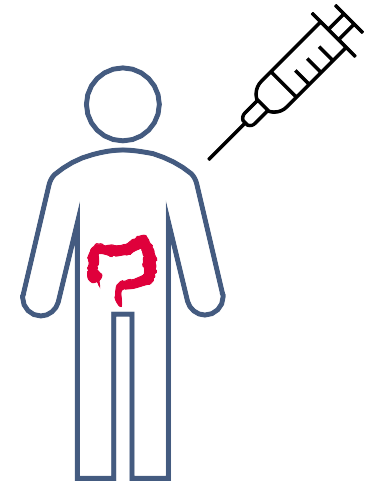


Ulcerative colitis



Baseline

vs

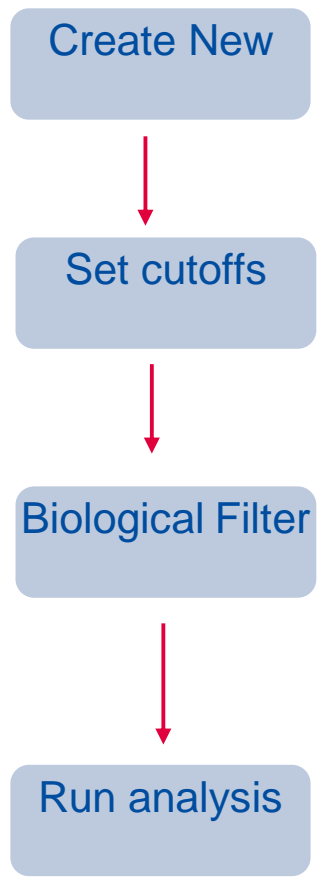


**52 weeks
Vedolizumab**

RNA samples were isolated from colonic biopsies.

Key Features of Tox Analysis

- **Tox Lists:** Identifies genes linked to known toxicity biomarkers.
- **Tox Functions:** Predicts toxicological effects based on functional annotations.
- **Tox Pathways:** Highlights molecular pathways involved in toxicity mechanisms.
- **Organ Toxicity Prediction:** Assesses potential adverse effects on specific organs (e.g., liver, kidney, heart).



Create Tox Analysis - [analysis: GSE73661-UC VZD with pval]

Set Cutoffs **Biological Filters**

General Settings ☐ Select all

Networks Interaction & Ca... ☒ Tissues and Primary Cells not otherwise specified

Node Types biologic drug... ☒ Cells

Data Sources All ☒ Nervous System

miRNA Confidence Experi... ☒ Organ Systems

Species Human ☒ Other Tissues and Primary Cells

Tissues & Cell Lines Activa... ☐ Cell Line

Mutation All ☐ Cell Line not otherwise specified

☐ Breast Cancer Cell Lines

☐ Cervical cancer cell line

☐ CNS Cell Lines

☐ Colon Cancer Cell Lines

☐ Fibroblast cell lines

3497 analysis-ready molecules across observations

Filter Summary

Consider only molecules and/or relationships where
(species = Human) AND
(confidence = Experimentally Observed) AND
(tissues = Stomach OR Dendritic cells not otherwise specified OR Other Immune cells OR Neurons not otherwise specified OR Putamen OR Activated CD56bright NK cells OR Brain OR Skin OR Organ Systems not otherwise specified OR Thalamus OR Keratinocytes OR Immature monocyte-derived dendritic cells OR B lymphocytes not otherwise specified OR Adipocytes OR Adipose OR Ovary OR Other Tissues and Primary Cells OR Lung OR Th17 cells OR Smooth muscle cells not otherwise specified OR Epithelial cells not otherwise specified OR Bone marrow-derived dendritic cells OR Intraepithelial T lymphocytes OR Mesenchymal stem cells OR Activated Vd1 Gamma-delta T cells OR Effector T cells OR Cardiomyocytes OR Hippocampus OR Mature monocyte-derived dendritic cells OR Ventricular Zone OR Subventricular Zone OR Monocyte-derived macrophage OR Plasmacytoid dendritic cells OR Other Neurons OR Spleen OR Other Granulocytes OR Spinal Cord OR Immune cells not otherwise specified OR Amygdala OR Mononuclear leukocytes not otherwise specified OR Heart OR Other Nervous System OR Purkinje cells OR Endothelial cells not otherwise specified OR Peripheral blood monocytes OR Nervous System not otherwise specified OR Activated CD56dim NK cells OR Hepatocytes OR Vd1 Gamma-delta T cells OR Megakaryocytes OR Langerhans cells OR Striatum OR Smooth Muscle OR Stem cells not otherwise specified OR Gray Matter OR Retina OR Cortical neurons OR Pro-B lymphocytes OR Other Smooth muscle cells OR Embryonic stem cells OR Kidney OR Neutrophils OR Splenocytes OR HUVEC cells OR Stromal cells OR Bone marrow cells not otherwise specified OR Cerebellum OR Other B lymphocytes OR Microvascular endothelial cells OR Effector memory helper T cells OR Lymphocytes not otherwise specified OR Other Epithelial cells OR Sertoli cells OR Olfactory Bulb OR Other NK cells OR Oocytes OR Memory T lymphocytes not otherwise specified)

☒ Stringent filter (filter molecules and relationships) ☐ Relaxed filter (filter molecules)

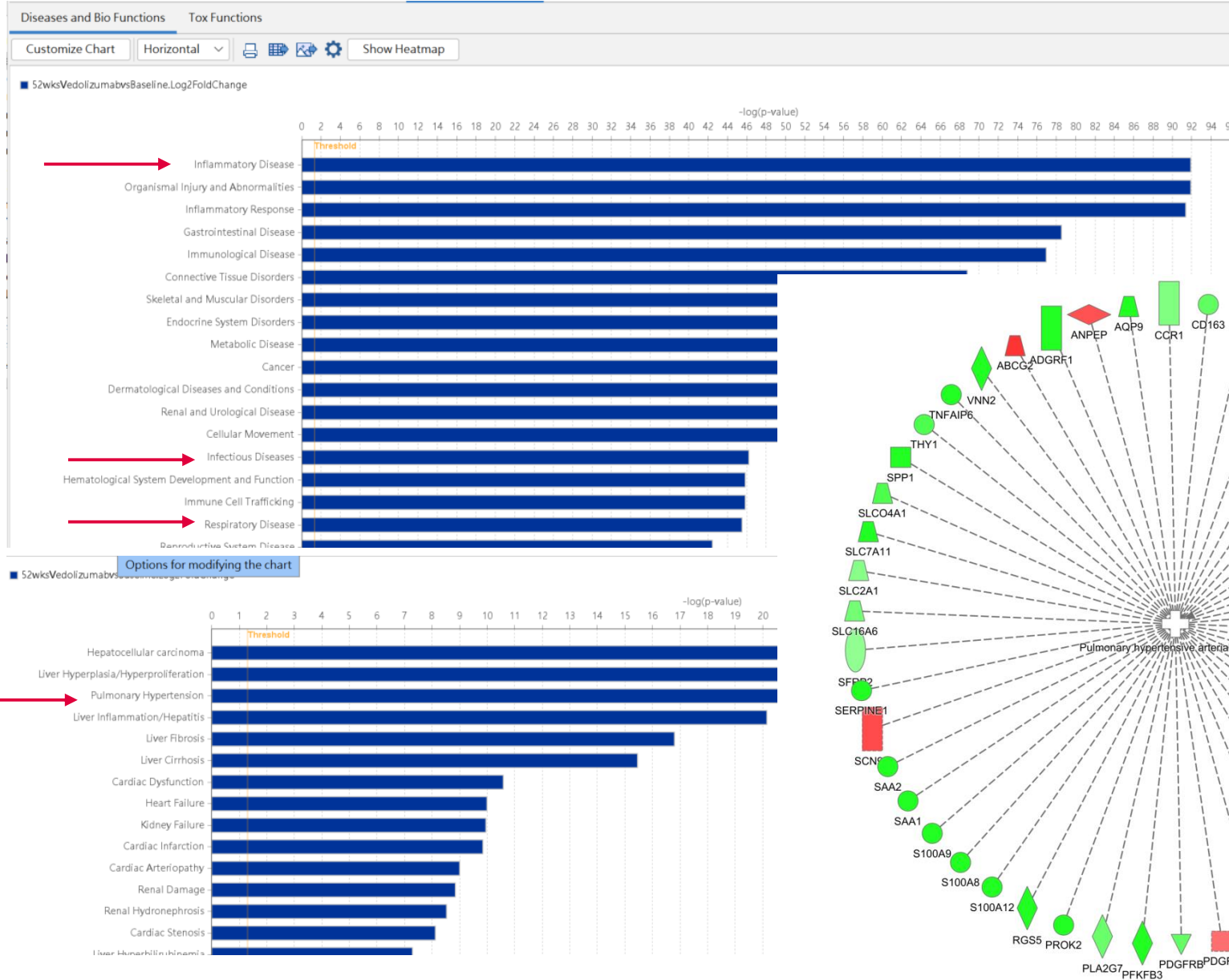
Preview Dataset GSE73661-UC VZD with pval Observation: UCvsNormal.Log2FoldChange (3458)

Analysis-Ready (3458) **Mapped IDs (20218)** **Unmapped IDs (1344)** **All IDs (21562)** **Metadata**

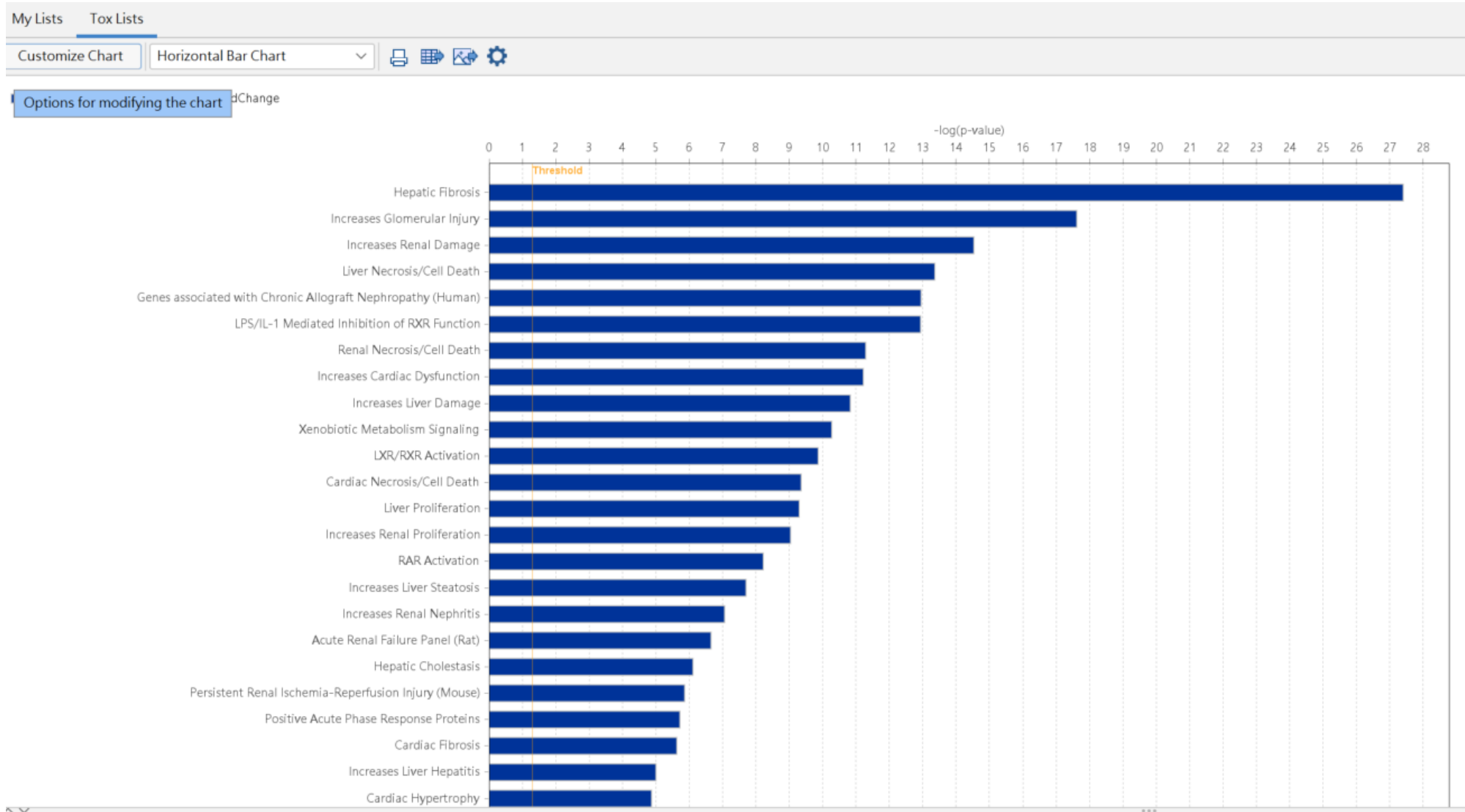
Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-1.543	4.72E-09	A1CF		A1CF	APOBEC1 complementation factor	Nucleus	other	
1.069	1.00E-04	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	other	
0.628	3.96E-07	A4GALT		A4GALT	alpha 1,4-galactosyltransferase (PIPK blood group)	Cytoplasm	enzyme	
-0.619	1.97E-11	AAK1		AAK1	AP2 associated kinase 1	Cytoplasm	kinase	LP-935509, SM1-71
-0.757	1.32E-19	AAMDC		AAMDC	adipogenesis associated Mth038 domain containing	Cytoplasm	other	
0.626	1.72E-09	AARS		AARS1	alanyl-tRNA synthetase 1	Cytoplasm	enzyme	
-1.083	2.94E-15	ABAT		ABAT	4-aminobutyrate aminotransferase	Cytoplasm	enzyme	theophylline/retinoin/valproic acid, valproic acid, ...

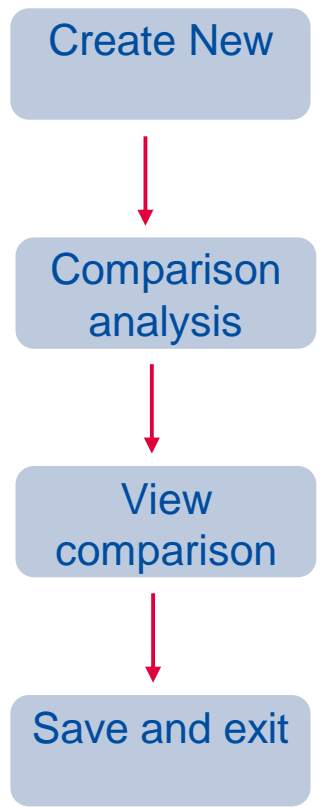
0 / 3458

Flags: **ABAT** Enzyme/molecule/Gene/Protein/Chemical identifier that meet the user-defined cutoff and map to the Global Molecular Network are displayed with bold text



Liver
Pulmonary
Heart
Renal





File Edit View Window Help

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

Create New...

Core Analysis...
Comparison Analysis...
Biomarker Filter...
Biomarker Comparison Analysis...
MicroRNA Target Filter...
BioProfiler
IsoProfiler
My Pathway
Path Designer
Filter Dataset
Upload Dataset...
Advanced Search
Project...
Compare
Import Pathway

Create Comparison Analysis

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

Create Comparison Analysis

Select Analyses

A-Z Sort

Analyses to Compare

▼ case_study

MOESEM_RNAseq - 2025-03-10 C

Naturecomm_protein - 2025-03-C

Naturecomm_phosphoprotein - 20

Naturecomm_phosphoprotein - 20

DEG summary statistics Neocorte

DEG summary statistics Neocorte

DEG_summary_statistics_hypotha

GSE73661-UC VZD with pval - 20

TREAM_m7 - 2024-12-12 10:28 上

CDAM_cluster - 2024-12-12 10:18

WT_EV_vs_LMP1_EV - 2024-11-22

mirna_target_mRna_ - 2024-11-1

colon miRNA after mRNA target f

maclur_sig_SNP_s_for_IPA - 2024-1

HBV_specific_CD8_pos_cluster8_C

HBV_specific_CD8_pos_cluster6_C

41586_2024_7187_MOESM7_ESM

41586_2024_7187_MOESM5_ESM

Endocrine DEP - 2024-08-15 12:06

Endocrinology Differentially expres

Add »

RNA.6h

RNA.12h

RNA.24h

protein.6

protein.12

protein.24

phsopho.6

phsopho.24

phsopho.12

Move Up ▲

Move Down ▼

« Remove

Senescence pathway

Deubiquitination

Human Embryonic Stem Ce...

Save & Exit

Provide Feedback | Support

Process RNA-seq data QIAGEN L


Comparison Settings

Please select a column (analysis) to displ

Canonical pathway comparison

Settings/Legend

Filter

Measurement: Activation z-score -8.216  12.926

Sort Method: Trend + Score Visualize: z-score

Insignificance Threshold: (absolute value)

Apply

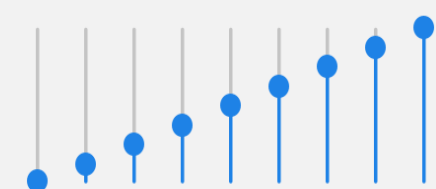
Clear

Trend Controls

Re-sort

Invert Trend

Reset Trend



View Report

Open Network

Gene Heatmap

Expand Header

Canonical Pathways

RNA 6h

RNA 12h

RNA 24h

protein 6

protein 12

protein 24

phospho 6

phospho 12

Coronavirus Pathogenesis Pathway

Pulmonary Fibrosis Idiopathic Signaling Pathway

Cell Cycle Checkpoints

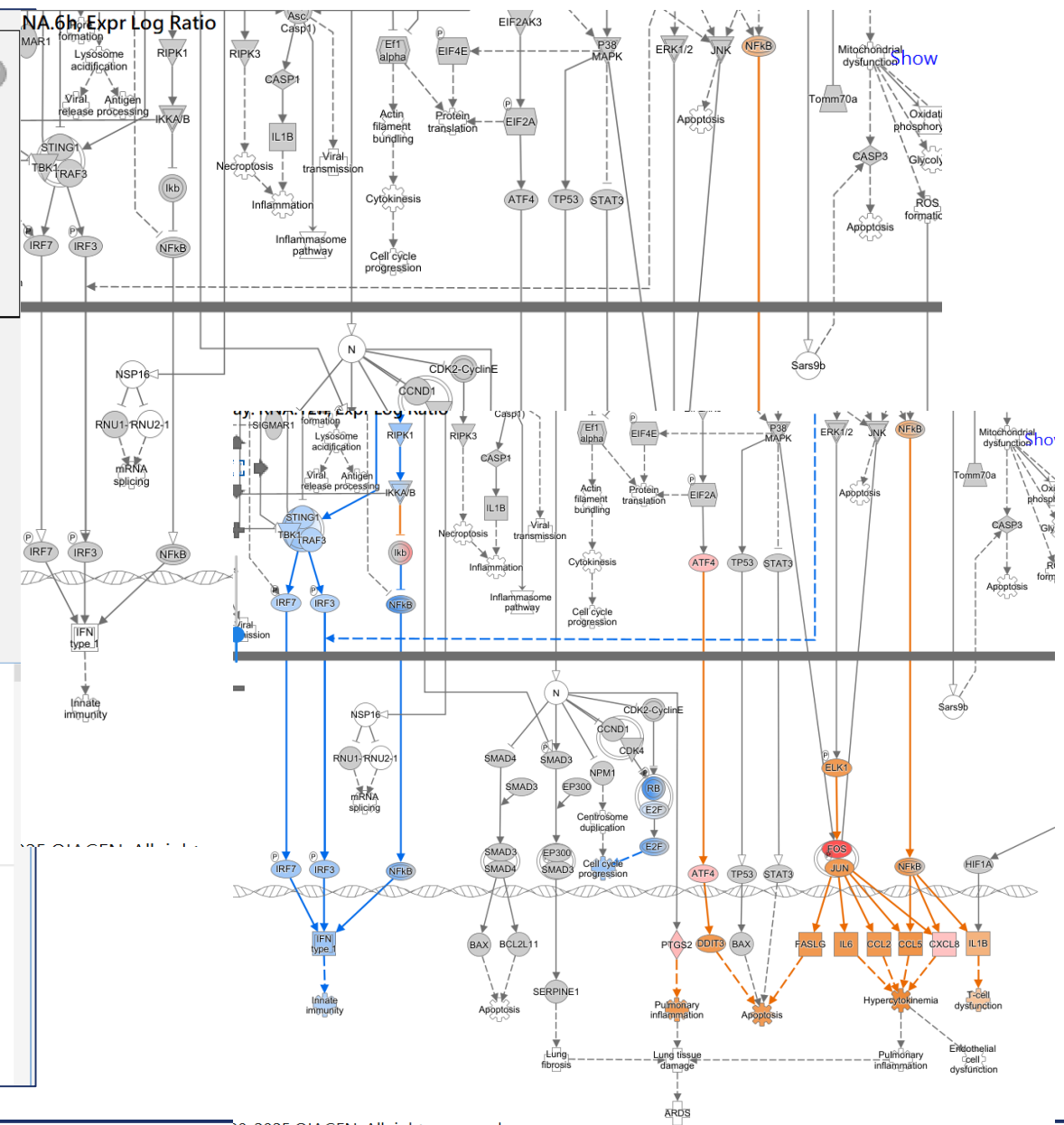
Chromatin organization

Deubiquitination

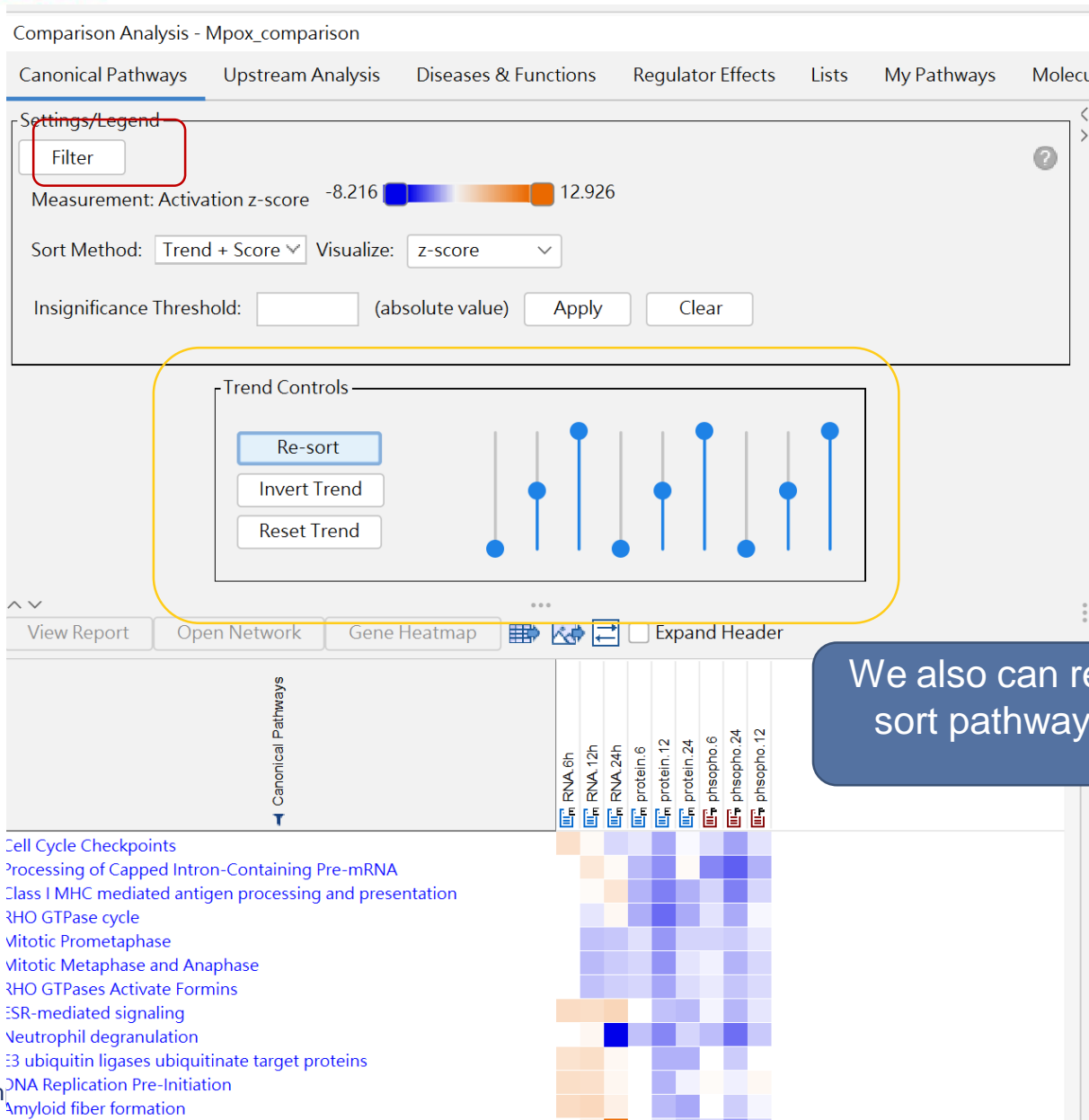
TCF dependent signaling in response to WNT

Activin Inhibin Signaling Pathway

Mitotic Prometaphase



Filtered canonical pathway



JB Filter

Pathways

Tree View List View

art typing to find Canonical Pathways that scored in your analysis

☐ Ingenuity Canonical Pathways

☐ Metabolic Pathways

☒ Reactome Pathways

☐ Signaling Pathways

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

Score Filter

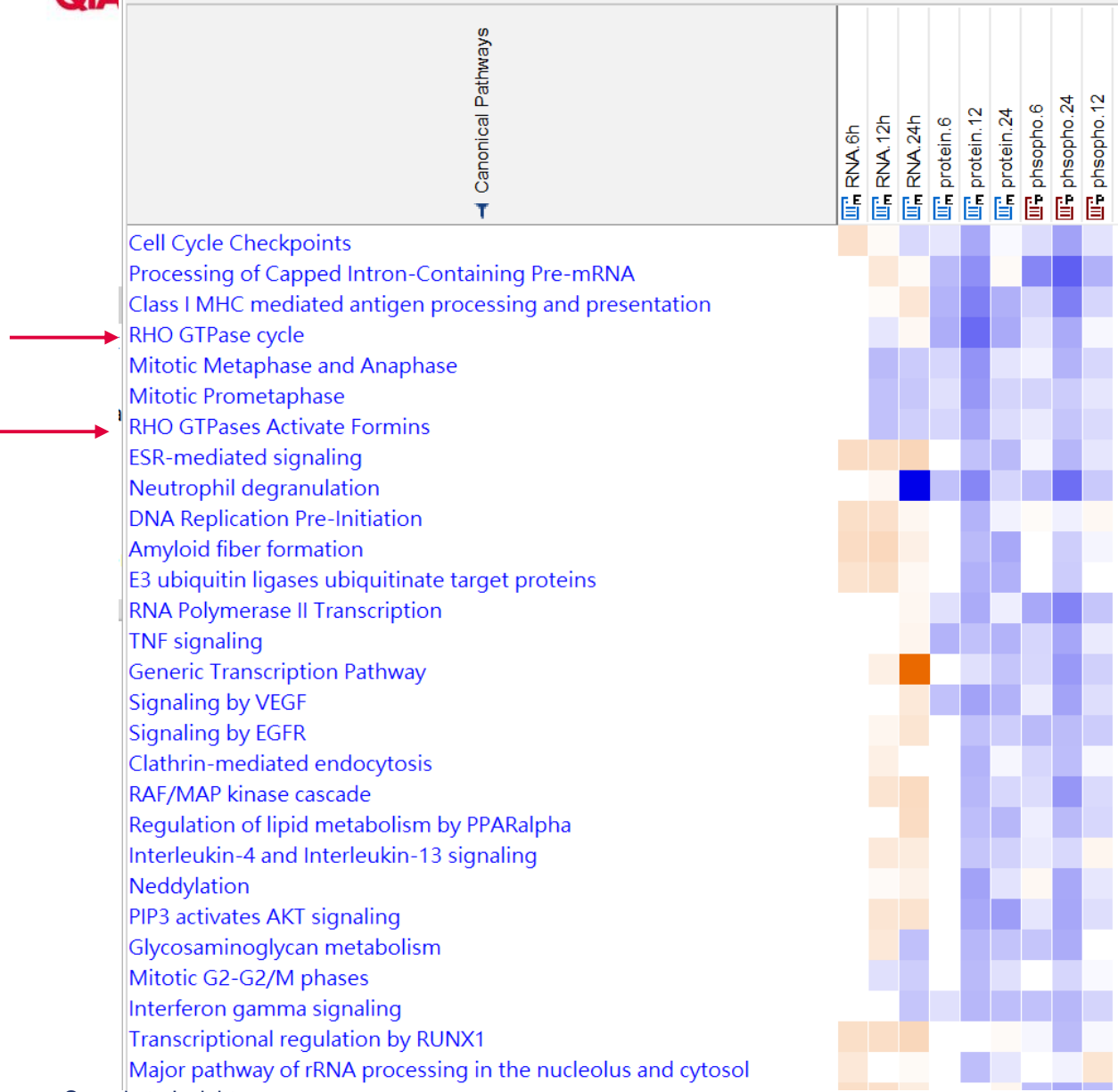
p-value Cutoff: 1.3 (log10)

z-score Cutoff: (absolute value)

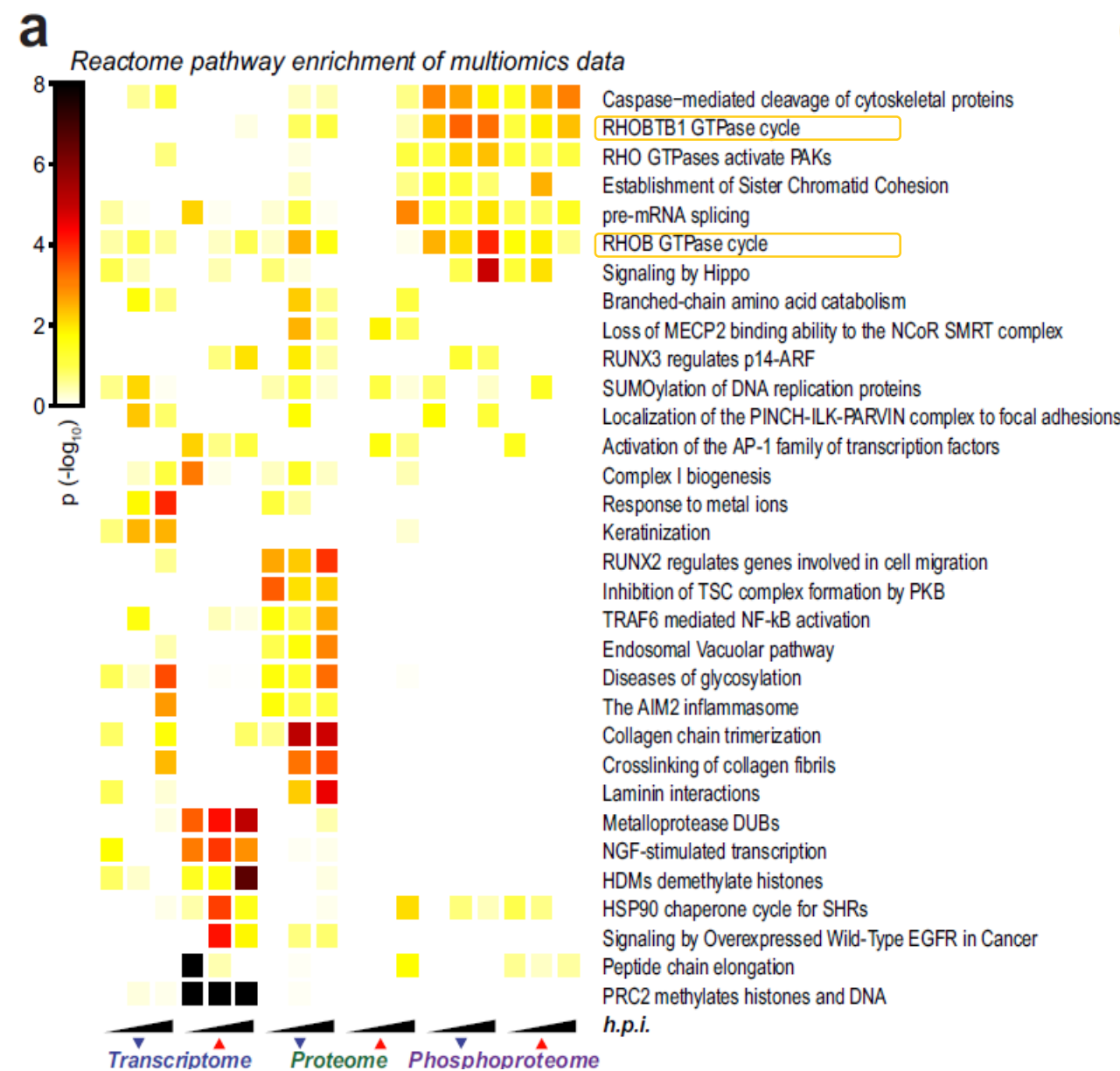
B-H p-value Cutoff: (log10)

We also can re-sort pathway

Reactome pathway



Sample to Insight





Upstream regulator comparison

Comparison Analysis - Mpox_comparison

Canonical Pathways Upstream Analysis Diseases & Fun

Upstream Regulators Causal Networks

Table Heatmap

Settings/Legend

Filter

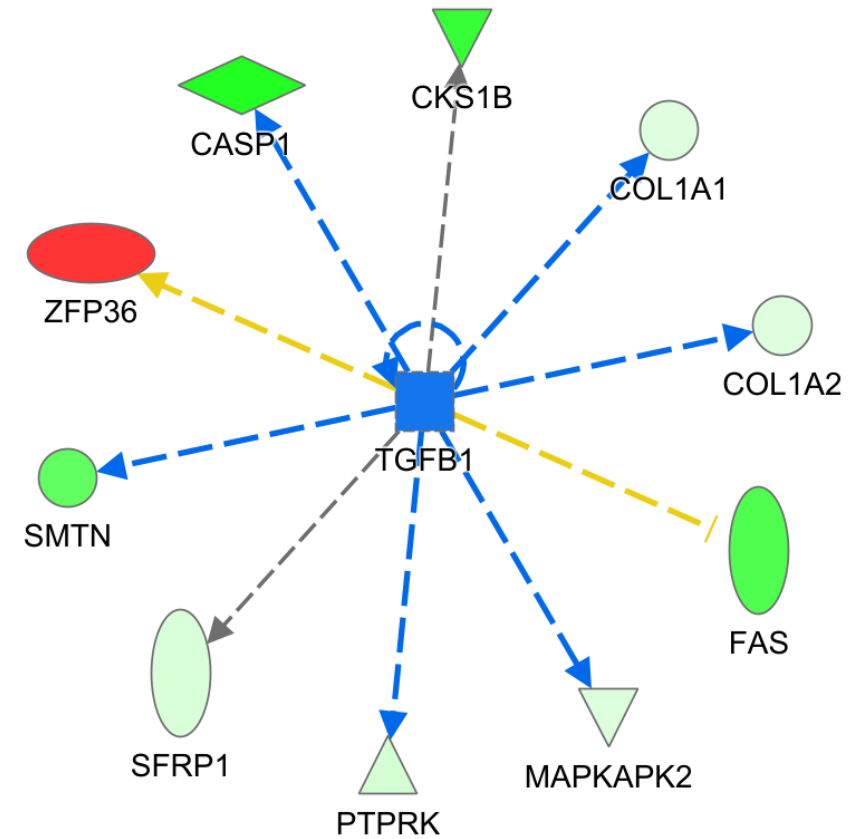
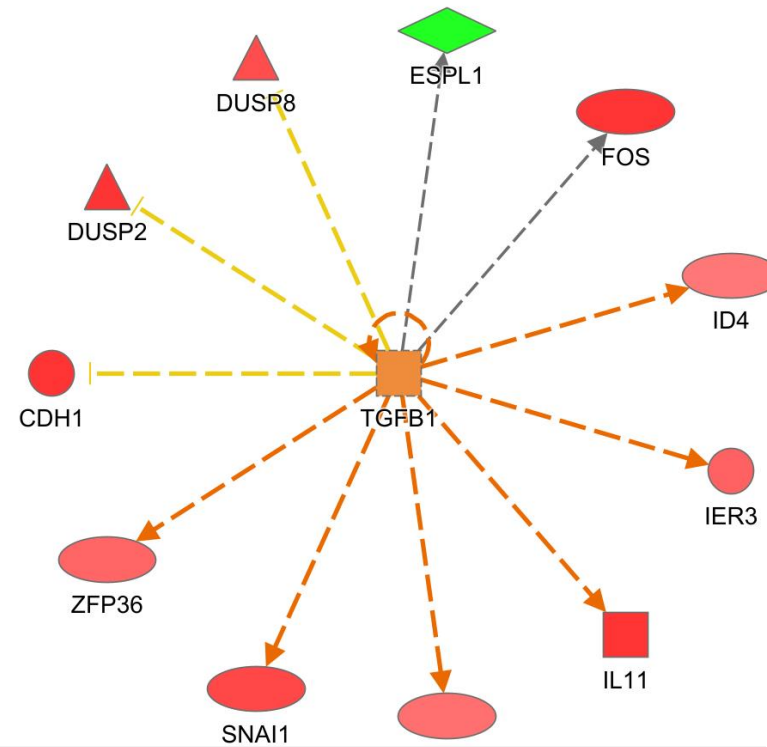
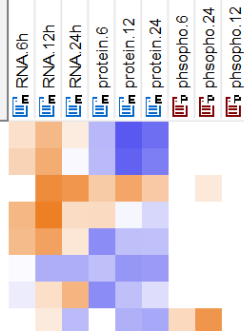
Measurement: Activation z-score -6.447

Sort Method: Trend + Score Visualize: z-score

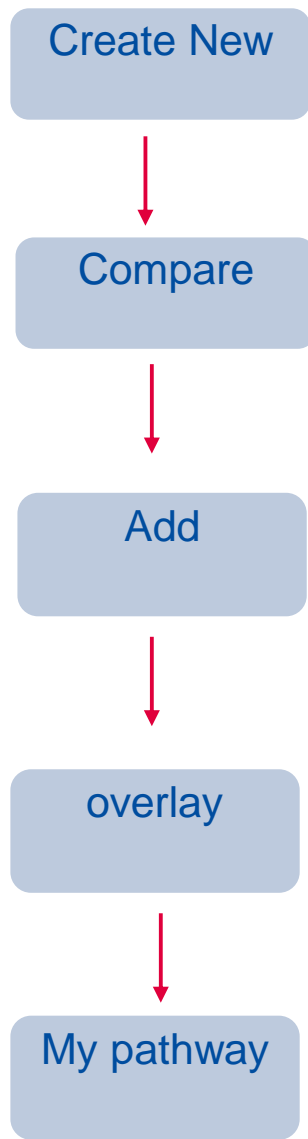
Insignificance Threshold: (absolute value)

Open Network Gene Heatmap Expand Header

Upstream Regulators



TNF
TGFB1
MAPK1
ERK
TP63
ARID1A
TP53
BSG



Genes and Chemicals

Diseases and Functions

Pathways and Lists

Datasets and Analyses

Create New...

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MicroRNA Target Filter...

BioProfiler

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My Pathway

Path Designer

Filter Dataset

Upload Dataset...

Advanced Search

Project...

Compare

Import Pathway

colon miRNA after miRNA target filter

maclur_sig_SNP_s_for_IPA

Custom Dataset miRNA - 2024-10-22 02:42 下午

Custom Dataset miRNA - 2024-10-22 02:39 下午

miRNA_miRNA_filteredDataset - 2024-09-24 02:36 下午

miRNA miRNA colon cancer

miRNA colon cancer

miRNA colon cancer

HBV_specific_CD8_pos_cluster8_DEG

HBV_specific_CD8_pos_cluster6_DEG

41586_2024_7187_MOESM7_ESM_sgAcyI

41586_2024_7187_MOESM5_ESM_sgEP300

S1PR3

Endocrine DEP

Endocrinology Differentially expressed genes

data_24vs2w

glaucoma_sig_snp_list

retinal_detachment_sig

catract_sig_snpList

scRNA_cluster2_in_MS_sample

DESeq2_exp_control

astrocyte_2IL-1B+TNF_vs_1IL-1B+TNF_bulk_RNA

female_bulk_rna

ADME_female_bulk_rna

聯醫部GWASstoIPA

leading_edge_SPATIAL_GENOME_deg_clean

Tumor_core_spatial_genome_DEG

PKCMT_vs_PKC

BHLHE40_cell_proliferation

somatic_mutation_sdc

DEP_for_CM

data_unique_sharm24hrs

trama_data_unique

GSE73661-UC_VDZ with pval

IPA_Phosphoproteomics_Data_PIMD23684622

GSE61566_isoform_exp1702521224092_c10.0_IPA

Nature_comm_2020_germline_variants_ACMG

QCIT_mod

myList

colon cancer-association

Ulcerative Colitis-associations

catract

catract.sig

HCC_CD8

HCC_relapse

HCC_relapse_downregulate

Analyses

Show All

Calculate intersections

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

A RNA.6h (Analysis)

B protein.6 (Analysis)

C phsopho.6 (Phospho Analysis)

102 0 181 3 1 7 682

Entities Comparison Results (11)

CRKL

CYBA

GPS2

H2BC14

LEO1

LFNG

PEAK1

SF1

TNP1

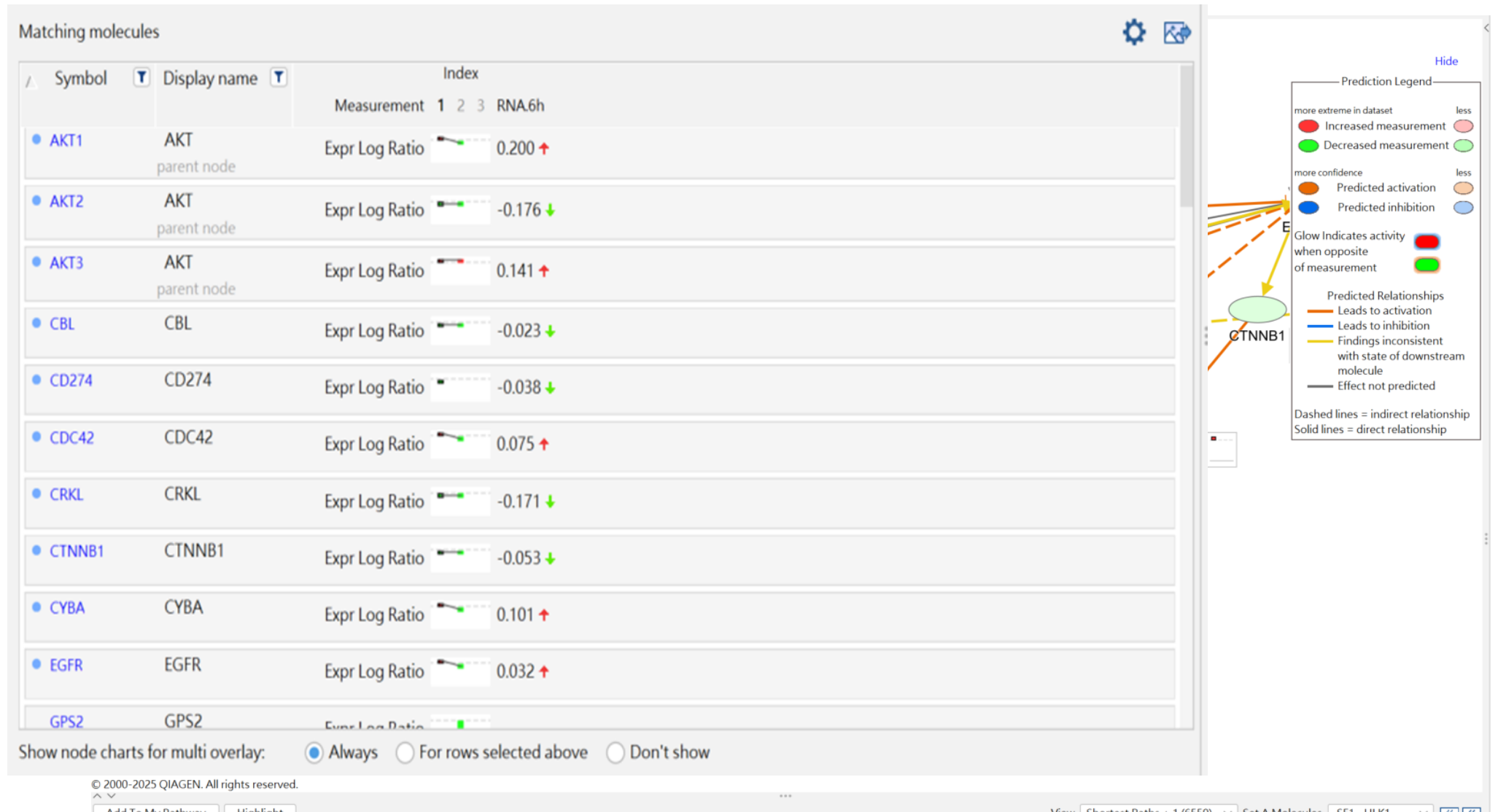
ULK1

ZFP36

BUILD

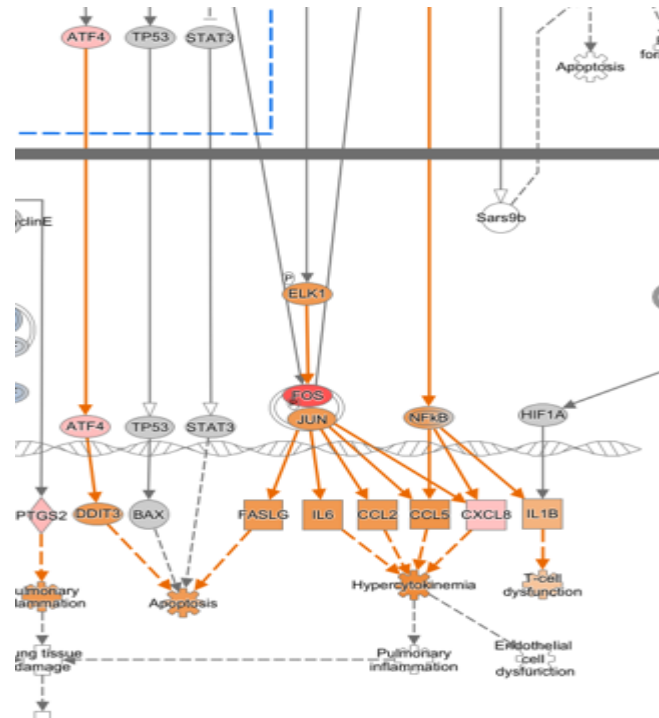
PATH
EXPLORE

OVERLAY

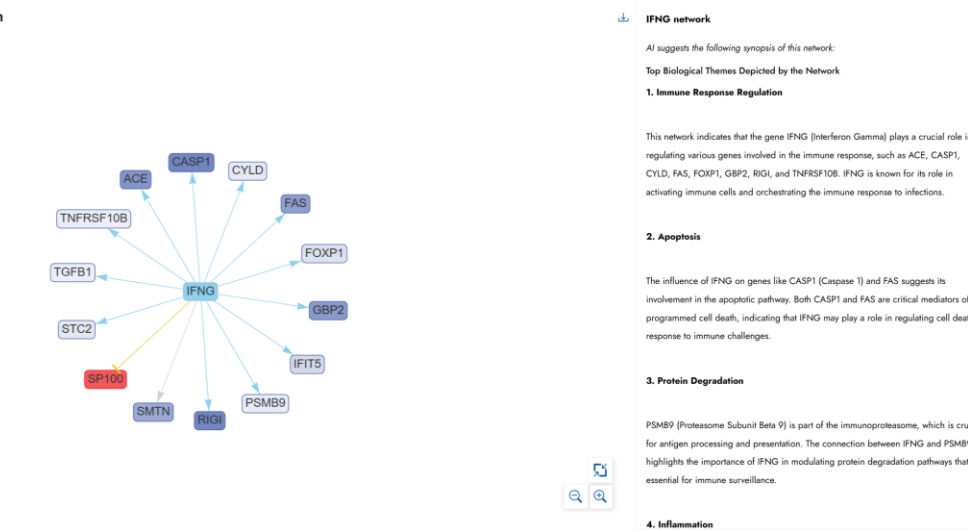
DATASET
AND
ANALYSIS

Summary: Evaluating your 'omics data using IPA

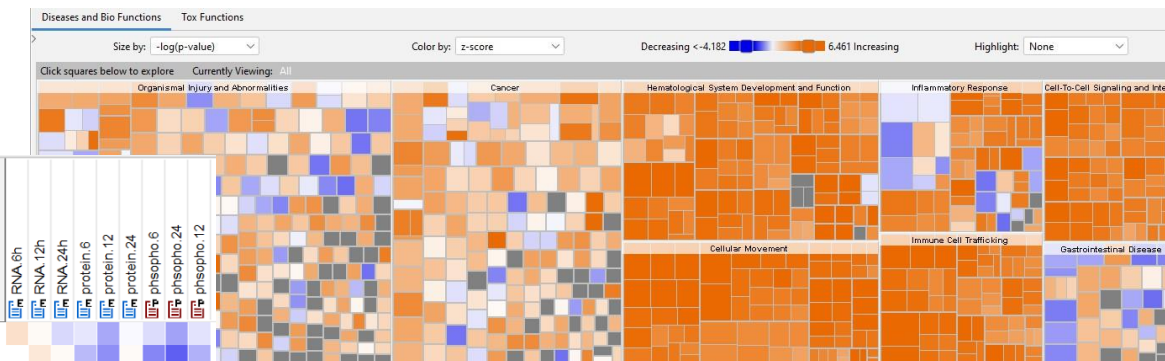
geneid	UCVsNormal.Log2FoldChange	UCVsNormal.pval
DDX11L1	-0.1067	0.2878
WASH7P	-0.1883	0.0097
FAM138F	-0.0761	0.4699
OR4F5	0.1474	0.5311
LOC729737	0.4789	0.0017
LOC100133331	0.4789	0.0017
LOC100132062	0.4789	0.0017
OR4F29	0.2495	0.2389
JA429831	0.1215	0.3338
JB137814	-0.674	1.6381E-06
M37726	-1.0551	0.0000576
LINC00115	-0.1866	0.021
LOC643837	0.1025	0.3021
FAM41C	0.2098	0.2554
SAMD11	-0.0552	0.4088
NOC2L	0.3408	1.2575E-06
KLHL17	0.1497	0.0082
PLEKHN1	0.1463	0.0088
C1orf170	-0.1649	0.0085
TTTY13	-0.3543	0.0003
RBMY1E	-0.3167	0.016
PRY2	-0.1792	0.0084
TTTY6	-0.2051	0.0005
RBMY1J	-0.3167	0.016
TTTY5	-0.105	0.0743
RBMY2FP	-0.5248	0.0939
RBMY1F	-0.5248	0.0939
PRY	-0.1792	0.0084
BPY2	-0.1446	0.0562
DAZ1	0.0734	0.5811
DAZ4	0.0734	0.5811
DAZ2	0.0734	0.5811
DAZ3	0.0734	0.5811
CDY1	-0.0319	0.6541
CSPG4P1Y	-0.0678	0.3043
GOLGA2P2Y	-0.0872	0.1077
U6_83	0.21	0.1



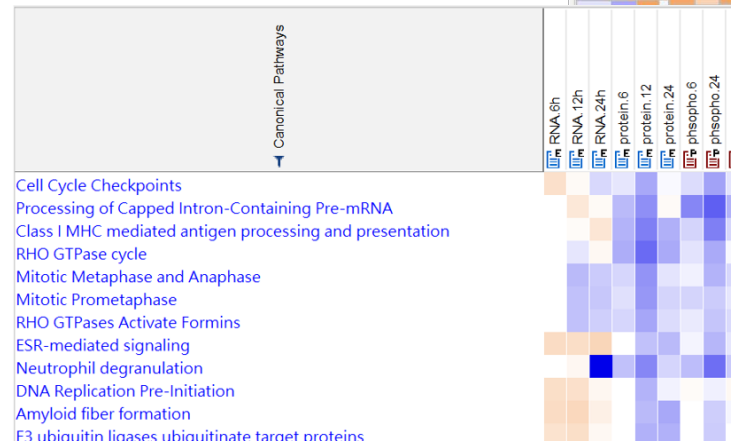
Upstream regulator representation



Dataset molecules



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





Better Care with Better Knowledge

若有需要進一步的資訊或在使用軟體上遇到問題歡迎聯繫以下窗口：
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熊嘉妮 專案主任 ChristineHsiung@gga.asia 02-2795 1777 #3028

Bioinfo@GGA.ASIA