

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

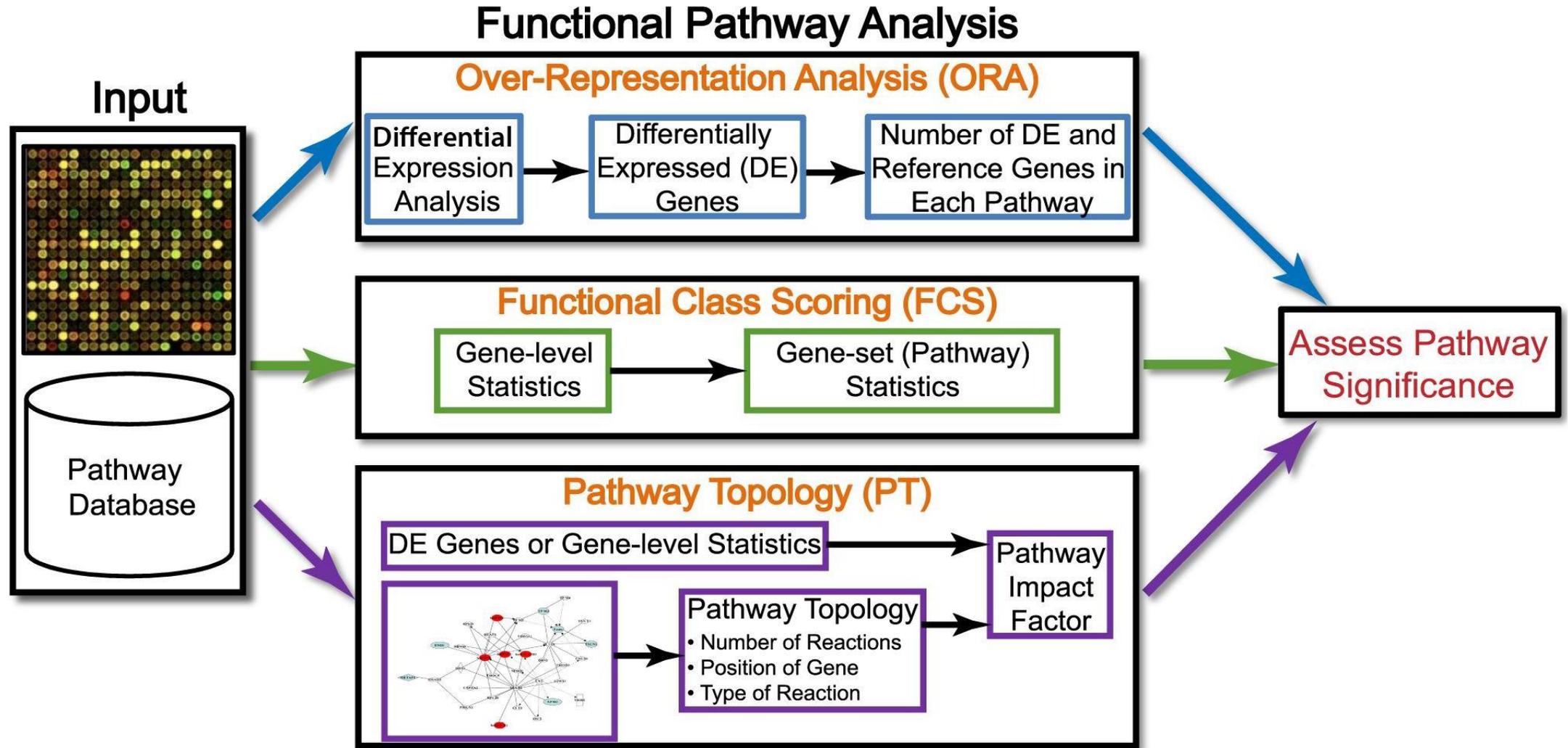
Test hypothesis in silico

Interpreting your 'omics data using IPA

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

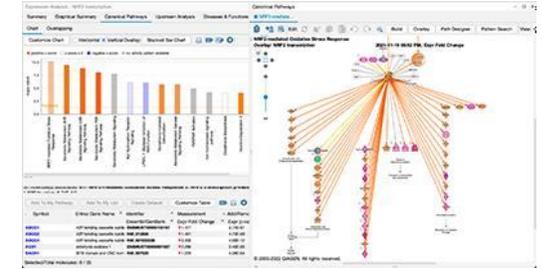
Creating networks from compare molecules

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**

Curated experiments

Knowledge to insight

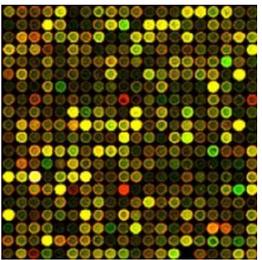
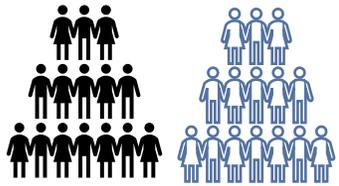
Interpretation
Pathway analysis

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

Variant interpretation

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

Drugs and chemicals

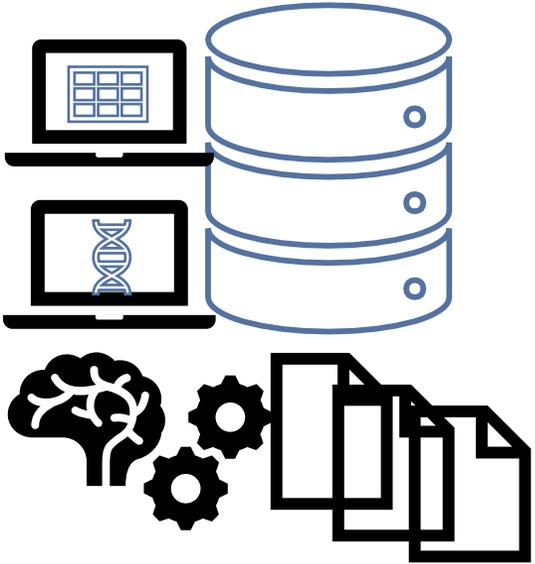
Pathway

Disease

Function

Network

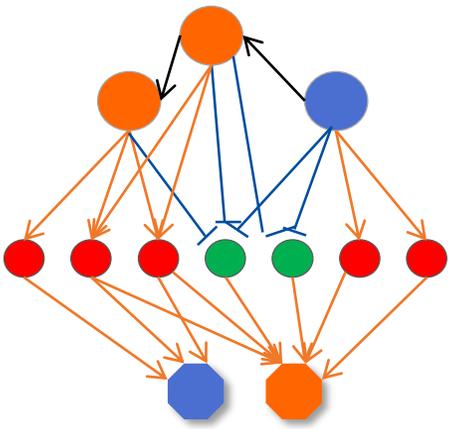
Public /commercial database



ORA/FCS/Topology Pathway Analysis

Machine learning

What do they relate to each other?



What are the relationship between each molecules?

From 2019-2025
1,738 literatures

> *Hepatol Commun.* 2020 Mar 15;4(5):724-738. doi: 10.1002/hep4.1497. eCollection 2020 May.
Integrated GWAS and mRNA Microarray Analysis Identified IFNG and CD40L as the Central Upstream Regulators in Primary Biliary Cholangitis

GWAS

> *J Neuroinflammation.* 2024 Mar 20;21(1):69. doi: 10.1186/s12974-024-03065-z.
Deletion of Slc9a1 in Cx3cr1⁺ cells stimulated microglial subcluster CREB1 signaling and microglia-oligodendrocyte crosstalk

transcriptomic

> *J Allergy Clin Immunol.* 2024 May;153(5):1268-1281. doi: 10.1016/j.jaci.2023.12.030. Epub 2024 Mar 29.
Galectin-10 in serum extracellular vesicles reflects asthma pathophysiology

proteomics

> *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

Single-cell RNA-seq

> *Stem Cells Transl Med.* 2024 Mar 15;13(3):293-308. doi: 10.1093/stcltm/szad090.
Histone Trimethylations and HDAC5 Regulate Spheroid Subpopulation and Differentiation Signaling of Human Adipose-Derived Stem Cells

The screenshot shows a PubMed search for "ingenuity pathway analysis" with 1,738 results. The search interface includes filters for "Save", "Email", "Send to", and "Sort by: Best match". The results list includes:

- 1** **Ingenuity pathway analysis** of alpha-synuclein predicts potential signaling pathways, network molecules, biological functions, and its role in neurological diseases. Suthar SK, Lee SY. *Front Mol Neurosci.* 2022 Nov 29;15:1029682. doi: 10.3389/fnmol.2022.1029682. eCollection 2022. PMID: 36523604 **Free PMC article.** We have taken the advantage of such a Bioinformatics tool, **ingenuity pathway analysis (IPA)** to decipher the signaling pathways, interactome, biological functions, and role of alpha-synuclein. ...
- 2** **Gene set enrichment analysis and ingenuity pathway analysis** to verify the impact of Wnt signaling in psoriasis treated with Taodan granules. Chen Y, Zhang Z, Zhang Y, Jiang J, Luo Y, Fei X, Ru Y, Li B, Zhang H, Liu T, Yang Y, Kuai L, Song J, Luo Y. *Am J Transl Res.* 2023 Jan 15;15(1):422-434. eCollection 2023. PMID: 36777818 **Free PMC article.** MATERIALS AND METHODS: Primarily, transcriptional profiling was applied to identify expressed genes (DEGs), proceeding with Gene ontology (GO) and Kyoto Encyclopedia of Genomes (KEGG) analysis. Gene Set Enrichment Analysis (GSEA) and **Ingenuity P...**
- 3** **Gene set enrichment analysis and ingenuity pathway analysis** to identify biomarkers in Sheng-ji Hua-yu formula treated diabetic ulcers. Ru Y, Zhang Y, Xiang YW, Luo Y, Luo Y, Jiang JS, Song JK, Fei XY, Yang D, Zhang Z, Li B, Kuai L. *J Ethnopharmacol.* 2022 Mar 1;285:114845. doi: 10.1016/j.jep.2021.114845. Epub 2022 Mar 1. PMID: 34800645 GO and KEGG enrichment analysis were used to identify the mechanisms underlying effect of SJHY formula, and then gene set enrichment analysis and **ingenuity pathway analysis** were conducted for functional analysis. ...



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

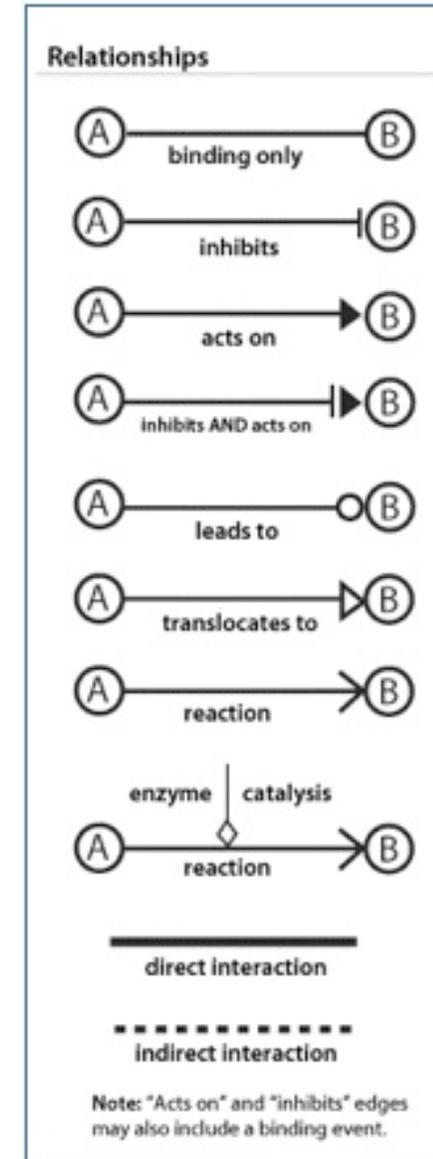
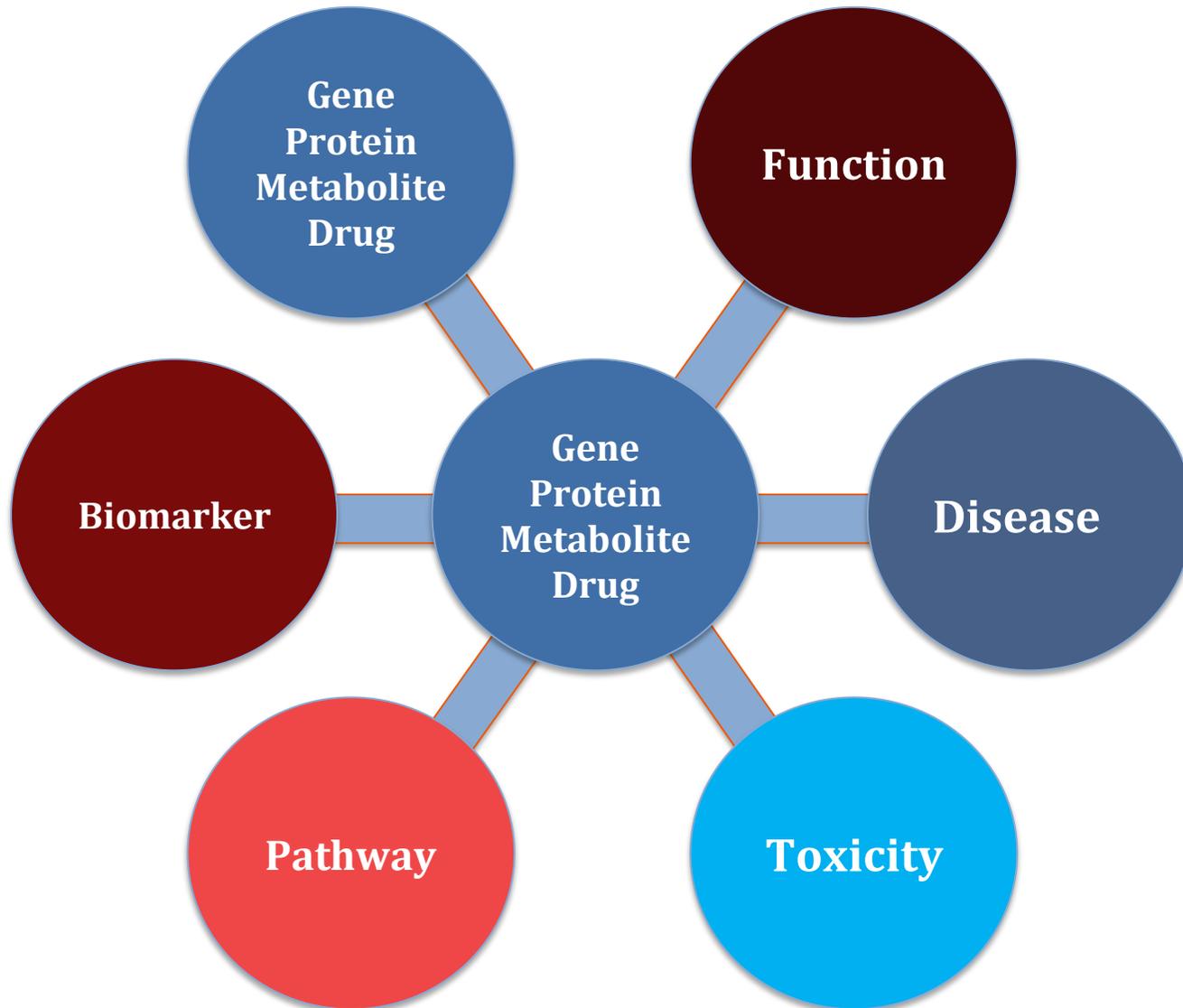
A massive, manually curated Knowledge Base updated weekly for the last ~20 years

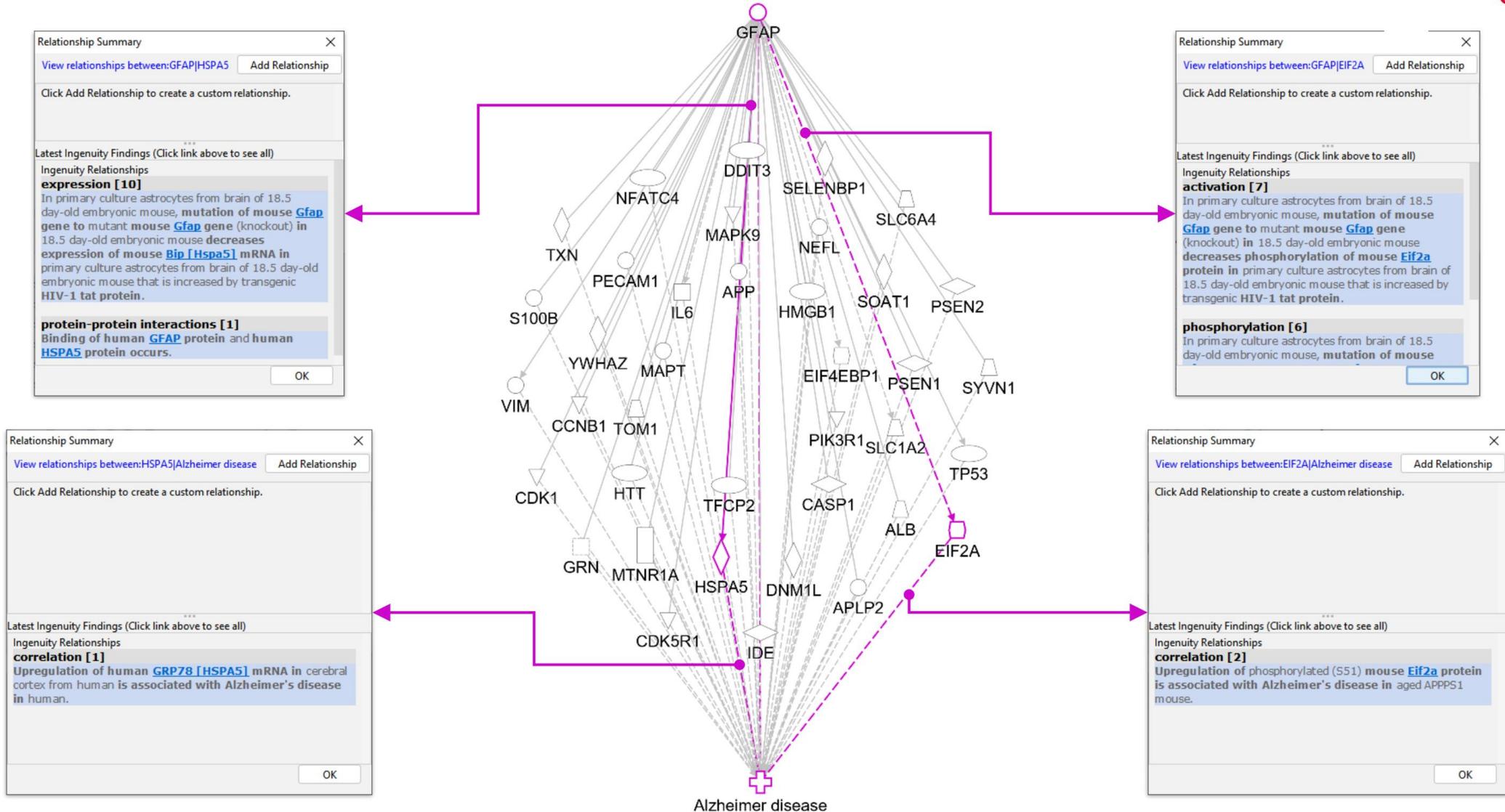


>12.6 million findings

Ingenuity Pathway Analysis







Fully supported:

What species identifiers are accepted for analysis by IPA?



Human

- ✓ Atlantic Salmon (*Salmo salar*)
- ✓ Thale cress (*Arabidopsis thaliana*)
- ✓ Bat (Greater horseshoe bat, *Rhinolophus ferrumequinum*)
- ✓ Brewer's yeast (*Saccharomyces cerevisiae*)
- ✓ Cat (domestic, *Felis catus*)
- ✓ Chicken (*Gallus gallus*)
- ✓ Chimpanzee (*Pan troglodytes*)
- ✓ Chinese hamster (*Cricetulus griseus*)
- ✓ Cow (*Bos taurus*)
- ✓ Crab-eating macaque (*Macaca fascicularis*)
- ✓ Dog (*Canis lupus familiaris*)
- ✓ Fission yeast (*Schizosaccharomyces pombe*)
- ✓ Fruit fly (*Drosophila melanogaster*)
- ✓ Golden hamster (*Mesocricetus auratus*)

- ✓ Guinea pig, domestic (*Cavia porcellus*)
- ✓ Horse (*Equus caballus*)
- ✓ Human (*Homo sapiens*)
- ✓ Mouse (*Mus musculus*)
- ✓ Pig (*Sus scrofa*)
- ✓ Rabbit (*Oryctolagus cuniculus*)
- ✓ Rainbow trout (*Oncorhynchus mykiss*)
- ✓ Rat (*Rattus norvegicus*)
- ✓ Rhesus Monkey (*Macaca mulatta*)
- ✓ Roundworm (*Caenorhabditis elegans*)
- ✓ Sheep (*Ovis aries*)
- ✓ Western clawed frog (*Xenopus tropicalis*)
- ✓ Zebrafish (*Danio rerio*)



Mouse



Rat

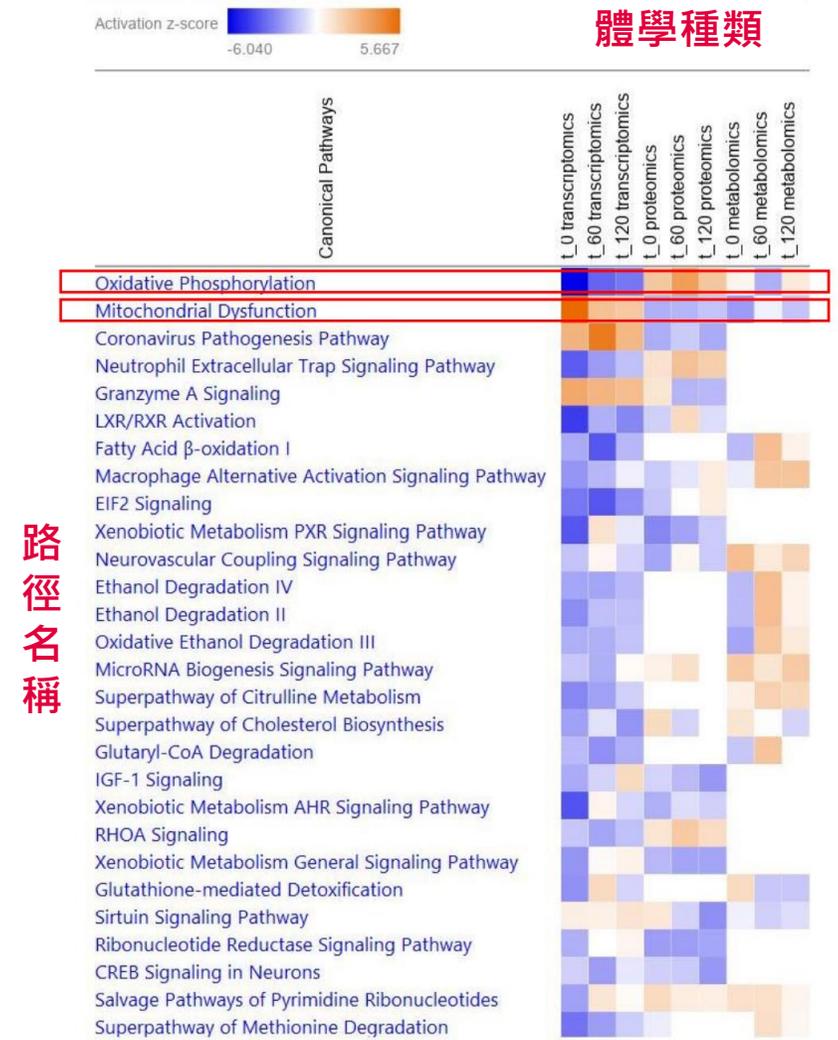
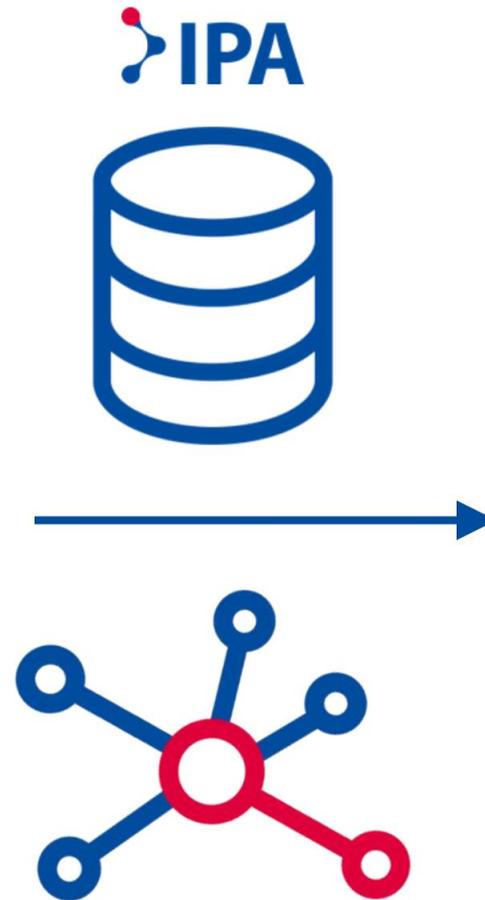
Orthologs Gene from NCBI Eukaryotic Genome Annotation Pipeline

Get more complete mapping during dataset upload!

Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2023/8)	GenPept	Ensembl (110)	miRbase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (257)	International Protein Index (IPI)	RefSeq (human, mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human (HUGO/ HGNC, EG)	UniProt/ Swiss-Prot Accession (2022_02)	UCSC (hg18)			KEGG
Codelink	Symbol- mouse (EG)		UCSC (hg19)			PubChem CID
Illumina	Symbol- rat (EG)		UCSC (hg38)			
Ingenuity	GI Number					
	UniGene					

Omics data type

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

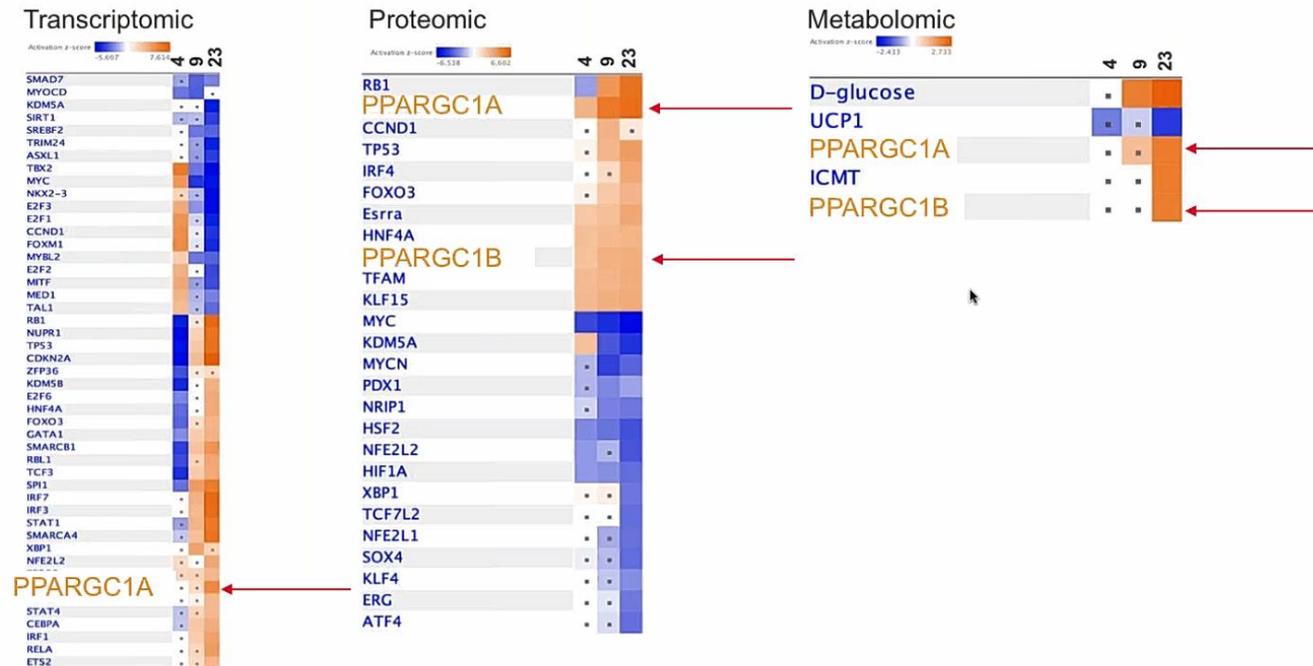


Integrate and compare genomics, transcriptomics, proteomics and metabolomics data to see the big picture on your focus research

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.



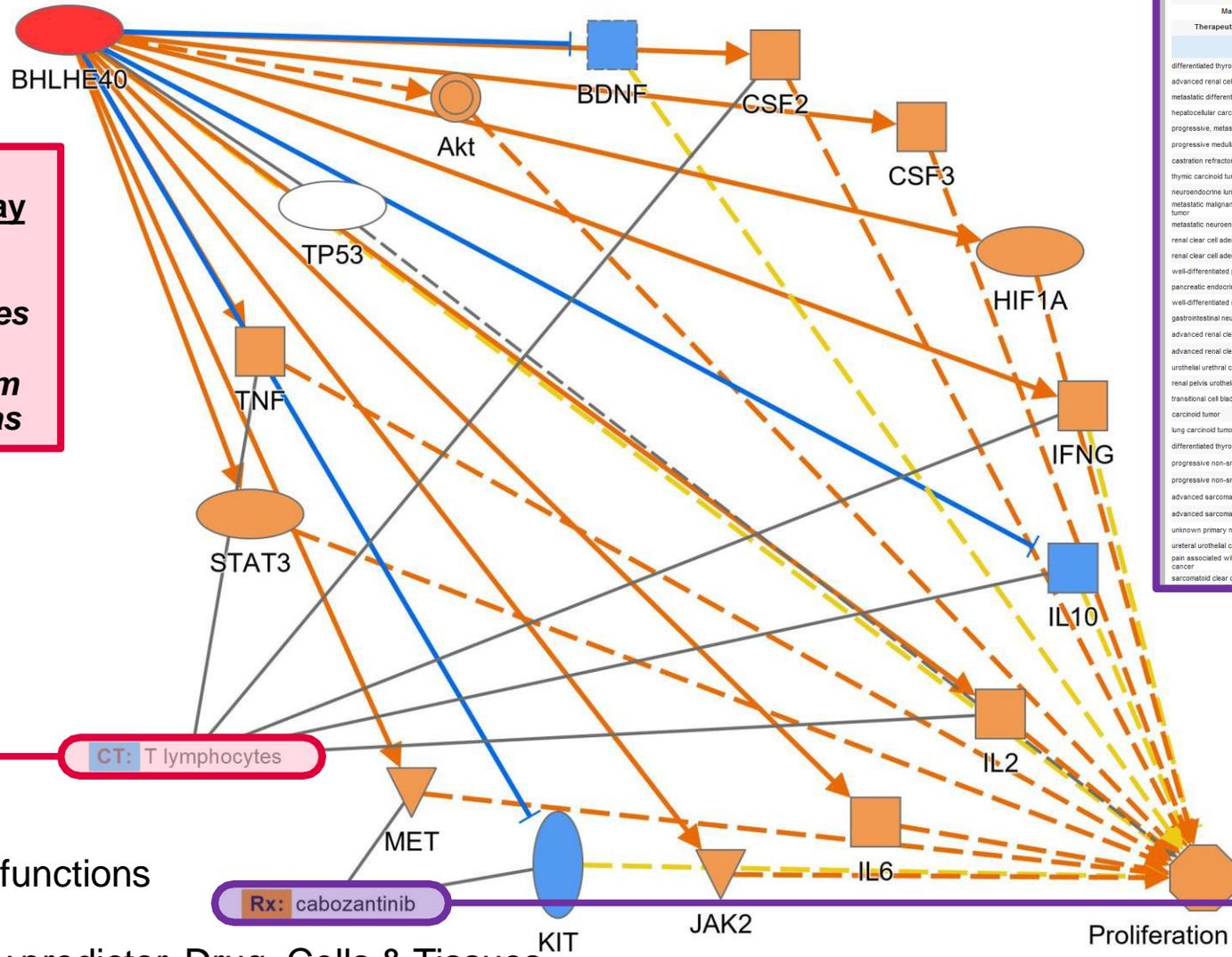
<https://go.qiagen.com/IPA-multi-omics-analysis-webinar>

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



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

Drug Information					
Brand Name(s): Cabometyx, Cometriq					
Manufacturer(s): EXELIXIS, EXELIXIS 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	Exelixis	NCT018864702022-09-28	—
castration refractory prostate cancer	Phase 3	Completed	Exelixis	NCT016652272018-02-14	—
thymic carcinosarcoma	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	NCT04582312023-01-09	—
renal clear cell adenocarcinoma	Phase 3	Recruiting	Merck Sharp & Dohme LLC	NCT04582312023-01-09	—
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)	NCT050929502023-01-07	—
renal pelvis urothelial cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050929502023-01-07	—
transitional cell bladder cancer	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT050929502023-01-07	—
carcinoid tumor	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
lung carcinosarcoma	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT033753202022-12-30	—
differentiated thyroid cancer	Phase 3	Active, not recruiting	Exelixis	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)	NCT050929502023-01-07	—
pain associated with castration refractory prostate cancer	Phase 3	Terminated	Exelixis	NCT015224422018-04-23	—
sarcomatoid clear cell renal cell adenocarcinoma	Phase 3	Recruiting	National Cancer Institute (NCI)	NCT037931662023-01-10	—

CT: T lymphocytes

Rx: cabozantinib

Step by Step slide 57-63

- Search for genes
- Search for diseases and functions
- Build: Path explorer
- Overlay: Molecule activity predictor, Drug, Cells & Tissues
- Drug: IPA Chem View

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



Processing, curation and QA

QIAGEN OmicSoft Studio



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



Curated Findings

Ingenuity Pathway Analysis



141,000+ comparison



- 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	
	ClinicalProteomicTumor	2,129	2,978	849
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	63,336	77,140	13,804
	SingleCellHumanHCL	1,476	1,469	-7*
	SingleCellMouse	81	81	
	SingleCellMouseUmi	13,135	13,135	
Normal Cells and Tissues	Human Tissues (GTEx)	1,312	1,312	

The screenshot shows the OmicSoft Land Explorer interface. At the top, the 'Genes and Chemicals' tab is selected, and a search for 'EGFR' is performed. The search results show 158 items, with the first result being EGFR. A blue arrow points from the 'EGFR' result in the search results 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

Land selection
Search bar
View selection

View controller

Download data for current view

Metadata filtering

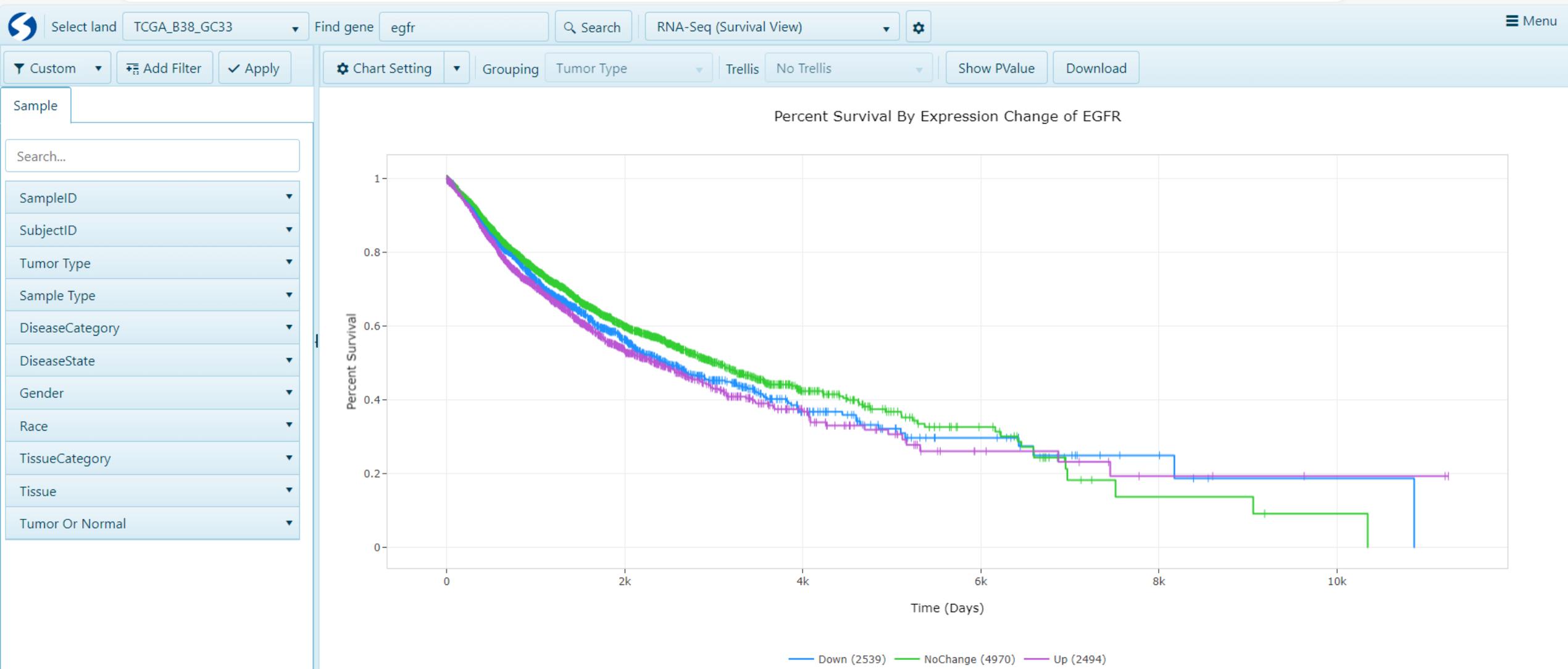
https://explorer.omicsoft.com/OPA/Home/MainPage?landName=TCGA_B38_GC33&qeneID=EGFR&viewID=RnaSeq_Transcript.GeneVariable&grouping=Tumor.Type&trellis=No.Trellis

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

The screenshot shows the OmicSoft Land Explorer interface. The top navigation bar includes 'Select land' (TCGA_B38_GC33), 'Find gene' (egfr), and 'Gene FPKM'. The left sidebar shows a filter menu with 'DiseaseState' selected. The main chart area displays a dot plot for EGFR gene expression, with data points colored by tumor type (LUAD, BRCA) and disease state (Metastatic, Primary Tumor, Recurrent Tumor, Solid Tissue Normal). A red box highlights a specific data point in the BRCA group, which is linked to a data table below.

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



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

Create New... Sleep Disorders [abnormal sleep pattern,sleep difficulties,...] Search Advanced Search

Project Manager A-Z So

- QCIT_mod
- selected_skin_re
- selected_miRN
- myList
- colon cancer-a
- Ulcerative Colit
- hsa_miRNA filte
- hsa_miRNA
- catarct
- catarct.sig
- HCC_CD8
- HCC_relapse
- HCC_relapse_d
- Analyses
 - Nature_comm_
 - Nature_comm_
 - QCIT_mod - 20
 - selected_skin_re
 - selected_miRN
 - colon cancer-a
 - Ulcerative Colit
 - hsa_miRNA - 20
 - catarct - 2024-0

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.

Diseases & 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 Molecu	
312	
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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 [hepatic organoid] 3-D cultu	SingleCellHuman...	normal control	kidney organ...	3-D culture	Cluster vs Ot...	nephron pro...	GSE110...	https://www...	50.00	52.09	46.92	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	46.62	13.41		
654- normal control [bronchial epithelium] air liq	SingleCellHuman...	normal control	bronchial epi...	air liquid int...	Cluster vs Ot...	pulmonary io...	GSE102580.UN	https://www...	55.90	48.99	30.00	51.57	13.41		
25- hepatocellular carcinoma (LIHC) [liver] NA 116	OncoHuman	hepatocellul...	liver	NA	Treatment1 v...	CellLine:Infer...	GSE20948.GPL5	http://www...	55.90	52.92	26.46	46.45	16.87		
5349- intrahepatic cholangiocarcinoma [liver] 53	SingleCellHuman...	intrahepatic ...	liver	NA	Cell Type vs ...	cytotoxic T ce...	GSE1427...	https://www...	55.90	51.12	24.49	46.28	31.02		
13- normal control [skeletal muscle] NA 8919	RatDisease	normal control	skeletal muscle	NA	Treatment vs...	TreatTime[da...	GSE57816.GPL1	https://www...	55.90	57.45	30.00	45.13	15.11		
3645- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cluster vs Ot...	embryonic st...	GSE110...	https://www...	50.00	56.67	31.62	44.96	27.78		
3682- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cell Type vs ...	embryonic st...	GSE110...	https://www...	50.00	56.67	31.62	44.96	27.78		
87- disease [airway epithelium] NA 20248	HumanDisease	disease contr...	airway epith...	NA	Treatment1 v...	SamplingTim...	GSE412...	https://www...	50.00	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...	GSE110...	https://www...	50.00	40.00	31.62	45.28	18.65		
20- normal control [skeletal muscle] NA 8925	RatDisease	normal control	skeletal muscle	NA	Treatment vs...	TreatTime[da...	GSE57816.GPL1	https://www...	55.90	50.14	30.00	45.25	14.43		
6657- normal control [osteoarthritis] NA 20248	SingleCellHuman...	normal control	osteoarthritis	NA	Cluster vs Ot...	synovial fibr...	GSE110...	https://www...	50.00	53.85	31.62	45.16	16.44		
23- normal control [foreskin] NA 2522	HumanDisease	normal control	foreskin	4-thiouridine	Treatment1 v...	SampleMater...	GSE59...	https://www...	50.00	53.96	30.00	46.13	15.61		
1- prostate cancer [prostate] NA 20248	MetastaticCancer	prostate can...	prostate	NA	Disease vs. N...	LandSam...	GSE6919.GPL8	https://www...	50.00	57.45	33.17	44.80	34.62		
2- nephrolithiasis [papillary duct] NA 20248	HumanDisease	nephrolithiasis	papillary duct	NA	Cluster vs Ot...	LandSam...	GSE73680...	https://www...	50.00	53.85	30.00	44.70	24.88		
8878- normal control [colorectal adenocarcinoma] NA 20248	SingleCellHuman...	normal control	colorectal adenocarcinoma	NA	Cluster vs Ot...	colorectal adenocarcinoma	GSE110...	https://www...	50.00	58.31	33.17	44.67	33.85		
1388- normal control [embryo] NA 20248	SingleCellMouse...	normal control	embryo	NA	Cluster vs Ot...	embryonic st...	GSE110...	https://www...	50.00	56.57	22.36	43.76	13.38		
10818- normal control [bladder] NA 20248	SingleCellHuman...	normal control	bladder	NA	Cluster vs Ot...	bladder	GSE110...	https://www...	50.00	54.77	22.36	43.31	26.44		
216- breast cancer [breast] NA 20248	OncoHuman	breast carcin...	breast	doxorubicin	Treatment vs...	CellLine:Infer...	GSE110...	https://www...	50.00	41.24	20.00	43.02	8.39		
1- normal control [lung] NA 1141	MouseDisease	normal control	lung	NA	Treatment vs...	ExperimentG...	GSE110...	https://www...	50.00	44.91	22.36	42.89	12.46		
161- lung adenocarcinoma [lung] NA 1141	SingleCellHuman...	lung adenoc...	lung	NA	Cell Type vs ...	unassigned c...	E-M...	https://www...	50.00	41.46	26.46	42.88	25.93		
5368- normal control [fetal testis] 5367	SingleCellHuman...	normal control	fetal testis	NA	Cluster vs Ot...	unassigned c...	GSE110...	https://www...	50.00	61.64	47.96	42.87	21.80		
23- normal control [heart] NA 6993	RatDisease	normal control	heart	NA	Treatment vs...	TreatTime:Su...	GSE110...	https://www...	50.00	42.00	36.06	42.76	12.79		
3- diet induced obesity [lung] NA 20248	MouseDisease	diet induced ...	lung	NA	Disease vs. N...	DiseaseState...	GSE38...	https://www...	50.00	45.83	33.57	42.66	10.20		
7902- normal control [foreskin] pellet culture; TGF	SingleCellHuman...	normal control	foreskin	pellet culture...	Cell Type vs ...	chondrocyte ...	GSE160625.UN	https://www...	40.82	46.00	30.00	42.60	14.20		
105- normal control [heart] NA 2522	RatDisease	normal control	heart	NA	Other Comp...	Tissue:Gend...	GSE53960.GPL1	https://www...	50.00	48.11	28.28	43.76	10.05		
7781- normal control [foreskin] pellet culture; TGF	SingleCellHuman...	normal control	foreskin	pellet culture...	Cluster vs Ot...	chondrocyte ...	GSE1606...	https://www...	50.00	50.00	26.46	42.25	20.41		
6271- normal control [embryo] differentiation me	SingleCellHuman...	normal control	embryo	differentiatio...	Cell Type vs ...	chondrogeni...	GSE110...	https://www...	50.00	41.46	30.00	42.18	14.89		
135- normal control [liver] cerivastatin 6363	RatDisease	normal control	liver	cerivastatin	Treatment vs...	TreatTime[da...	GSE57...	https://www...	50.00	45.83	26.46	42.10	8.52		
7640- idiopathic pulmonary fibrosis [bronchoalveolar] NA 1141	SingleCellHuman...	idiopathic p...	bronchoalve...	NA	Cluster vs Ot...	epithelial cell...	GSE15...	https://www...	50.00	56.57	24.49	42.06	27.33		
10- non-small cell lung carcinoma [lung] NA 1141	OncoHuman	non-small cel...	lung	NA	Other Comp...	SmokingStat...	GSE15...	https://www...	50.00	37.71	20.00	42.05	13.28		
EEC P32 Tumor vs Norm RPKM - 2018-09-28 04:03 AS123									50.00	57.45	30.00	42.04			
EEC P32 Tumor vs Norm RPKM - 2020-02-13 11:12 NDMC-0212									50.00	45.39	30.00	41.93			
28- colon carcinoma [colon] recombinant hTGF al	OncoHuman	colon carcin...	colon	recombinant ...	Treatment1 v...	CellLine:Trea...	GSE10...	https://www...	50.00	38.38	31.62	41.82	9.24		
1- normal control [umbilical cord vein] mechanica	HumanDisease	normal control	umbilical cor...	mechanical s...	Treatment vs...	Treatment:Tr...	GSE178...	https://www...	50.00	41.24	43.59	41.75	7.59		
EEC P32 Tumor vs Norm RPKM123 - 2020-02-14 11 NDMC-0212									50.00	86.60	42.43	41.64			
3- normal control [small airway epithelium] 3132	HumanDisease	normal control	small airway ...	NA	Other Comp...	SmokingStat...	GSE77658.GPL5	http://www...	50.00	48.99	26.46	41.35	8.66		
MetastaticMelanoma mRNA_vs_Normal PMID_204 CT20190116									50.00	61.24	44.72	41.30			

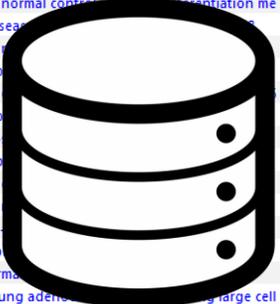
Selected 0 / 140569

Your datasets

Analysis

Donor datasets

Analysis



compare

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Mapping Your Results to OmicSoft Datasets by IPA Analysis Match

Project

Cell & Tissue

Datasets information

similar

opposite

Analysis Name	Project	Cell & Tissue	Datasets information	z-scores
127- breast carcinoma [breast] human marrow strom HumanDisease	breast	breast	human marro... Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	23.33
67- breast carcinoma [breast] human marrow strom HumanDisease	breast	breast	human marro... Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	55.90
129- breast carcinoma [breast] IL-6;siltuximab 27511 HumanDisease	breast	breast	IL-6;siltuximab Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	20.00
101- breast carcinoma [breast] IL-6;siltuximab 27481 HumanDisease	breast	breast	IL-6;siltuximab Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	41.23
east carcino...	breast	breast	IL-6;siltuximab Treatment vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-20.00
east carcino...	breast	breast	TRE28786.GPL93 Dosage:Experi... GSE28786.GPL93 https://www.n...	43.59
east carcino...	breast	breast	none CellType1 vs. C... SamplingTime... GSE54329.GPL18 https://www.n...	10.00
east cancer	breast	breast	ethanol Treatment1 vs. ... Treatment:Tra... GSE64536.GPL57 https://www.n...	47.96
east carcino...	breast	breast	IL-6 Treatment vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-18.86
east carcino...	breast	breast	IL-6 Treatment vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-11.34
east cancer	breast	breast	ethanol Treatment1 vs. ... Treatment:Tra... GSE64536.GPL57 https://www.n...	42.43
east carcino...	breast	breast	IL-6;siltuximab Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	20.00
east carcino...	breast	breast	IL-6;siltuximab Treatment vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-28.40
east carcino...	breast	breast	human marro... Treatment vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-38.38
east carcino...	breast	breast	none Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-37.42
east carcino...	breast	breast	human marro... Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-38.73
east carcino...	breast	breast	none Treatment1 vs. ... CellLine:Sampli... GSE54329.GPL18 https://www.n...	-42.43

Project

- Select Projects
- Shared Projects
- Libraries
 - OmicSoft
 - OncoLand
 - DiseaseLand
 - SingleCellLand
 - Normal Cells and Tissues

Or filter using wild card search

include: (use * for wildcard)

[comma-separated list]

exclude:

[comma-separated list]

Apply Cancel

atasets
ta

z-scores

Match Analyses Heatmap: treat2_vs_untreat

Settings/Legend

Filter

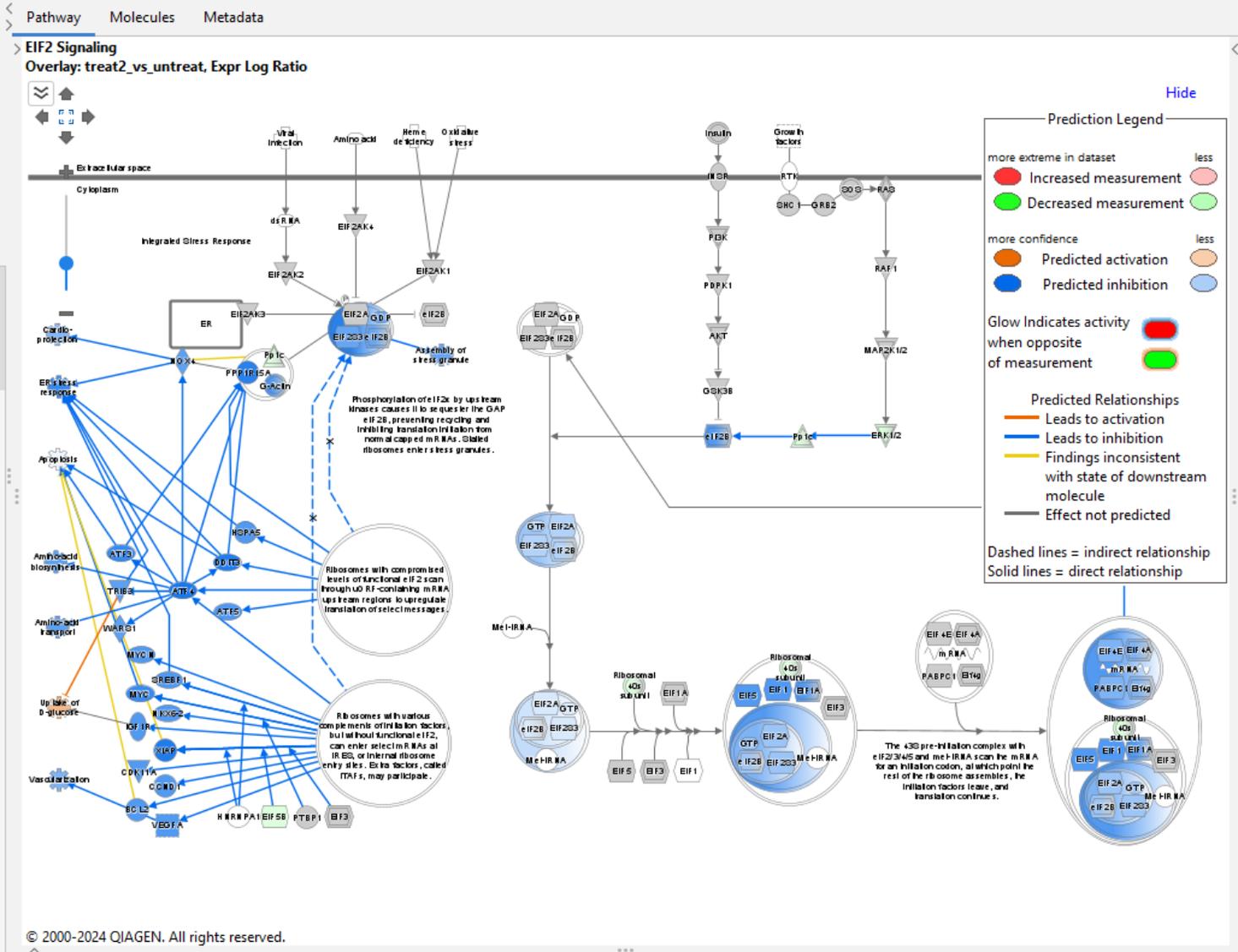
Measurement: Activation z-score -9.075 34.771

Sort Method: Hierarchical Clustering Visualize: z-score

Insignificance Threshold: (absolute value) Apply

View Report Open Network Expand Header

Entity Type	Entity Name	treat2_vs_untreat	treat2_vs_untreat
DM	Analysis-ready genes		
UR	RICTOR		
CN	RICTOR		
CN	SIGLEC8		
CP	Oxidative Phosphorylation		
CP	EIF2 Signaling		
UR	MYC		
CN	MYC		
CN	MLXIP		
UR	MLXIP		
CP	Eukaryotic Translation Initi...		
CP	Response of EIF2AK4 (GCN...		
CP	Major pathway of rRNA pro...		
CP	Nonsense-Mediated Decay ...		
CP	Selenoamino acid metaboli...		
CP	SRP-dependent cotranslati...		
CP	Eukaryotic Translation Elon...		
DE	Organismal death		
UR	NPC1		
CN	NPC1		
DE	Necrosis of tumor		
DE	Cell death of cancer cells		
DE	Cell death of tumor cells		
DE	Cell death of osteosarcoma...		
CP	Coronavirus Pathogenesis ...		



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

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

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

Search Results - [] X

Diseases and Functions **Datasets and Analyses**

Search Results

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

Folder Types

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

4

Open **Add to Comparison** Customize Table Crea... 2024/... - 2024/... (1/125) << >>

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

Libraries > OmicSoft > SingleCellLand > SingleCellHumanUmi > Analyses

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

Case/Control Differences

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

Comparison Context

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

All Experiment Metadata

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

3

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

Project Manager

My Projects

Shared Projects

Libraries

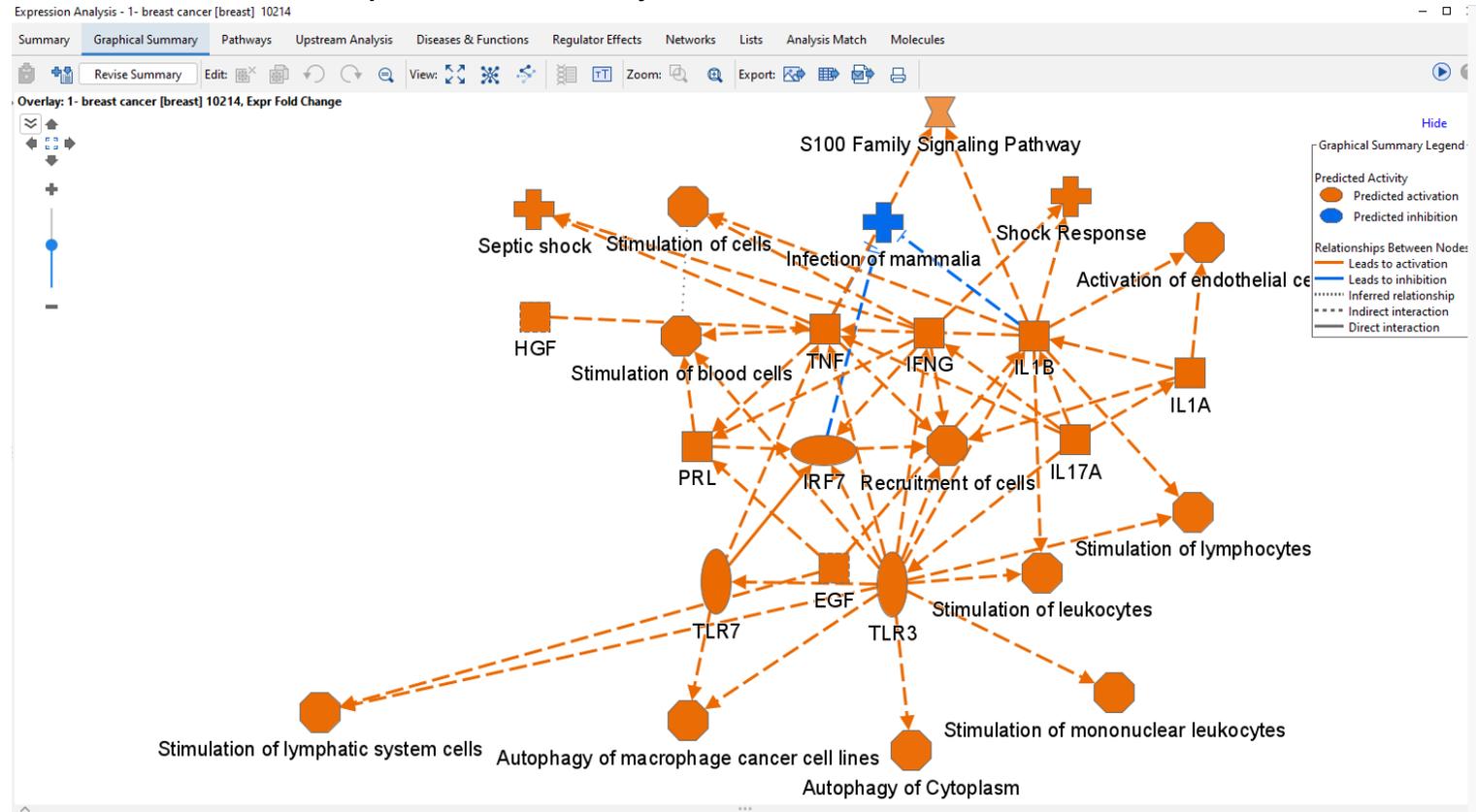
- OmicSoft
 - OncoLand
 - DiseaseLand
 - SingleCellLand
 - Normal Cells and Tissues
 - Ingen
 - ML D
 - My P
 - Ingen
 - My Li

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] 2886

Graphical summary



RNA-seq analysis portal



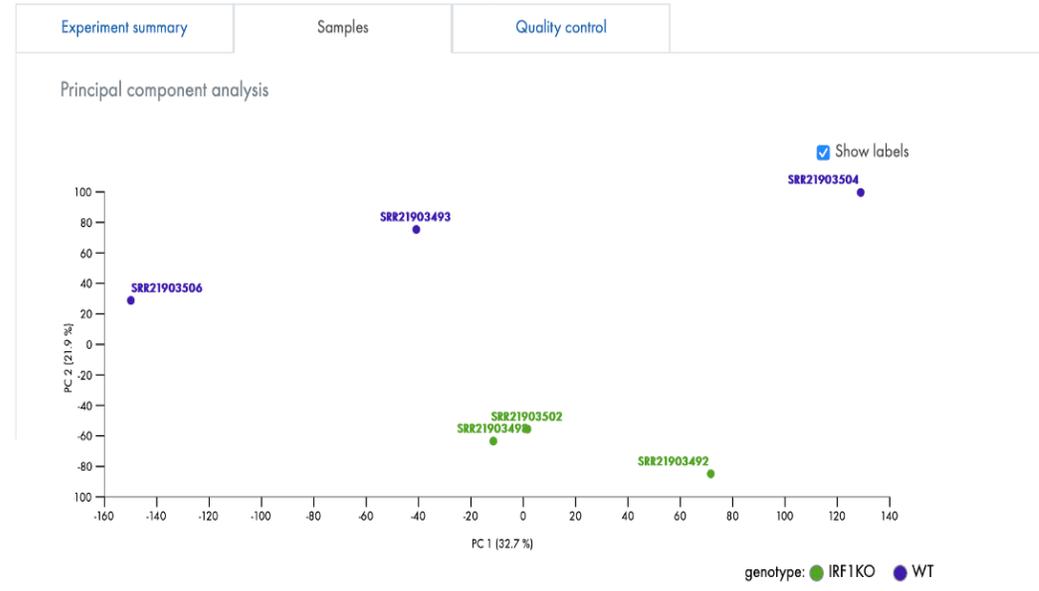
For the easy three step
You can analyze your RNA-seq
via IPA

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

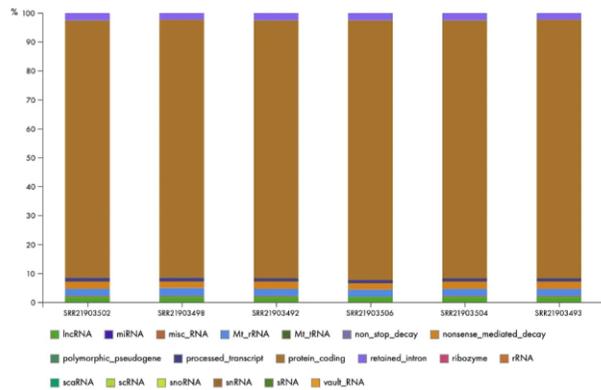
Summary of experiment setup, samples and attributes, and sample quality control [Print view](#)



Mapped by type

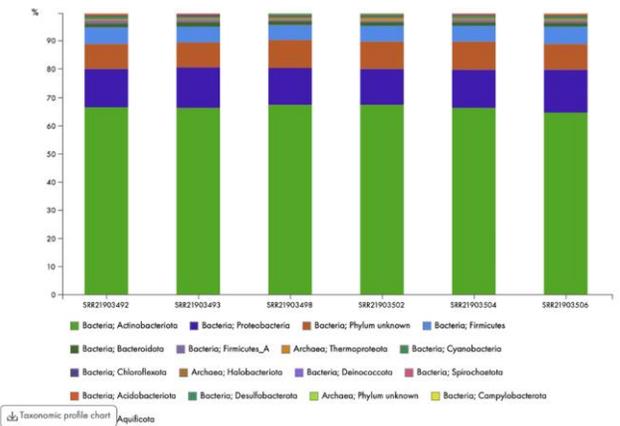
Sample name	Mapped to gene (intron + exon)	Mapped to intron	Mapped to exon	Mapped to intergenic region
SRR21903502	93.76%	11.29%	82.47%	6.24%
SRR21903498	93.59%	11.70%	81.89%	6.41%
SRR21903492	94.13%	10.79%	83.35%	5.87%
SRR21903506	94.12%	10.89%	83.23%	5.88%
SRR21903504	93.71%	11.65%	82.06%	6.29%
SRR21903493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

Biotype distribution



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 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).



[Taxonomic profile chart](#)

Sample name	Archaea: Halobacteriota	Archaea: Phylum unknown	Archaea: Thermoproteota	Bacteria: Acidobacteriota	Bacteria: Actinobacteriota	Bacteria: Aquificota	Bacteria: Bacteroidota	Bacteria: Campylobacterota
SRR21903502	0.40%	5.92e-3%	0.70%	0.02%	67.42%	6.62e-3%	1.34%	9.16e-3%
SRR21903498	0.49%	5.34e-3%	0.53%	0.03%	67.37%	-	1.29%	-
SRR21903492	0.34%	8.02e-3%	0.78%	0.05%	66.46%	-	1.61%	-
SRR21903506	0.44%	0.01%	0.54%	0.07%	64.55%	-	1.42%	-

RNA-seq portal results

Analysis Portal Samples Help

All Projects > CDDO-me in mouse liver > test2 > CDDO-Me vs. Vehicle

Treatment: CDDO-Me vs. Vehicle

Features: 864 of 30841
Sort by: Name (Asc) Full feature list

Name	Fold change	FDR p-value	P-value	Biotype
1700001105Rik	-1.47	0.07	3.44e-3	lincRNA
1700018102Rik	1.82	9.85e-3	2.65e-4	antisense
1810008118Rik				lincRNA
1810058124Rik				protein_coding
2310001117Rik				lincRNA
2310015A16Rik	1.60	0.01	4.09e-4	lincRNA
2410002F23Rik	1.32	0.07	3.15e-3	protein_coding
2810459M11Rik	1.29	0.02	6.58e-4	protein_coding
3110082117Rik	-2.39	3.07e-7	1.90e-9	protein_coding

Differentially expressed genes table

Biological insights: Canonical pathways

Pathway	-log10 of p-value	z-score
NRF2-mediated Oxidative Stress Response	17.812	3.873
LPS/IL-1 Mediated Inhibition of RXR Function	17.735	-0.832
Nicotine Degradation II	16.712	1.964

Ingenuity Pathway Analysis (IPA)
10 most enriched pathways, regulators, diseases
See more with your IPA account

Xenobiotic Metabolism: PXR Signaling Pathway	12.879	3.402
PXR/RXR Activation	12.622	1.886

[View details](#)

Volcano plot

Heatmap

Filter data by fold change & p-value

Filters: FDR p-value ≤ 0.1, -1.1, 1.1, Filter not saved

Biological insights filter: None selected Advanced filters Save

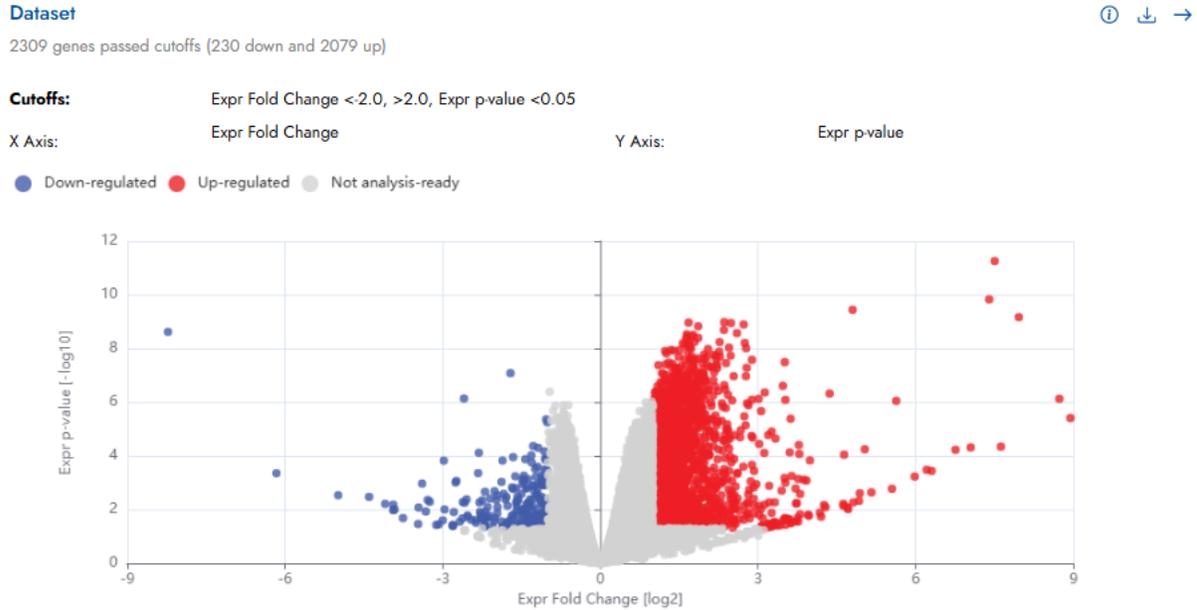
Send to QIAGEN IPA
Analyze the selected features further in QIAGEN IPA Send

Send the data to your IPA account!

IPA interpret

early vs norm

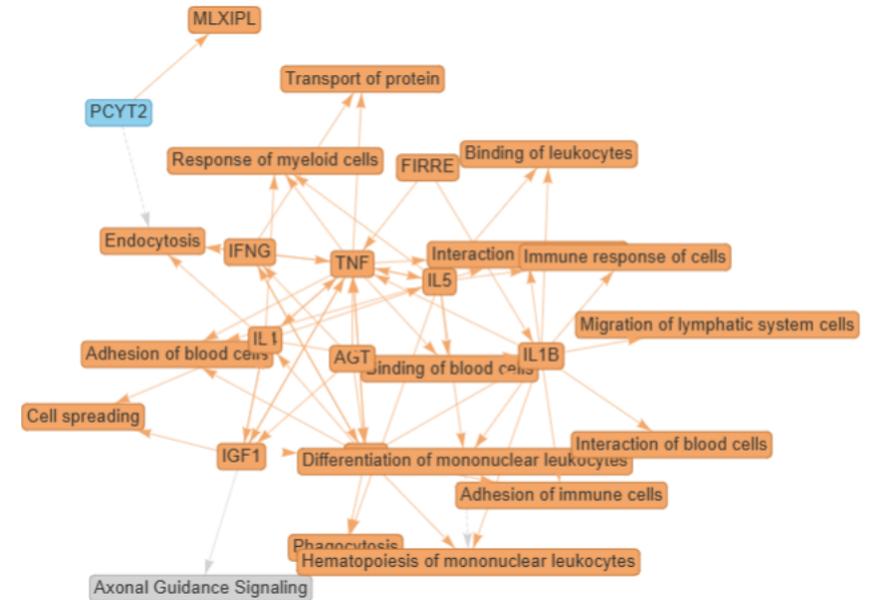
Created on September 30, 2024, from observation "early vs norm" in dataset "All MSG Levels"



Dataset molecules

Name	P-value ▲	Fold Change	Molecule Type
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
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
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
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
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

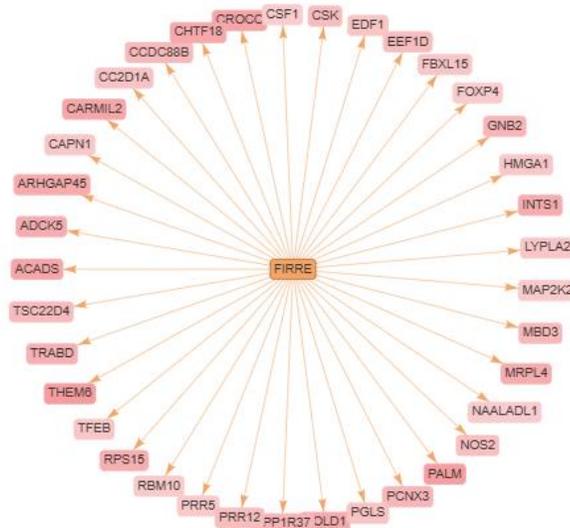
Upstream Regulators

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

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

Upstream regulator representation

FIRRE Figure Legend OFF



FIRRE network

AI suggests the following synopsis of this network:

Top Biological Themes in the given Biological Network

Gene Regulation and Expression

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

Metabolic Pathways

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

Signal Transduction

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

Immune Response

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

Label gene names of interest in the volcano plot

Dataset

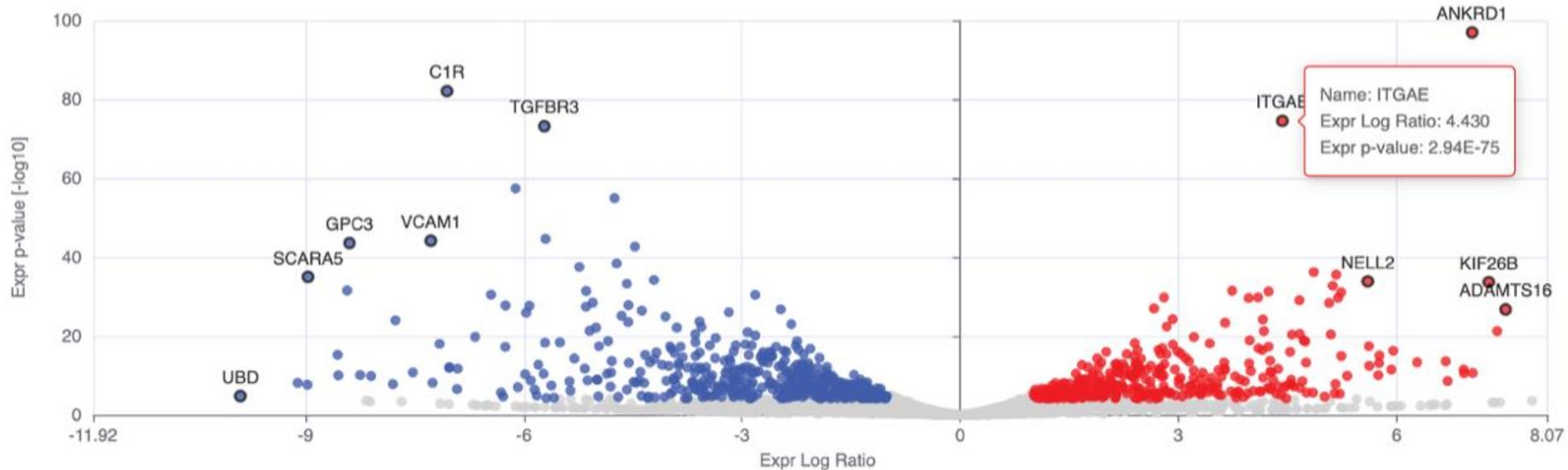
882 genes passed cutoffs (491 down and 391 up)

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

QIAGEN IPA Interpret

Dataset molecules

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

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

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

Analyte identifier **REQUIRED** to explore enrichment

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

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

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

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

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

Accepted file formats:

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

Multiple comparisons or observations may be uploaded in one file

IDs (required)

	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

Ratio, fold change, etc. (recommended)

Significance (optional)

Common protein IDs

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

UniProt ID conversion tool:

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

IDs (required)

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

Observation 1

Ratio, fold change, etc. (recommended)

Significance (optional)

Common protein IDs

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

UniProt ID conversion tool:

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

Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

	A	B	C	D	E	F	G	H
	Pubchem	Kegg	HMDB	CAS	Metabolites	Fold change	P_value	P_value_adjust
1								
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

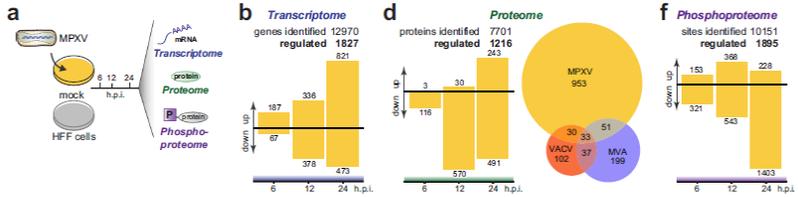
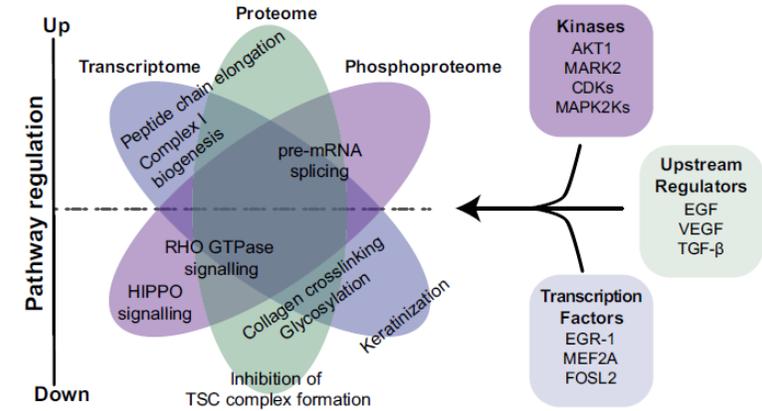
Common metabolite IDs

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

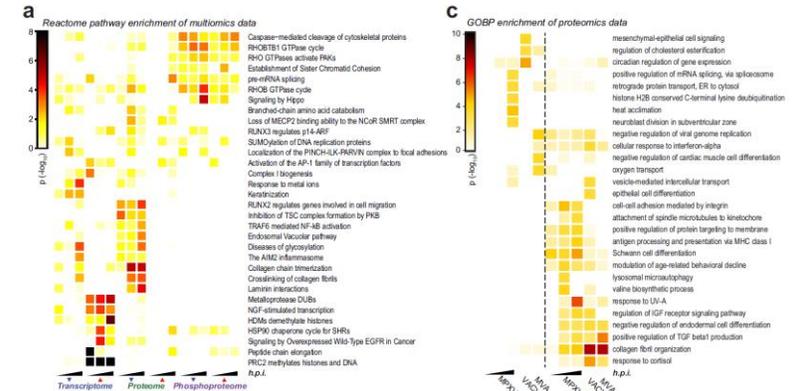
Metabolite ID conversion tools:

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

b



DEG, DEP,
DEphospho



Pathway
analysis

nature communications

Article

<https://doi.org/10.1038/s41467-024-51074-6>

Multi-omics characterization of the monkeypox virus infection

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Check for updates

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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/IKBKB, and splicing factor kinases with potent antiviral efficacy against MPXV and VACV.

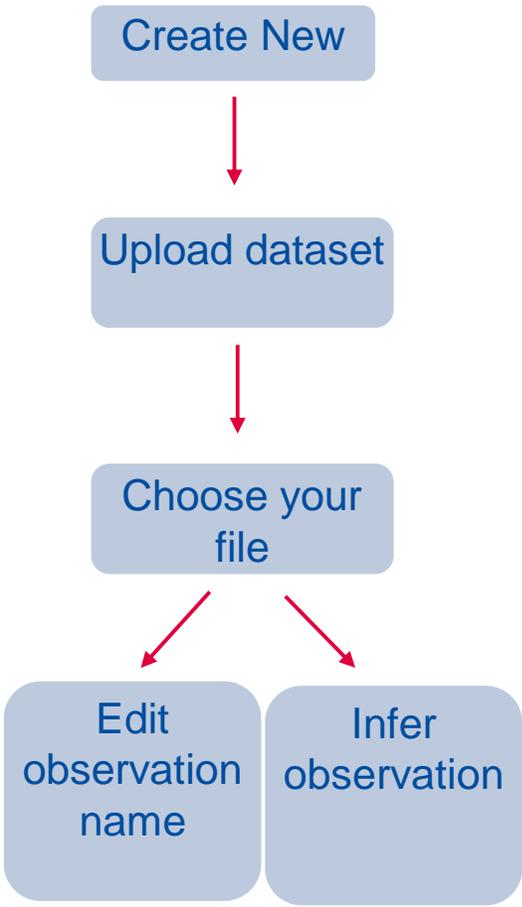
Monkeypox (mpox) virus (MPXV) is a pathogenic orthopoxvirus and etiological agent of the zoonosis mpox, first identified in 1970¹. The virus species is separated into clade I (Central African, Congo basin) and clade II (West African), the latter of which includes the 2022 mpox

outbreak strain that caused the first widespread community transmission of MPXV outside Africa^{2,3}. 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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Upload dataset protein

gene_names	majority_protein_acs	protein_descriptions	fold_change_log2.6h	p_value.6h	sd_log2.6h	fold_change_log2.12	p_value.12h	sd_log2.12h	fold_change_log2.24	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	Q60814;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	Q9NWX9	Uncharact	-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	Q8I WV8;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



Dataset Upload - MOESEM_protein.xlsx

- Select File Format:
- Contains Column Header: Yes No
- Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
- Array platform used for experiments: Select relevant array platform as a reference set for data analysis.
- Use the dropdown menus to specify the column names that contain identifiers and observations. For observations, select the appropriate measurement value type.

Raw Data (7702) Dataset Summary (0) Metadata

Edit Observation Names

ID/Observation Name	Ignore	Ignore
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	Q9H944;Q9H944-2
15	C14orf119	Q9NWW9
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	STEAP2	Q8NFT2;Q8NFT2-2...
25	TAX1BP3	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

-
-
-
-
-
-
-

Ignore	Ignore	Ignore
fold_change_log2.2...	p_value.24h	sd_log2.24h
-0.2674955500000000...	7.5430876500756699...	9.28915038320519E-2
-0.4940649999999999...	0.4576397276695309...	1.2088366425480001
-9.574999999999889...	0.9720591511091649...	0.4524954842321570...
0.2707499999999999...	0.380341728316895	0.3562806529816229...
0.4861150000000000...	1.4394252647286301...	0.1678519601499839...
-4.234709999999999...	5.3837009198685302...	1.8836548463955201
-3.905000000000039...	0.9877520642211119...	0.5171131399459959...
-0.346074999999999...	0.5723601284551610...	1.64431208954147
-4.617750000000000...	0.5812464974222110...	7.8768809979468196...
4.2799999999999699...	0.8605141383867239...	0.4336125290605820...
8.63037849999999902	1.999999999999999E...	0.458489081433477
0.1104749999999999	0.634492908667461	0.1992221002607250...
-7.8502855	0.1299470877263939...	2.9851368758577999
1.500000000320301...	0.9969694623128220...	0.4998669027721590...
5.7999999999998001...	0.9841780900094929...	0.6861339143223850...
0.1401350000000000...	0.1054355947707039...	0.401042192027527
3.2350000000000898...	0.9915485814740040...	0.5030443827824170...
-0.724079999999999...	0.362523190756112	1.8756340543427601...
0.2825934999999999	4.8404147917430397...	0.1472934103667830...
-3.663774999999999	1.58972622239568E...	1.8290275854350899
1.1515560499999999	3.4266735339520999...	0.2599574173142100...
-3.821999999999899...	0.8666968915045030...	0.3798707638404609...
-0.227585000000000...	0.5082650323241549...	0.4080403041260199...
-9.536050000000000...	0.5279445437520450...	0.1768228456816919...
0.6107599999999999...	7.4747780841027302...	0.117401839985863
8.737999999999999...	0.8632089953956040...	1.25799626205648
9.510499999999999...	0.6605636001239140...	0.3202115717559749...
7.9237015992669496...	0.352280272453129...	

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	AASDHPPT		AASDHPPT	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	sulfipyrazone
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, filgrastin/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 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	trimebutin
0.001	9.45E-01	ACAA2		ACAA2	acetyl-CoA acyltransferase 2	Cytoplasm	enzyme	

0 / 7186

Flags: *ID* - 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 - Overrides 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.

Symbol: A1BG - ACPY2 (1/72)

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

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	<input type="text" value="-0.58"/>	Down <input type="text" value="0.58"/> Up
p_value.6h	Expr p-value	0.0 to 1.0	<input type="text" value="0.05"/>	

Recalculate

Advanced

Recalculate 1110 analysis-ready molecules across observations

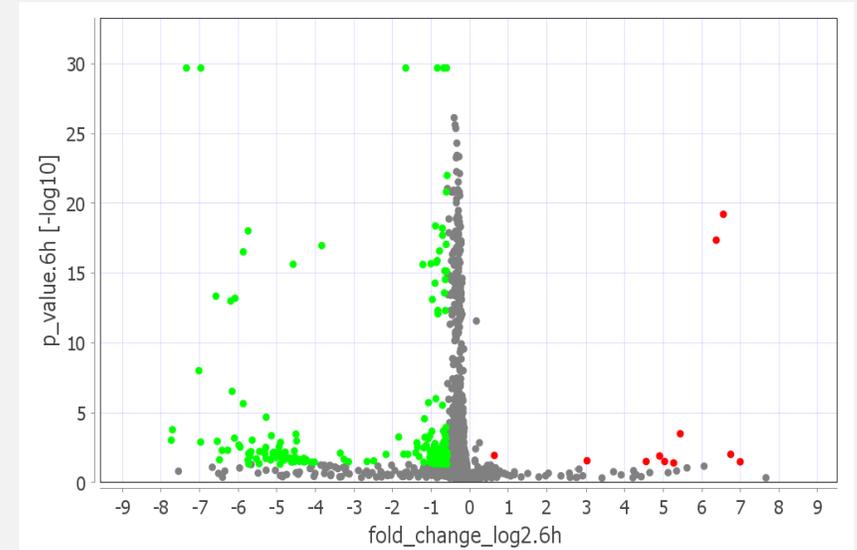
Preview Dataset Naturecomm_protein Observation:

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

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

Volcano plot

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



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

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 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

- 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

Causal networks

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

Score using causal paths only

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 OR node OR transcription regulator OR translation

←

You can put interesting disease or gene

 1110 analysis-ready molecules across observations

Preview Dataset Naturecomm_protein Observation:

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

Symbol

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) ▾ ⏪ ⏩

> Experiment Metadata

> Analysis Settings

∨ 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 >

∨ Top Upstream Regulators

∨ Upstream Regulators

Name	p-value	Predicted Activation
IFNG	1.14E-05	Inhibited
IFNA2	1.22E-05	
RETREG3	6.94E-05	
TSIX	6.94E-05	
PARP2	6.94E-05	

1 2 3 4 5 6 7 8 9 >

∨ Causal Network

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

Pathway or gene activity predicted by IPA



Actual measurement of gene expression in your dataset



What do z-scores mean in IPA?

Actual dataset measurement

vs.

What IPA expects if pathway is activated

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

Pathway inhibited

- Z score

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

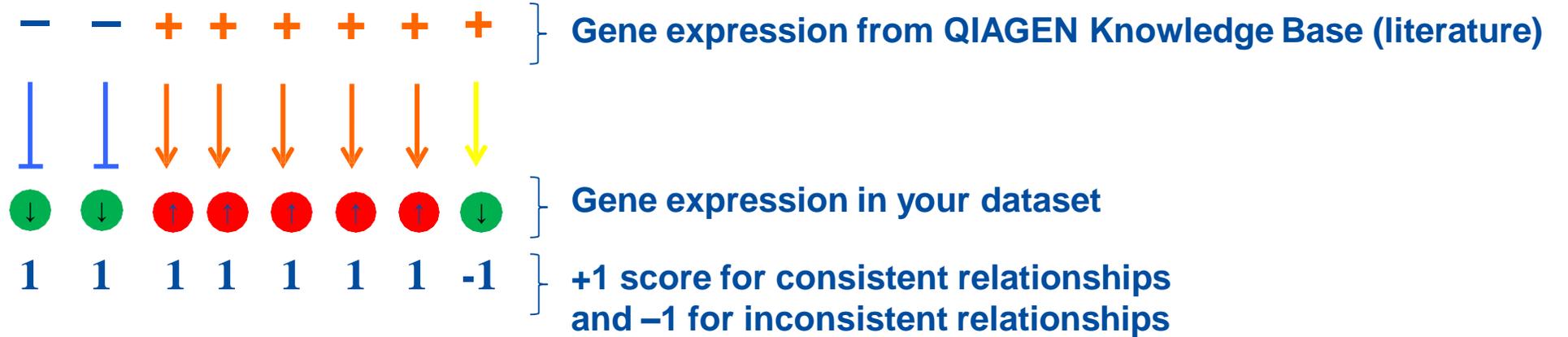
No clear signal for prediction
Z score = 0

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

Pathway activated

+ Z score

How well do the actual measurements match the expected measurements?



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

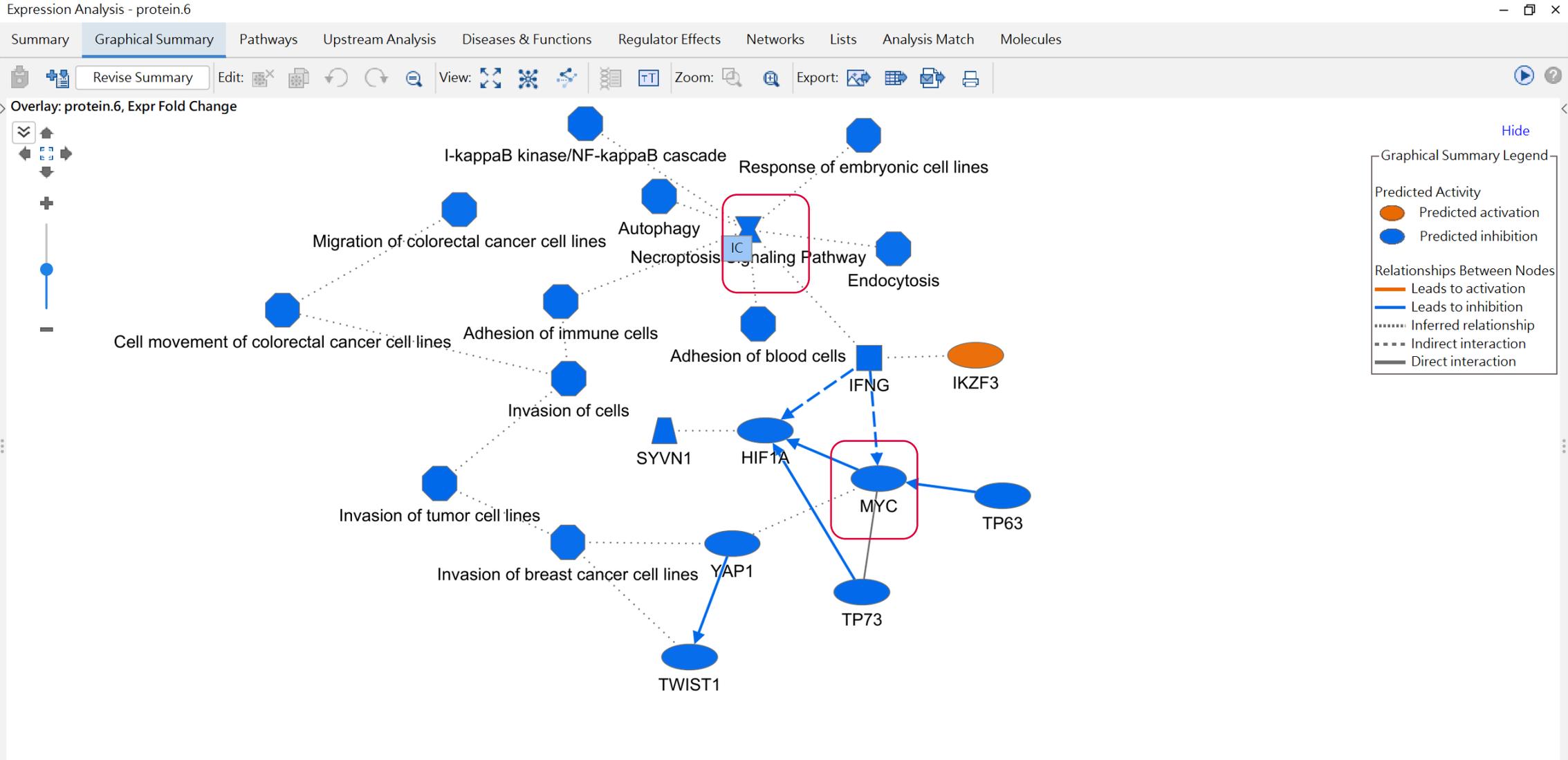
- z-score is a statistical measure of the match between expected relationship direction and observed gene expression
- z-score greater than 2 or less than -2 is considered significant
- Note that the actual z-score is weighted by the underlying findings, the relationship bias and dataset bias

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

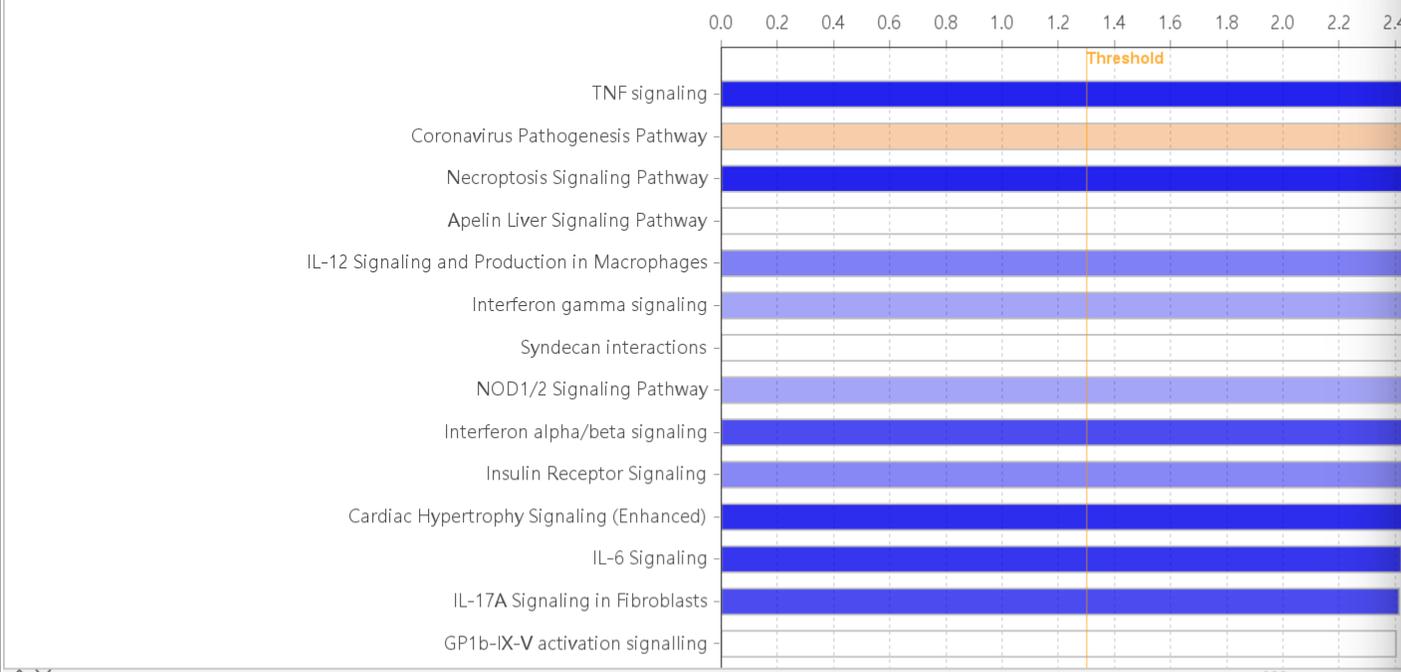
Symbol	Measurement Expr Log Ratio	+ △ ×	Expected
CREB3L3	↓ -1.536	↑	Up
IHH	↓ -1.173	↑	Up
PBX1	↓ -1.037	↑	Up
CD86	↑ 1.016	↓	Down
IL1RAP	↑ 1.046	↓	Down
PKM	↑ 1.082	↑	Up
HLA-DMB	↑ 1.106	↓	Down
IL18RAP	↑ 1.124	↓	Down
CREB5	↑ 1.148	↑	Up
CREB3L2	↑ 1.179	↑	Up
CCN4	↑ 1.204	↑	Up
TLR4	↑ 1.213	↓	Down

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

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



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



Click on a data point in the chart above to see which molecules are associated with that pathway

Customize Chart

Select Canonical Pathways to Display

Tree View List View

- 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:

P-Value Type to Determine Bar Length

Fisher's Exact Test p-value

Score Cutoff

Display only entities that have a -log(p-value) greater than: (between 0 and 5.21)

an absolute value z-score greater than: (between 0 and 2.83)

Select Sort Order

-log(p-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**

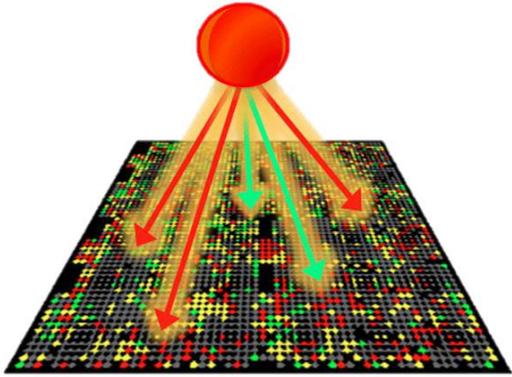
Customize Chart Horizontal Bar Chart    

?

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



Click on a disease name 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

Expression Analysis - protein.6

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

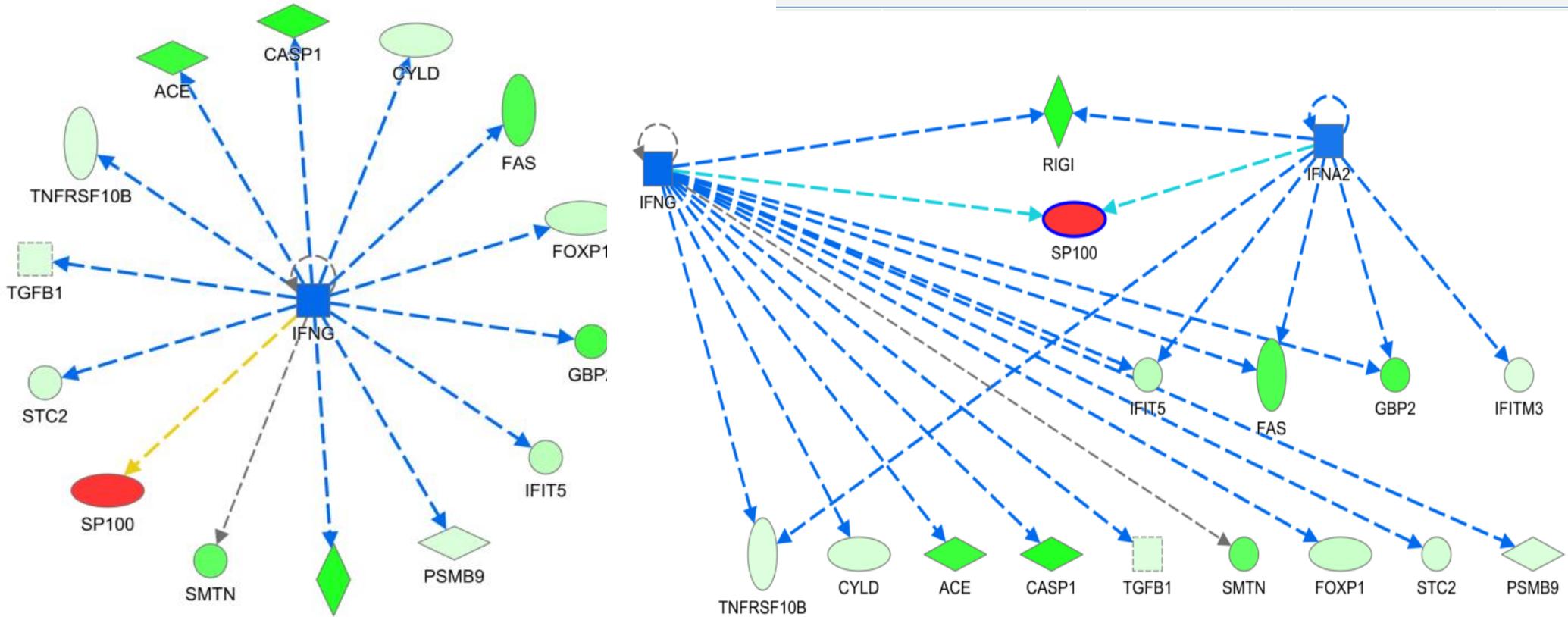
Upstream Regulators Causal Networks

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
- RETREG3
- 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



Regulator	Description	Activity	Score	Significance	Targets
IFNG	transcription regulator	Activated	2.000	0.92E-07	↓IFIT5, ↓PSMB9, ↓RIGI, ...all 9
IFNA2	complex			9.33E-04	↓IFIT5, ↓PSMB9, ↓RIGI, ...all 4
				1.00E-03	↑AKT2, ↑CCN1, ↑COL...all 5
				1.02E-03	↓COL1A1, ↓COL1A2 ...all 2

Expression Analysis - protein.6

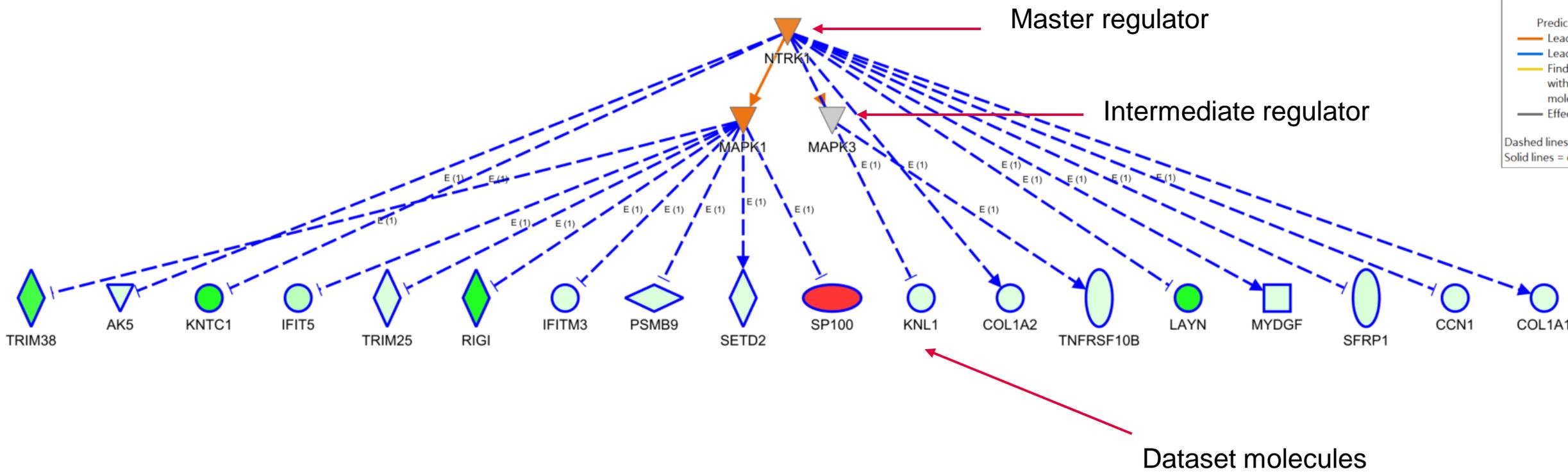
Summary Graphical Summary Pathways Upstream Analysis Diseases & Functions Regulator Effects Networks Lists Analysis Match Molecules

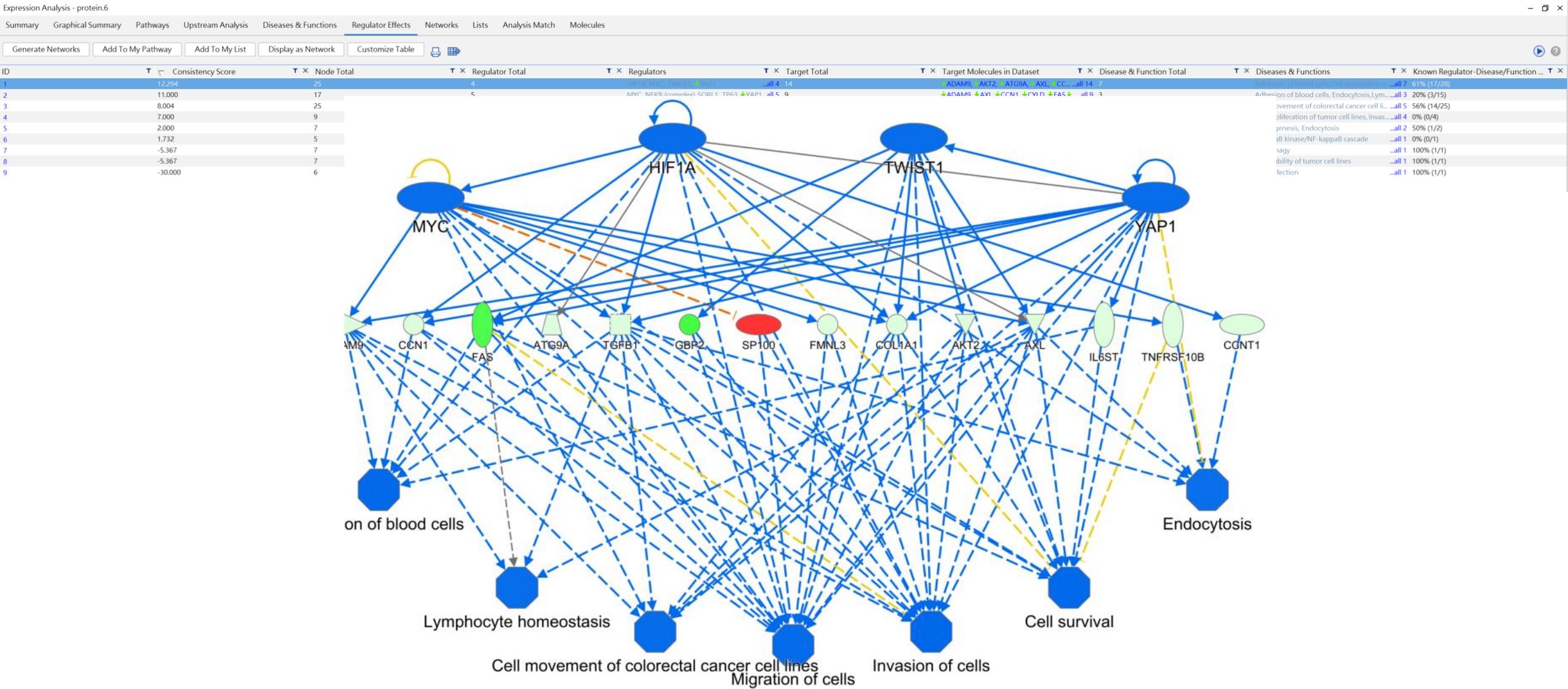
Upstream Regulators Causal Networks

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

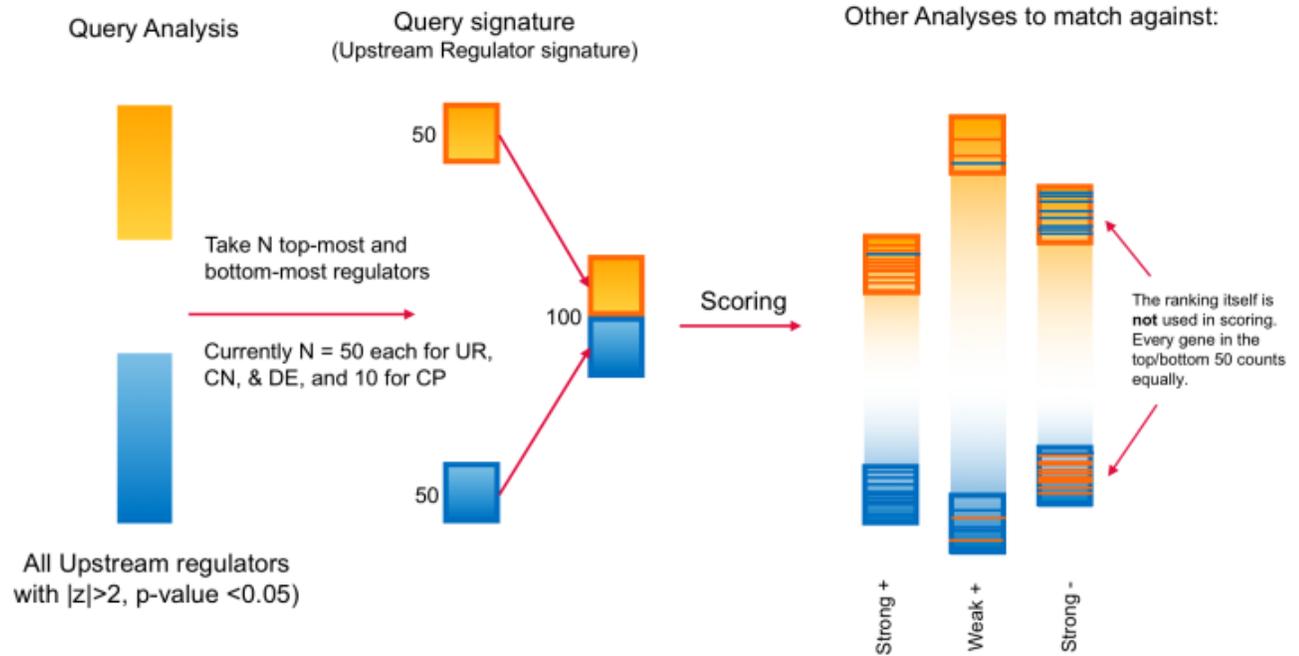
Canonical Pathways (up to 20 pathways)

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-score: 52.76 - 35.53 (1/954)

Analysis Name	Project	case.disea...	case.tissue	case.treat...	compariso...	compariso...	compariso...	compariso...	weblink	CP (z-score)	UR (z-score)	CN (z-score)	DE (z-score)	z-score...	DM (z-score...)
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...	63.25	88.64	42.64	79.77	52.76	
12527- normal control [eye] CMP_0sU52dlyhxp	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	erythroid cell vs ker...	TabulaSapiens_UMI...	CMP:0sU52dlyhxp	https://tabula-sapi...	63.25	75.59		67.42	51.56	22.93
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...	63.25	59.76	30.15	47.67	50.21	20.57
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...	63.25	80.18	39.89	73.85	48.48	
161- exudative age-related macular degeneration[norm	SingleCellHumanUmi	normal control	macula lutea,periph...		Cell Type vs Cell Ty...	melanocyte vs peric...	GSE135922_UMI.GPL	CMP:hS3RTLjyCXT	https://www.ncbi.n...	63.25	59.76		70.71	48.43	20.63
2701- normal control [pancreas] CMP_g3f5CvYOqOW	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:g3f5CvYOqOW	https://tabula-sapi...	63.25	59.76	15.08	47.67	46.44	25.46
3- normal control [artificial human skin tissue] UV	HumanDisease	normal control	artificial human ski...	UV	Treatment vs. Contr...	Treatment => UV v...	GSE48586.GPL13938	CMP:UwefEkmJm6p	http://www.ncbi.n...	63.25	53.45		67.42	46.03	25.46
13135- normal control [large intestine;small intestine]	SingleCellHumanUmi	normal control	large intestine;smal...		Cell Type vs Cell Ty...	goblet cell vs radia...	TabulaSapiens_UMI...	CMP:RbjvrDeo5pn3	https://tabula-sapi...	63.25	59.76		60.30	45.83	15.43
17642- normal control [pancreas] CMP_kqOXsVGNAl6	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:kqOXsVGNAl6	https://tabula-sapi...	63.25	65.47		52.22	45.23	13.80
18318- normal control [lung] CMP_wUCWD82OJVP	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	pulmonary ionocyt...	TabulaSapiens_UMI...	CMP:wUCWD82OJVP	https://tabula-sapi...	63.25	53.45		63.96	45.16	13.75
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...	63.25	53.45		63.96	45.16	
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...	63.25	53.45		63.96	45.16	26.02
14147- normal control [large intestine] CMP_jLoD3Vf1f	SingleCellHumanUmi	normal control	large intestine		Cell Type vs Cell Ty...	intestinal crypt ste...	TabulaSapiens_UMI...	CMP:jLoD3Vf1fA4c	https://tabula-sapi...	63.25	53.45	20.23	42.64	44.89	28.17
18604- normal control [eye] CMP_kkBY6IZsYVfI	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	retinal pigment epi...	TabulaSapiens_UMI...	CMP:kkBY6IZsYVfI	https://tabula-sapi...	63.25	59.76		56.41	44.85	21.71
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...	63.25	53.45		60.30	44.25	21.82
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...	63.25	65.47		47.67	44.10	23.33
5674- normal control [salivary gland] CMP_hooytsBn5k	SingleCellHumanUmi	normal control	salivary gland		Cell Type vs Cell Ty...	acinar cell of salivar...	TabulaSapiens_UMI...	CMP:hooytsBn5kEr	https://tabula-sapi...	63.25	65.47		47.67	44.10	24.00
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...	63.25	59.76		52.22	43.81	
2351- normal control [eye] CMP_BeCmsjZGgoM	SingleCellHumanUmi	normal control	eye		Cell Type vs Cell Ty...	erythroid cell vs ker...	TabulaSapiens_UMI...	CMP:BeCmsjZGgoM	https://tabula-sapi...	63.25	59.76		52.22	43.81	20.57
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...	63.25	59.76		52.22	43.81	13.80
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...	63.25	59.76		52.22	43.81	12.12
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...	63.25	59.76		52.22	43.81	25.46
1466- normal control [skin] CMP_VsM4rDaErGC0	SingleCellHumanUmi	normal control	skin		Cell Type vs Cell Ty...	mast cell vs smooth...	TabulaSapiens_UMI...	CMP:VsM4rDaErGC0	https://tabula-sapi...	63.25	59.76		52.22	43.81	26.02
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...	63.25	75.59	33.71	63.96	43.32	19.52
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...	63.25	65.47	33.71	73.85	43.26	20.57
15579- normal control [lung] CMP_UesQfKuIzd5Y	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	lung ciliated cell vs ...	TabulaSapiens_UMI...	CMP:UesQfKuIzd5Y	https://tabula-sapi...	63.25	65.47		42.64	42.64	26.23
12000- normal control [small intestine] CMP_3d7qj0B8J	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	enterocyte of epith...	TabulaSapiens_UMI...	CMP:3d7qj0B8JcV	https://tabula-sapi...	63.25	65.47		42.64	42.84	25.20
18776- normal control [small intestine] CMP_ieTZeErz	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	small intestine gobl...	TabulaSapiens_UMI...	CMP:ieTZeErzJbB	https://tabula-sapi...	63.25	59.76		47.67	24.42	
17983- normal control [small intestine] CMP_3yZc8Y	SingleCellHumanUmi	normal control	small intestine		Cell Type vs Cell Ty...	paneth cell of epith...	TabulaSapiens_UMI...	CMP:3yZc8YtZdNN	https://tabula-sapi...	63.25	59.76		47.67	42.67	27.43
17625- normal control [pancreas] CMP_nmhz2E659CsJ	SingleCellHumanUmi	normal control	pancreas		Cell Type vs Cell Ty...	pancreatic acinar ce...	TabulaSapiens_UMI...	CMP:nmhz2E659CsJ	https://tabula-sapi...	63.25	59.76		47.67	42.67	25.46
83- disease control [secondary auditory cortex] NA	HumanDisease	disease control	secondary auditory...	NA	Tissue1 vs. Tissue2	ExperimentGroup =...	GSE127898.GPL2030	CMP:j6Cypd5j78	https://www.ncbi.n...	63.25	65.47	30.15	73.85	42.37	16.27
14- normal control [peripheral blood] CL097 CMP_PXQ	HumanDisease	normal control	peripheral blood	CL097	Treatment vs. Contr...	AgeCategory;CellSu...	GSE94496.GPL10558	CMP:PXQY00t3Niv	https://www.ncbi.n...	63.25	65.47	33.71	67.42	41.65	15.35
84- coronavirus disease 2019 (COVID-19);disease contr	SingleCellHumanUmi	normal control	peripheral blood		Cell Type vs Cell Ty...	airway mucous cell...	GSE171524_UMI.GPL	CMP:ew1sokI7fj	https://www.ncbi.n...	63.25	59.76		42.64	41.41	19.74
16361- normal control [eye;skin] CMP_5bN4EomZj0y	SingleCellHumanUmi	normal control	eye;skin		Cell Type vs Cell Ty...	melanocyte vs retin...	TabulaSapiens_UMI...	CMP:5bN4EomZj0y	https://tabula-sapi...	63.25	59.76		42.64	41.41	6.58
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...	63.25	59.76		42.64	41.41	25.46
6- ovarian cancer [ovary] NA CMP_LVelpNWagJOO	OncoHuman	ovarian cancer	ovary	NA	Treatment1 vs. Trea...	SubjectTreatment =...	GSE112798.GPL570.t	CMP:LvelpNWagJOO	https://www.ncbi.n...	63.25	70.71	30.15	63.96	41.21	12.12
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...	63.25	70.71	33.71	60.30	41.18	6.05
10125- normal control [lung] CMP_ILl8jGEMalk1	SingleCellHumanUmi	normal control	lung		Cell Type vs Cell Ty...	club cell vs pericyte...	TabulaSapiens_UMI...	CMP:ILl8jGEMalk1	https://tabula-sapi...	63.25	53.45		47.67	41.09	23.00
16- breast cancer [breast] CMP_RLS4ZqwMMSX	SingleCellHumanUmi	breast cancer	breast		Cluster vs Others	B cell (cluster) vs o...	GSE135710_UMI.GPL	CMP:RLS4ZqwMMSX	https://www.ncbi.n...	63.25	59.76	30.15	73.85	40.94	22.93
5- normal control [peripheral blood] IL-2 CMP_p4wFO8J	HumanDisease	normal control	peripheral blood	IL-2	CellType1 vs. CellTy...	CellDescription => ...	GSE118165.GPL2030	CMP:p4wFO8J3dfa	https://www.ncbi.n...	63.25	59.76	30.15	73.85	40.94	7.27
97- diffuse scleroderma;normal control [skin] CMP_sTG	SingleCellHumanUmi	diffuse scleroderma...	skin		Cluster vs Others	epidermal keratino...	GSE138669_UMI.GPL	CMP:sTGsdj80wyVE	https://www.ncbi.n...	63.25	43.64		56.41	40.82	16.68
7- diffuse scleroderma;normal control [skin] CMP_BTFI	SingleCellHumanUmi	diffuse scleroderma...	skin		Cell Type vs Others	epidermal keratino...	GSE138669_UMI.GPL	CMP:8TFHlUJLZGGO	https://www.ncbi.n...	63.25	43.64		56.41	40.82	16.68
62- NA [peripheral blood] NA CMP_HBEKic46qHz	HumanDisease	NA	peripheral blood	NA	Other Comparisons	ExperimentGroup =...	GSE198449.GPL24671	CMP:HBEKic46qHz	https://www.ncbi.n...	63.25	65.47	33.71	63.96	40.78	4.20
230- normal control [peripheral blood] S_aureus (heat	HumanDisease	normal control	peripheral blood	S. aureus (heat killed)	Other Comparisons	TreatmentAgeCate...	GSE103500.GPL10551	CMP:hY6dEg7MZzZ	https://www.ncbi.n...	63.25	65.47	33.71	63.96	40.78	16.90
104- keloid [skin] CMP_F29ddQGONZ5E	SingleCellHumanUmi	keloid	skin		Cluster vs Others	epidermal keratino...	HRA000425_UMI.GPL	CMP:F29ddQGONZ5E	https://ngdc.cncb.a...	63.25	35.86		63.96	40.77	23.76
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...	63.25	70.71	30.15	60.30	40.29	4.60
15- normal control [peripheral blood] lipopolysaccharid	HumanDisease	normal control	peripheral blood	lipopolysaccharide ...	Treatment vs. Contr...	AgeCategory;CellSu...	GSE94496.GPL10558	CMP:05i3I2MUTly	https://www.ncbi.n...	63.25	59.76	33.71	67.42	40.22	16.80
60- pulmonary tuberculosis [peripheral blood] NA	HumanDisease	pulmonary tubercu...	peripheral blood	NA	Other Comparisons	DiseaseStateExper...	GSE42832.GPL10558	CMP:ciCVOLxkfbco	https://www.ncbi.n...	63.25	59.76		67.42	40.22	25.46
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:bQvBN7HzYt	https://www.ncbi.n...	63.25	59.76		70.71	40.16	24.00
48- acute myeloid leukemia (AML) [peripheral blood] r	HumanDisease	acute myeloid leuk...	peripheral blood	none	Treatment1 vs. Trea...	ExperimentGroup =...	GSE133317.GPL1679	CMP:XLwA70GLKjot	https://www.ncbi.n...	63.25	59.76	30.15	70.71	40.16	2.02
17- type 1 diabetes mellitus [peripheral blood] NA	HumanDisease	type 1 diabetes mel...	peripheral blood	NA	Treatment vs. Contr...	ExperimentGroupS...	GSE124284.GPL1679	CMP:fuRm15MJNd4h	https://www.ncbi.n...	63.25	59.76	30.15	70.71	40.16	20.66
67- cervical squamous cell carcinoma (CESC) [cervix] NA	TCGA	cervical squamous ...	cervix	NA	Other Comparisons	DNASeqSomaticMut...	TCGA_CESC.GPLnaD	CMP:l0o4Q6BTGVe2	https://www.cancer...	63.25	65.47	30.15	63.96	39.89	15.55
5- bladder transitional cell carcinoma [bladder] PD1730	OncoHuman	bladder transitiona...	bladder	PD173074	Treatment vs. Contr...	CellDescription:Trea...	GSE201395.GPL1758	CMP:Ox8o1m9bsX	https://www.ncbi.n...	63.25	65.47	33.71	60.30	39.87	10.97

Biomarker Application

Drug

Expression Analysis - protein.6

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

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		
AAMDC	adipogenesis associated Mth938 domain...	AAMDC	↓-0.003	Cytoplasm	other		LP-935509, SM1-71
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

ptmngroup_id	ptmngroup_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	0.236049
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	0.00328	9.65E-04	0.9170780	0.9597367	0.2700707	0.0024	0.005105	0.909206	0.9676906	0.4174601	0.036688	0.00877	0.902123	0.9693272	0.638054

Create New

Upload dataset

Choose your file

Edit observation name

Infer observation

Dataset Upload - MOESEM_protein.xls

- Select File Format: Flexible Format
- Contains Column Header: Yes No
- Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s). Assign additional columns as ID to improve mapping coverage if desired.
- Array platform used for experiments: Not specified/applicable
- 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			
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	Q6Y7W6;Q6Y7W6-3...	GRB10-interacting ...	-0.128
21	MED18	Q9BUE0	Mediator of RNA po...	-5.308000000000000...
22	SLC30A1	Q9Y6M5	Zinc transporter 1	2.905000000000000399...
23	UBR2	Q8IWW8;Q8IWW8-2...	E3 ubiquitin-protei...	-2.920000000000047E...
24	STEAP2	Q8NFT2;Q8NFT2-2...	Isoform 2 of Metallo...	-0.322019999999999...
25	TAX1BP3	O14907	Tax1-binding protei...	-3.271881499999999...
26	SRSF7	Q16629;Q16629-2;Q...	Isoform 2 of Serine/...	-0.144449999999999...
27	SFSWAP	Q12872;Q12872-2	Isoform 2 of Splicin...	0.429499999999999...
28	ANXA13	P27216;P27216-2	Annexin A13;Isofor...	3.17599999999998401...
29	TERF1	P54274;P54274-2	Isoform 2 of Telome...	0.2908350000000000...

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

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

OK Cancel

sd_log2.12h	fold_change_log2.2...	p_value.24h	sd_log2.24h
1696...	-0.2674955500000000...	7.5430876500756699...	9.28915038320519E-2
12559...	-0.4940649999999999...	0.4576397276695309...	1.2088366425480801
17779...	-9.5749999999999889...	0.9720591511091649...	0.4524954842321570...
15570...	0.2707499999999999...	0.380341728316895	0.3562806529816229...
6929...	0.4861150000000000...	1.4394252647286301...	0.1678519601499839...
11580...	-4.2347099999999999...	5.3837009198685302...	1.8836548463955201
4069...	-3.9050000000000039...	0.9877520642211119...	0.5171131399459959...
8150...	-0.3460749999999999...	0.5723601284551610...	1.64431208954147
171E...	-4.6177500000000000...	0.5812464974222110...	7.8768809979468196...
16610...	4.2799999999999699...	0.8605141383867239...	0.4336125290605820...
0501...	8.6303784999999902...	1.99999999999999E...	0.458489081433477
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12670...	-0.7240799999999999...	0.362523190756112	1.8756340543427601

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

Symbol A1BG - ACYP2 (1/72)

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	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/matinib, ...
0.001	9.60E-01	ABL2		ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase	Cytoplasm	kinase	nilotinib, dasatinib
0.074	6.36E-01	ABLIM1		ABLIM1	actin binding LIM protein 1	Cytoplasm	other	
-0.253	1.36E-01	ABLIM3		ABLIM3	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, BRIS 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	

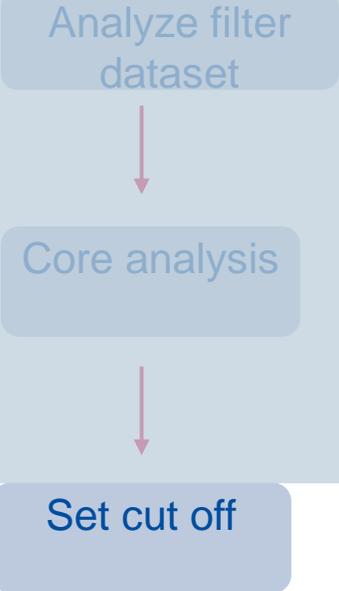
0 / 7186

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.

Core Analysis
 Biomarker Filter
 Filter Dataset
 microRNA Target Filter
 BioProfiler
 IsoProfiler

Edit Dataset Settings Analyze/Filter Dataset Close

Load Volcano plot



Create Phosphorylation Analysis - [analysis : Naturecomm_phosphprotein]

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

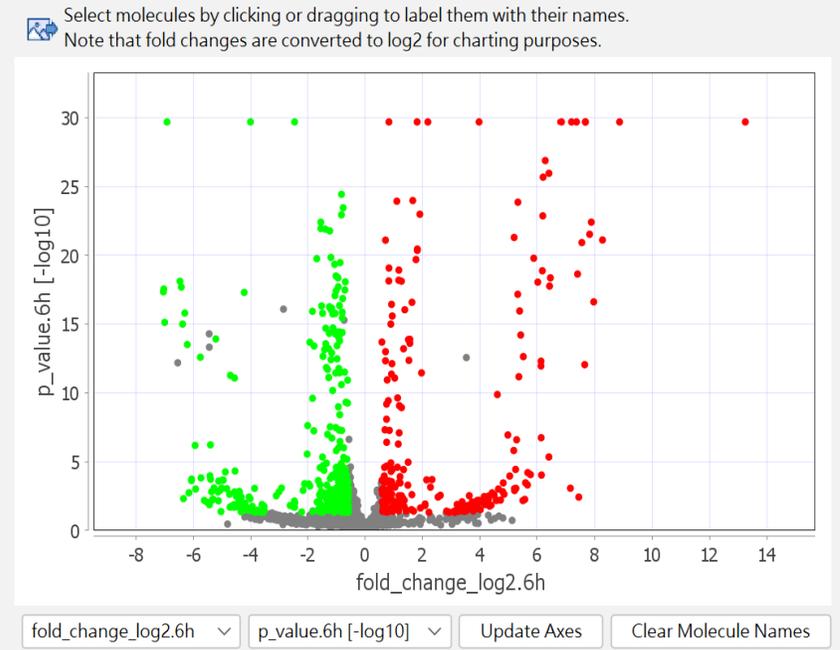
Advanced Recalculate 2216 analysis-ready molecules across observations

Preview Dataset Naturecomm_phosphprotein Observation:

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

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

Load volcano plot





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**

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: **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

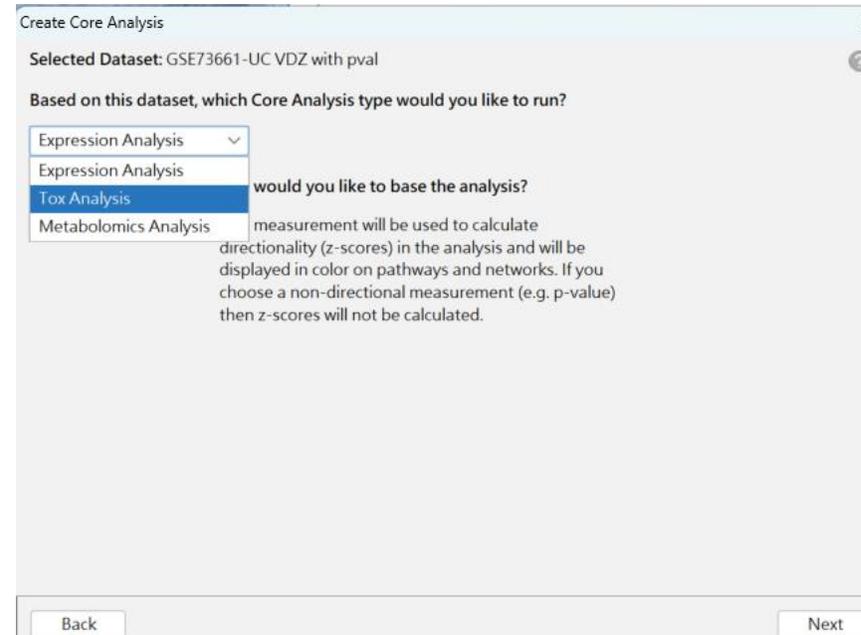
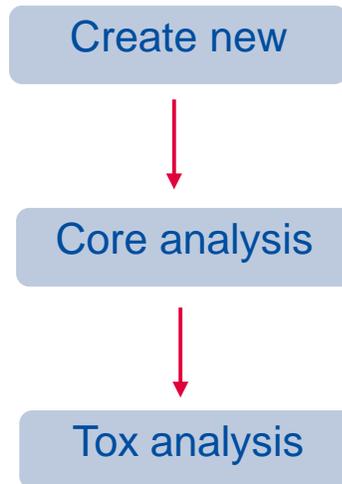
Phospho Log Ratio	Phospho p-value	Phospho Site	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-1.336	5.14E-04	S679	11297		AAMP	angio associated migrat...	Plasma Membrane	other	
-1.294	3.45E-02	T18	8647	D	ABCB11*	ATP binding cassette su...	Plasma Membrane	transporter	
-1.340	6.03E-03	S443	8308	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	

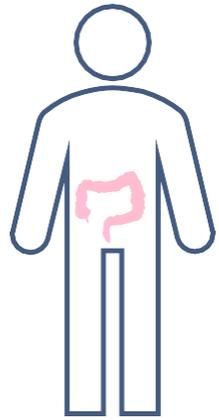
Run Analysis Cancel

- 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

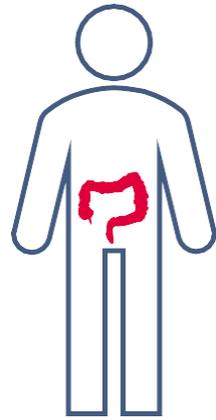
- Drug Development:** Evaluating potential toxicity of drug candidates.
- Environmental Toxicology:** Assessing gene expression changes in response to pollutants.
- Disease Research:** Understanding toxicity-related pathways in various diseases



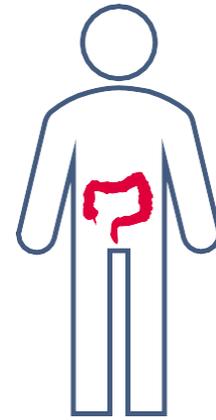


Control

vs

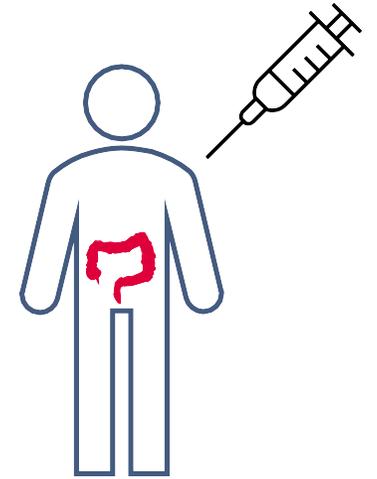


Ulcerative colitis



Baseline

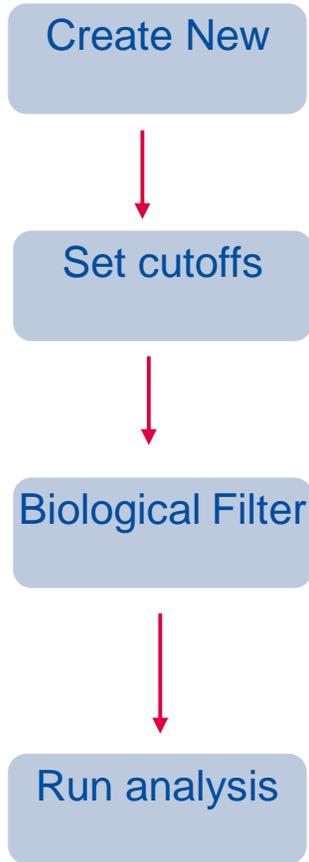
vs



**52 weeks
Vedolizumab**

RNA samples were isolated from colonic biopsies.

- **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

- 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

Save As Default

Stringent filter (filter molecules and relationships)

Relaxed filter (filter molecules)

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)

Recalculate 3497 analysis-ready molecules across observations

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

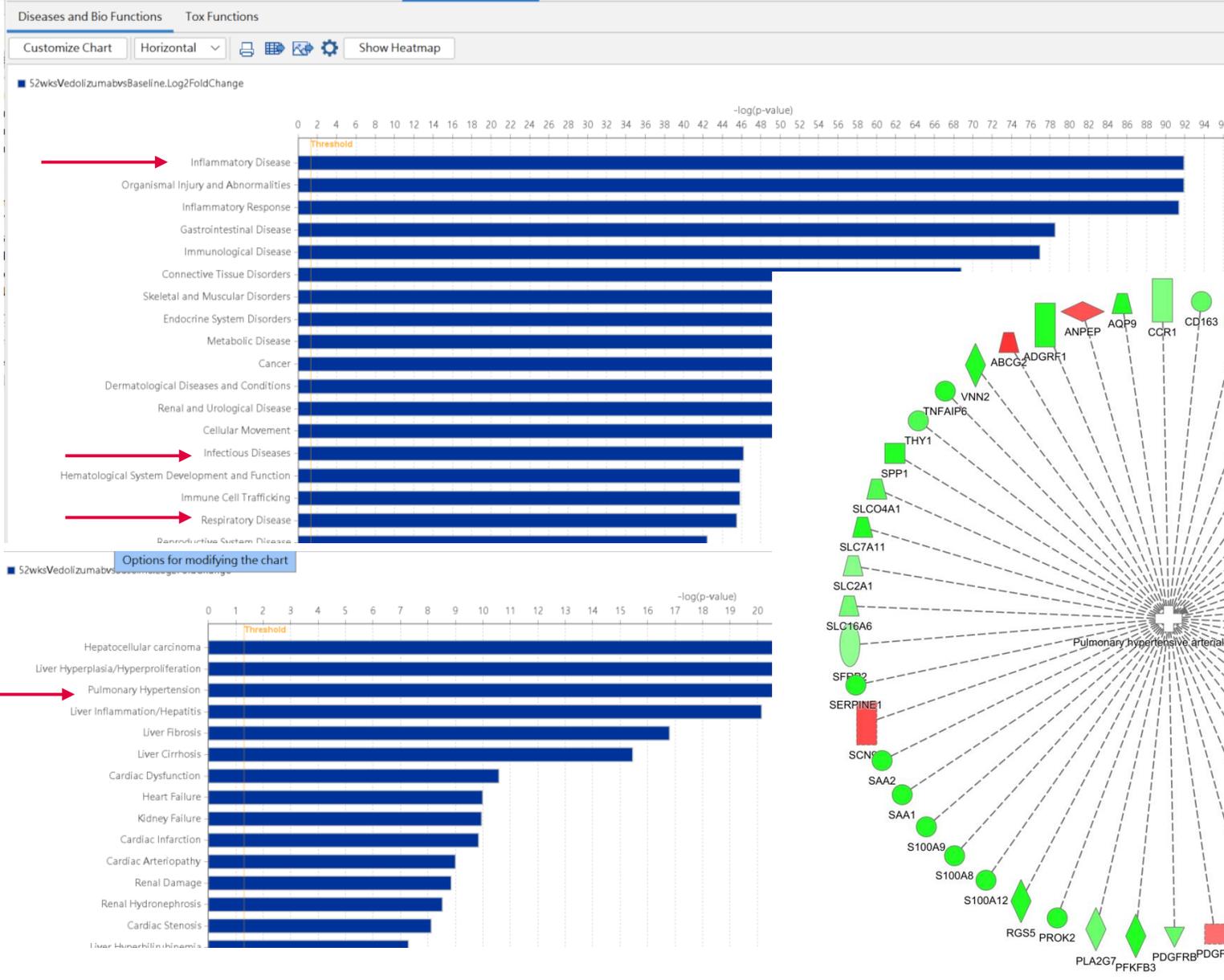
Analysis-Ready (3458) Mapped IDs (20218) Unmapped IDs (1344) All IDs (21562) Metadata

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

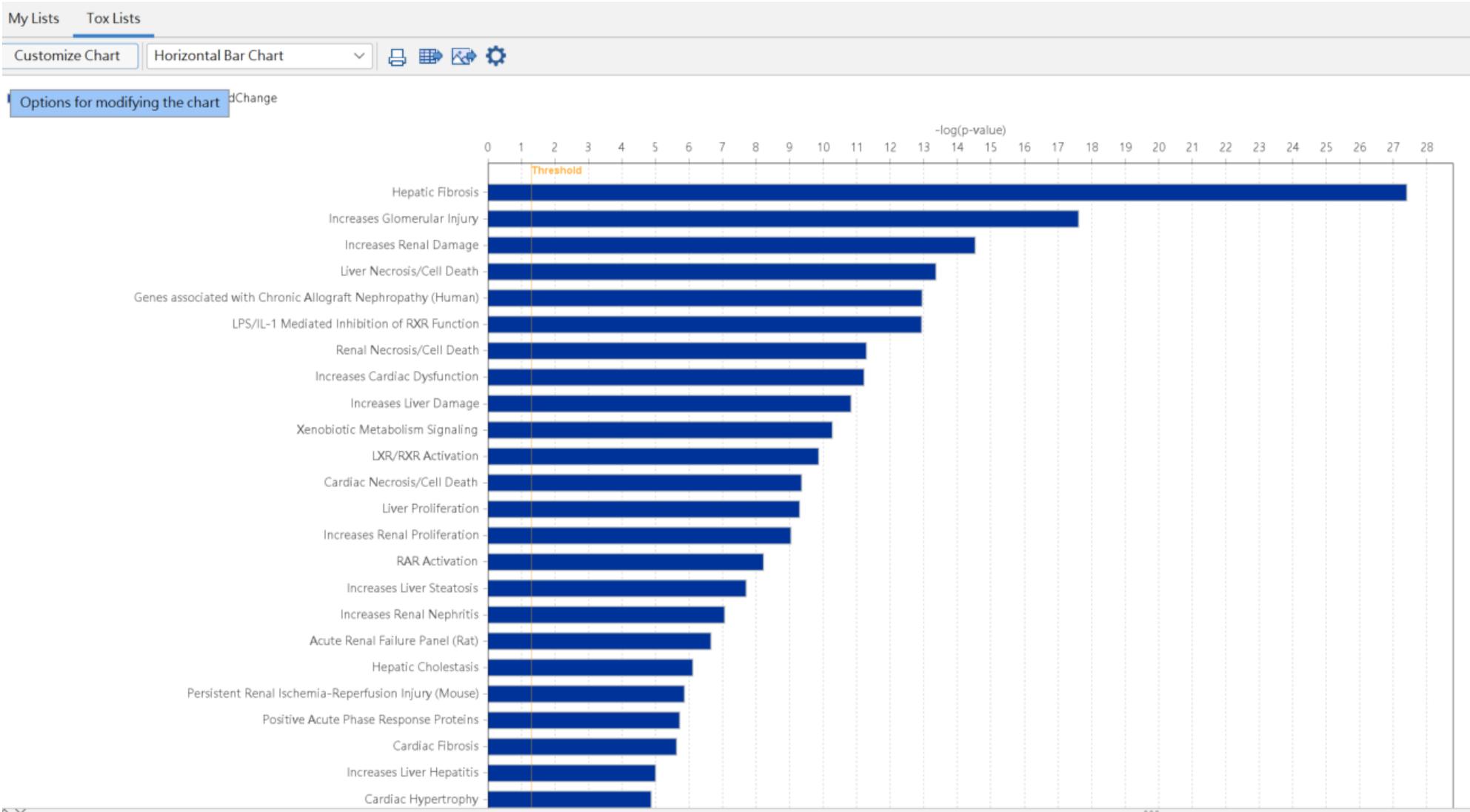
Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
-1.543	4.72E-09	A1CF		A1CF	APOBEC1 complementation factor	Nucleus	other	
1.069	1.00E-04	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	other	
0.628	3.96E-07	A4GALT		A4GALT	alpha 1,4-galactosyltransferase (PIPK blood 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 MH038 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/tretinoin/valproic acid, valproic acid, ...

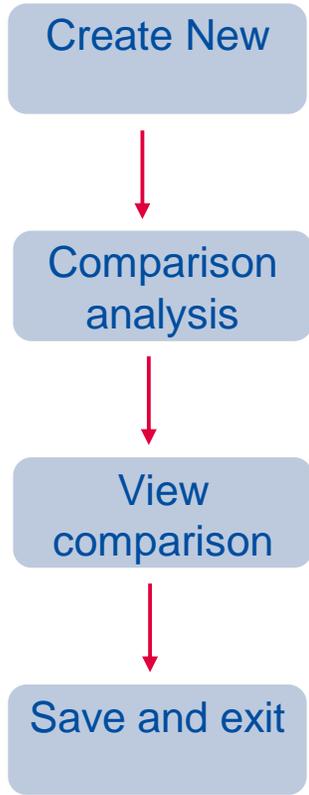
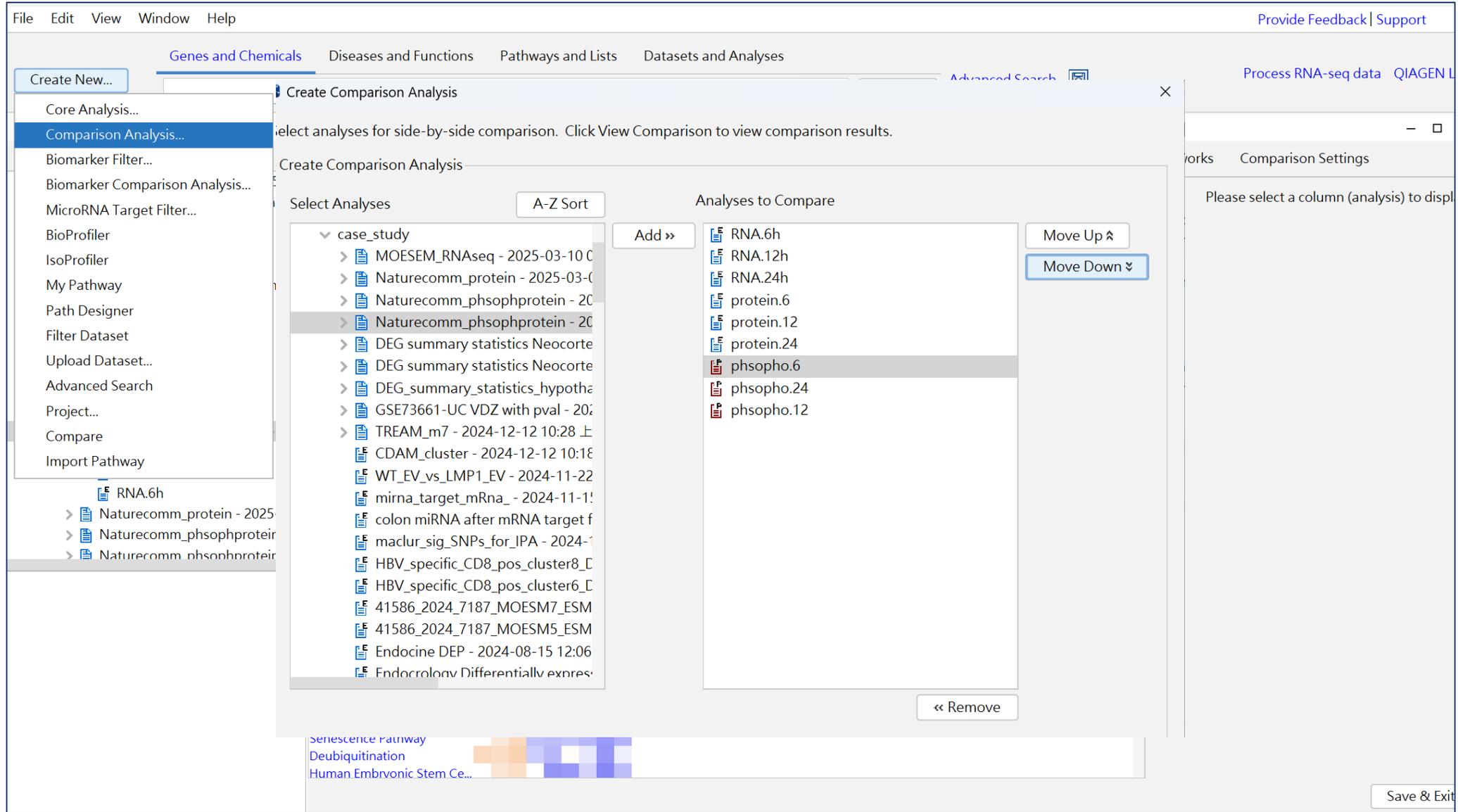
0 / 3458

Flags: **Real** Four molecules (Gene/Protein/Chemical Identifier) that meet the user-defined cutoff and map to the Global Molecule 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... 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

- case_study
 - MOESEM_RNAseq - 2025-03-10 C
 - Naturecomm_protein - 2025-03-10 C
 - Naturecomm_phosphoprotein - 2025-03-10 C
 - Naturecomm_phosphoprotein - 2025-03-10 C
 - DEG summary statistics Neocort
 - DEG summary statistics Neocort
 - DEG_summary_statistics_hypotha
 - GSE73661-UC VDZ with pval - 2025-03-10 C
 - 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_ - 2024-11-11
 - colon miRNA after mRNA target f
 - maclur_sig_SNPs_for_IPA - 2024-11-11
 - 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

Analyses to Compare

- RNA.6h
- RNA.12h
- RNA.24h
- protein.6
- protein.12
- protein.24
- phospho.6
- phospho.24
- phospho.12

Move Up ▲ Move Down ▼

<< Remove

Save & Exit

serenescence pathway
 Deubiquitination
 Human Embryonic Stem Ce...

Canonical pathway comparison

Settings/Legend

Filter

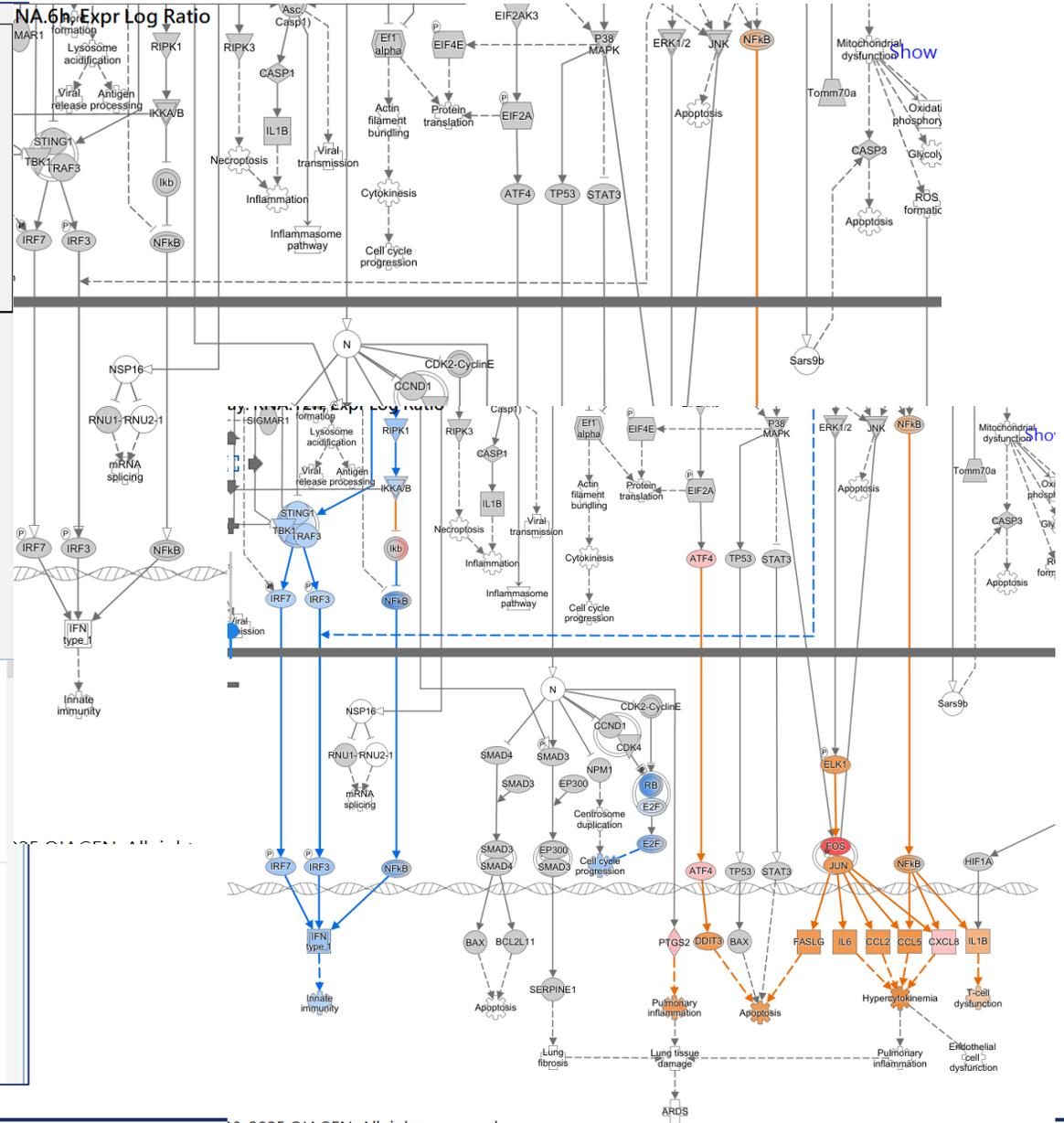
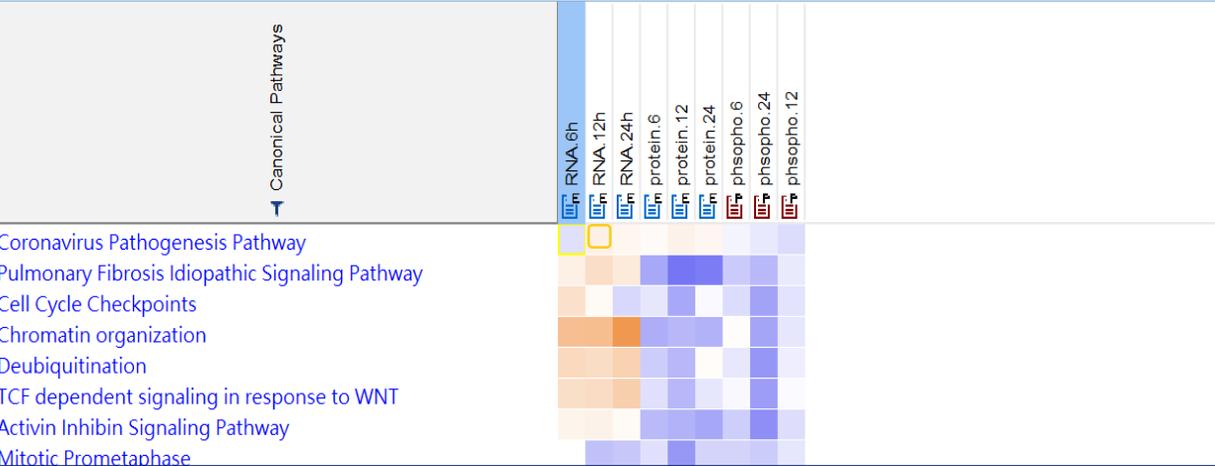
Measurement: Activation z-score -8.216 12.926

Sort Method: Trend + Score Visualize: z-score

Insignificance Threshold: (absolute value)

Trend Controls

View Report Open Network Gene Heatmap Expand Header



Filtered canonical pathway

Comparison Analysis - Mpox_comparison

Canonical Pathways | Upstream Analysis | Diseases & Functions | Regulator Effects | Lists | My Pathways | Molec...

Settings/Legend

Filter

Measurement: Activation z-score -8.216  12.926

Sort Method: Trend + Score | Visualize: z-score

Insignificance Threshold: (absolute value)

Trend Controls

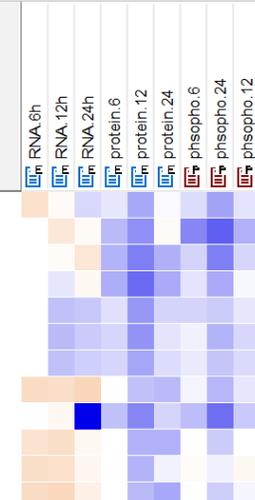


View Report | Open Network | Gene Heatmap | Expand Header

Canonical Pathways

- Cell Cycle Checkpoints
- Processing of Capped Intron-Containing Pre-mRNA
- Class I MHC mediated antigen processing and presentation
- RHO GTPase cycle
- Mitotic Prometaphase
- Mitotic Metaphase and Anaphase
- RHO GTPases Activate Formins
- ESR-mediated signaling
- Neutrophil degranulation
- E3 ubiquitin ligases ubiquitinate target proteins
- DNA Replication Pre-Initiation
- Amyloid fiber formation

RNA 6h, RNA 12h, RNA 24h, protein 6, protein 12, protein 24, phospho.6, phospho.24, phospho.12



We also can re-sort pathway

Filter

Pathways

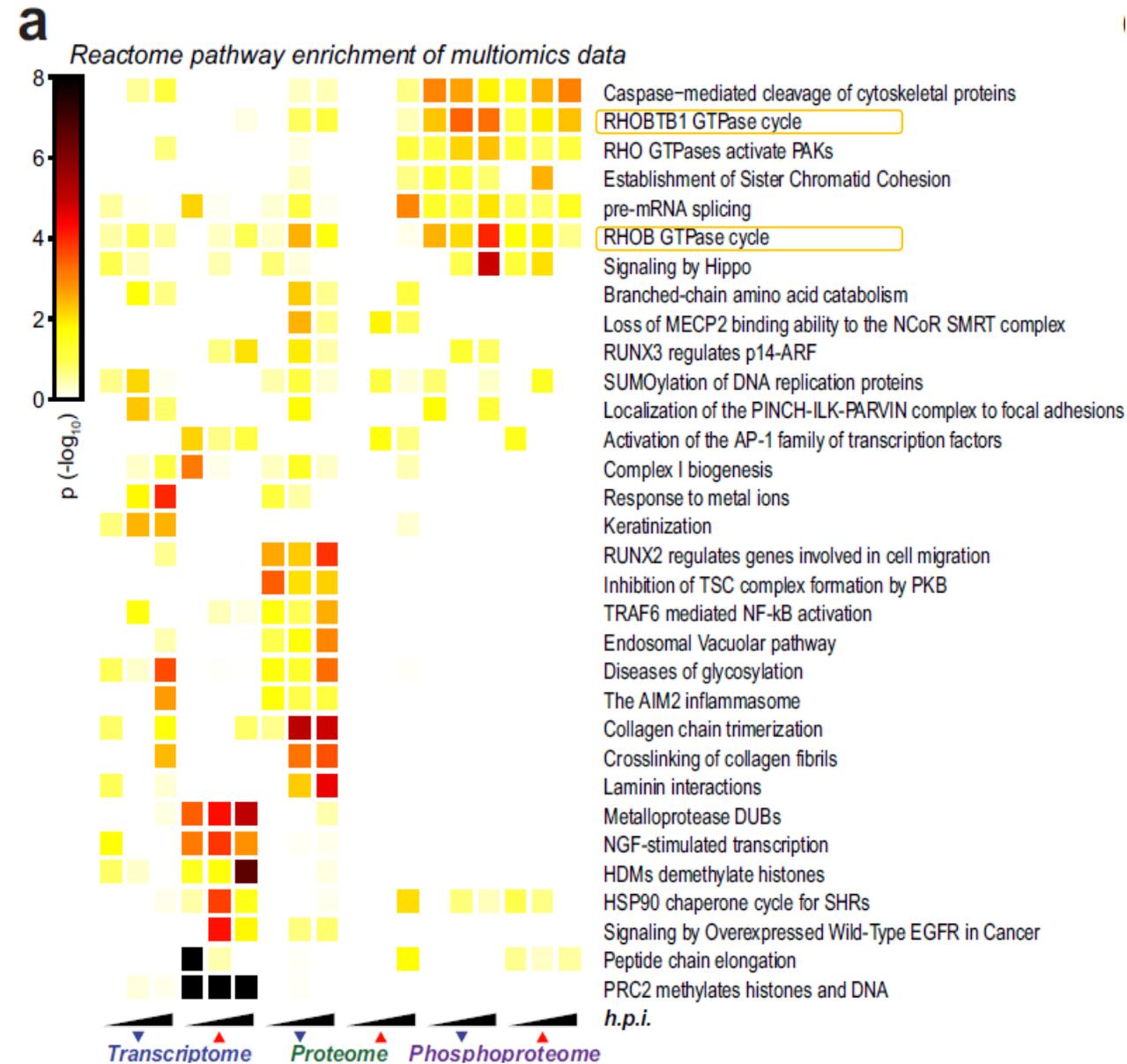
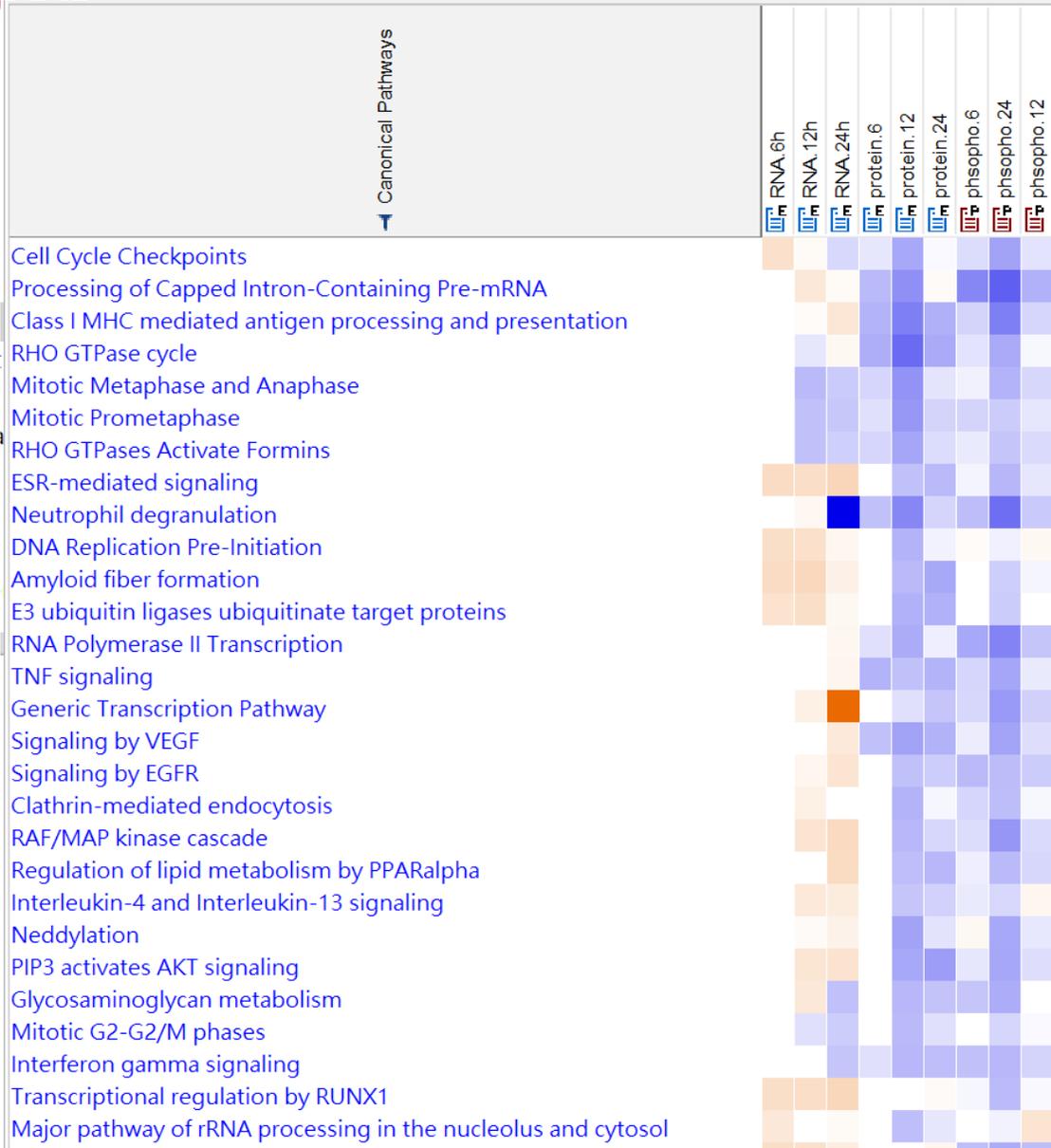
Tree View List View

- Ingenuity Canonical Pathways
- Metabolic Pathways
- Reactome Pathways
- Signaling Pathways

Score Filter

p-value Cutoff:	1.3	(log10)
z-score Cutoff:	<input type="text"/>	(absolute value)
B-H p-value Cutoff:	<input type="text"/>	(log10)

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





Upstream regulator comparison

Comparison Analysis - Mpox_comparison

Canonical Pathways Upstream Analysis Diseases & Fun

Upstream Regulators Causal Networks

Table Heatmap

Settings/Legend

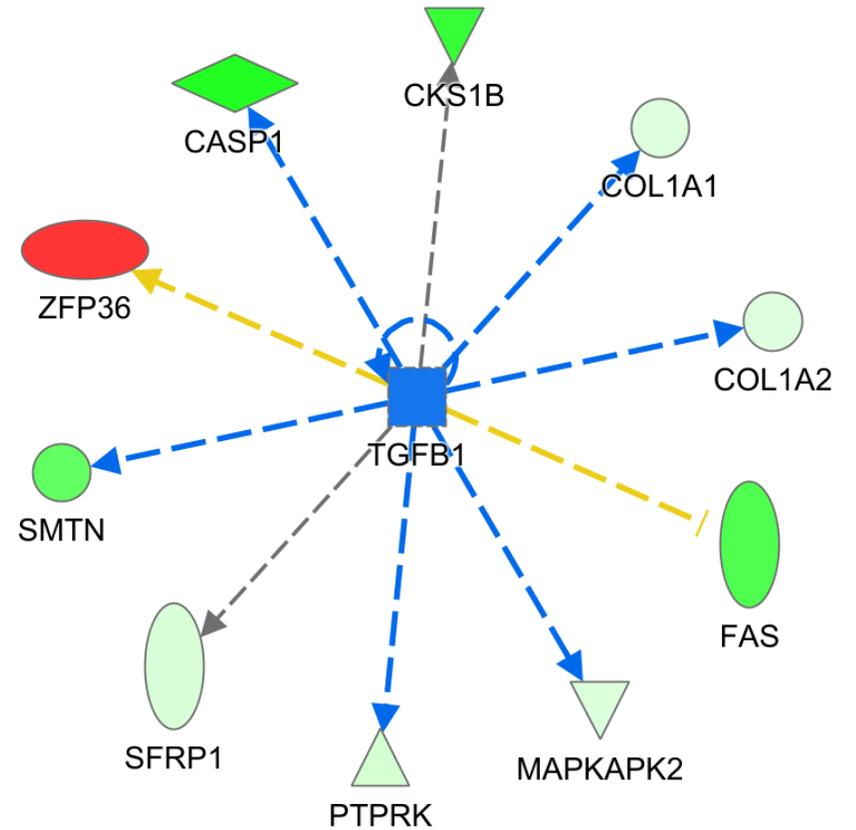
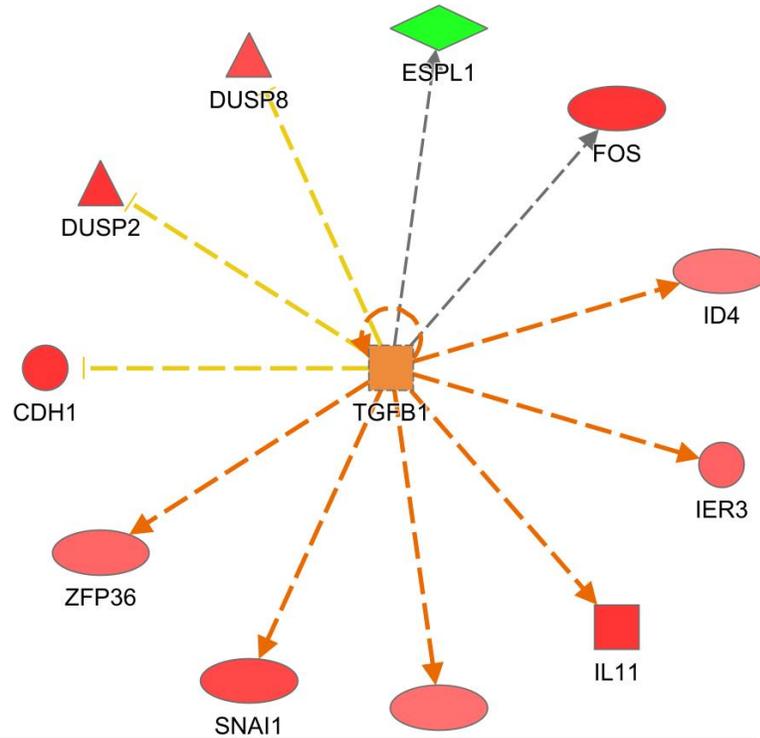
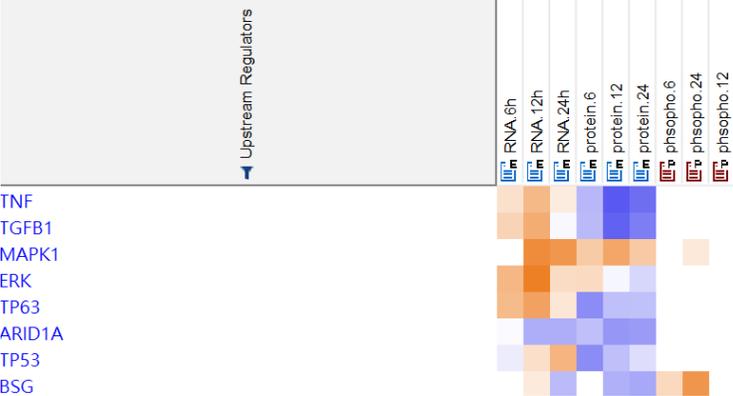
Filter

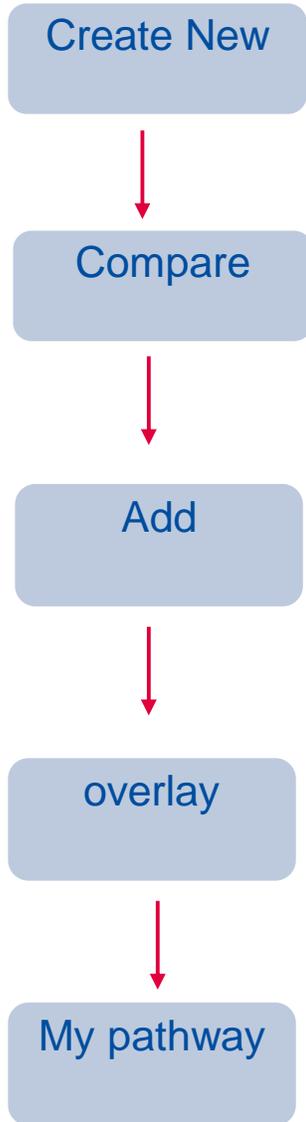
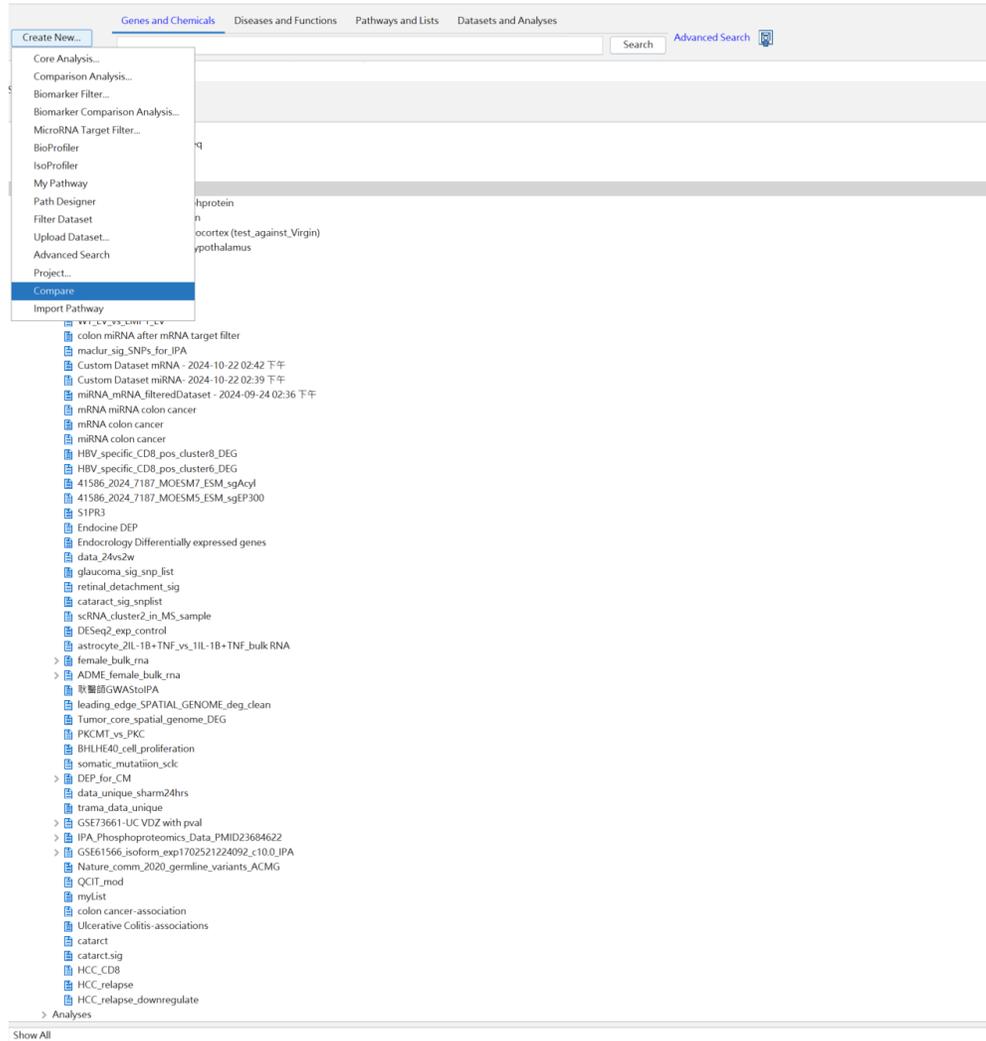
Measurement: Activation z-score -6.447

Sort Method: Trend + Score Visualize: z-score

Insignificance Threshold: (absolute value)

Open Network Gene Heatmap Expand Header



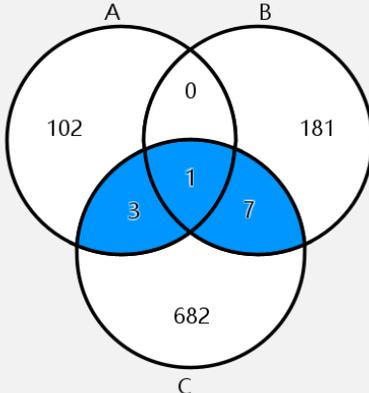
The screenshot shows the 'Create New...' dropdown menu with the following items:

- 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

Calculate intersections 

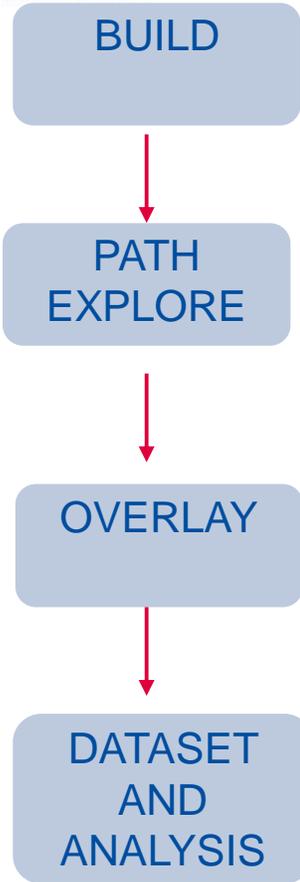
Click in the Venn diagram below to compare different sets. Keep the Ctrl key down to select multiple areas.

- A RNA.6h (Analysis)
- B protein.6 (Analysis)
- C phsopho.6 (Phospho Analysis)



Entities Comparison Results (11)

CRKL
CYBA
GPS2
H2BC14
LEO1
LFNG
PEAK1
SF1
TNP1
ULK1
ZFP36



Matching molecules

Symbol	Display name	Index	Measurement		
			1	2	3 RNA.6h
AKT1	AKT parent node	Expr Log Ratio		0.200	↑
AKT2	AKT parent node	Expr Log Ratio		-0.176	↓
AKT3	AKT parent node	Expr Log Ratio		0.141	↑
CBL	CBL	Expr Log Ratio		-0.023	↓
CD274	CD274	Expr Log Ratio		-0.038	↓
CDC42	CDC42	Expr Log Ratio		0.075	↑
CRKL	CRKL	Expr Log Ratio		-0.171	↓
CTNNB1	CTNNB1	Expr Log Ratio		-0.053	↓
CYBA	CYBA	Expr Log Ratio		0.101	↑
EGFR	EGFR	Expr Log Ratio		0.032	↑
GPS2	GPS2	Expr Log Ratio			

Show node charts for multi overlay: Always For rows selected above Don't show

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Prediction Legend

more extreme in dataset

- Increased measurement (red circle)
- Decreased measurement (green circle)

more confidence

- Predicted activation (orange circle)
- Predicted inhibition (blue circle)

Glow Indicates activity when opposite of measurement

- Red glow
- Green glow

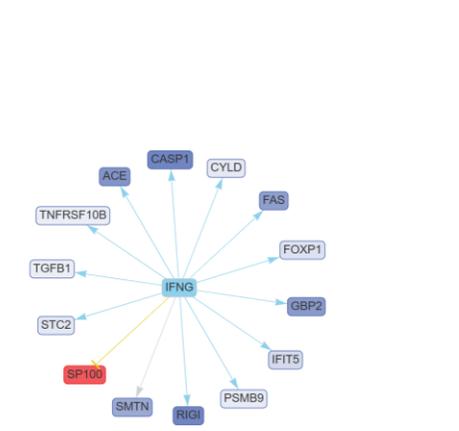
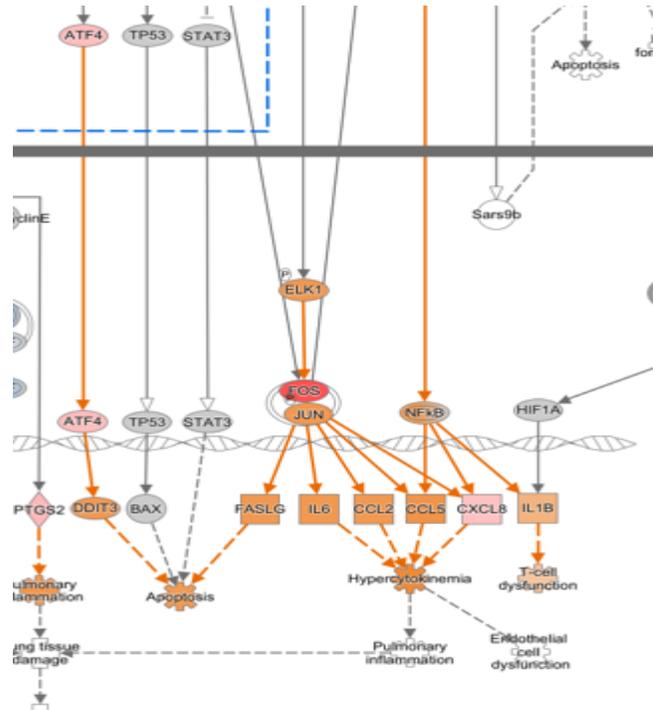
Predicted Relationships

- Leads to activation (orange line)
- Leads to inhibition (blue line)
- Findings inconsistent with state of downstream molecule (yellow line)
- Effect not predicted (grey line)

Dashed lines = indirect relationship
 Solid lines = direct relationship

Summary: Evaluating your 'omics data using IPA

	A	B	C
1	geneid	UCvsNormal.Log2FoldChange	UCvsNormal.pval
2	DDX11L1	-0.1067	0.2878
3	WASH7P	-0.1883	0.0097
4	FAM138F	-0.0761	0.4699
5	OR4F5	0.1474	0.5311
6	LOC729737	0.4789	0.0017
7	LOC100133331	0.4789	0.0017
8	LOC100132062	0.4789	0.0017
9	OR4F29	0.2495	0.2389
10	JA429831	0.1215	0.3338
11	JB137814	-0.674	1.6381E-06
12	M37726	-1.0551	0.0000576
13	LINC00115	-0.1666	0.021
14	LOC643837	0.1025	0.3021
15	FAM41C	0.2098	0.2554
16	SAMD11	-0.0552	0.4088
17	NOC2L	0.3408	1.2575E-06
18	KLHL17	0.1497	0.0082
19	PLEKHN1	0.1463	0.0088
20	C1orf170	-0.1649	0.0085
1546	TTY13	-0.3543	0.0003
1547	RBMY1E	-0.3167	0.016
1548	PRY2	-0.1792	0.0084
1549	TTY6	-0.2051	0.0005
1550	RBMY1J	-0.3167	0.016
1551	TTY5	-0.105	0.0743
1552	RBMY2FP	-0.5248	0.0939
1553	RBMY1F	-0.5248	0.0939
1554	PRY	-0.1792	0.0084
1555	BPY2	-0.1446	0.0562
1556	DAZ1	0.0734	0.5811
1557	DAZ4	0.0734	0.5811
1558	DAZ2	0.0734	0.5811
1559	DAZ3	0.0734	0.5811
1560	CDY1	-0.0319	0.6541
1561	CSPG4P1Y	-0.0678	0.3043
1562	GOLGA2P2Y	-0.0872	0.1077
1563	U6_83	0.21	0.1



IFNG network

AI suggests the following synopsis of this network:

Top Biological Themes Depicted by the Network

- Immune Response Regulation**
- Apoptosis**
- Protein Degradation**
- Inflammation**

PSMB9 (Proteasome Subunit Beta 9) is part of the immunoproteasome, which is crucial for antigen processing and presentation. The connection between IFNG and PSMB9 highlights the importance of IFNG in modulating protein degradation pathways that are essential for immune surveillance.



- Canonical Pathways
- Cell Cycle Checkpoints
 - Processing of Capped Intron-Containing Pre-mRNA
 - Class I MHC mediated antigen processing and presentation
 - RHO GTPase cycle
 - Mitotic Metaphase and Anaphase
 - Mitotic Prometaphase
 - RHO GTPases Activate Formins
 - ESR-mediated signaling
 - Neutrophil degranulation
 - DNA Replication Pre-Initiation
 - Amyloid fiber formation
 - F3 ubiquitin ligases ubiquitinate target proteins

- 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