QIAGEN IPA
系統生物學分析軟體

IPA以數據演算及人工閱讀的資料庫文獻，
提供您快速的在數千萬筆的研究分析資料中，
找到最關鍵的生物途徑與分子間調控關係。

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Agenda

1. Introduction to IPA
2. Learn how to search database in IPA
3. Draw the relationship between 3 nodes (Gene/Disease/Pathway)
4. Upload dataset to IPA and create core analysis
5. Realize the meaning of the IPA analysis result

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Sample to Insight Workflow

Sample

Insight

Sample Prep → Assay Data → Sequence-Level Statistics → Biology of Interest (Genes, Variants, etc) → Comparative Statistical Analysis → Biological Interpretation

Upstream Analysis | "primary" | "secondary" | "tertiary"

QIAGEN

QIAcube
GeneRead™ Panel

Sequencer

CLC bio A QIAGEN Company

Genomics
Workbench

POWERED BY INGENUITY

Variant/Pathway
Analysis

Streamline Integration and Workflow Embedding

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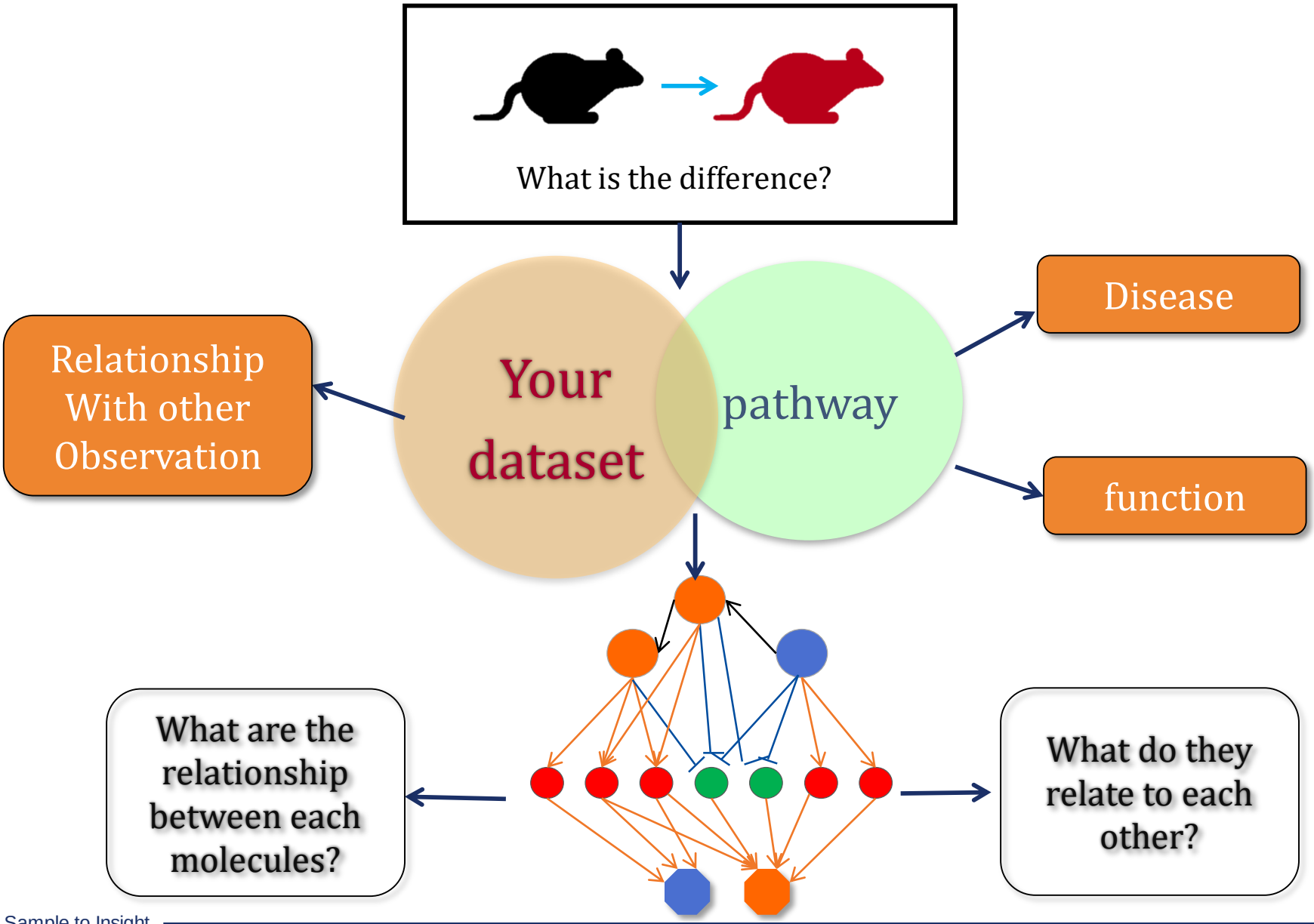
Why are we using IPA?



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IPA Supported

IPA orthologous (25 species):

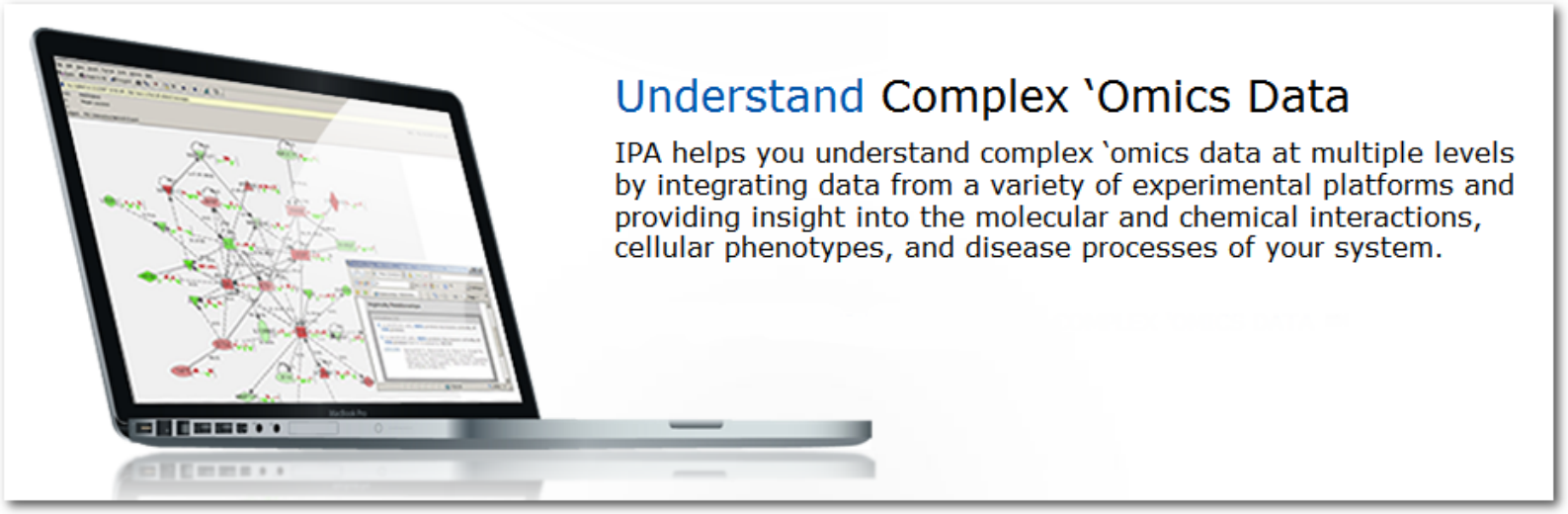
- Arabidopsis thaliana
- Bos taurus (bovine)
- Caenorhabditis elegans
- Gallus gallus (chicken)
- Pan troglodytes (chimpanzee)
- Danio rerio (zebrafish)
- Canis lupus familiaris (canine)
- Drosophila melanogaster
- Macaca mulatta (Rhesus Monkey)
- Saccharomyces cerevisiae
- Schizosaccharomyces pombe

IPA supported platform :

- **Gene expression:**
  - qPCR analysis
  - Microarray
  - RNA-Seq (NGS)
  - microRNA
  - mRNA
- **Proteomics**
  - PhosphoProteomics
- **Metabolomics**

IPA application:

- Biomarker finding
- Toxicity functions
- Diseases regulation



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Supported Identifiers for Data Upload

Get more complete mapping during dataset upload!

Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2020/10)	GenPept	Ensembl (101)	miRBase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (239)	International Protein Index (IPI)	RefSeq (human、mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human (HUGO/ HGNC, EG)	UniProt/ Swiss-Prot Accession (2020_03)	UCSC (hg18)			KEGG
Codelink	Symbol- mouse (EG)		UCSC (hg19)			PubChem CID
Illumina	Symbol- rat (EG)		UCSC (hg38)			
Ingenuity	GI Number					
	UniGene					

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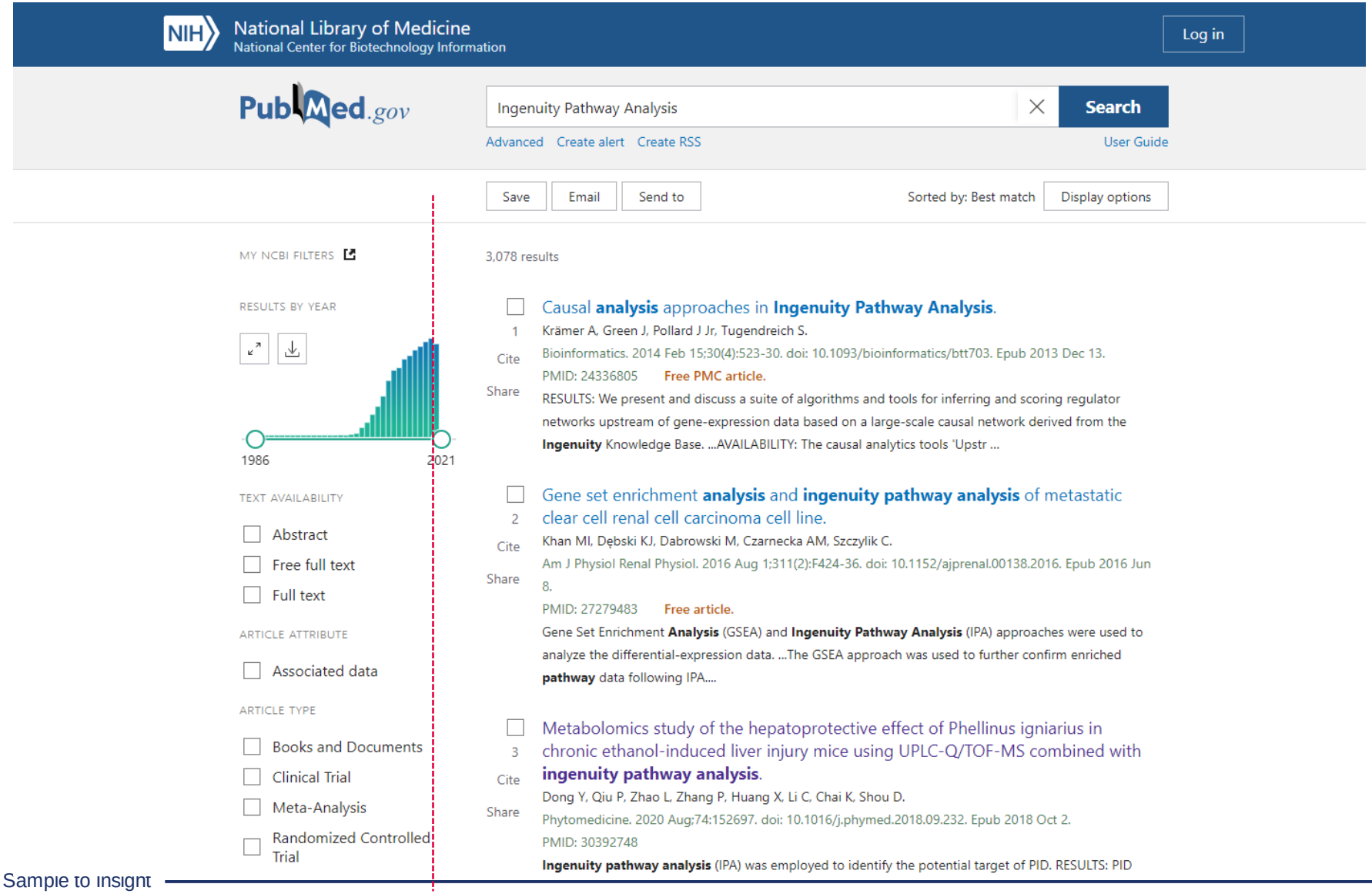
Peer-reviewed publications citing Ingenuity apps

>53,800 publications that used IPA and growing! (Search Google Scholar for publications that cite IPA.)



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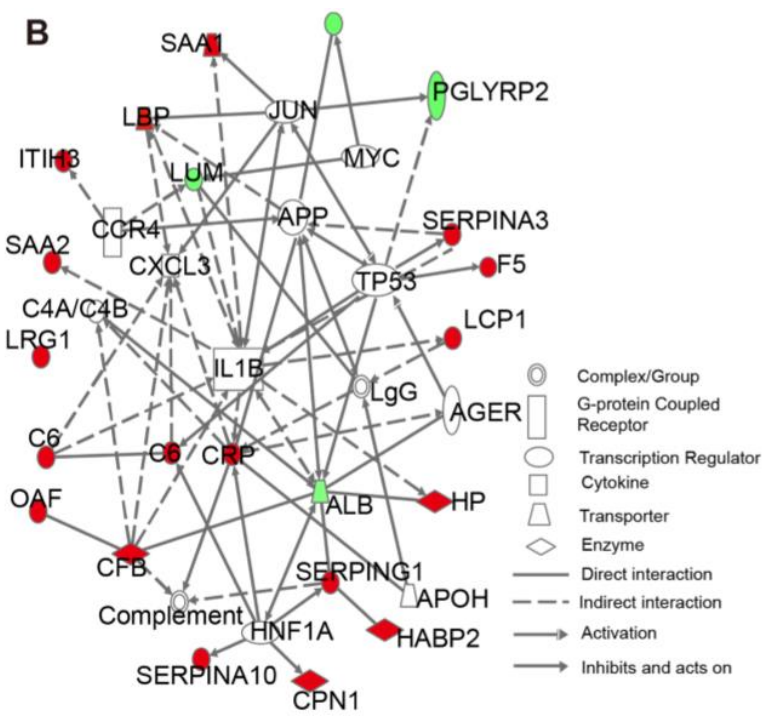
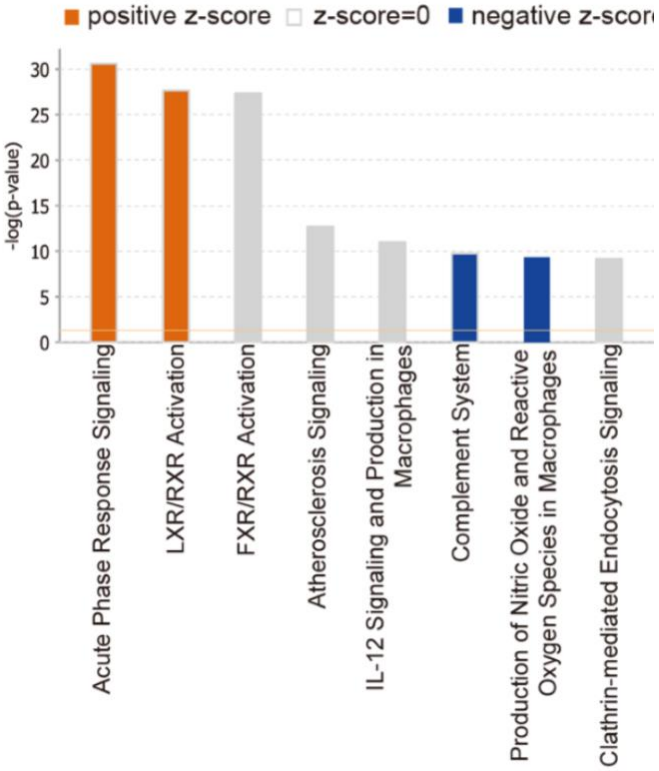
IPA was cited in paper to study severe COVID-19

Here is one latest paper submitted to medRxiv using IPA to identify potential protein and metabolite biomarkers in severe COVID-19 disease. In this study, IPA was used to identify most significantly relevant pathways and build regulation networks. It is welcome to share with your customers or distributor, and please let me know if you need further help.





https://www.medrxiv.org/content/10.1101/2020.04.07.20054585v1

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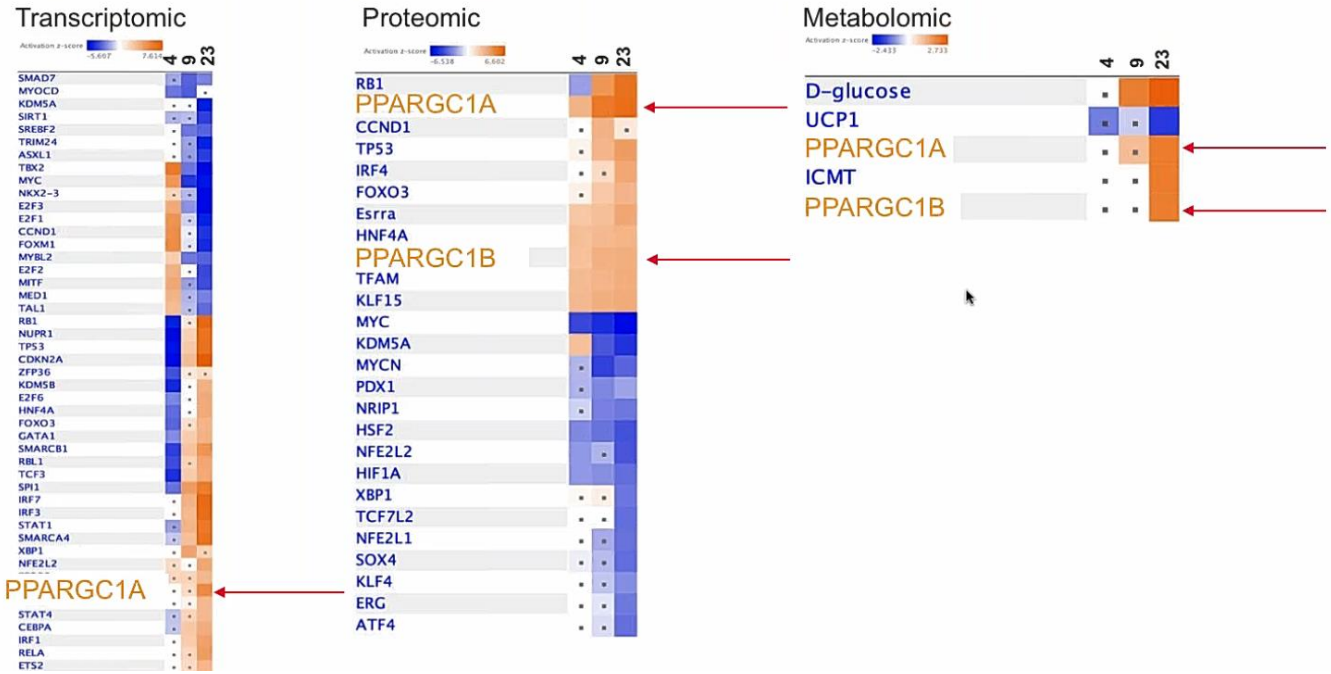
Multi-Omics Analysis using IPA

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

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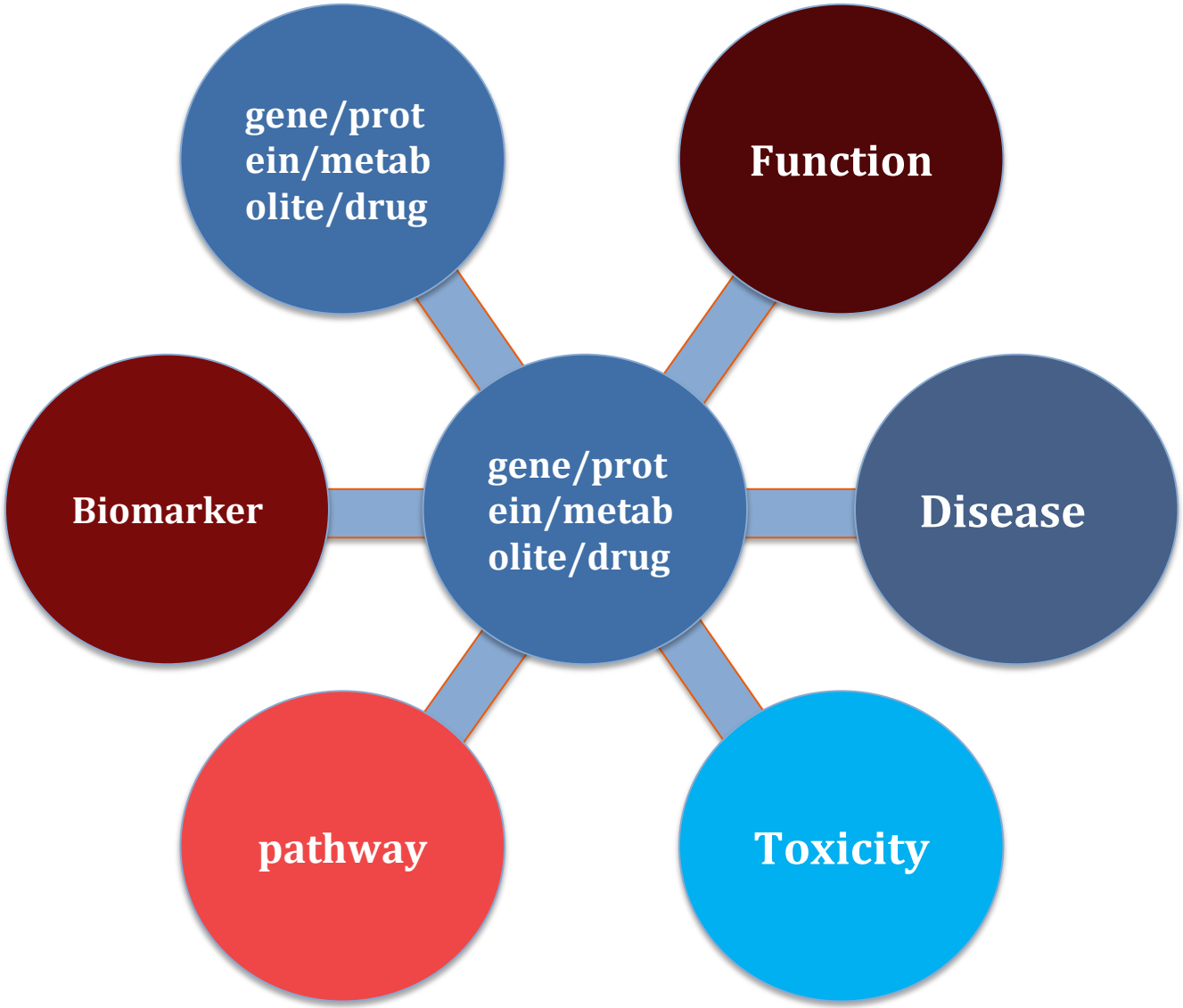
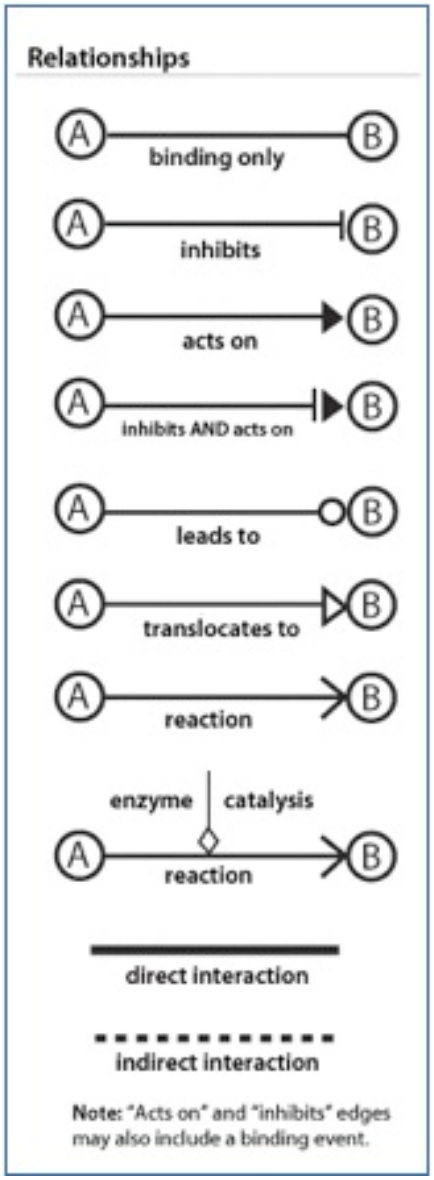
Using IPA to Discover Relationships in Experimental Data





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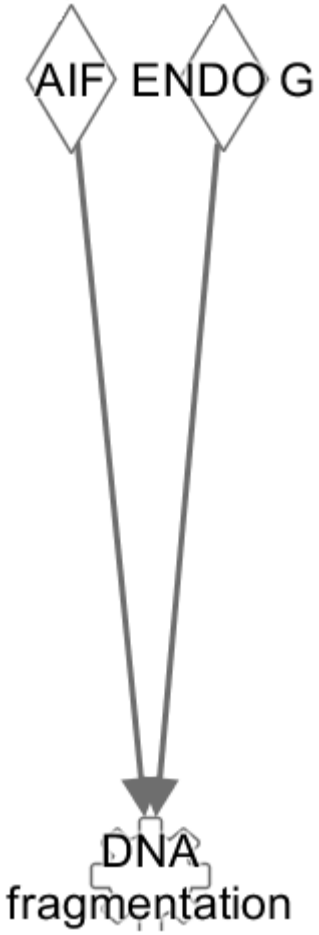
How IPA content is different: context and direction of effect



IPA Relationships: ENDO G|DNA fragmentation

Review the information that supports the gene-to-function relationship. Click the plus icon to view the reference infor

EndNote ▼ EXPORT REFERENCES

Ingenuity Relationships

causation [16]

Translocation of ENDONUCLEASE G [ENDOG] protein to nuclei from mammal cultured hepatocytes **increases**

18691057 Gómez-Lechón MJ, O'Connor JE, Lahoz A, Castell JV, Donato MT. Identification of apo 2008;15(20):2071-85.

Source: Ingenuity Expert Findings

Rat Endog protein in a cell free system **increases fragmentation of** nucleosomal **Deoxyribonucleic Acid** in nuc

Experiment Type: agarose gel electrophoresis

16407272 Ishihara Y, Shimamoto N. Involvement of endonuclease G in nucleosomal DNA fragm 10;281(10):6726-33. Epub 2006 Jan 4.

Source: Ingenuity Expert Findings

In cytoplasm, **Endo G protein increases fragmentation of DNA**.

15182854 Lemarié A, Lagadic-Gossmann D, Morzadec C, Allain N, Fardel O, Vernhet L. Cadmiur oxidative stress-related impairment of mitochondria and relocation of endonuclease C

Source: Ingenuity Expert Findings

ENDOG protein in a cell-free system **increases fragmentation of DNA** in nuclei.

15077142 Cregan SP, Dawson VL, Slack RS. Role of AIF in caspase-dependent and caspase-ind

Source: Ingenuity Expert Findings

zVAD causes little or no change in fragmentation of DNA that is mediated by **ENDOG protein**.

15077142 Cregan SP, Dawson VL, Slack RS. Role of AIF in caspase-dependent and caspase-ind

Source: Ingenuity Expert Findings

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Third Party Database

- **Synonyms, Protein Family, Domains**
  - GO, Entrez Gene, Pfam
- **Tissue and Biofluid Expression & Location**
  - GNF, Plasma Proteome
- **Molecular Interactions**
  - BIND, DIP, MIPS, IntAct, Biogrid, MINT, Cognia, etc.
- **miRNA/mRNA target databases**
  - TarBase, TargetScan, miRecords
- **Gene to Disease Associations**
  - OMIM, GWAS databases
- **Metabolomics**
  - HumanCyc
- **Clinical Trial information**
  - ClinicalTrials.gov

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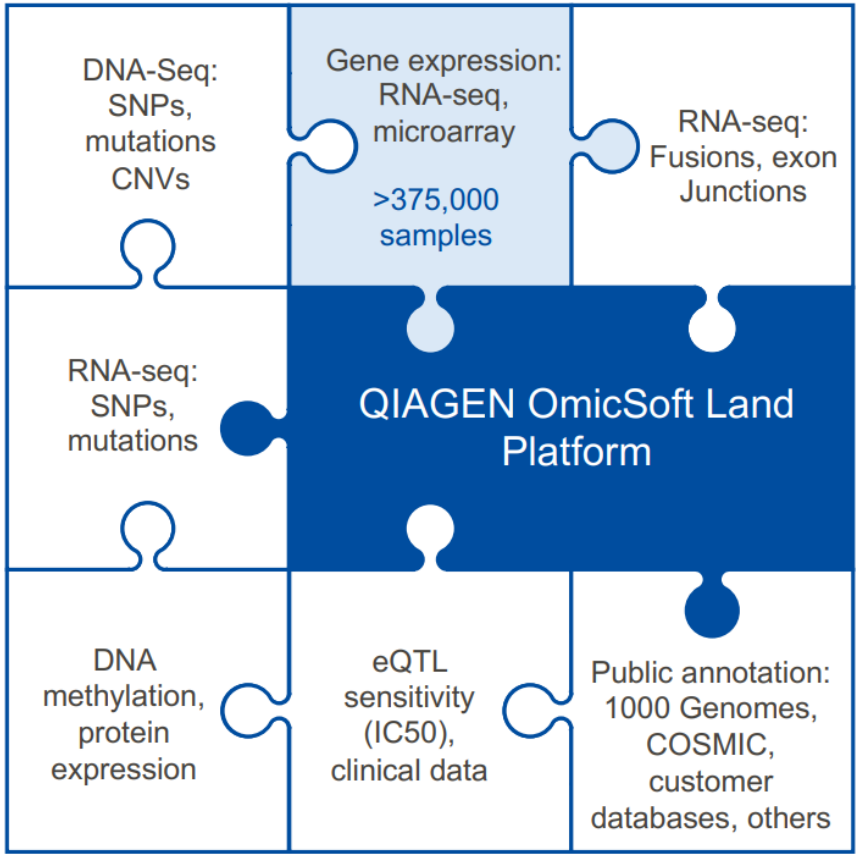
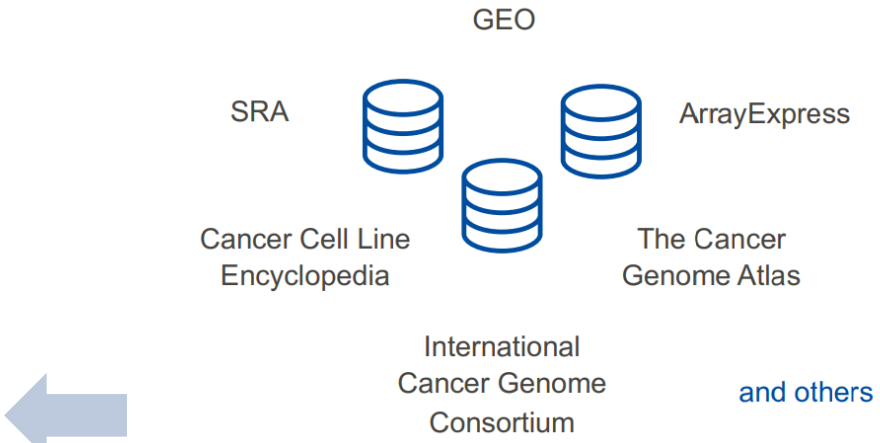
OmicSoft Lands and findings in QIAGEN IPA

- More than **12 million** findings from literature source or database.
- More than **124,927** comparison datasets from QIAGEN OmicSoft Lands.

Lands provide expression data to QIAGEN IPA





Land	Repository	Datasets Q3 2022	Datasets Q4 2022	Increase
DiseaseLand	HumanDisease	31,041	32,092	1,051
	MouseDisease	24,411	24,506	95
	RatDisease	7,900	7,900	
	LINCS	28,234	28,234	
OncoLand	OncoHuman (Formerly OncoGEO)	13,360	14,131	771
	OncoMouse	1,054	1,054	
	TCGA	4,438	4,438	
	MetastaticCancer	81	81	
	Hematology	4,267	4,267	
	Pediatrics	444	444	
	ENCODE RNA Binding	486	486	
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	2056	2056	
	SingleCellHumanUmiLite	603	603	
	SingleCellHumanHCL	1,476	1,476	
	SingleCellMouse	81	81	
	SingleCellMouseUmi	1,457	1,457	
	SingleCellMouseUmiLite	115	115	
Normal Cells and Tissues	Human Tissues (GTEx)	52	1,312	1,260

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What's New in the IPA Fall Release (September 2022)

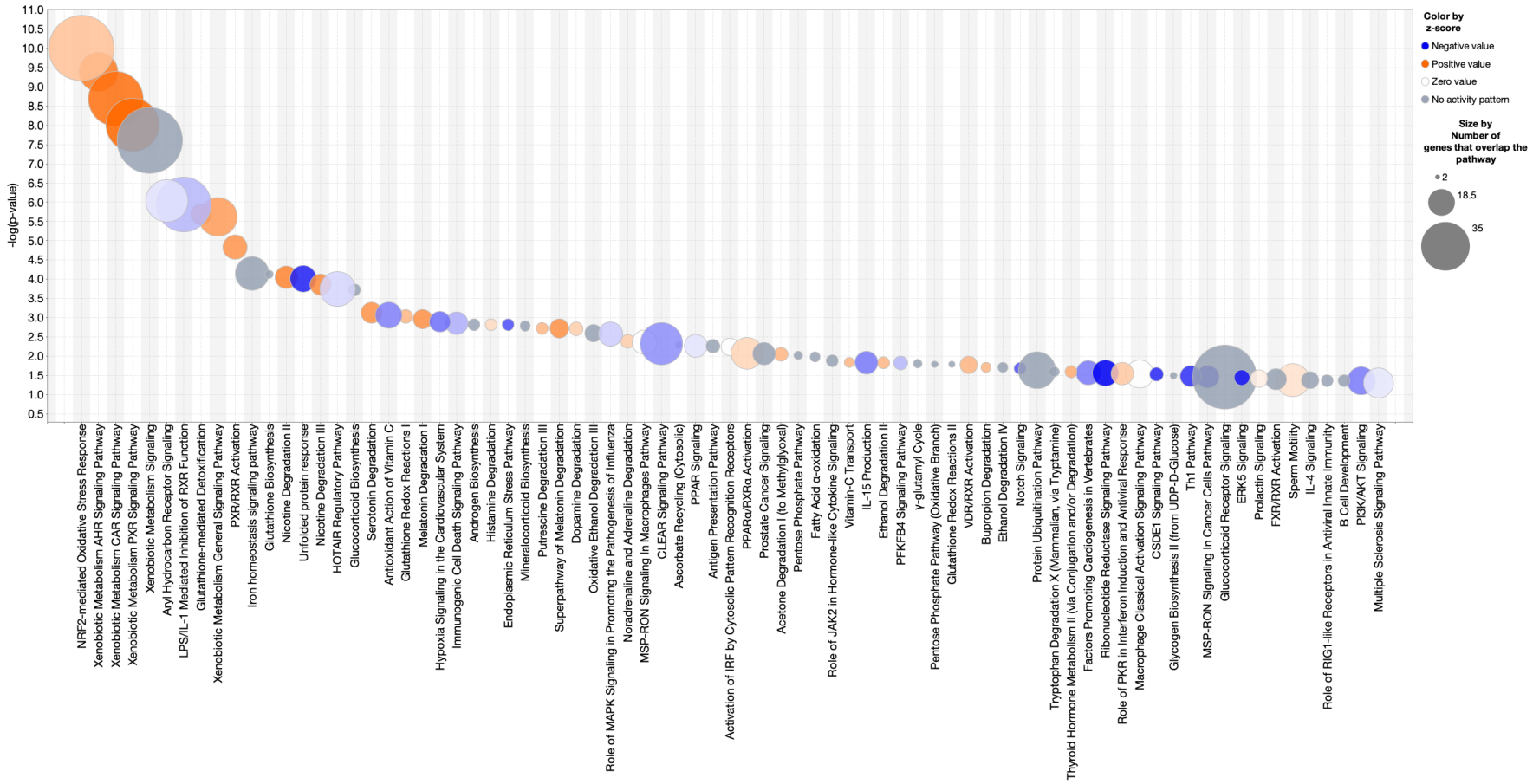

Figure 1. Nrf2-activator Canonical Pathway scores plotted as pathway name vs. significance.

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What's New in the IPA Fall Release (September 2022)

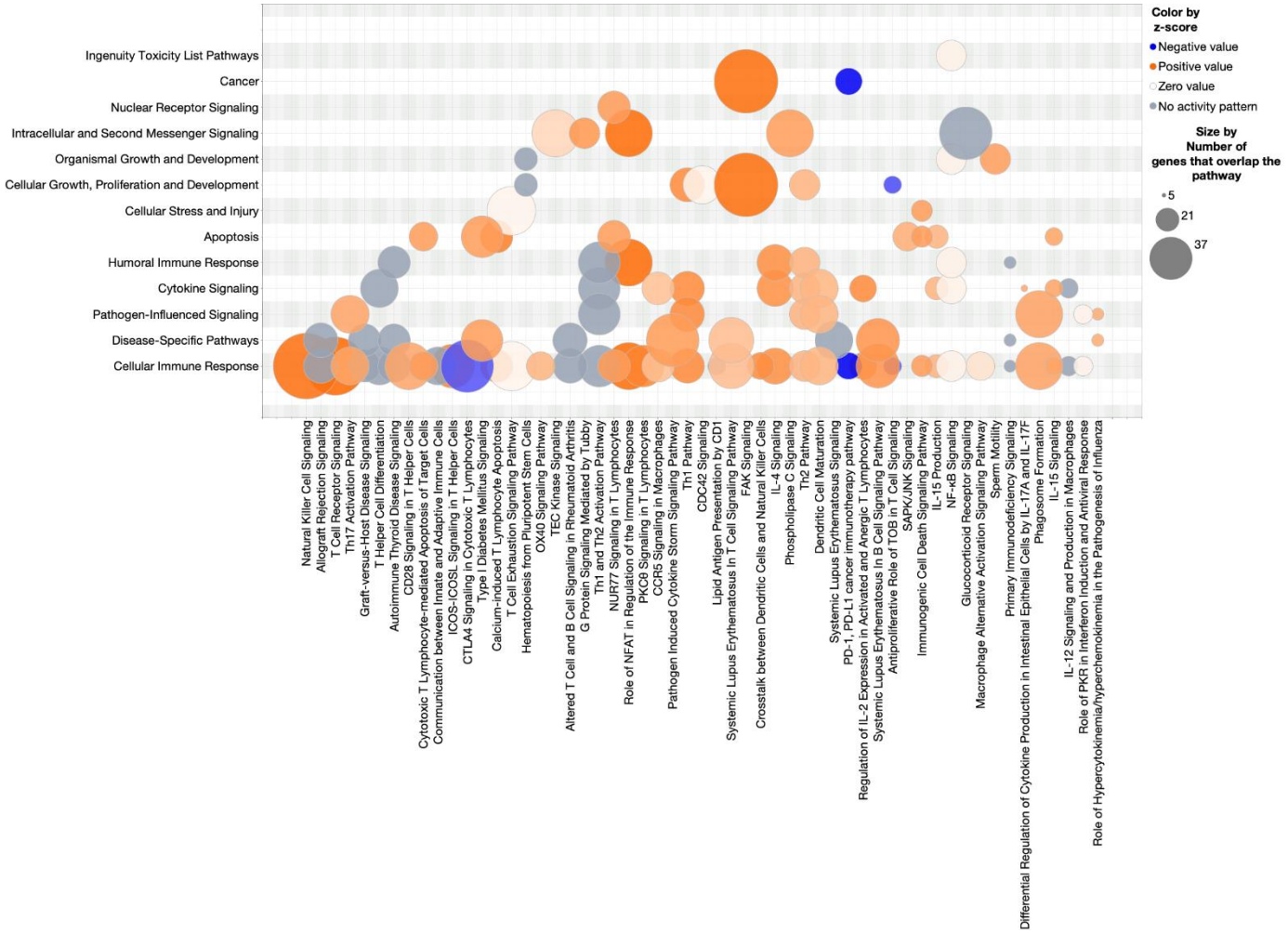

Figure 2. Canonical Pathway scores from single-cell data plotted as pathway name versus pathway category.

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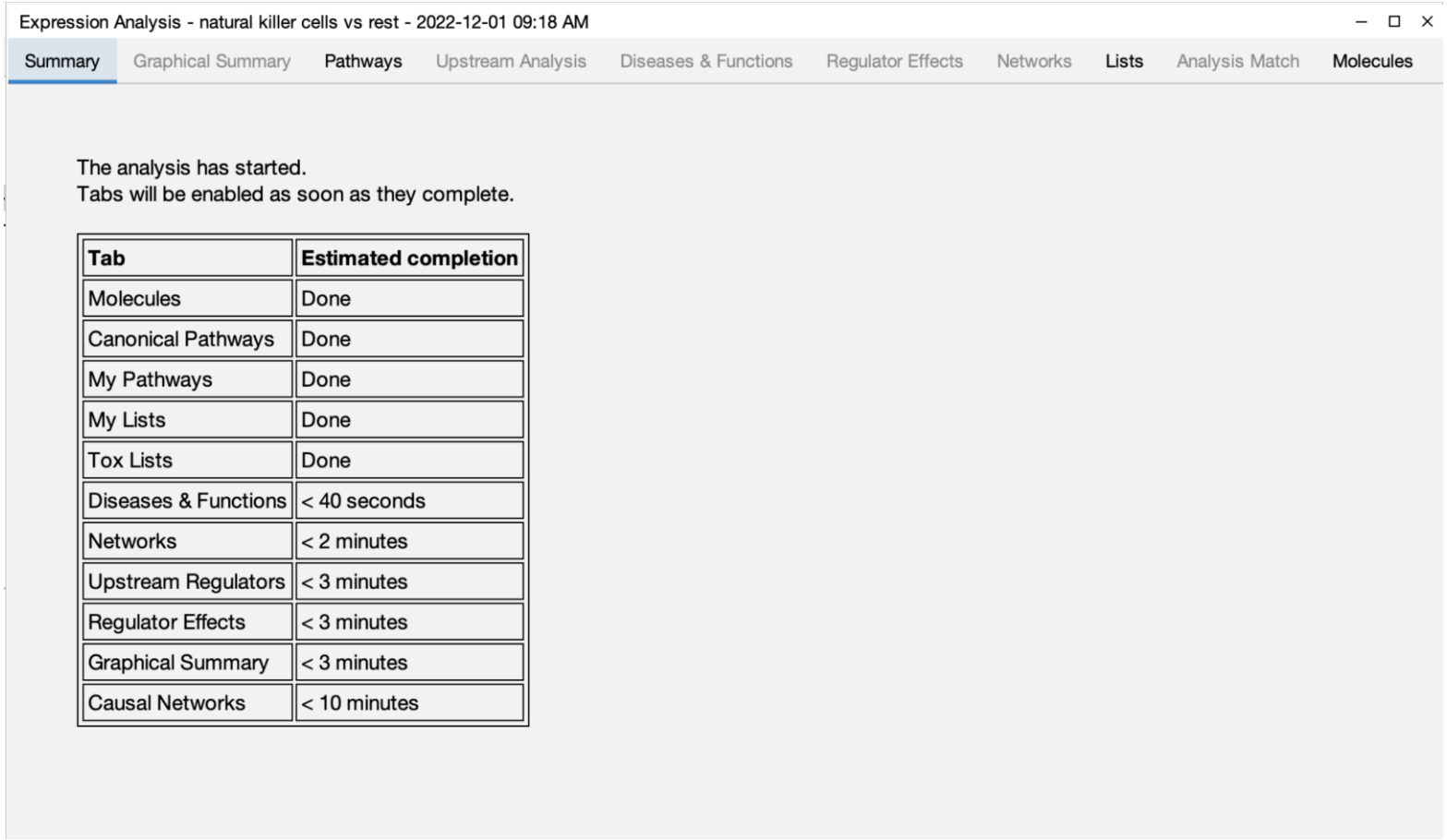
What's New in the IPA Winter Release (December 2022)



Tab	Estimated completion
Molecules	Done
Canonical Pathways	Done
My Pathways	Done
My Lists	Done
Tox Lists	Done
Diseases & Functions	< 40 seconds
Networks	< 2 minutes
Upstream Regulators	< 3 minutes
Regulator Effects	< 3 minutes
Graphical Summary	< 3 minutes
Causal Networks	< 10 minutes

Figure 1. Start viewing your Core Analysis results even as it is running.

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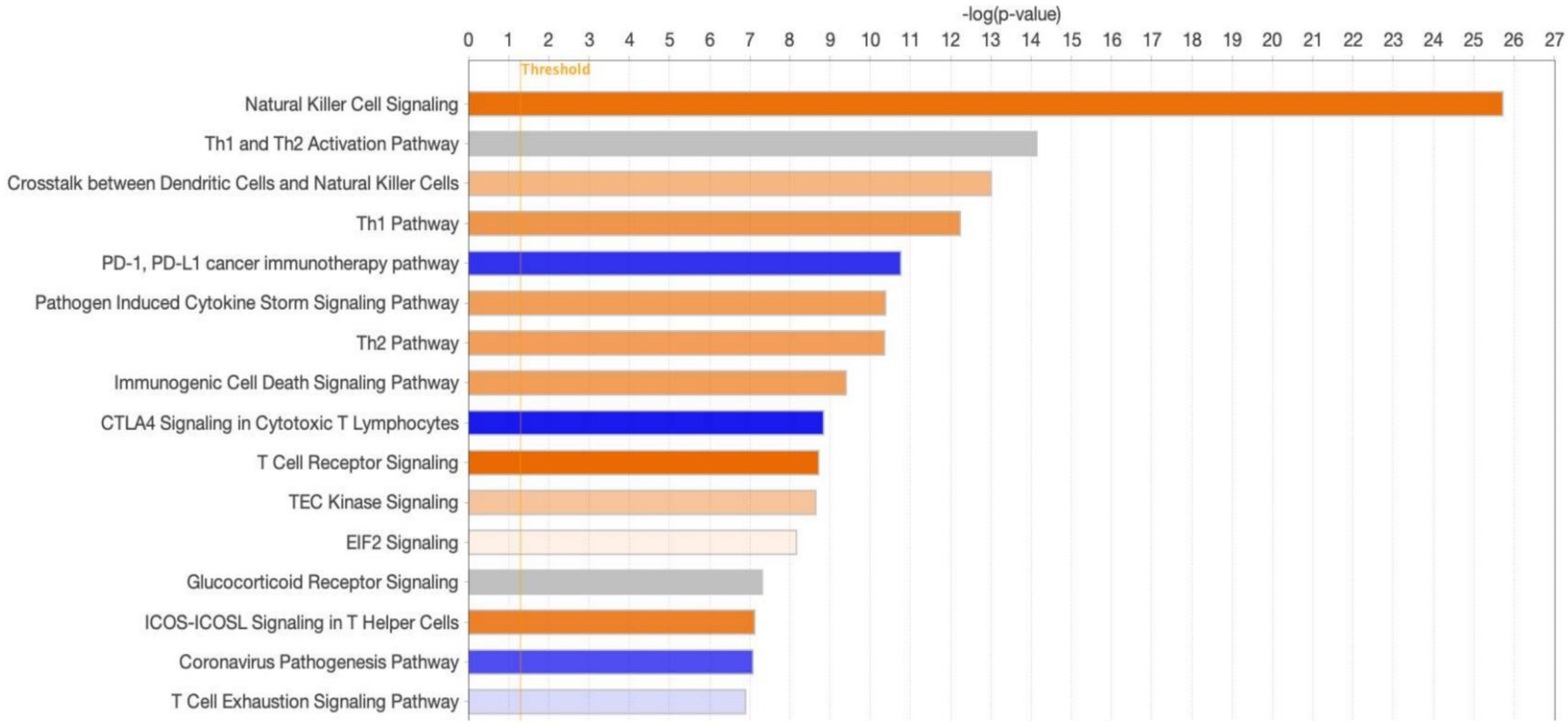

Figure 2. New compact layout for horizontal bar charts.

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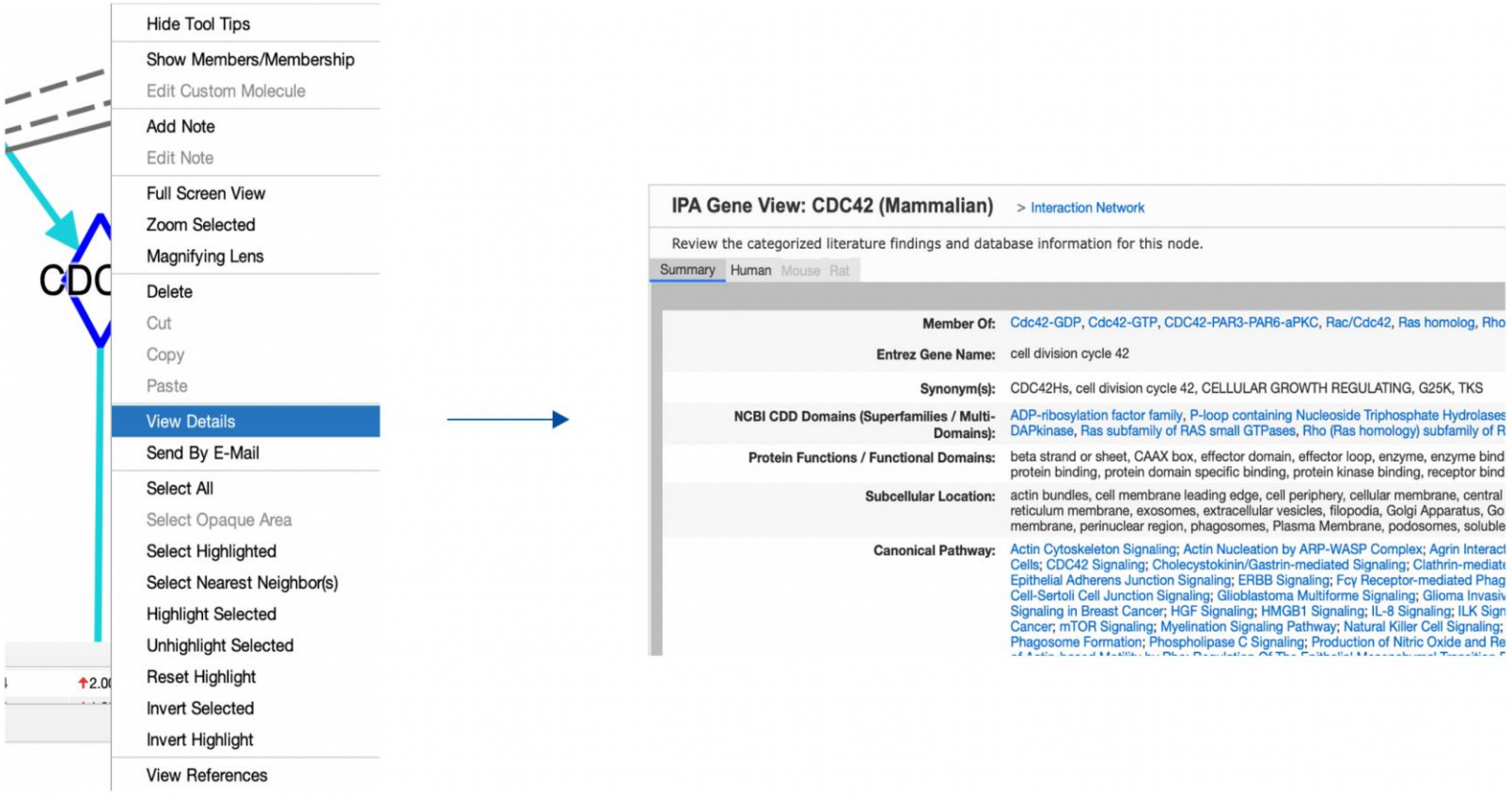

Figure 3. Right-click on a node to view the details for a gene, chemical, or disease / function node on a network or pathway.

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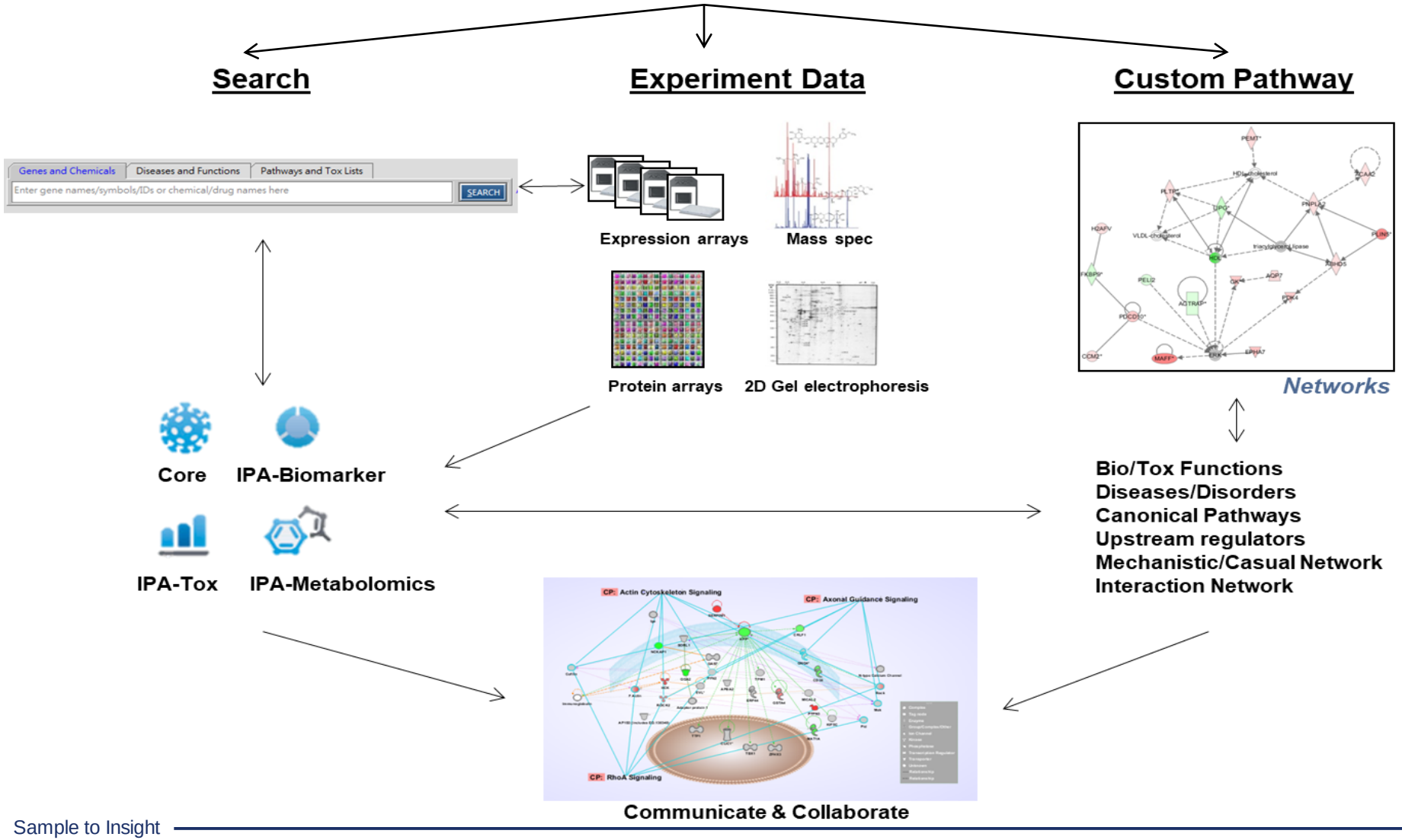
Entry Points in IPA

1) What does the data reveal about the underlying biology in the sampled cells or tissues?
2) What relevance does that biological information have with respect to other biological samples?



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Agenda

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3. Draw the relationship between 3 nodes (Gene/Disease/Pathway)
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Live Demo

Learn how to search database in IPA

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Search gene database

- Search (Genes and Chemicals) : IL1B

Search Results

Genes and Chemicals | Diseases and Functions

Add To My Pathway | Add To My List | Create Dataset | BioProfiler | Interaction Network | Activity Plot

The search for IL1B matched 1 items.

#	Symbol	Matched Term	Synonym(s)	Entrez Gene Name	Location
1	IL1B	IL1B, Il1b	IL-1, IL1-BETA, IL-1F2, IL-1 β, interleukin 1 beta, Interleukin 1 β, OAF, Osteoclast-Activating Factor, Pro-IL-1beta, Pro-IL-1β	interleukin 1 beta	Extracellular Spac

IPA Gene View

IPA Gene View: IL1B (Mammalian) > Interaction Network — Contact Support | Help Documentation

Review the categorized literature findings and database information for this node.

Summary | Human | Mouse | Rat

Member Of:	cytokine, IL1, IL1/IL6/TNF, Pro-inflammatory Cytokine
Entrez Gene Name:	interleukin 1 beta
Synonym(s):	IL-1, IL1-BETA, IL-1F2, IL-1 β, interleukin 1 beta, Interleukin 1 β, OAF, Osteoclast-Activating Factor, Pro-IL-1beta, Pro-IL-1β
NCBI CDD Domains (Superfamilies / Multi-Domains):	IL1, Interleukin-1 propeptide
Protein Functions / Functional Domains:	cytokine, integrin binding, protein binding, protein domain specific binding
Subcellular Location:	axons, cell surface, cellular membrane, Cytoplasm, cytosol, endosomes, Extracellular Space, granules, intracellular space, lysosome, Nucleus, plasma, Plasma Membrane, secretory granules, vesicles
Canonical Pathway:	Acute Phase Response Signaling; Adrenomedullin signaling pathway; Agranulocyte Adhesion and Diapedesis; Airway Pathology in Chronic Obstructive Pulmonary Disease; Altered T Cell and B Cell Signaling in Rheumatoid Arthritis; Aryl Hydrocarbon Receptor Signaling; Atherosclerosis Signaling; Cardiac Hypertrophy Signaling (Enhanced); CDX Gastrointestinal Cancer Signaling Pathway; Cholecystokinin/Gastrin-mediated Signaling; Communication between Innate and Adaptive Immune Cells; Coronavirus Pathogenesis Pathway; Dendritic Cell Maturation; Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F; Differential Regulation of Cytokine Production in Macrophages and T Helper Cells by IL-17A and IL-17F; Docosahexaenoic Acid (DHA) Signaling; Erythropoietin Signaling Pathway; FXR/RXR Activation; GADD45 Signaling; Glucocorticoid Receptor Signaling; Graft-versus-Host Disease Signaling; Granulocyte Adhesion and Diapedesis; Granzyme A Signaling; Hepatic Cholestasis; Hepatic Fibrosis / Hepatic Stellate Cell Activation; Hepatic Fibrosis Signaling Pathway; HMGB1 Signaling; IL-10 Signaling; IL-17 Signaling; IL-23 Signaling Pathway; IL-6 Signaling; Immunogenic Cell Death Signaling Pathway; Inflammasome pathway; LPS/IL-1 Mediated Inhibition of RXR Function; LXR/RXR Activation; Macrophage Alternative Activation Signaling Pathway; Macrophage Classical Activation Signaling Pathway; Multiple Sclerosis Signaling Pathway; Neuroinflammation Signaling Pathway; Neutrophil Extracellular Trap Signaling Pathway; NF-κB Signaling; Osteoarthritis Pathway; Oxytocin In Brain Signaling Pathway; p38 MAPK Signaling; Pathogen Induced Cytokine Storm Signaling Pathway; PPAR Signaling; PPARα/RXRα Activation; Pulmonary Fibrosis Idiopathic Signaling Pathway; Pyroptosis Signaling Pathway; Role Of Chondrocytes In Rheumatoid Arthritis Signaling Pathway; Role of Cytokines in Mediating Communication between Immune Cells; Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza; Role of IL-17F in Allergic Inflammatory Airway Diseases; Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis; Role of MAPK Signaling in Inhibiting the Pathogenesis of Influenza; Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis; Role Of Osteoblasts In Rheumatoid Arthritis Signaling Pathway; Role Of Osteoclasts In Rheumatoid Arthritis Signaling Pathway; Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses; Role of PKR in Interferon Induction and Antiviral Response; Role of Tissue Factor in Cancer; S100 Family Signaling Pathway; STAT3 Pathway; Systemic Lupus Erythematosus In B Cell Signaling Pathway; Systemic Lupus Erythematosus Signaling; Th17 Activation Pathway; Toll-like Receptor Signaling; TREM1 Signaling; Tumor Microenvironment Pathway; Type I Diabetes Mellitus Signaling; Wound Healing Signaling Pathway; Xenobiotic Metabolism AHR Signaling Pathway; Xenobiotic Metabolism Signaling
Targeted By miRNA Functional Cluster: (showing 50 out of 120) show all	miR-1178-3p (miRNAs w/seed UGCUCAC), miR-1199-5p (and other miRNAs w/seed CUGAGCC), miR-1202 (and other miRNAs w/seed UGCCAGC), miR-1233-5p (and other miRNAs w/seed GUGGGAG), miR-1256 (miRNAs w/seed GGCAUUG), miR-125b-1-3p (miRNAs w/seed CGGGUUA), miR-125b-5p (and other miRNAs w/seed CCCUGAG), miR-1291 (and other miRNAs w/seed GGCCCUG), miR-135a-1-3p (and other miRNAs w/seed AUAGGGA), miR-138-5p (miRNAs w/seed GCUGGUG), miR-144-3p (miRNAs w/seed ACAGUAU), miR-149-5p (miRNAs w/seed CUGGCUC), miR-152-5p (miRNAs w/seed AGGUUCU), miR-185-5p (and other miRNAs w/seed GGAGAGA), miR-190a-3p (miRNAs w/seed UAUAUAU), miR-1912-5p (miRNAs w/seed GCUCAUU), miR-1966-5p (miRNAs w/seed AGGGAGC), miR-204-5p (and other miRNAs w/seed UCCCUUU), miR-205-3p (miRNAs w/seed AUUUCAG), miR-21-5p (and other miRNAs w/seed AGCUUAU), miR-221-5p (and other miRNAs w/seed CCUGGCA), miR-2682-5p (and other miRNAs w/seed AGGCAGU), miR-26b-3p (and other miRNAs w/seed CUGUUCU), miR-27b-5p (miRNAs w/seed GAGCUUA), miR-28b (and other miRNAs w/seed GGAGCUC), miR-297a-3p (and other miRNAs w/seed AUACAUA), miR-298-3p (miRNAs w/seed AGGAACU), miR-299a-3p (and other miRNAs w/seed AUGUGGG), miR-29b-5p (and other miRNAs w/seed UGGUUUC), miR-3063-5p (and other miRNAs w/seed GGAGAUC), miR-3064-5p (and other miRNAs w/seed CUGGCUG), miR-3066-5p (miRNAs w/seed UGGUUGC), miR-3070-2-3p (and other miRNAs w/seed GGUGCUA), miR-3072 (and other miRNAs w/seed GCCCCCU), miR-3083-5p (and other miRNAs w/seed GGCUGGG), miR-3084a-3p (and other miRNAs w/seed UCUGCCA), miR-3099-5p (miRNAs w/seed CAGCUUC), miR-30a-3p (and other miRNAs w/seed UUUCAGU), miR-3100-3p (miRNAs w/seed UGUGACA), miR-3145-3p (miRNAs w/seed GAUAUUU), miR-3147 (miRNAs w/seed GUUGGGC), miR-3174 (miRNAs w/seed AGUGAGU), miR-3194-5p (miRNAs w/seed GCCAGCC), miR-3200-5p (miRNAs w/seed AUCUGAG), miR-328-3p (and other miRNAs w/seed UGGCCCU), miR-330-3p (and other miRNAs w/seed CAAAGCA), miR-331-3p (miRNAs w/seed CCCCUGG), miR-344a-5p (and other miRNAs w/seed CAGGCUC), miR-3473f (miRNAs w/seed AAAUAGG), miR-3542 (and other miRNAs w/seed AGGCUCU)...(more)
Targeted By miRNA Family:	mir-21

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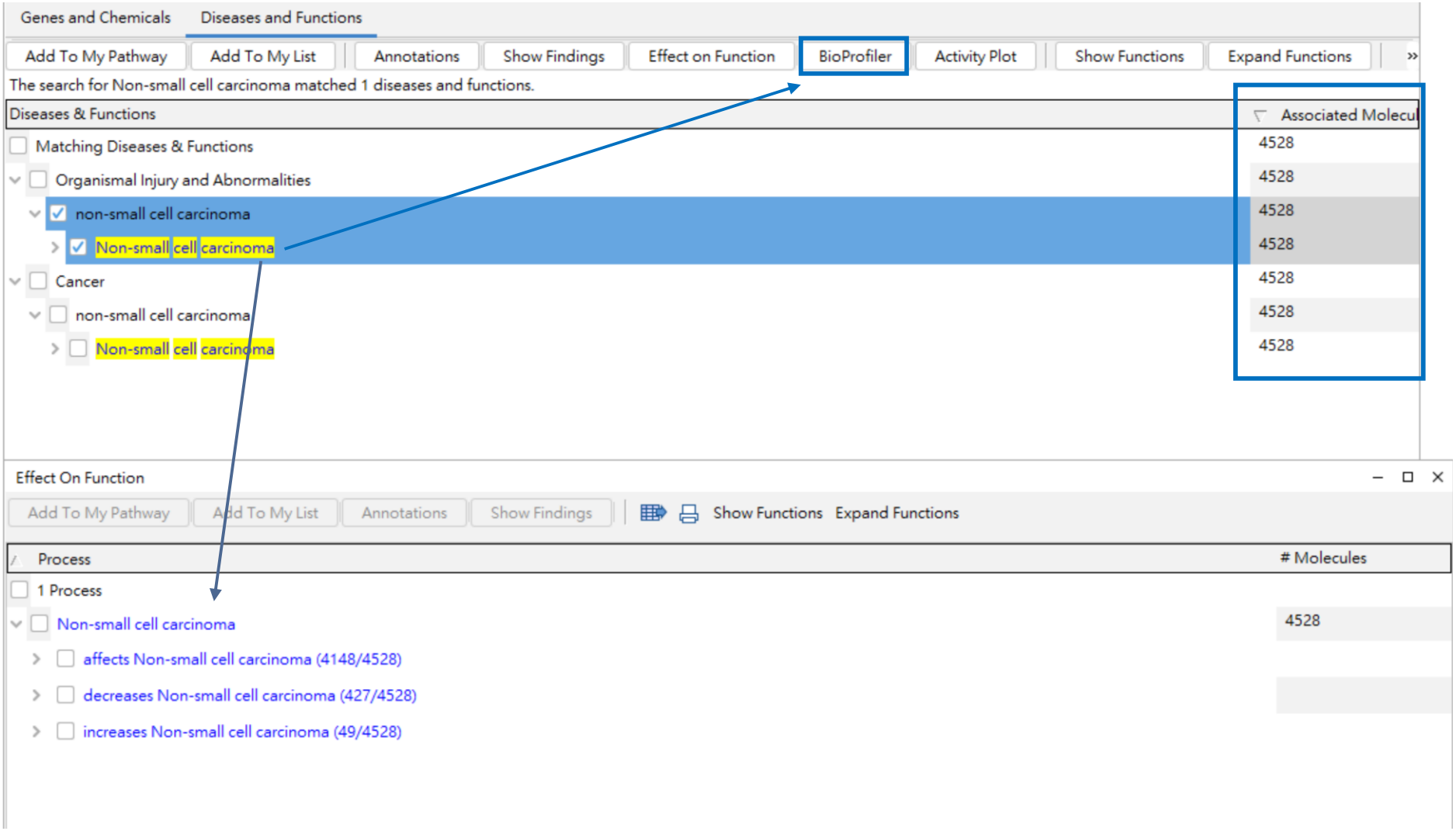
Search diseases and functions

- Search (Diseases and functions) : Non-small cell lung carcinoma



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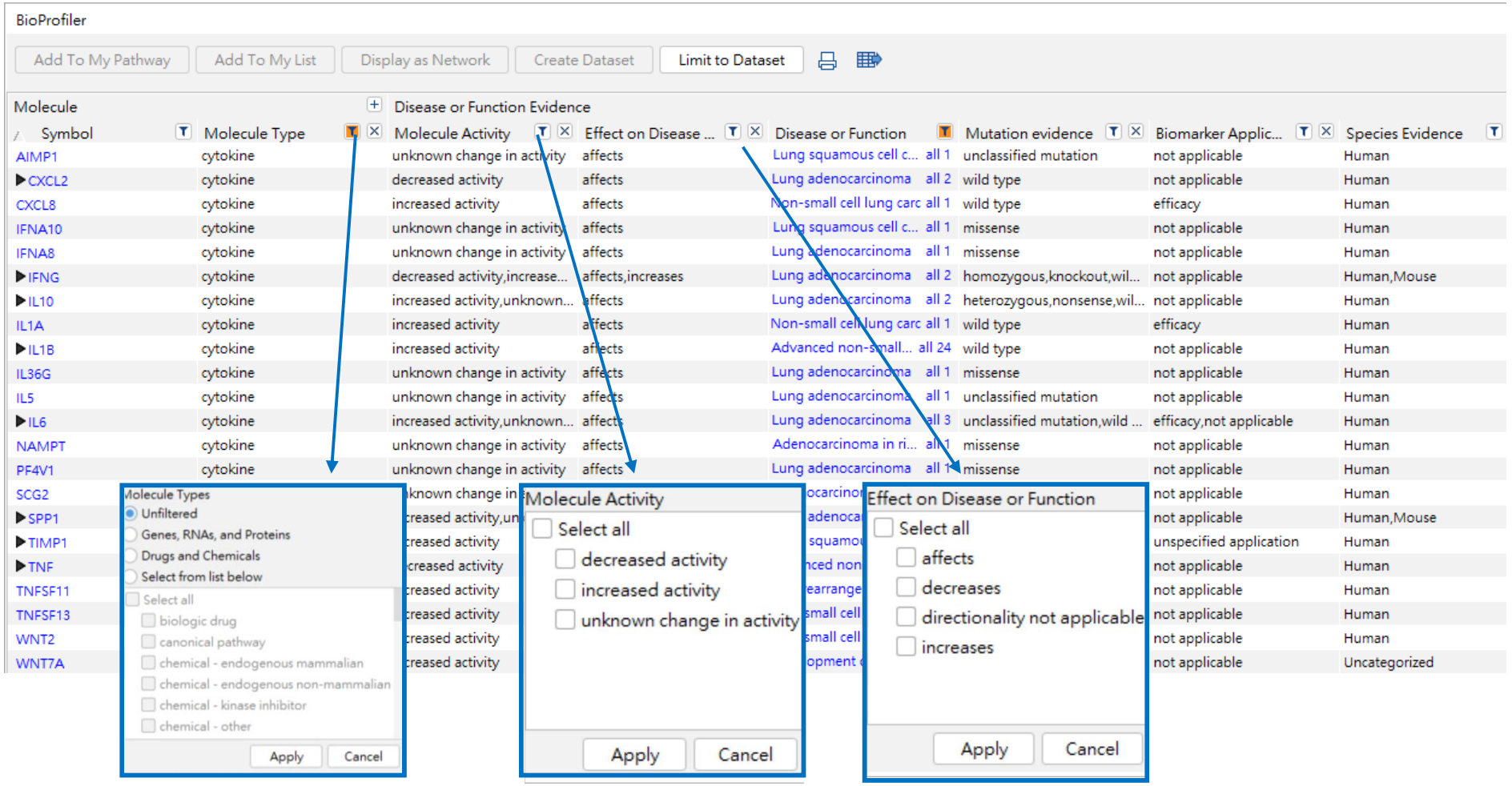
Profile key immune molecules in the context of cancer

- Search (Diseases and functions) : Non-small cell lung carcinoma
- BioProfiler: Cytokine



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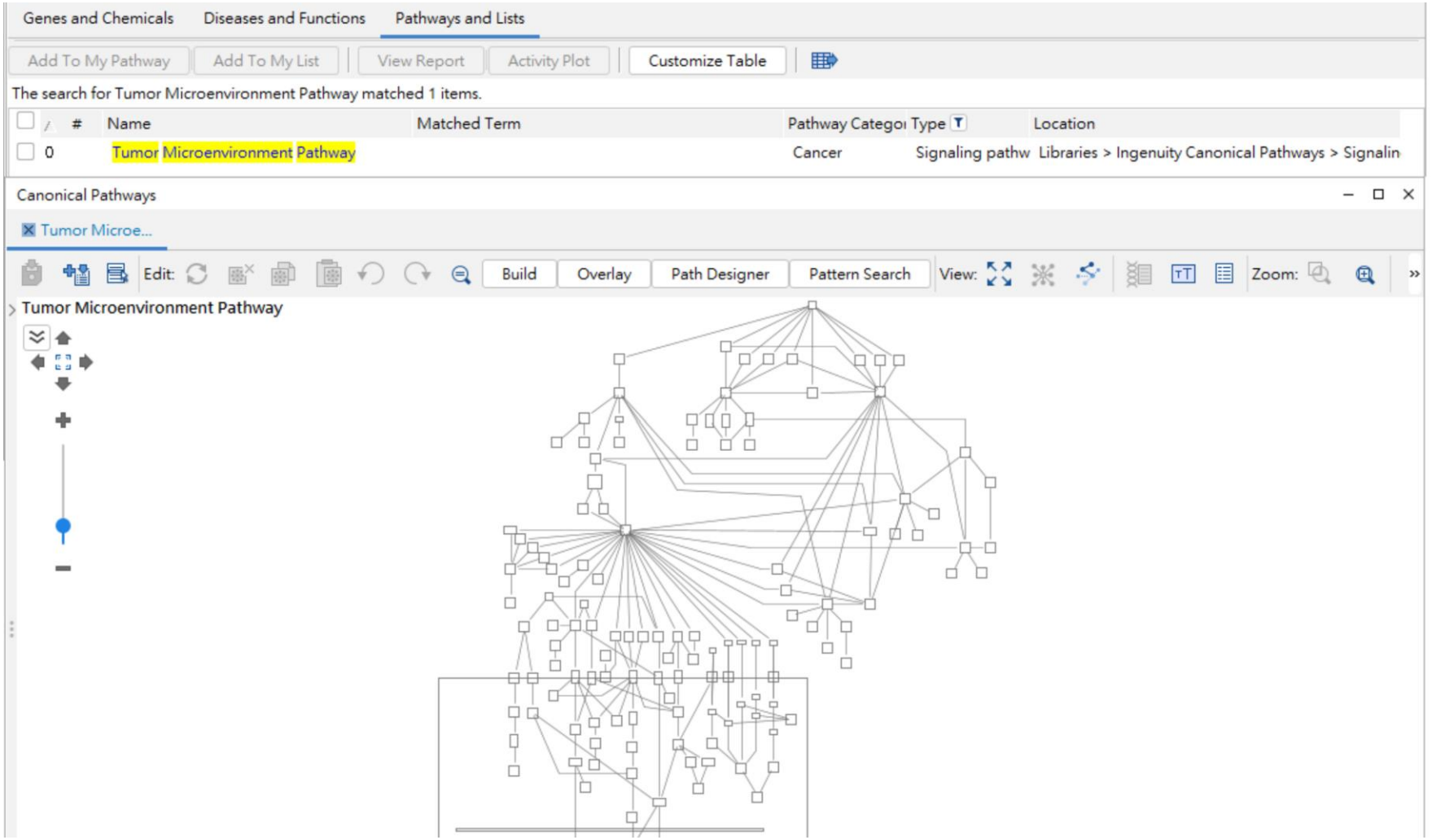
Search pathways and lists

- Search : Tumor Microenvironment Pathway



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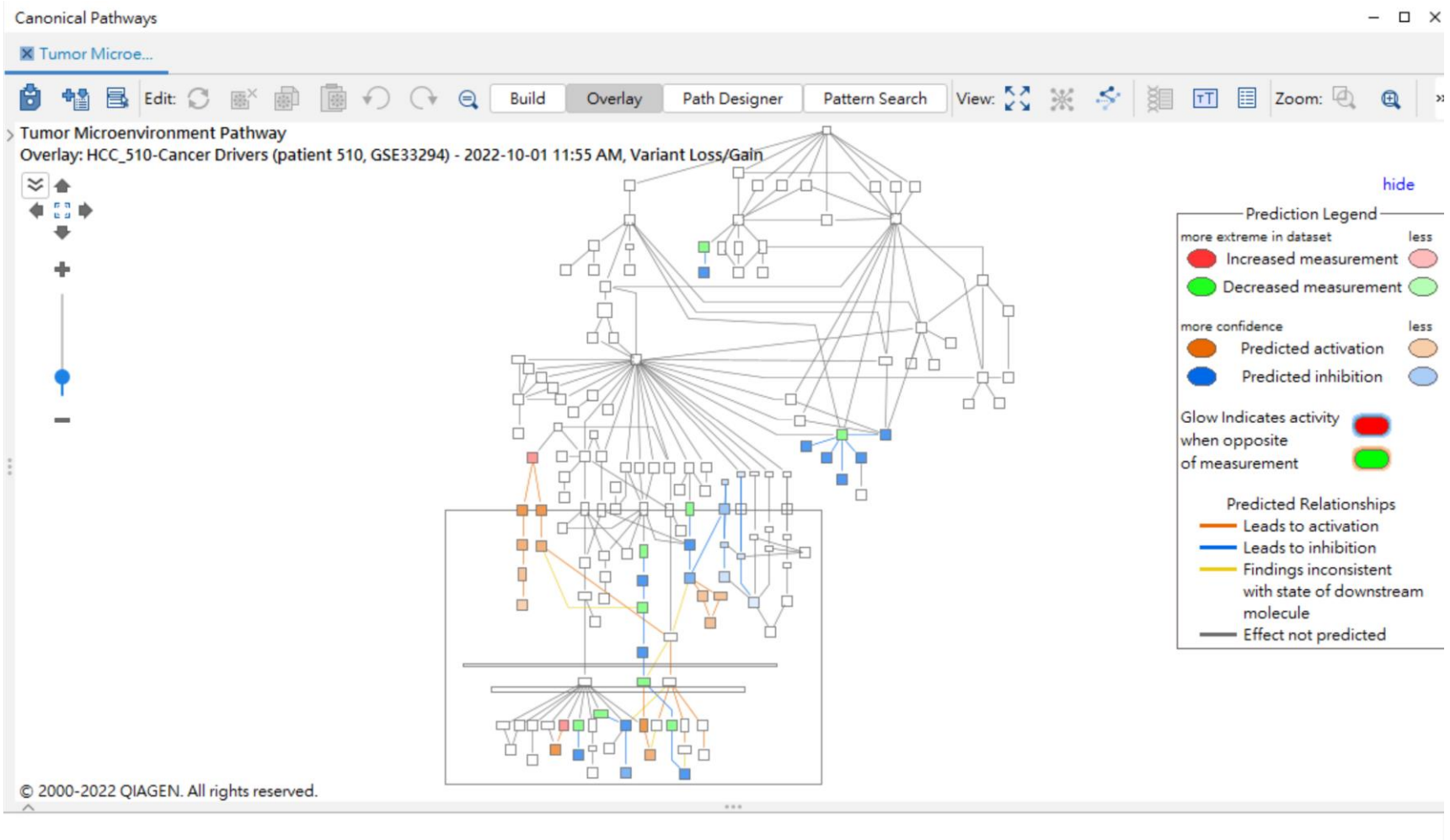
Search pathways and lists : pathway overlay

- Search : Tumor Microenvironment Pathway
- pathway overlay



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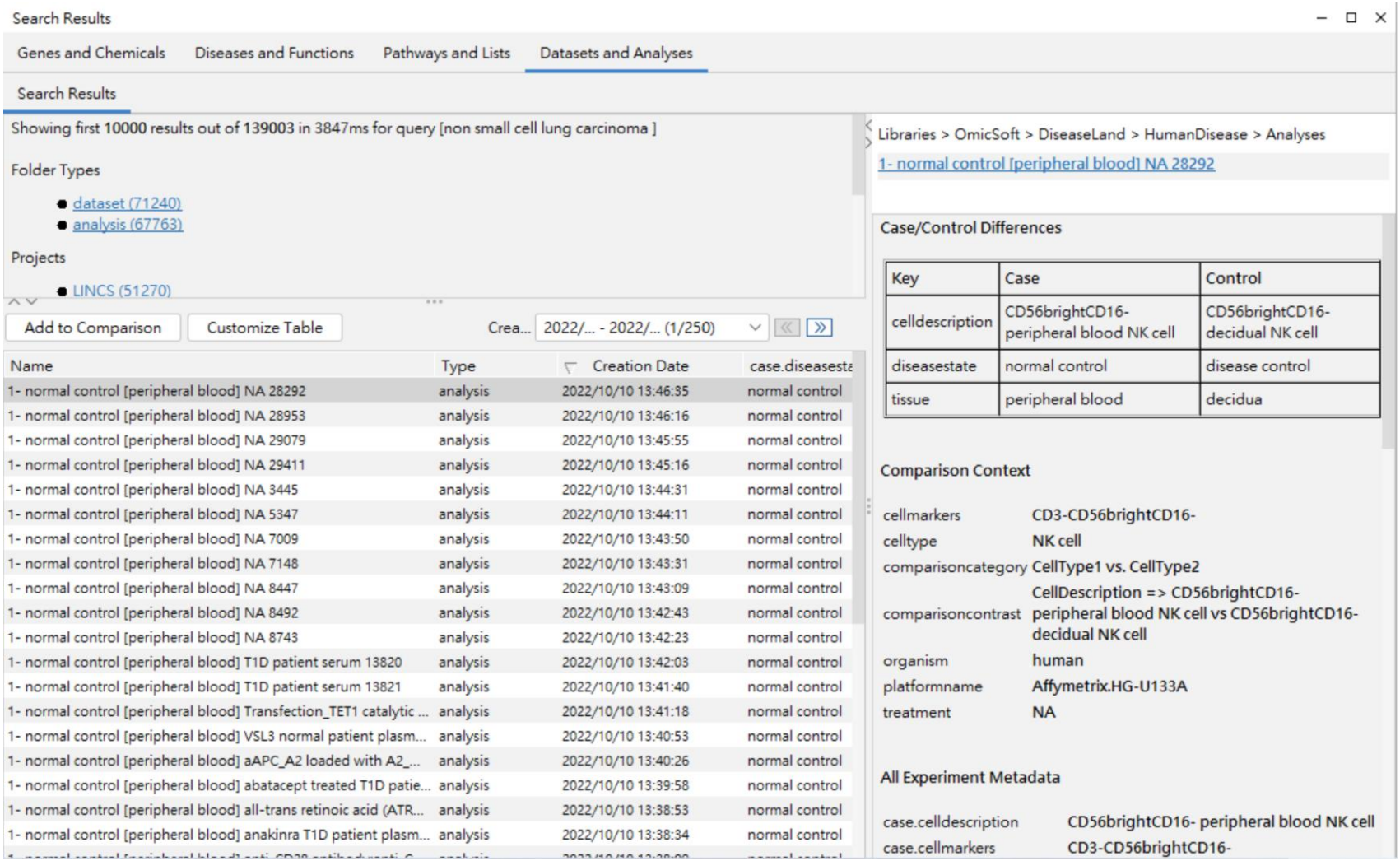
Search databases and analyses

- Search : non small cell lung carcinoma



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Live Demo

Case Study: Investigating the tumor microenvironment

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Explore key target molecules and disease indications

Construct networks based on key targets and predict molecule activity

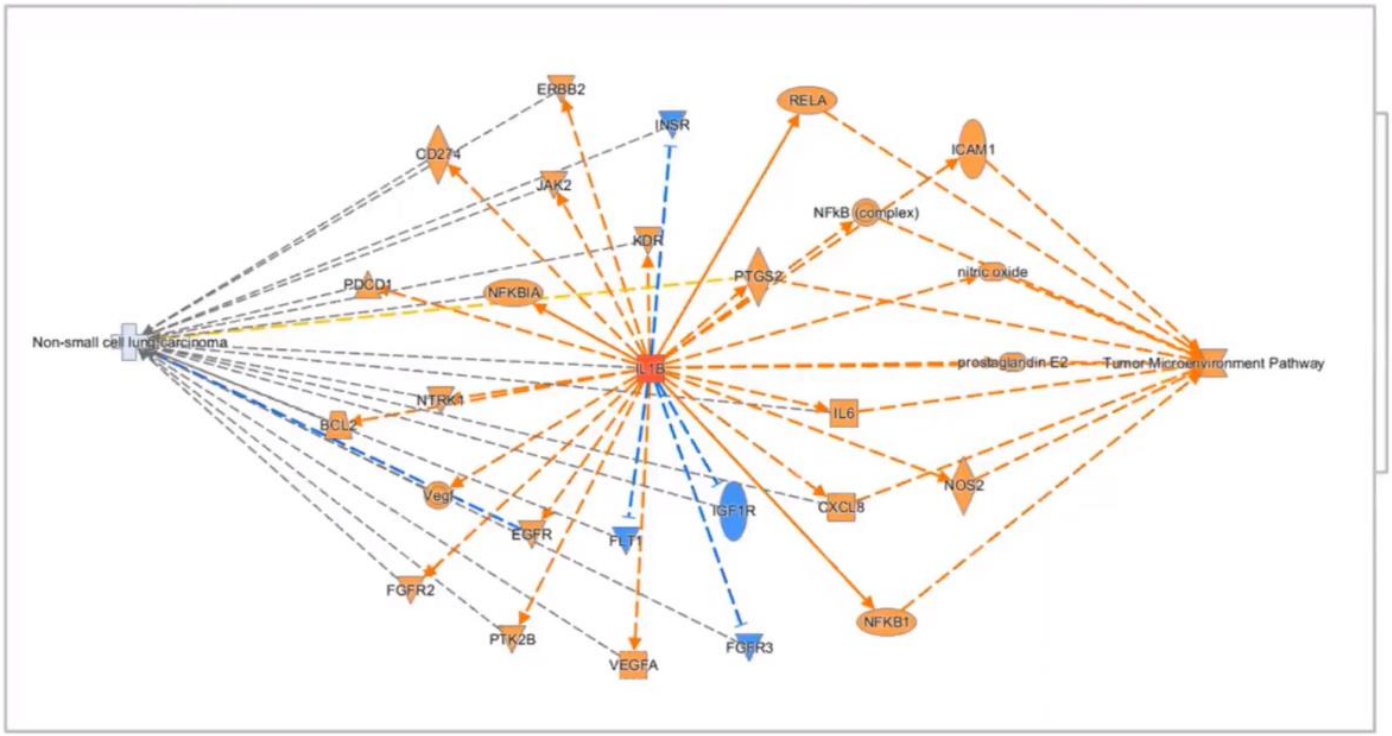
Review > Curr Pharm Des. 2017;23(32):4893-4905. doi: 10.2174/1381612823666170613080919.

Targeting the Tumor Microenvironment by Intervention in Interleukin-1 Biology

Elena Voronov [1], Ron N Apte [1]

Affiliations + expand

PMID: 28606052 DOI: 10.21



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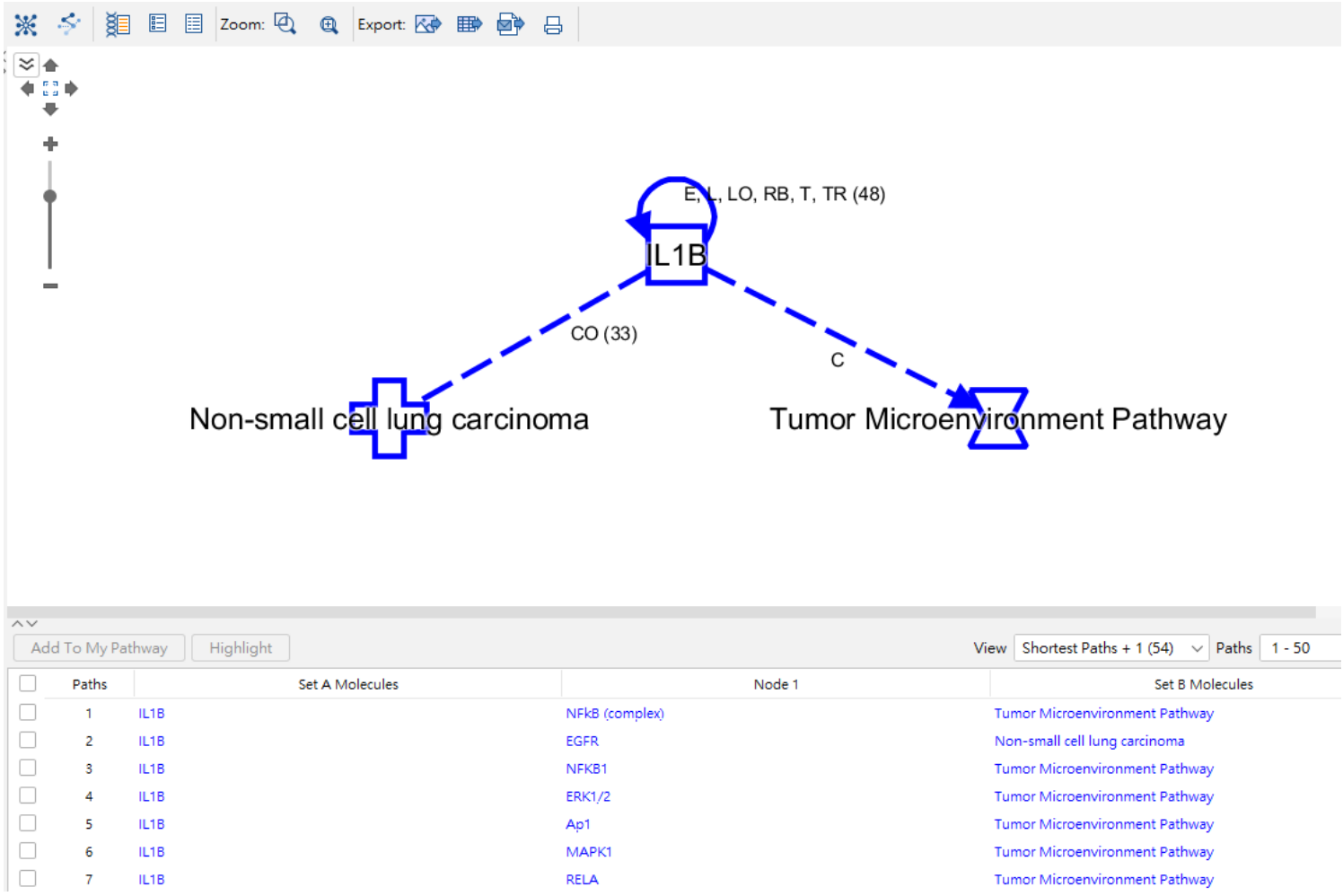
Build networks linking molecules to the TME and disease endpoints

- Search: IL1B、Non-small cell lung carcinoma、Tumor Microenvironment Pathway
- Path Explore: activation、causation、inhibition



Paths	Set A Molecules	Node 1	Set B Molecules
1	IL1B	NFkB (complex)	Tumor Microenvironment Pathway
2	IL1B	EGFR	Non-small cell lung carcinoma
3	IL1B	NFKB1	Tumor Microenvironment Pathway
4	IL1B	ERK1/2	Tumor Microenvironment Pathway
5	IL1B	Ap1	Tumor Microenvironment Pathway
6	IL1B	MAPK1	Tumor Microenvironment Pathway
7	IL1B	RELA	Tumor Microenvironment Pathway

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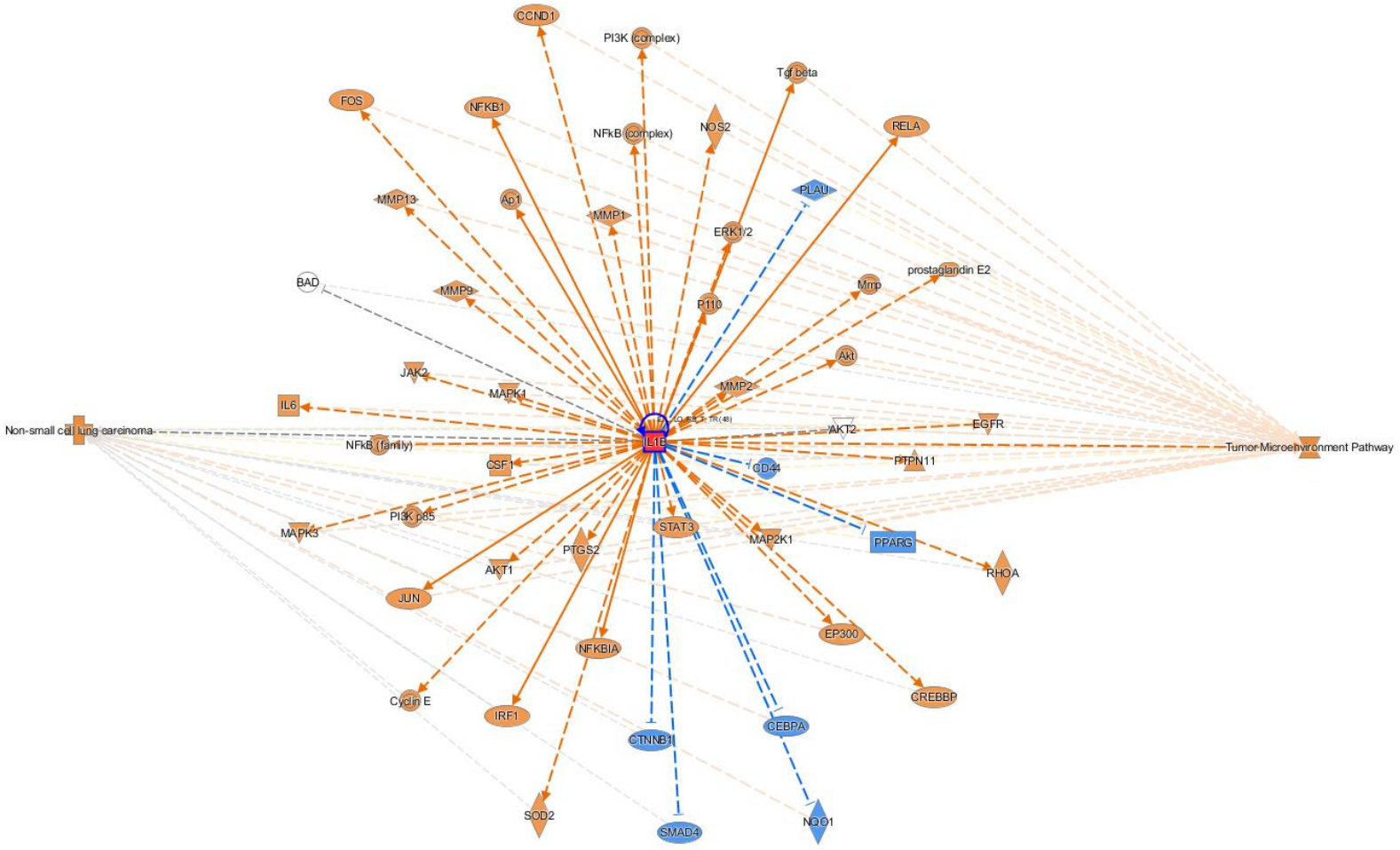
Predict molecule activity of IL1B

- MAP: IL1B Increased
- Lead to Tumor Microenvironment Pathway activation
- Correlation Non-small cell lung carcinoma activation



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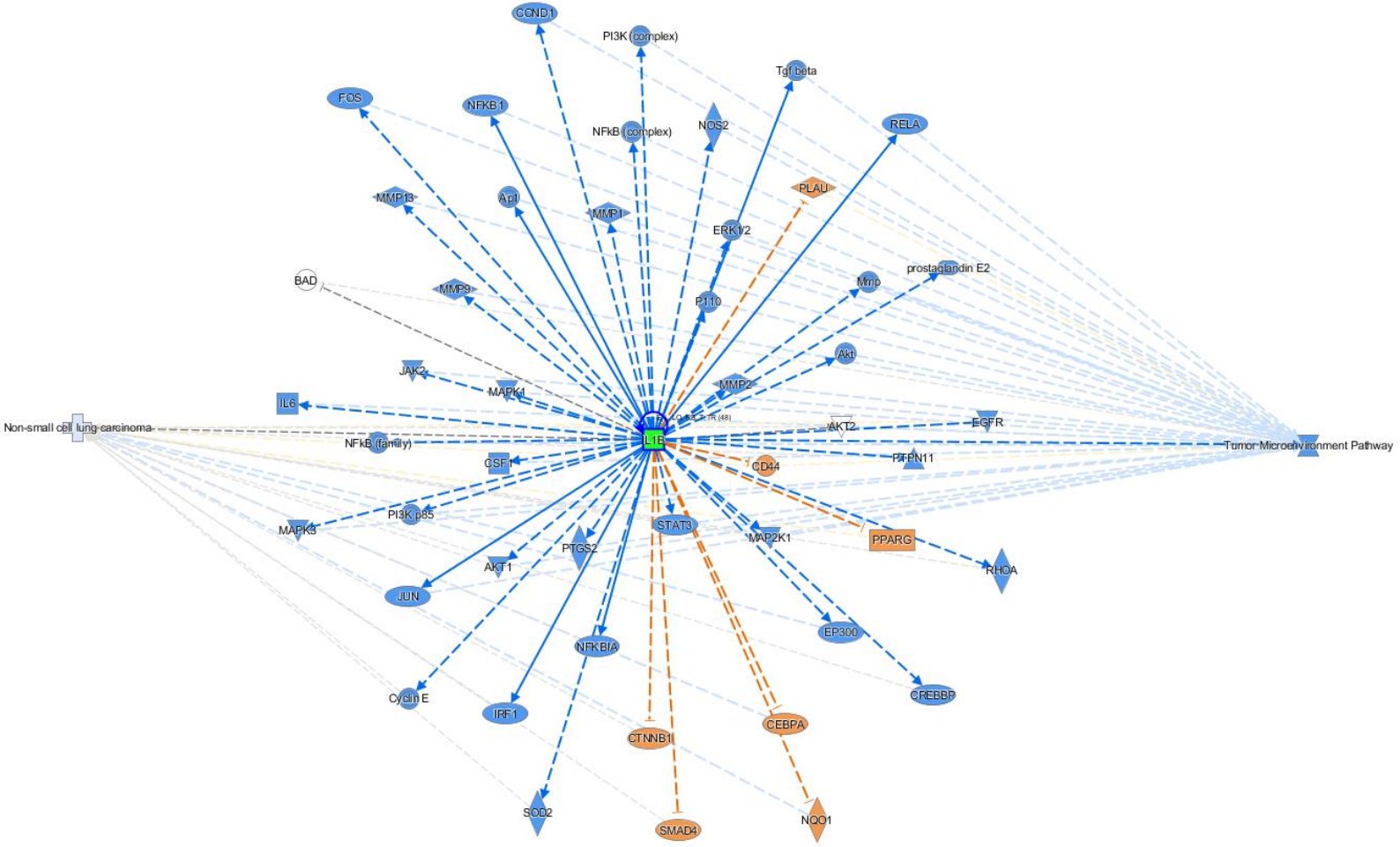
Predict molecule activity of IL1B

- MAP: IL1B Decreased
- Lead to Tumor Microenvironment Pathway inhibition
- Correlation Non-small cell lung carcinoma inhibition



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Live Demo

Data Upload

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Data Upload Workflow

- ID、Observation
- Annotated Dataset

Dataset Preparation

- Create Core Analysis
  - Expression type
  - Measurement type
- Create Expression Analysis
  - Criteria
  - Cutoffs

Analyze Dataset

- Summary
- Diseases/Disorders
- Canonical Pathways
- Upstream regulators
- Interaction Network

Expression Analysis

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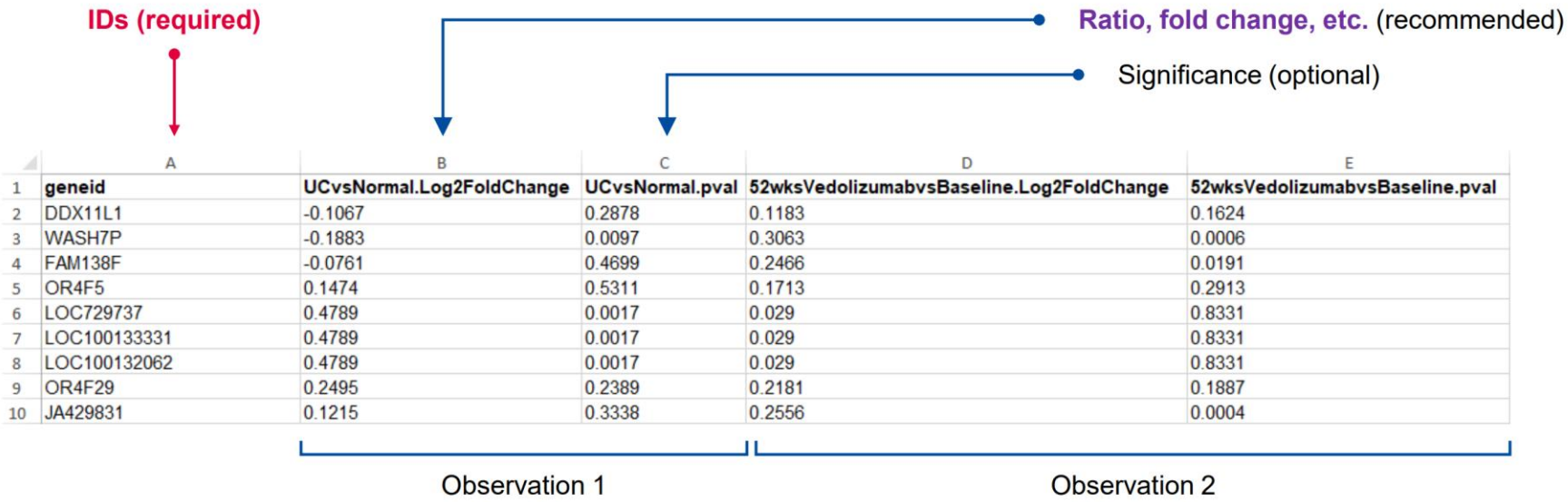
Formatting transcriptomics data before uploading to IPA



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

Common identifier types

- Arrays from Affymetrix, Illumina, etc.
- Gene symbols (Entrez or HUGO)
- Ensembl, RefSeq, UCSC, etc.

Accepted file formats

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

IDs are the only **required** column

Change measurements are needed for IPA to make activity predictions

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Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)

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

Observation 1

Common protein IDs

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

UniProt ID conversion tool:

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

Phosphorylation changes (ratio, fold change, etc.) and sites are supported, but these columns **must be assigned**

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Formatting metabolomics data before uploading to IPA

Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

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

Observation 1

Common metabolite IDs

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

Metabolite ID conversion tools:

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

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Formatting omics data before uploading to IPA

Observation 1

Observation 2

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

Analyte identifier REQUIRED to explore enrichment

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

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

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

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

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

Accepted file formats:

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

Multiple comparisons or observations may be uploaded in one file

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準備IPA分析用的Dataset

- 重複性實驗的數值平均、p-value或fold-change等統計計算，要先在IPA分析之前完成。

- 將實驗資料用 Excel 表格檔案儲存，檔案裡面只能有一個Sheet存在。
  - Excel Sheet當中必須要有一欄是列出**分子的ID** (如Gene Symbol, Refseq number, Uniprot number, HMDB等常用命名皆支援)
  - 每個Excel Sheet 最多可以放入 **20個 observations** (即20個實驗變因的資料欄的意思)
  - 每個Observation可以有3個不同的表現值種類 (ex. p-Value，fold-change等)
  - **表格欄位最上方只能有一個Head row (首行)**
  - 資料上傳到IPA後，可以在cut-off 值欄位進行設定，讓使用者決定門檻來決定**表現顯著有差異**的生物分子。意味著原始實驗資料中有些分子的數值不夠顯著，可以用cut-off值作為門檻排除於分析運算中。那些通過cut-off值的分子們在IPA中稱之為Analysis-Ready Molecules。

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What do colors mean in IPA?

Pathway or gene activity predicted by IPA

Actual measurement of gene expression in your dataset

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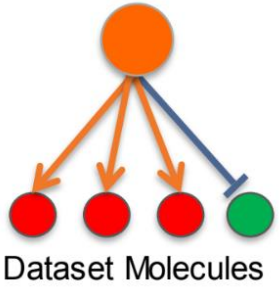
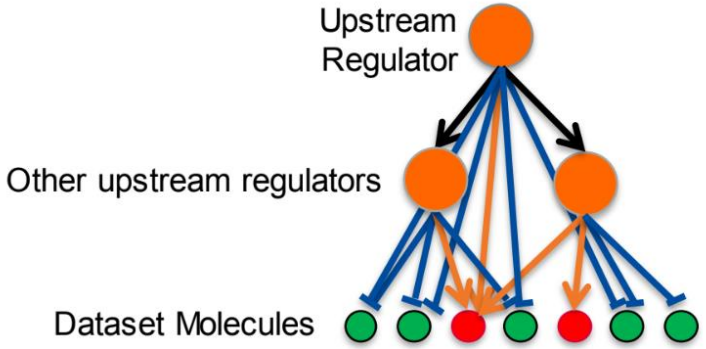
Network types in IPA Core Analysis

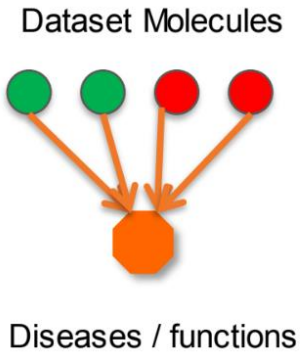
Upstream Analysis



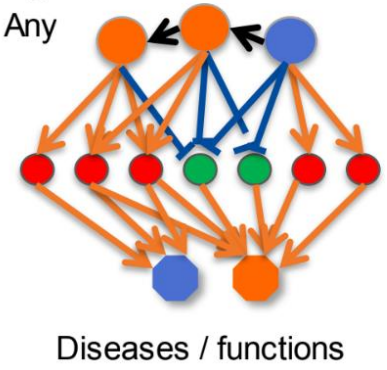
Mechanistic Network of Upstream Regulators



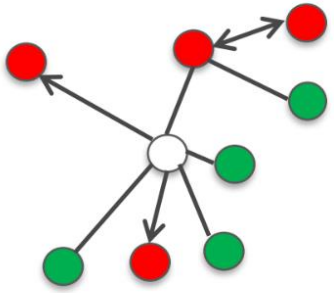
Function Analysis



Regulator Effect Network



Interaction Network



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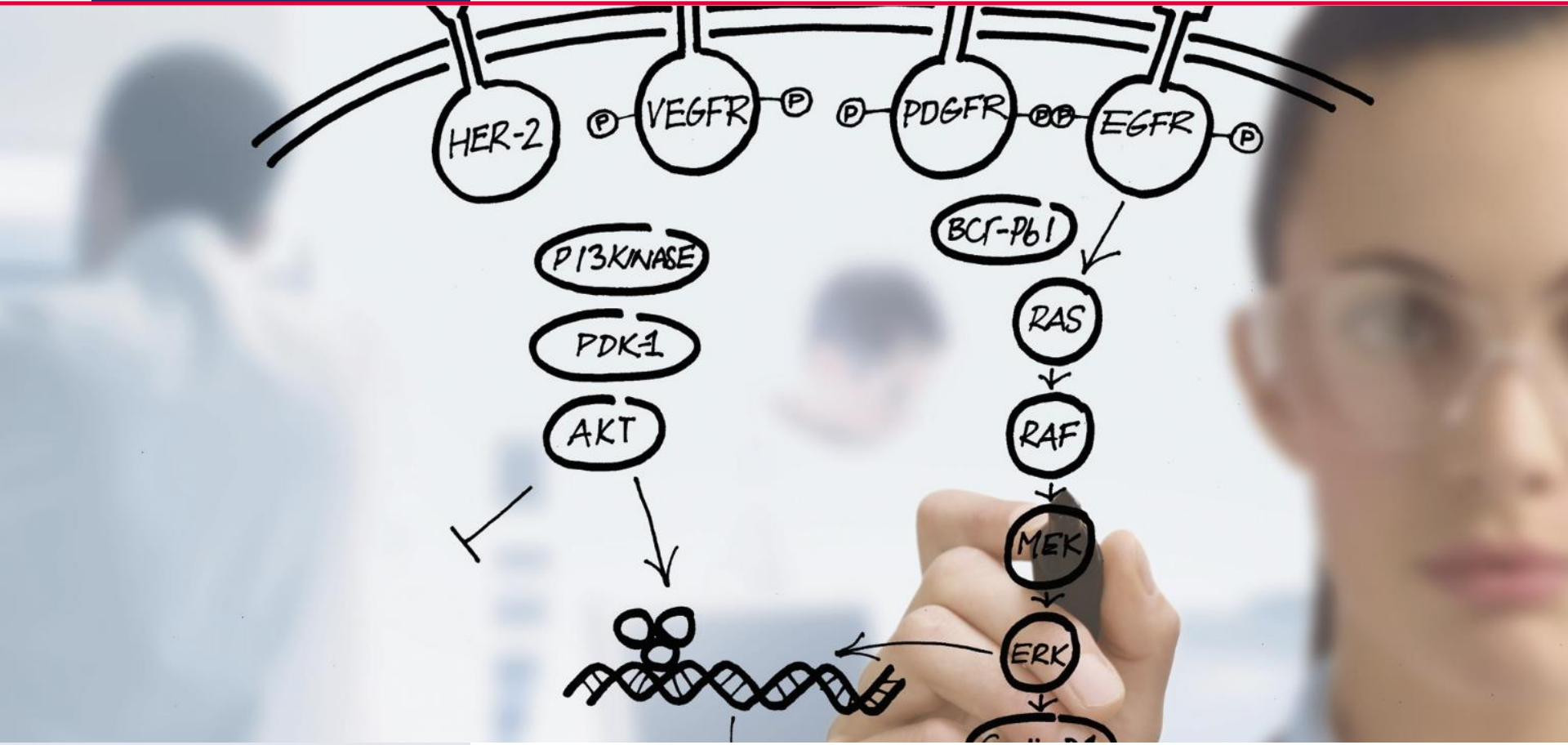
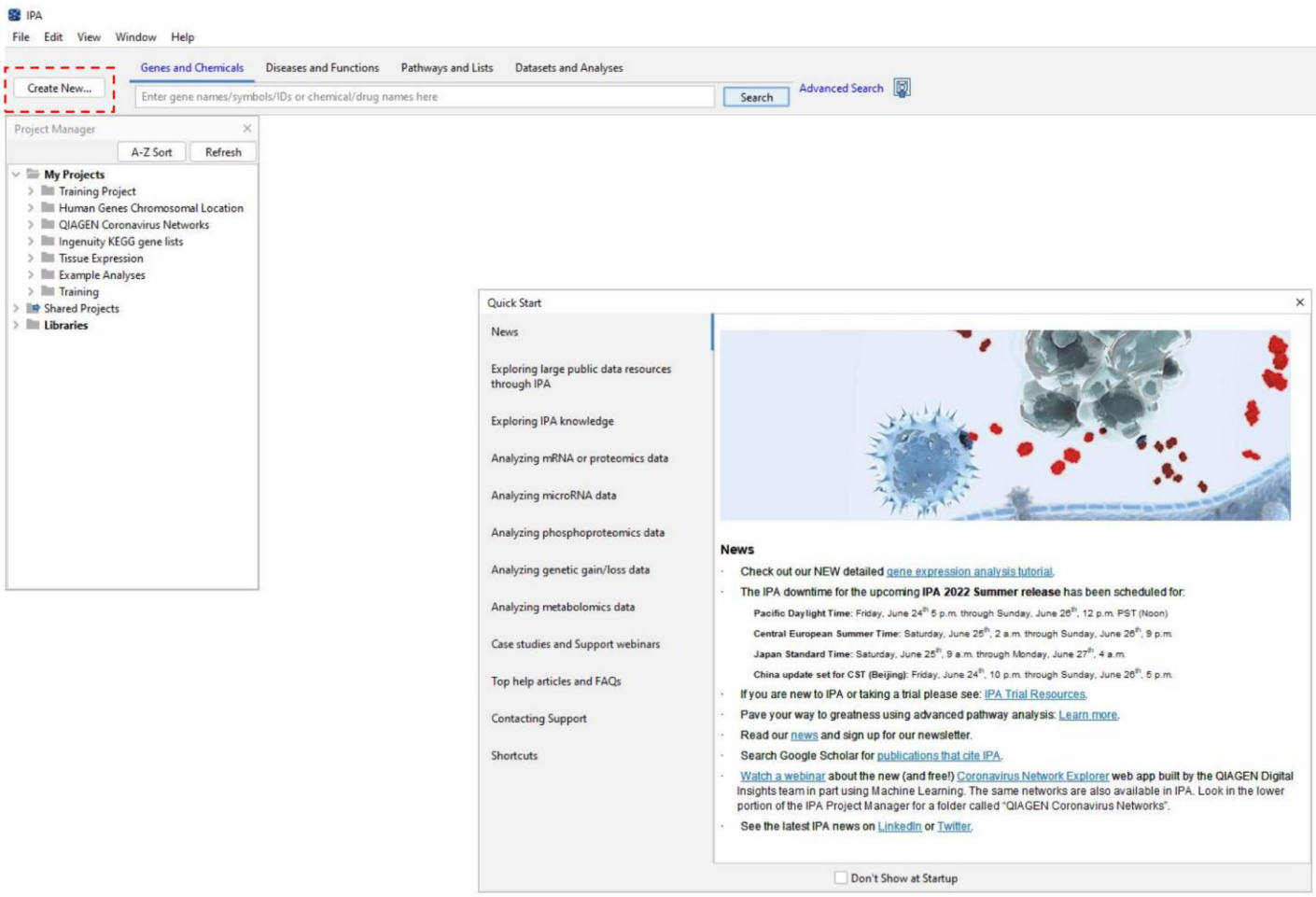


歡迎與我們聯絡

創源生技 GGA

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:

徐竹君 業務專員 LenaHsu@gga.asia 02-2795 1777 #3013
黃柔諭 產品專員 ZoeHuang@gga.asia 02-2795 1777 #3024



1. Click on Create New.

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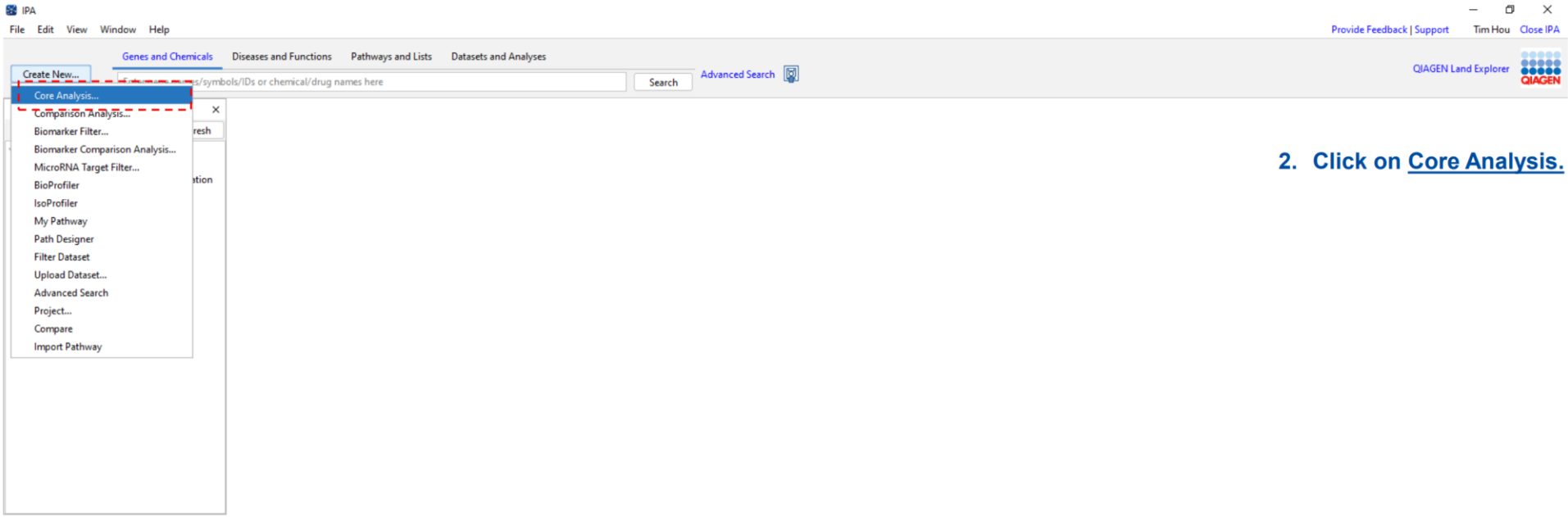

2. Click on Core Analysis.

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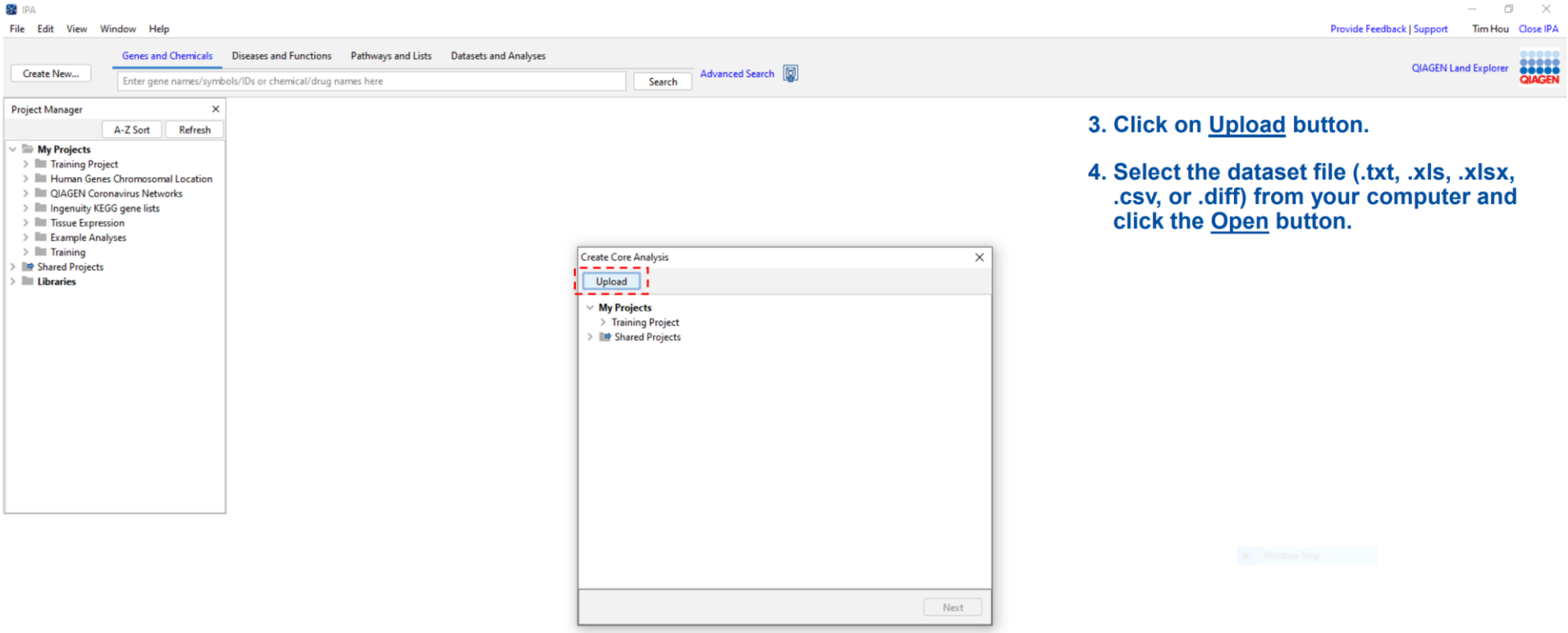

3. Click on Upload button.

4. Select the dataset file (.txt, .xls, .xlsx, .csv, or .diff) from your computer and click the Open button.

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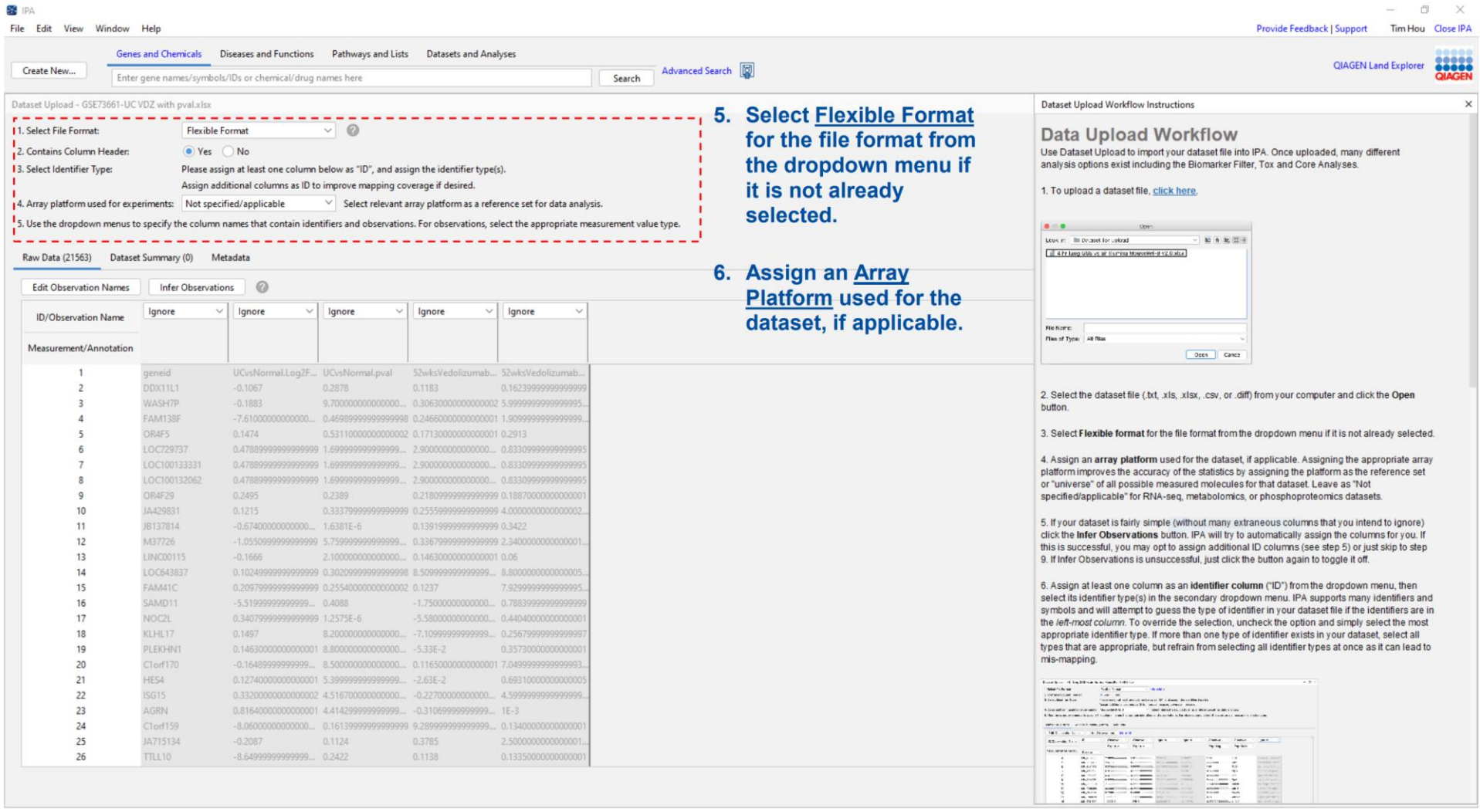

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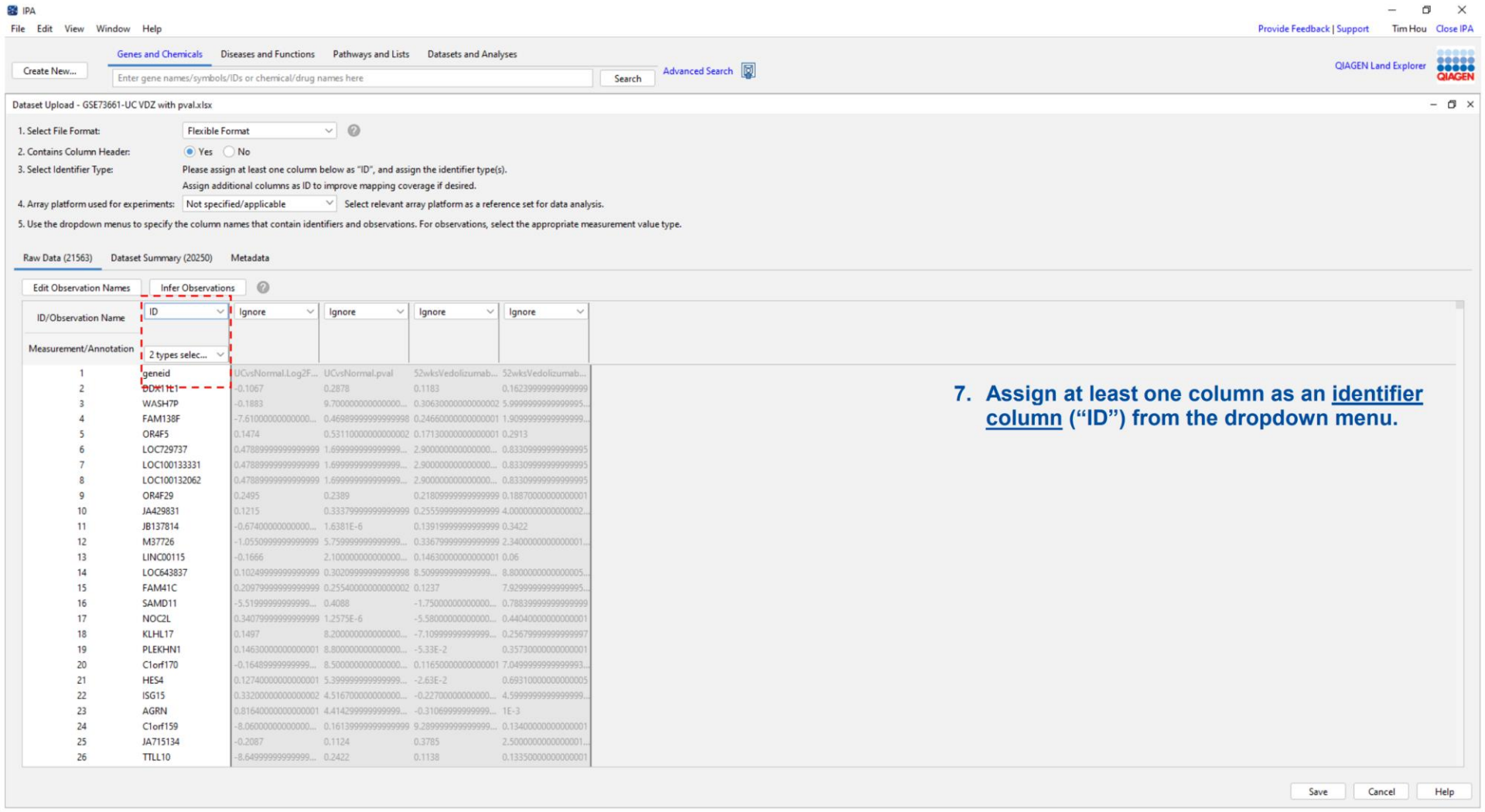

7. **Assign at least one column as an identifier column ("ID") from the dropdown menu.**

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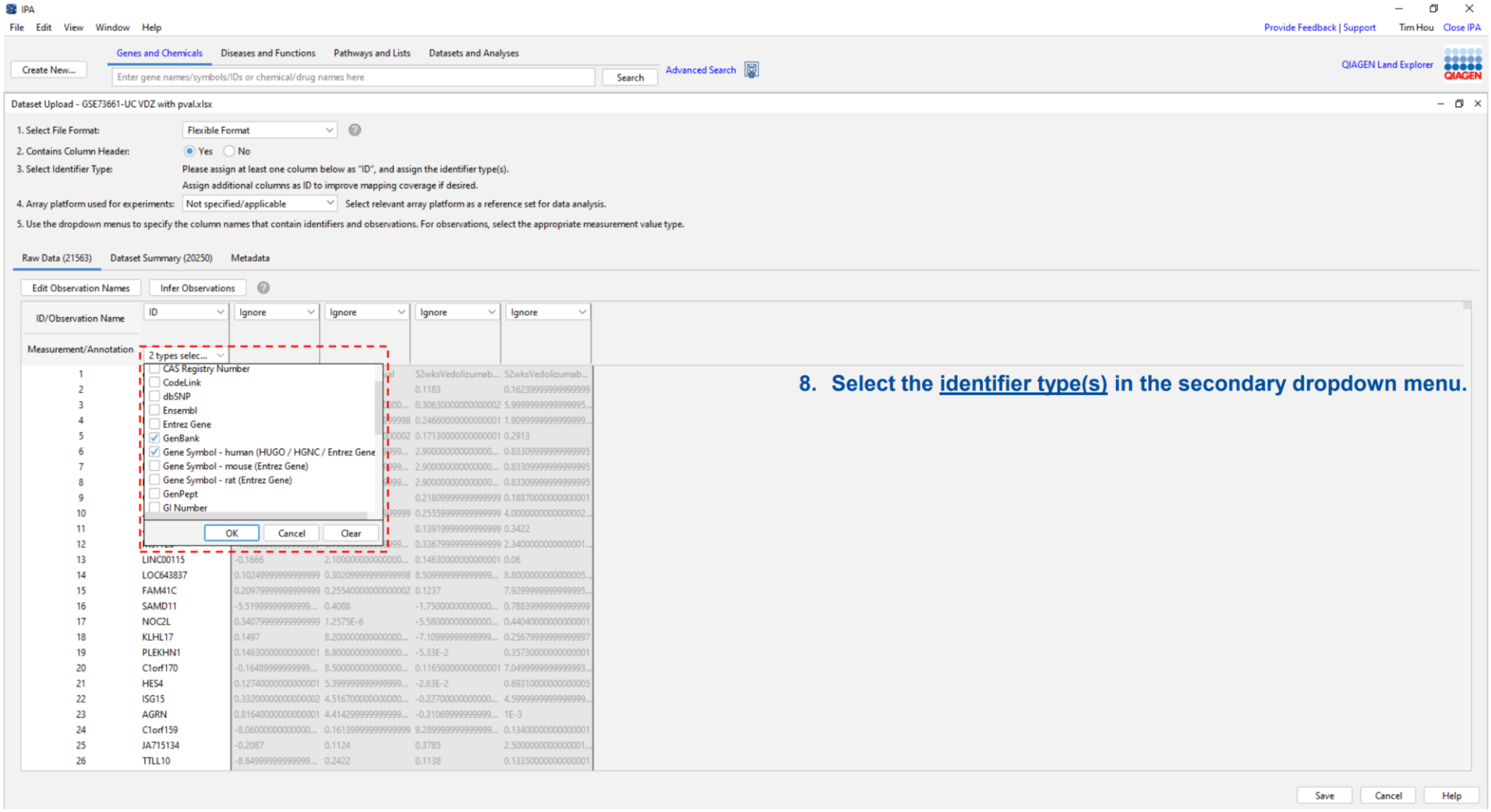

8. Select the identifier type(s) in the secondary dropdown menu.

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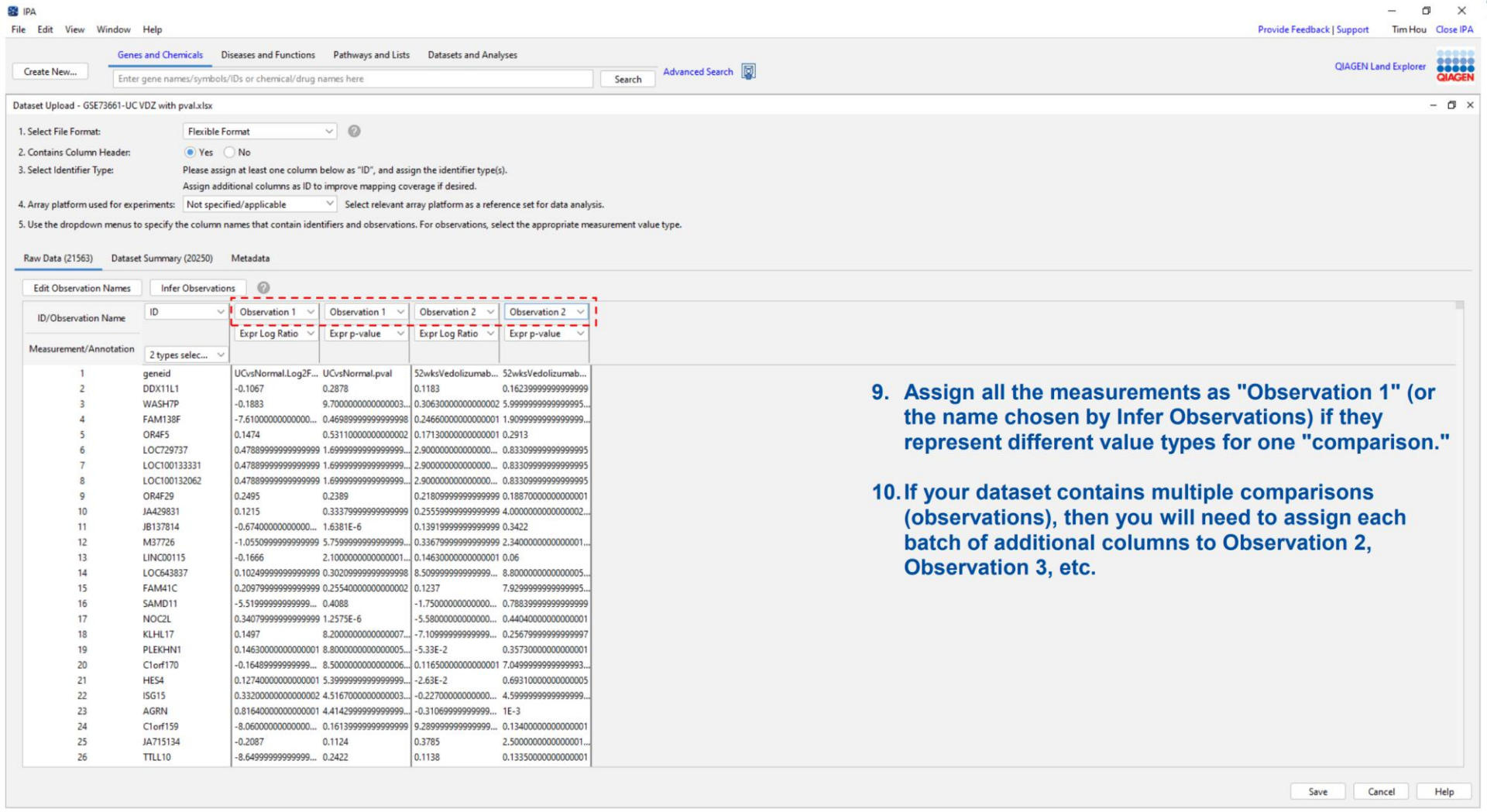

1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1	-0.1067	0.2878	0.1183	0.162399999999999
3	WASH7P	-0.1883	9.7000000000000003...	0.306300000000000002	5.99999999999999...
4	FAM138F	-7.610000000000000...	0.469899999999999998	0.246600000000000001	1.90999999999999...
5	OR4F5	0.1474	0.531100000000000002	0.171300000000000001	0.2913
6	LOC729737	0.478899999999999999	1.699999999999999...	2.900000000000000...	0.833099999999999995
7	LOC100133331	0.478899999999999999	1.699999999999999...	2.900000000000000...	0.833099999999999995
8	LOC100132062	0.478899999999999999	1.699999999999999...	2.900000000000000...	0.833099999999999995
9	OR4F29	0.2495	0.2389	0.218099999999999999	0.188700000000000001
10	JA429831	0.1215	0.333799999999999999	0.255599999999999999	4.000000000000002...
11	JB137814	-0.674000000000000...	1.6381E-6	0.139199999999999999	0.3422
12	M37726	-1.055099999999999999	5.759999999999999...	0.336799999999999999	2.340000000000001...
13	LINC00115	-0.1666	2.100000000000001...	0.146300000000000001	0.06
14	LOC643837	0.102499999999999999	0.302099999999999998	8.509999999999999...	8.800000000000005...
15	FAM41C	0.209799999999999999	0.255400000000000002	0.1237	7.929999999999995...
16	SAMD11	-5.519999999999999...	0.4088	-1.750000000000000...	0.788399999999999999
17	NOC2L	0.340799999999999999	1.2575E-6	-5.580000000000000...	0.440400000000000001
18	KLHL17	0.1497	8.200000000000007...	-7.109999999999999...	0.256799999999999997
19	PLEKHN1	0.146300000000000001	8.800000000000005...	-5.33E-2	0.357300000000000001
20	C1orf170	-0.164899999999999...	8.500000000000006...	0.116500000000000001	7.049999999999993...
21	HES4	0.127400000000000001	5.399999999999999...	-2.63E-2	0.693100000000000005
22	ISG15	0.332000000000000002	4.516700000000003...	-0.227000000000000...	4.599999999999999...
23	AGRN	0.816400000000000001	4.414299999999999...	-0.310699999999999...	1E-3
24	C1orf159	-8.060000000000000...	0.161399999999999999	9.289999999999999...	0.134000000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.500000000000001...
26	TTLL10	-8.649999999999999...	0.2422	0.1138	0.133500000000000001

9. **Assign all the measurements as "Observation 1" (or the name chosen by Infer Observations) if they represent different value types for one "comparison."**

10. **If your dataset contains multiple comparisons (observations), then you will need to assign each batch of additional columns to Observation 2, Observation 3, etc.**

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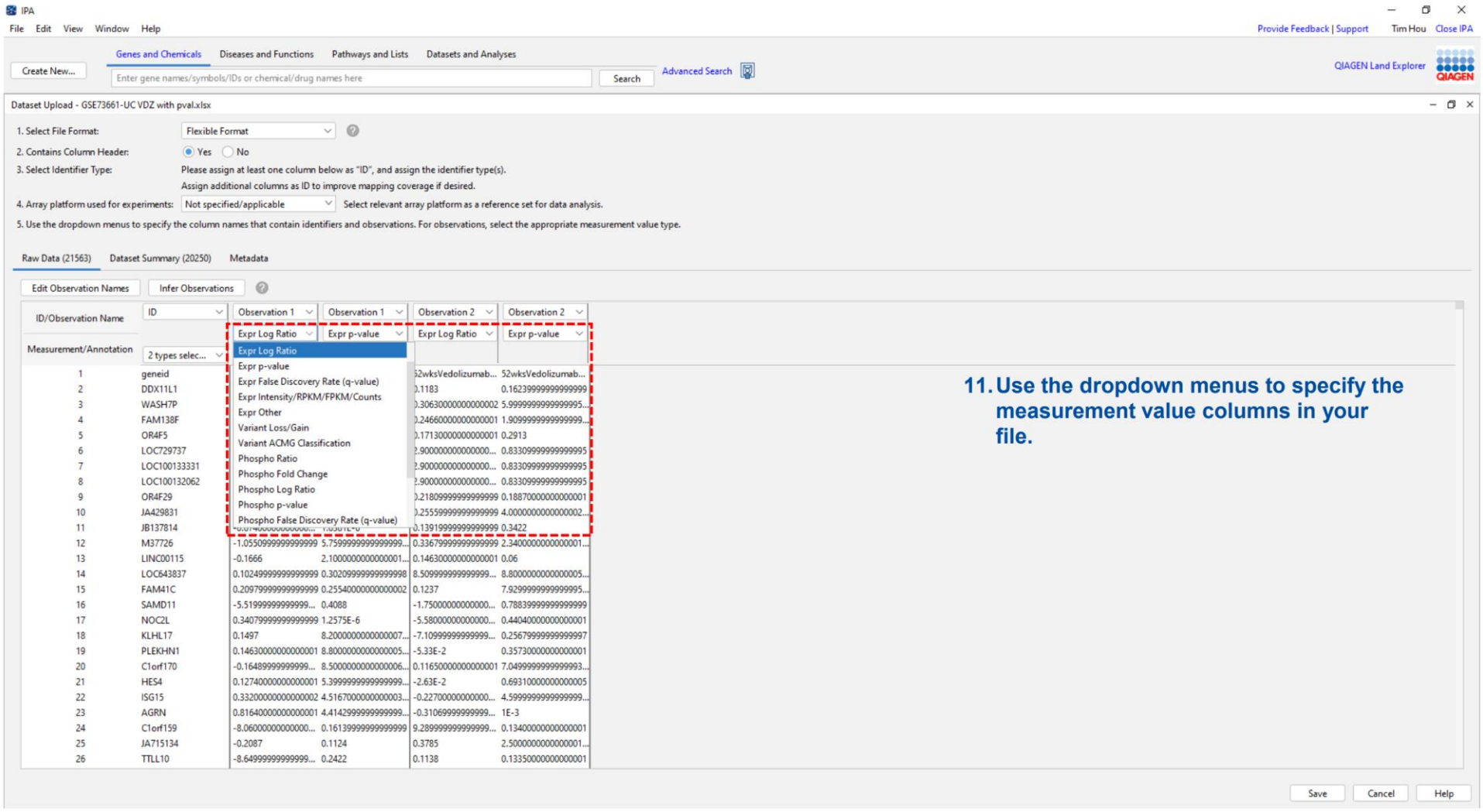

11. Use the dropdown menus to specify the measurement value columns in your file.

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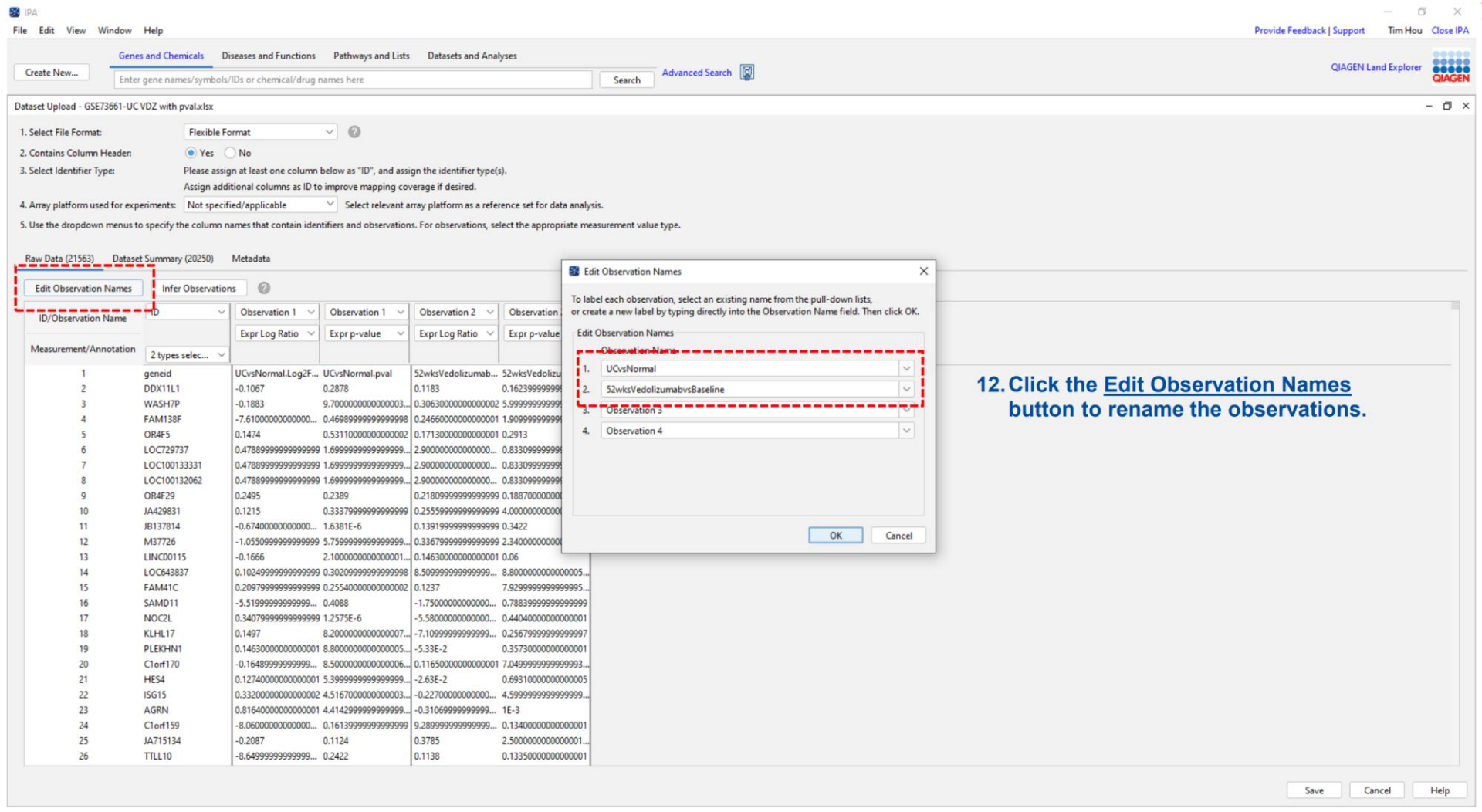

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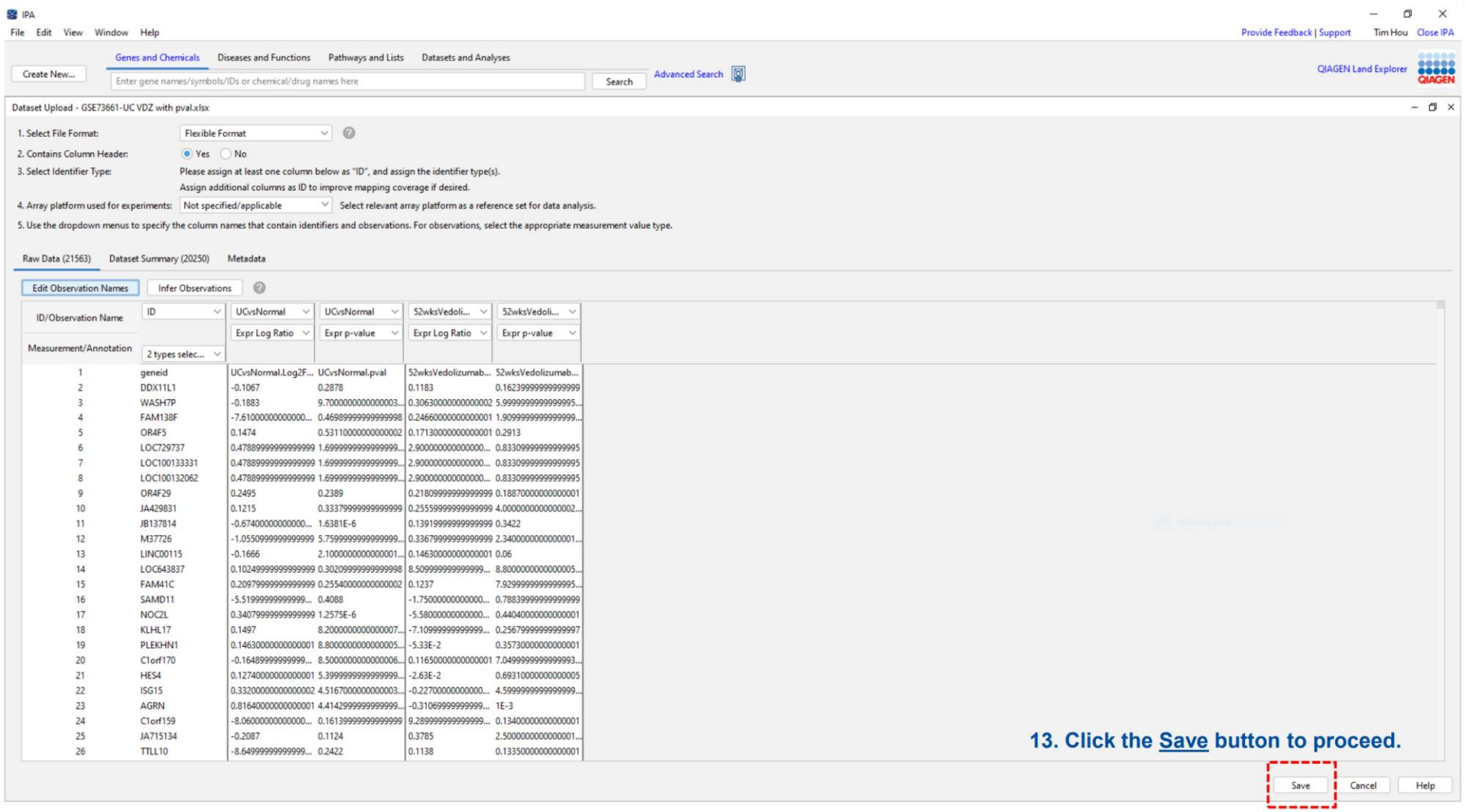

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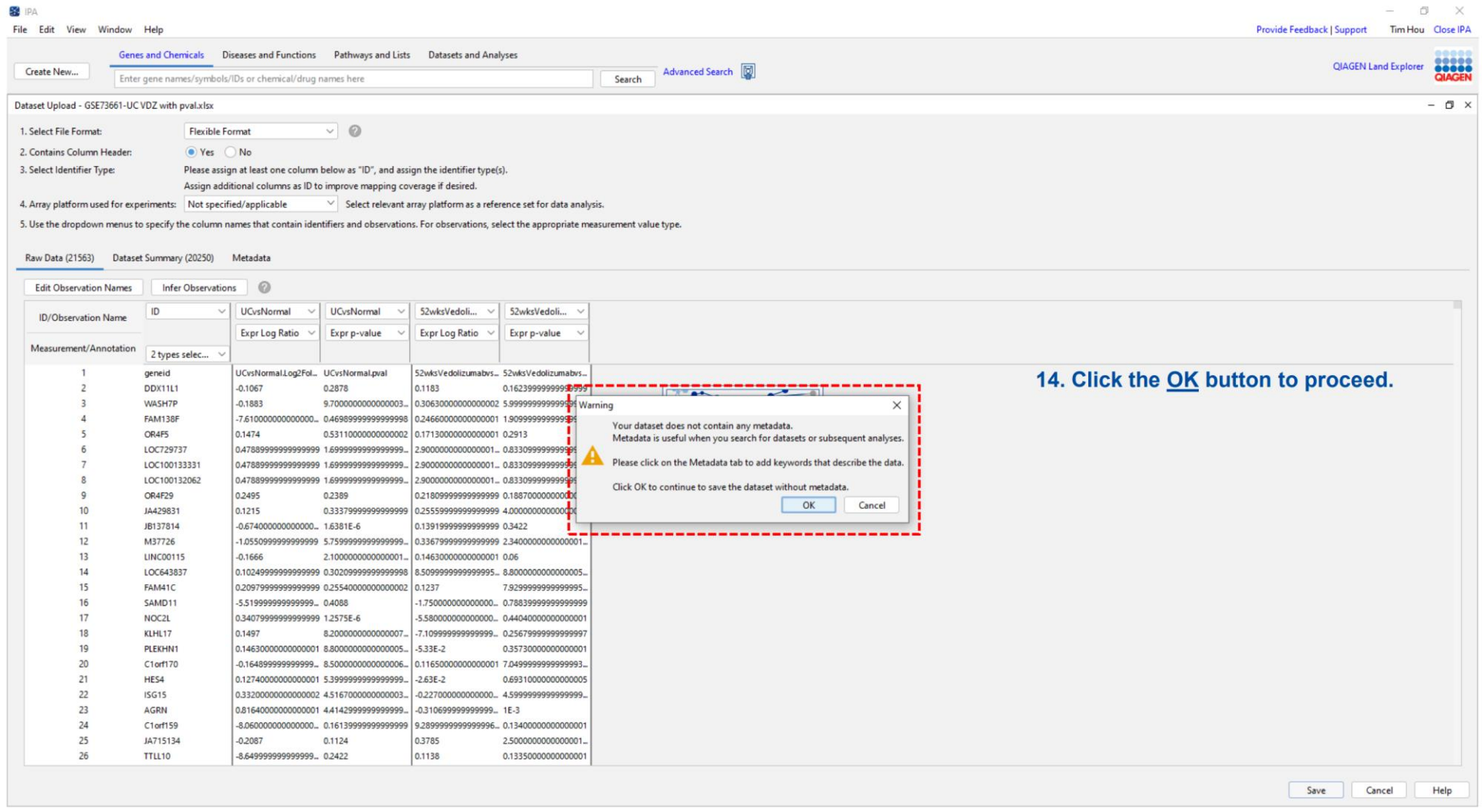

14. Click the OK button to proceed.

Sample to Insight

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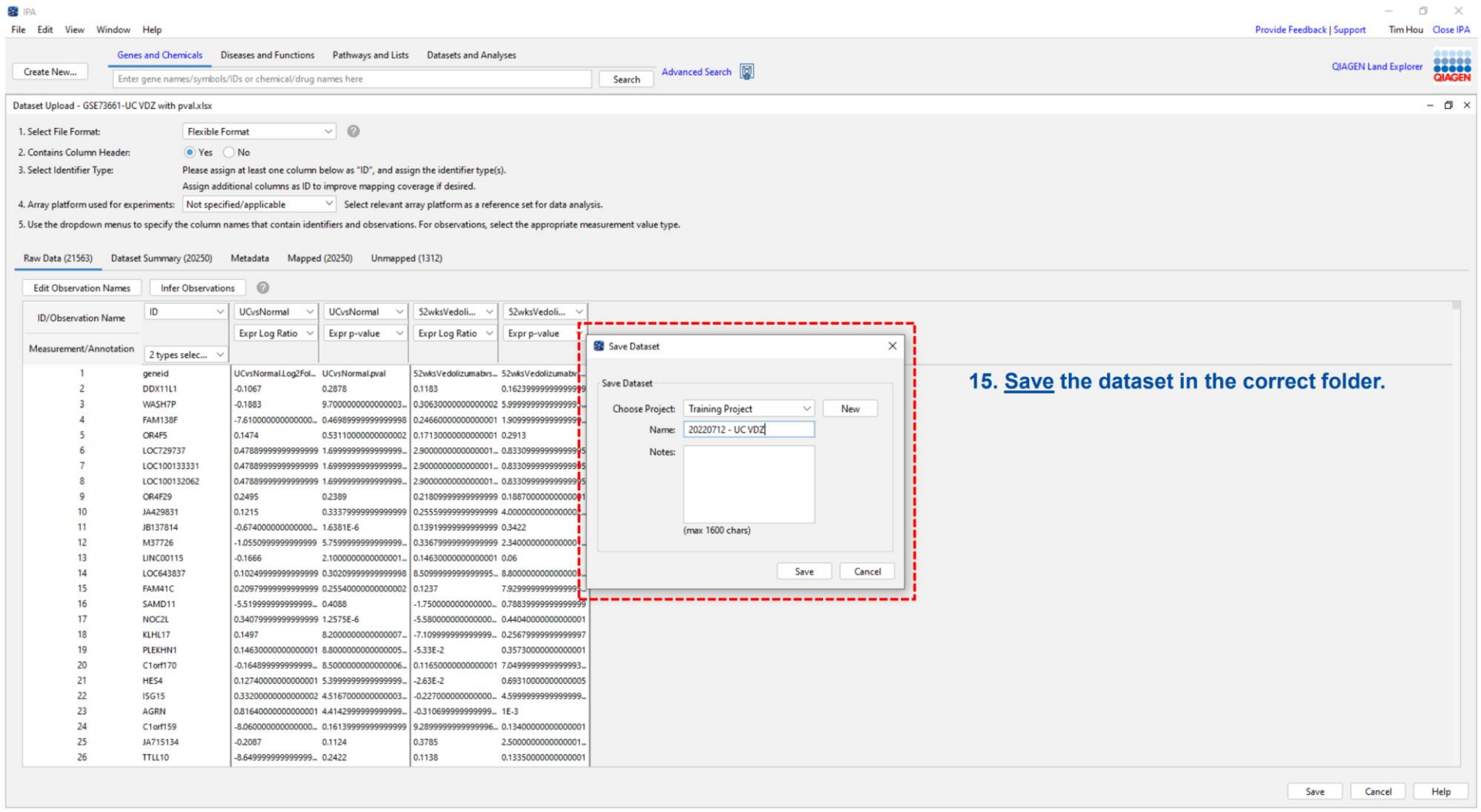

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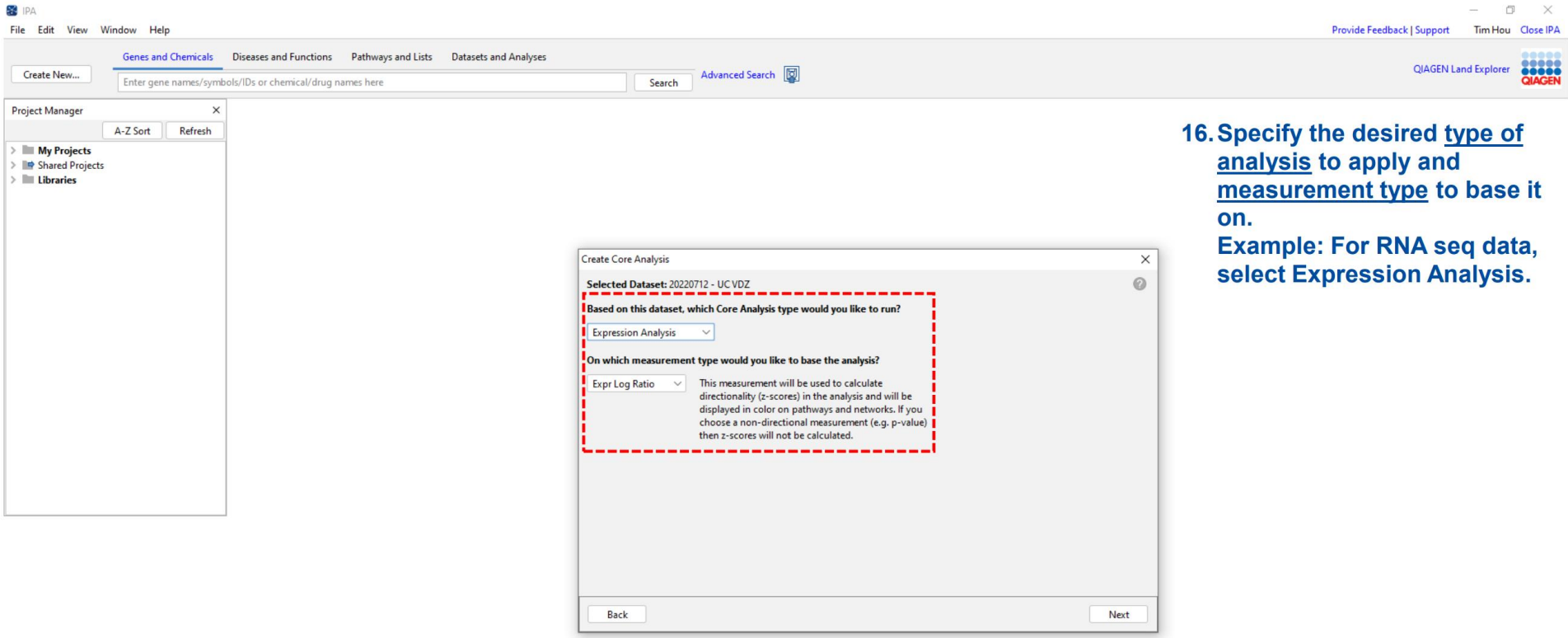

16. Specify the desired type of analysis to apply and measurement type to base it on.
    Example: For RNA seq data, select Expression Analysis.

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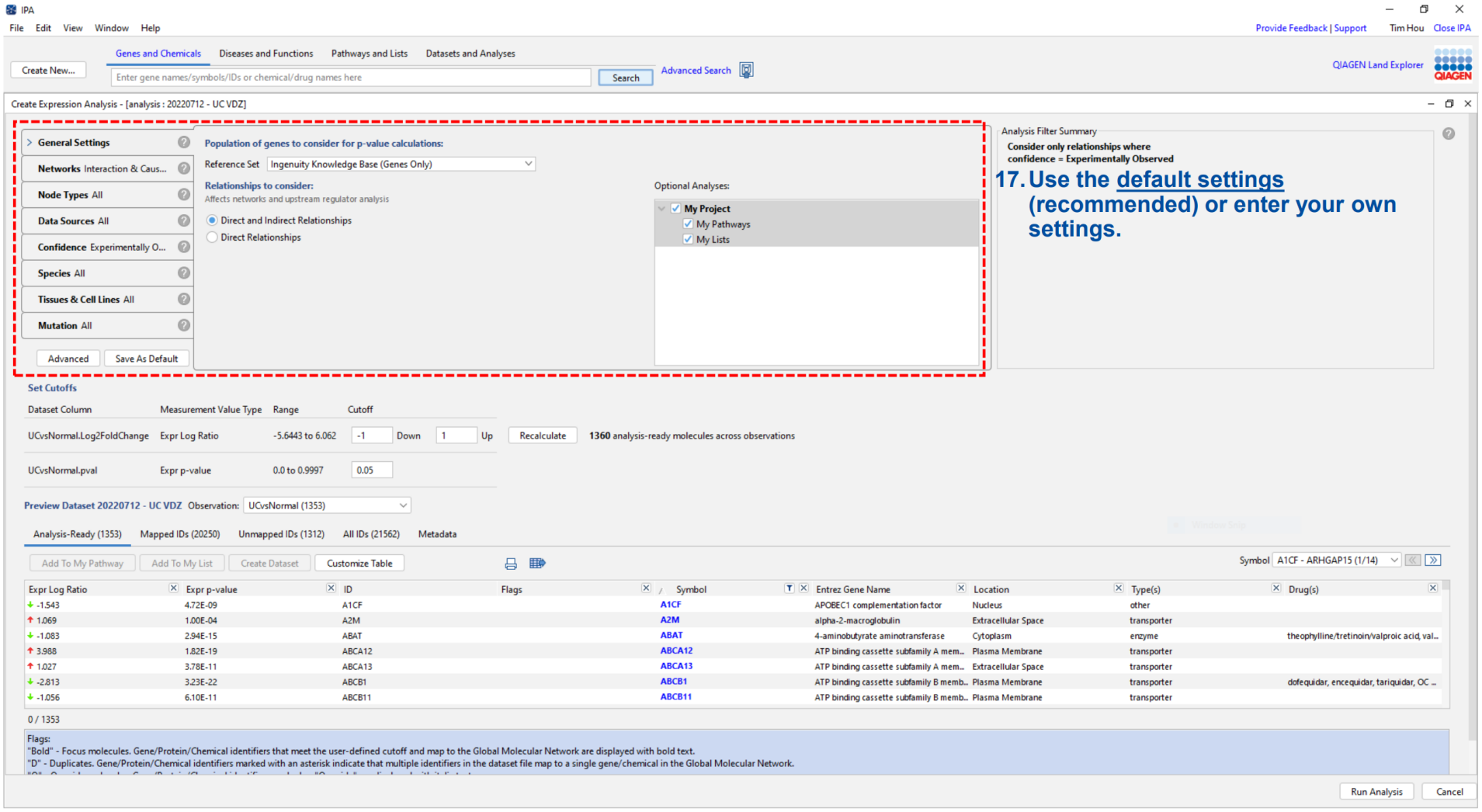

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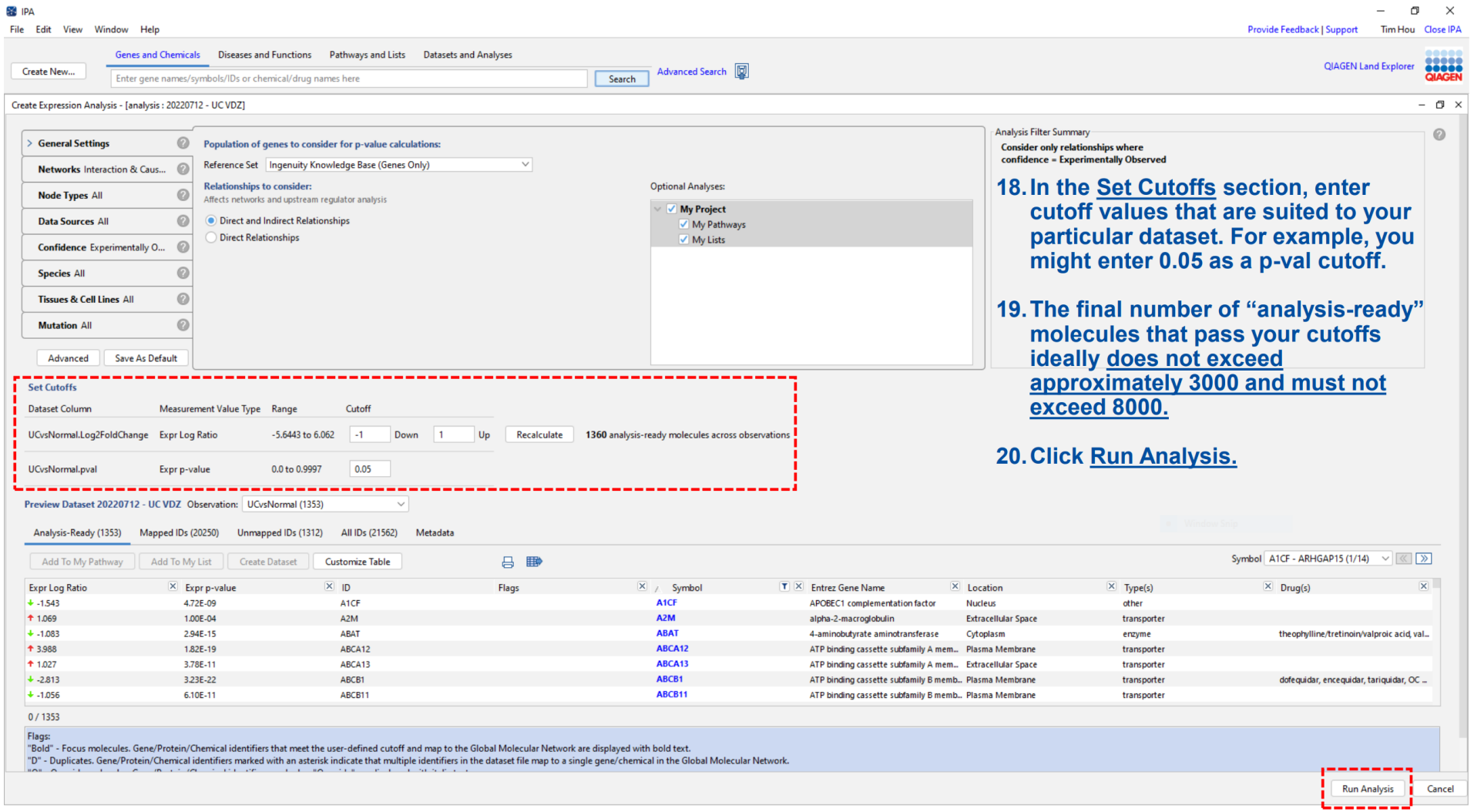

18. In the Set Cutoffs section, enter cutoff values that are suited to your particular dataset. For example, you might enter 0.05 as a p-val cutoff.

19. The final number of "analysis-ready" molecules that pass your cutoffs ideally does not exceed approximately 3000 and must not exceed 8000.

20. Click Run Analysis.

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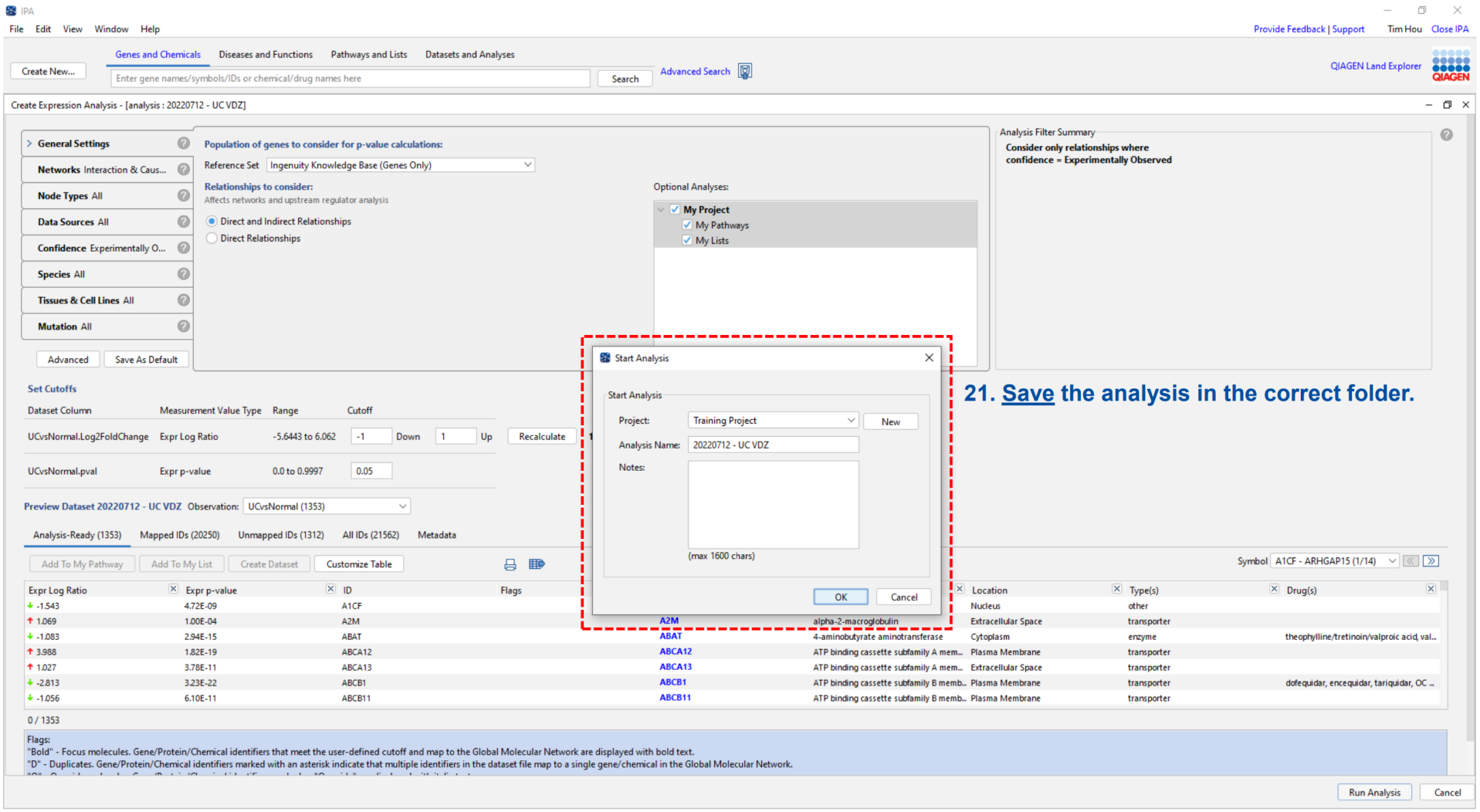

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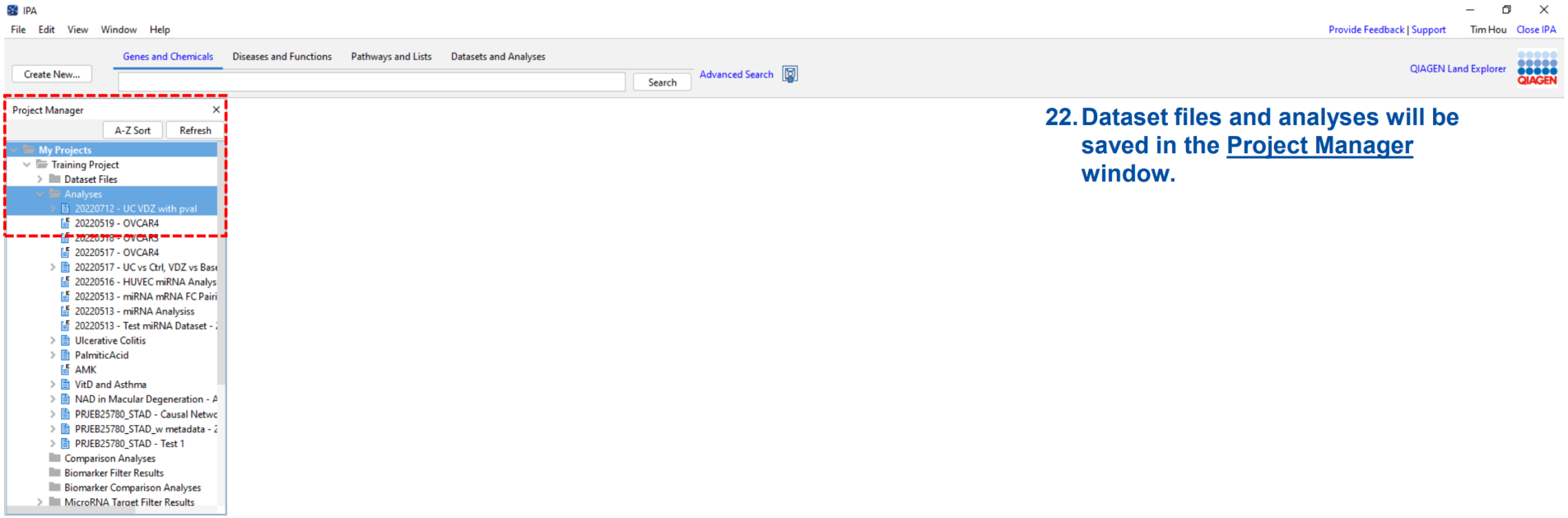

22. **Dataset files and analyses will be saved in the Project Manager window.**

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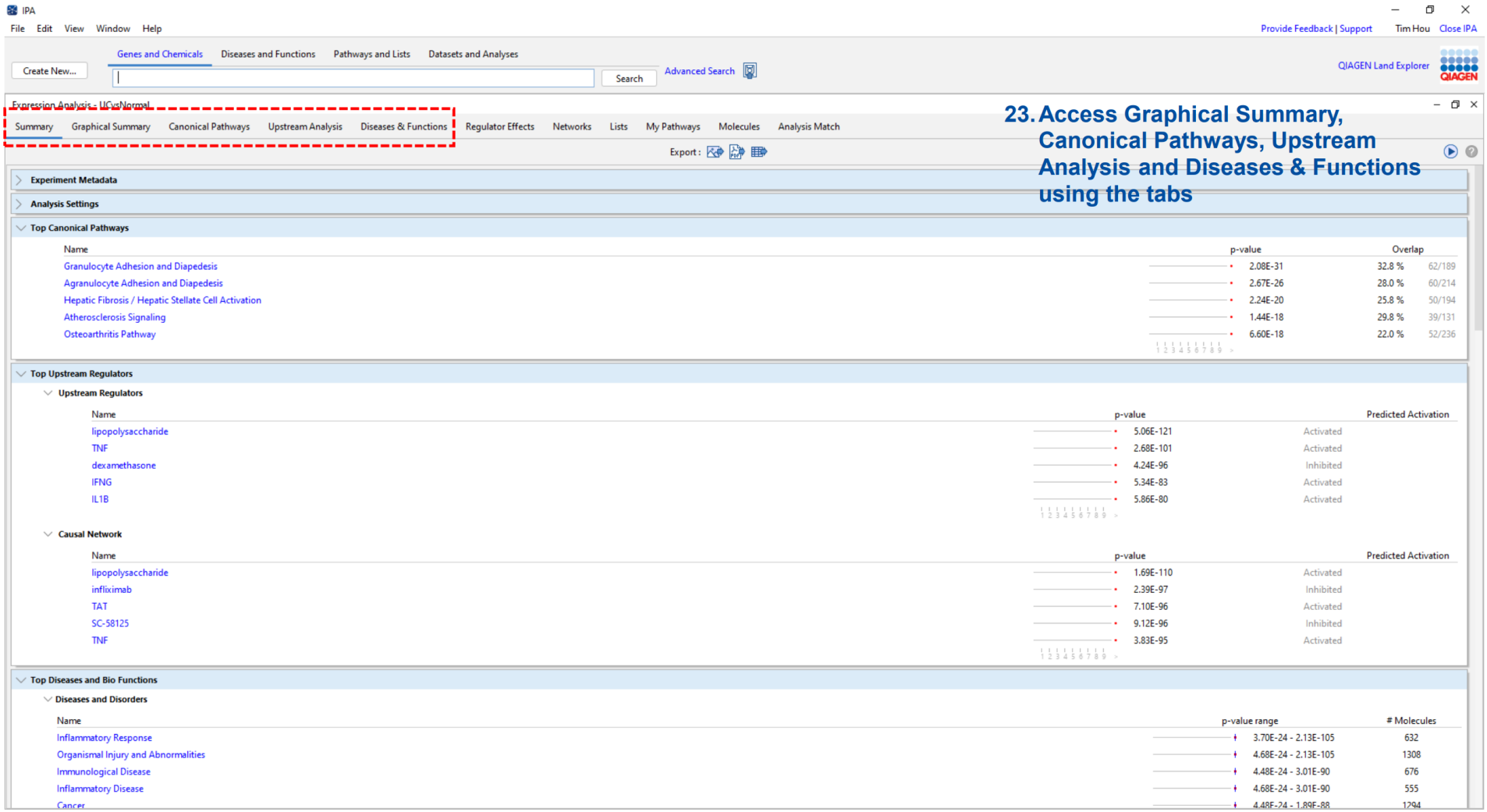

23. Access Graphical Summary, Canonical Pathways, Upstream Analysis and Diseases & Functions using the tabs

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