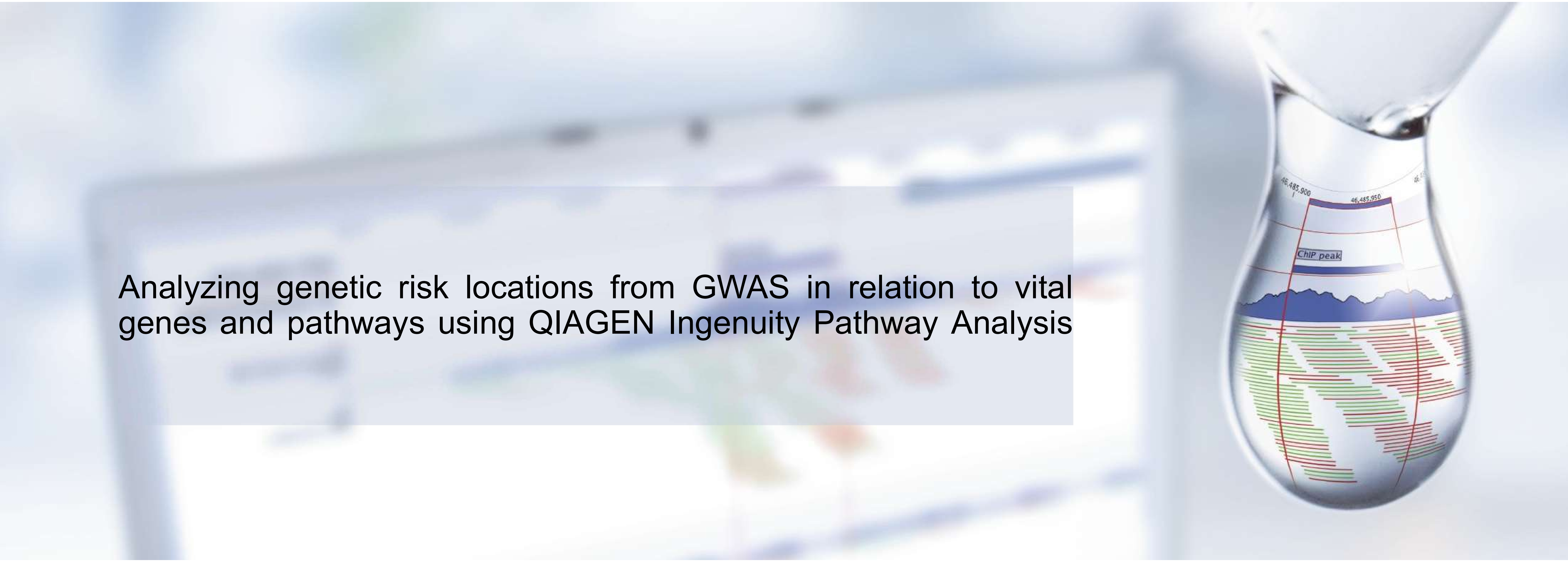


Analyzing genetic risk locations from GWAS in relation to vital genes and pathways using QIAGEN Ingenuity Pathway Analysis

Grace Chou 周儀柔 資深業務專員

Bryce Lin 林文賢 經理 Bioinfo@GGA.ASIA

Agenda

- Introduction to QIAGEN Ingenuity Pathway Analysis
- Analyzing risk loci using IPA
  - Data format
  - Data upload and analysis setup
  - Core analysis
- Comparing between risk loci analysis
  - Comparison Analysis
  - Compare
- Querying IPA's Knowledge base
  - Custom network construction for risk loci associated genes
  - Contextualization using public data
- Summary

IPA Training Account & Demo Data

Account: ipaXX@ingenuity.com
(XX= 01~45)
Password: **9-Str0ngP@&&IPA**

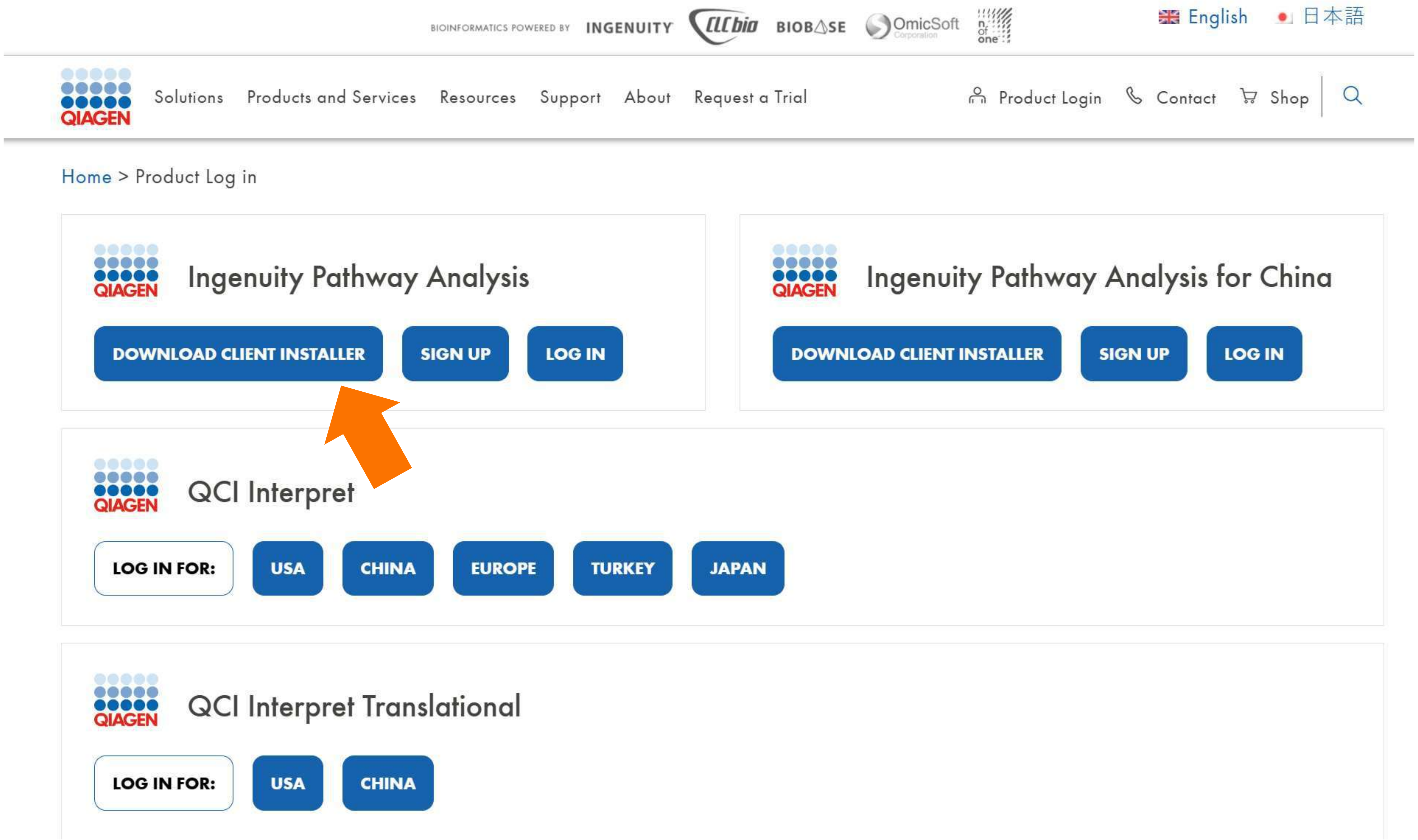
Expired until 10/20

Download website: https://tinyurl.com/**GGAIPA**

Dataset: https://tinyurl.com/**GGAdataset**

Client: (IPA Login)

IPA Download webpage



Home > Product Log in

Ingenuity Pathway Analysis

DOWNLOAD CLIENT INSTALLER SIGN UP LOG IN

Ingenuity Pathway Analysis for China

DOWNLOAD CLIENT INSTALLER SIGN UP LOG IN

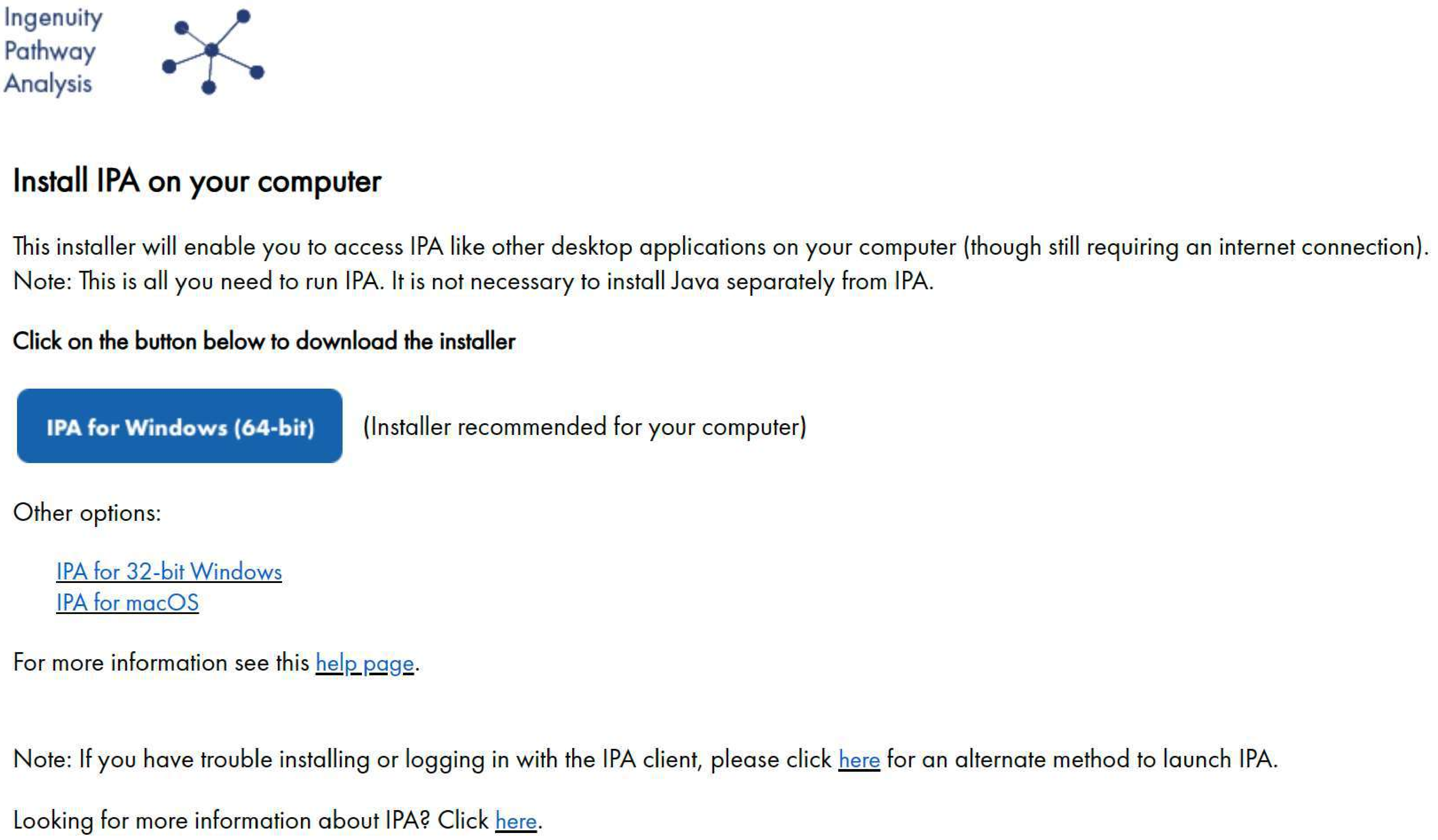
QCI Interpret

LOG IN FOR: USA CHINA EUROPE TURKEY JAPAN

QCI Interpret Translational

LOG IN FOR: USA CHINA

Choose your IPA installer



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.

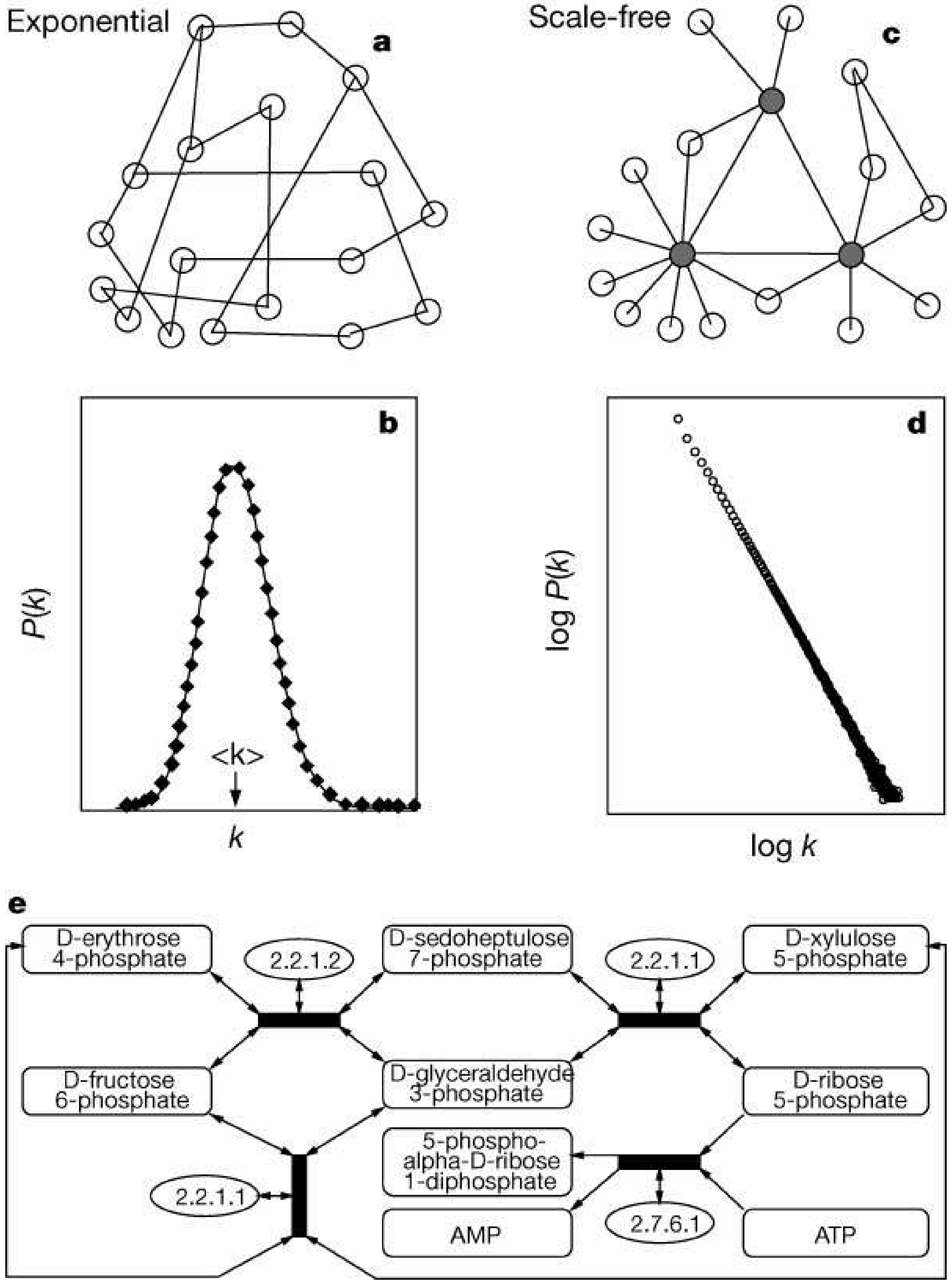
Note: If you have trouble installing or logging in with the IPA client, please click here for an alternate method to launch IPA.

Looking for more information about IPA? Click here.

The large-scale organization of metabolic networks

Despite significant variation in their individual constituents and pathways, these metabolic networks have the same topological scaling properties and show striking similarities to the inherent organization of complex non-biological systems. This may indicate that metabolic organization is not only identical for all living organisms, but also complies with the design principles of robust and error-tolerant scale-free networks, and may represent a common blueprint for the large-scale organization of interactions among all cellular constituents.

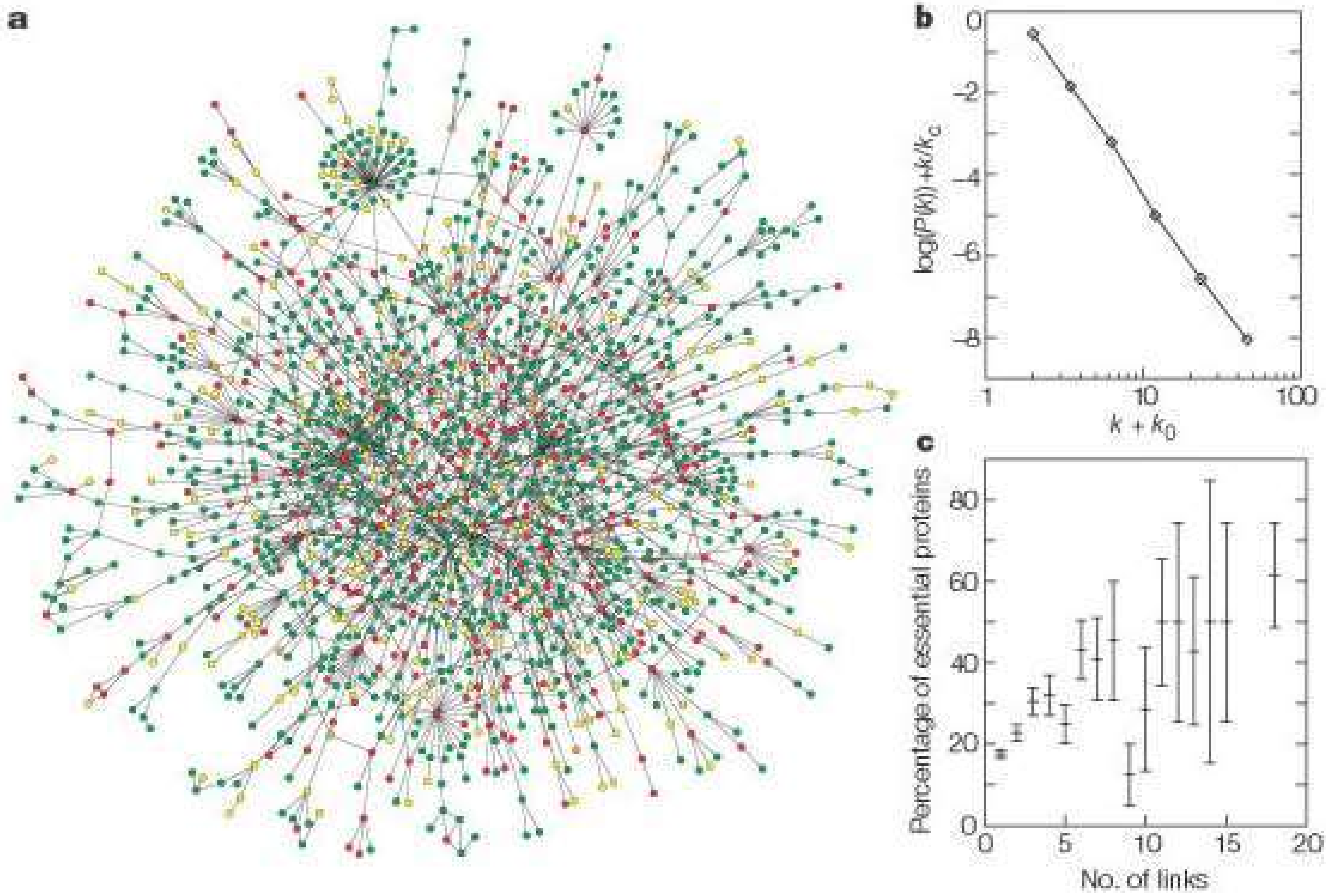
Nature 407, 651-654 (2000)



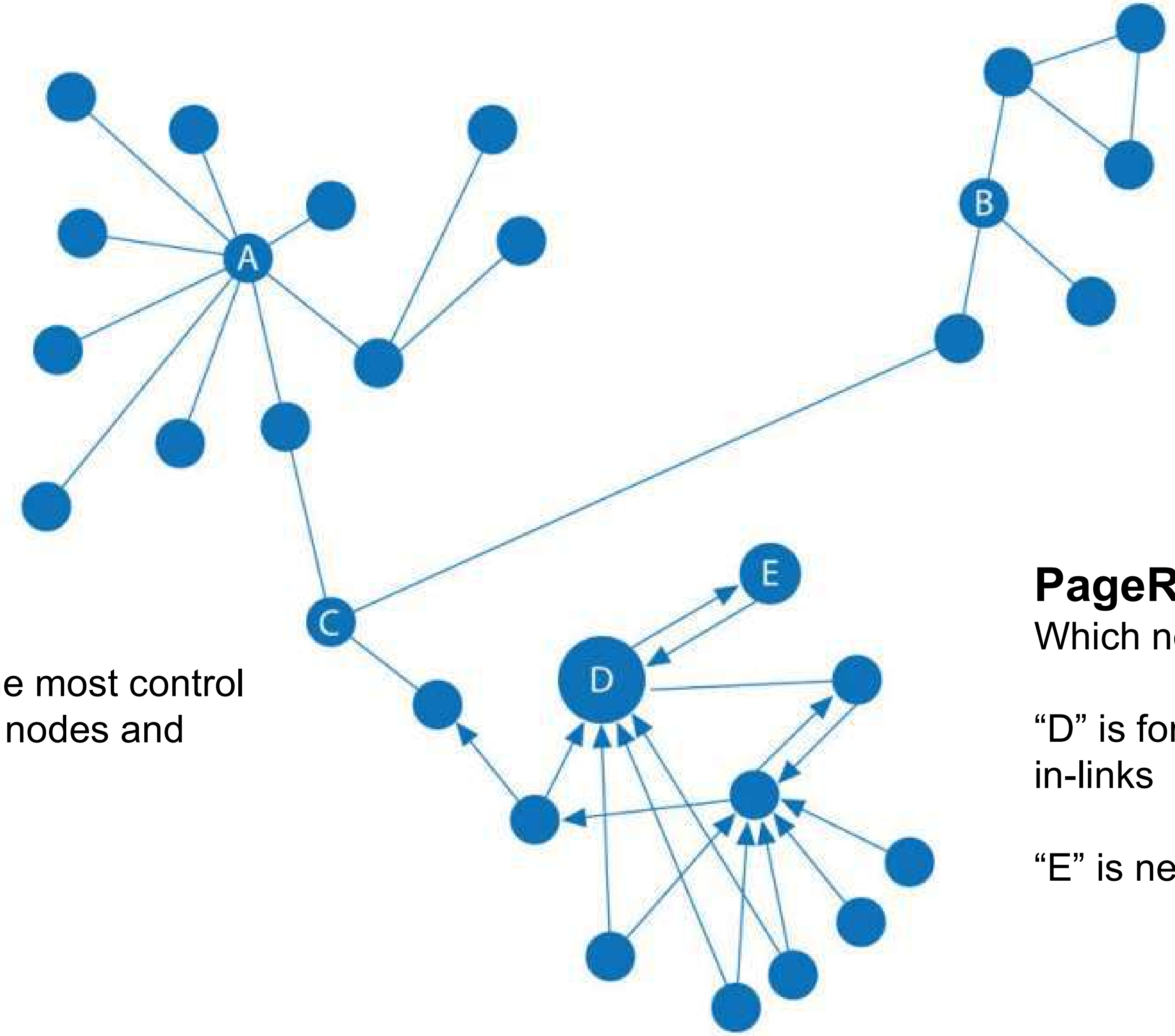
Lethality and centrality in protein networks

The most highly connected proteins in the cell are the most important for its survival.

Nature 411, 41-42 (2001)



Measurement of topology



Degree
Number of connections?

"A" has a high degree

Closeness
Which node can most easily reach all other nodes in a graph or subgraph?

"B" is closest with the fewest hops in its subgraph

Betweenness
Which node has the most control over flow between nodes and groups?

"C" is a bridge

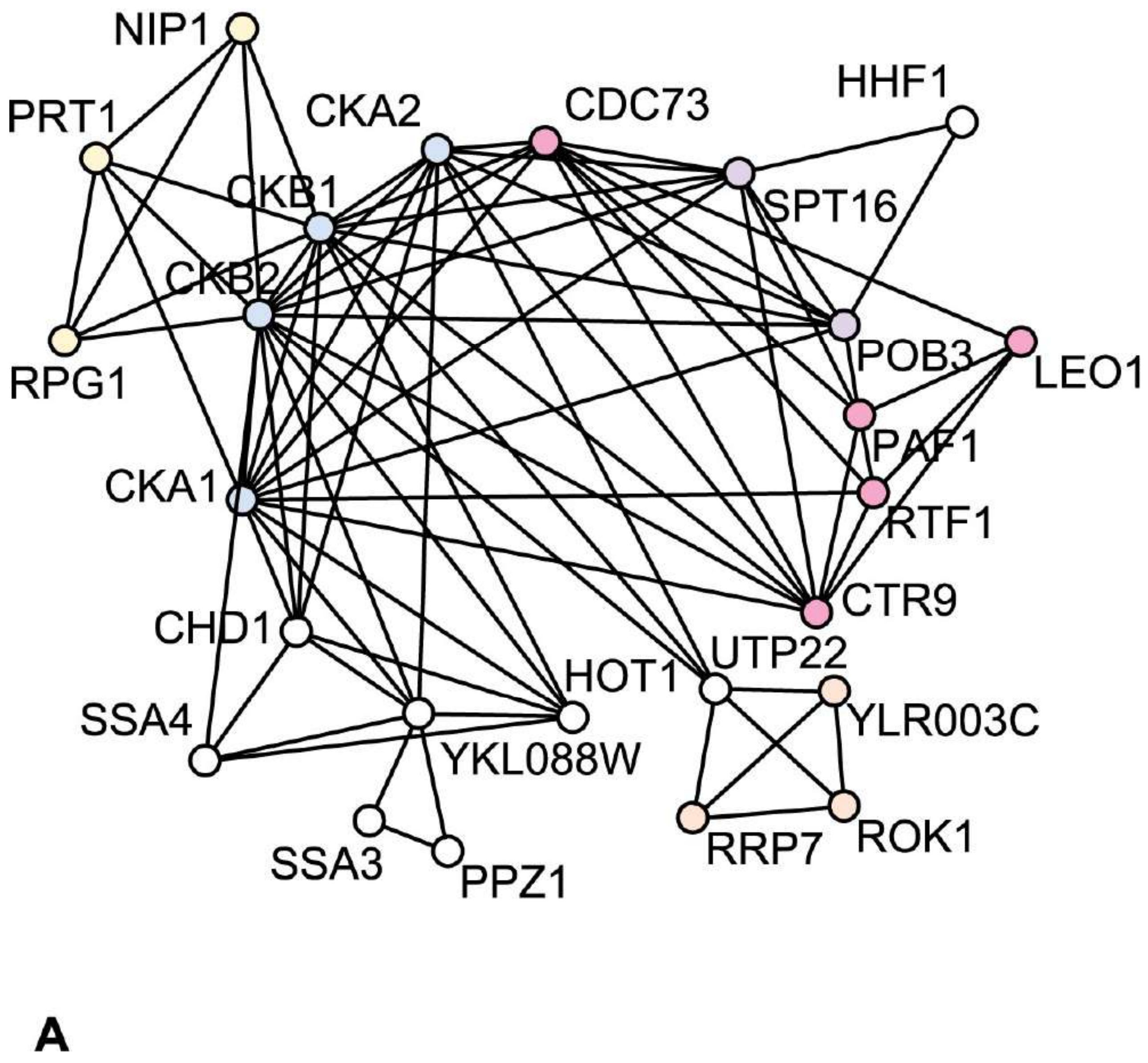
PageRank
Which node is the most important?

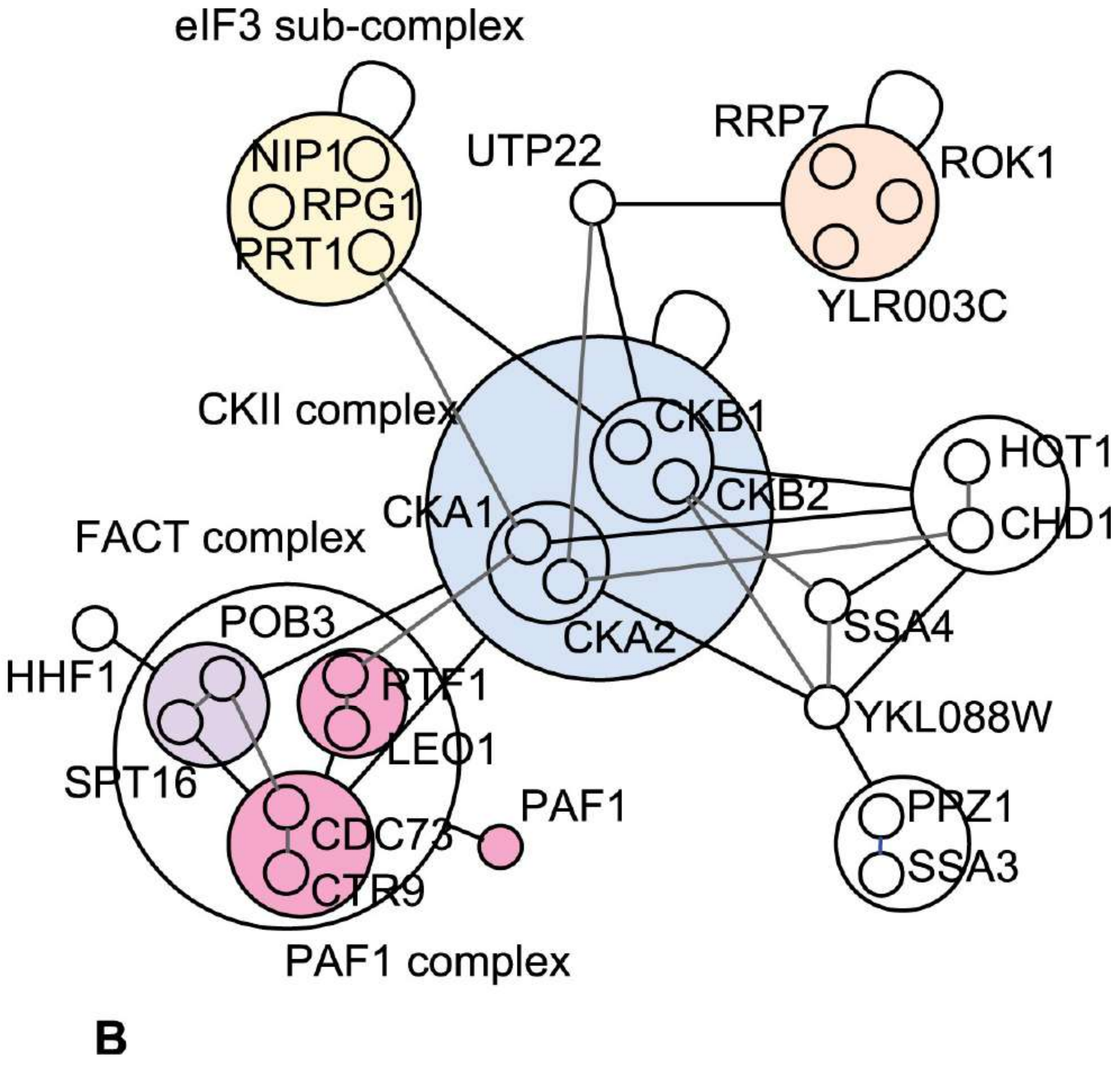
"D" is foremost based on number & weighting of in-links

"E" is next, due to the influence of D's link

(Source: Needham & Hodler, 2019)

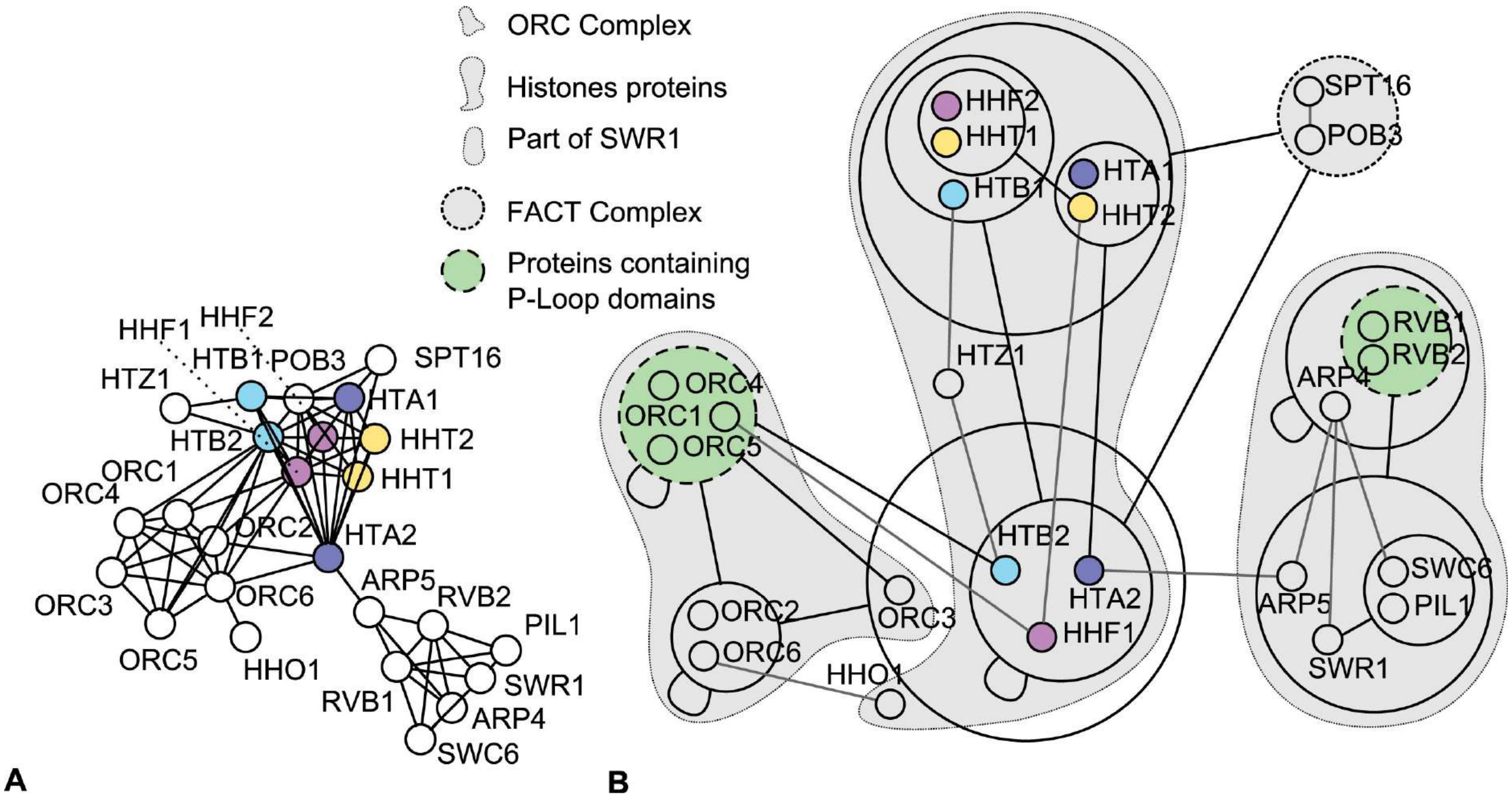
Casein Kinase II Complex





•https://doi.org/10.1371/journal.pcbi.1000108

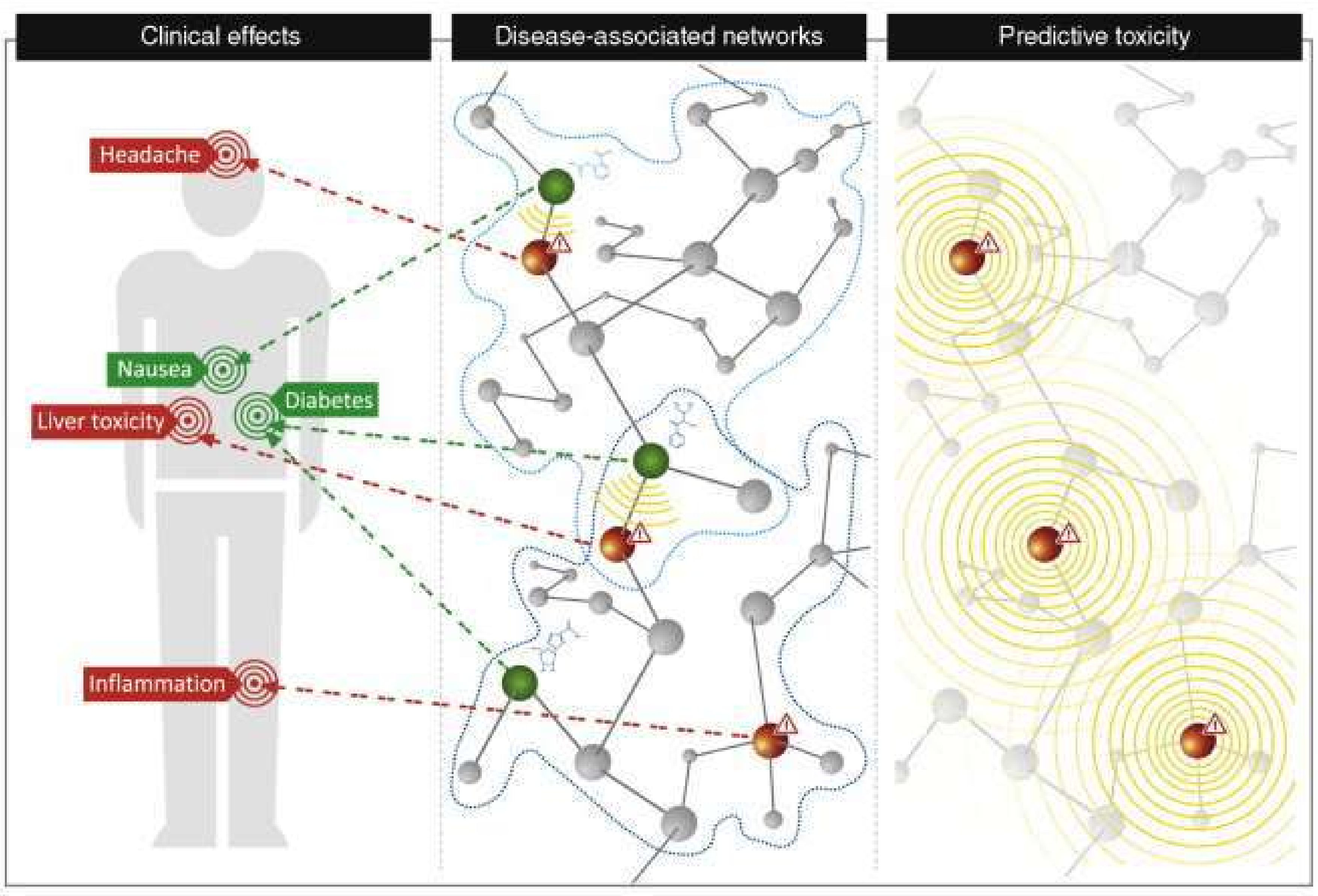
Histone Protein Interactions and Neighbouring Proteins



•https://doi.org/10.1371/journal.pcbi.1000108

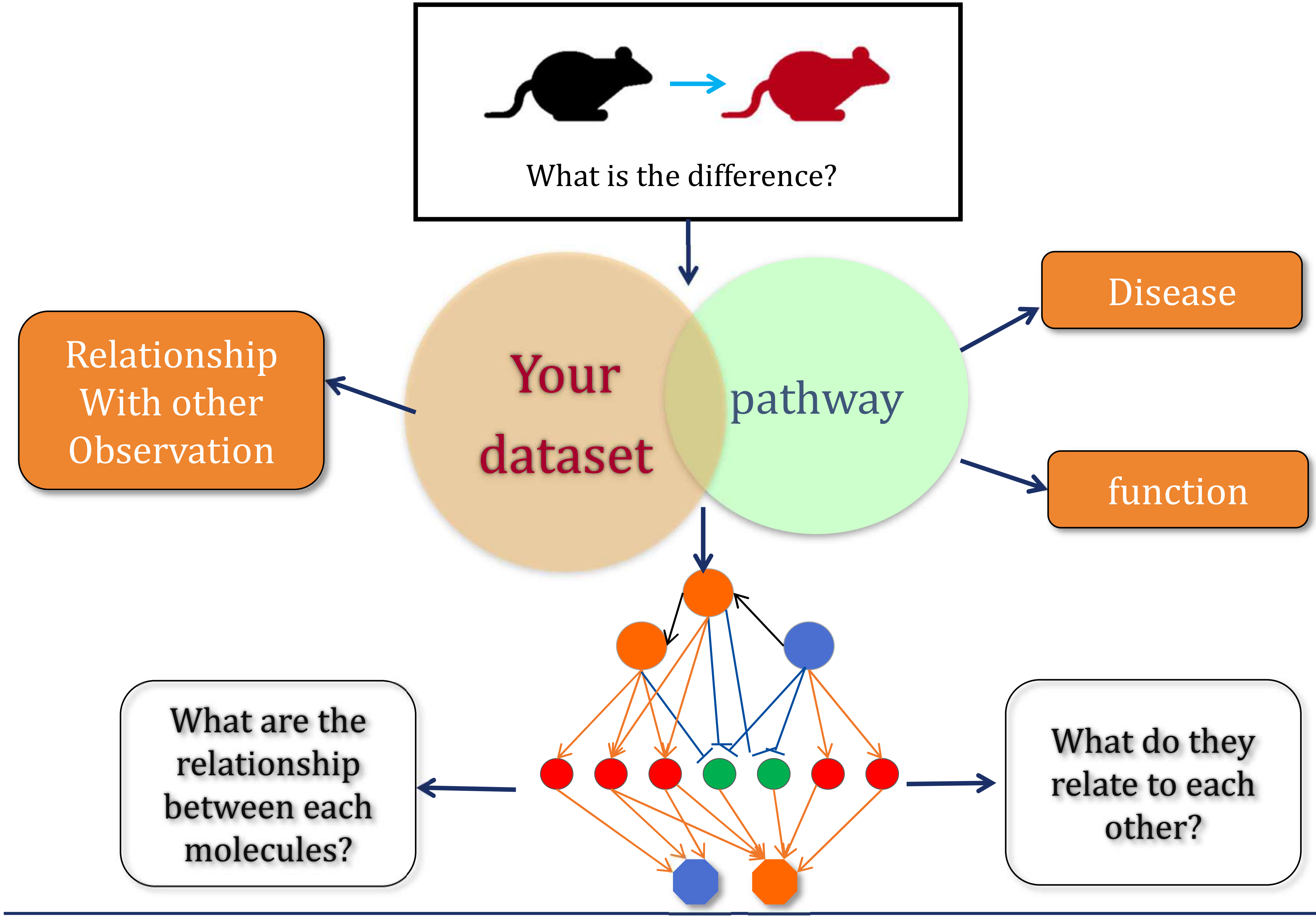
Models can identify the areas of influence of proteins leading to undesired effects, and to explore how they are related to network connectivity.

- Identifying potential drug targets
- Designing the toxicity tests
- Highlighting the existence of validated drug targets for a given therapeutic indication in key enclaves of the network describing a different disease, thereby suggesting candidates for drug repurposing (i.e. finding new indications for a target).



TRENDS in Pharmacological Sciences

Why are we using IPA?



What is the difference?

Your dataset

pathway

Relationship
With other
Observation

Disease

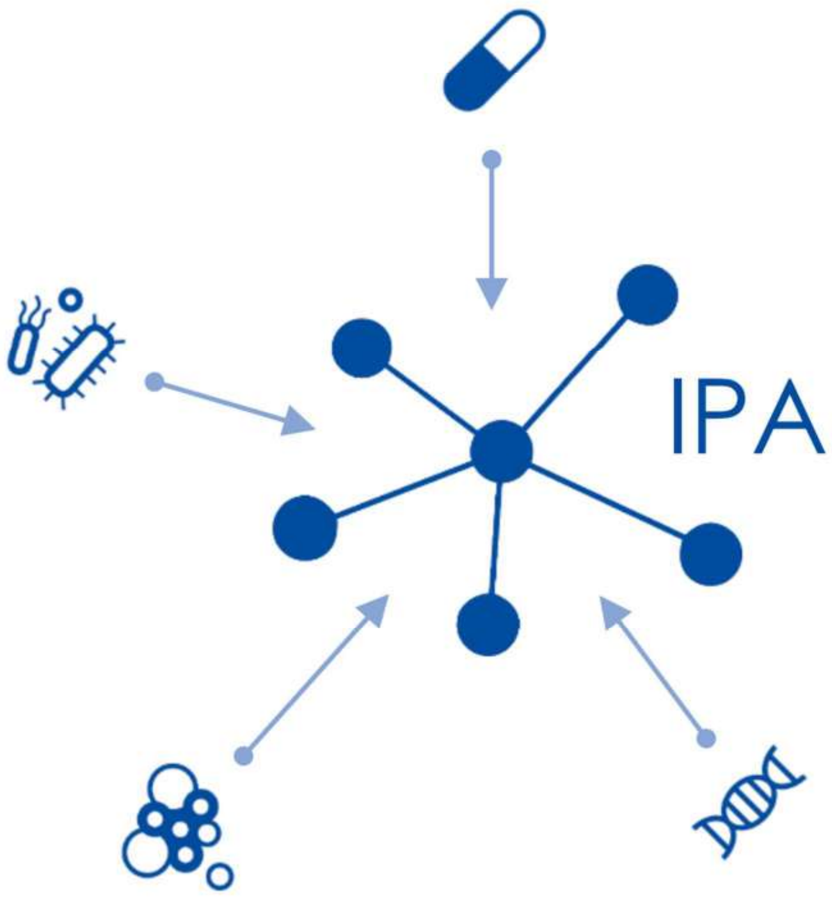
function

What are the relationship between each molecules?

What do they relate to each other?

Ingenuity Pathway Analysis is powered by our knowledge base

Updated weekly with the latest clinical trials and manuscripts



12+ million findings curated using controlled vocabulary

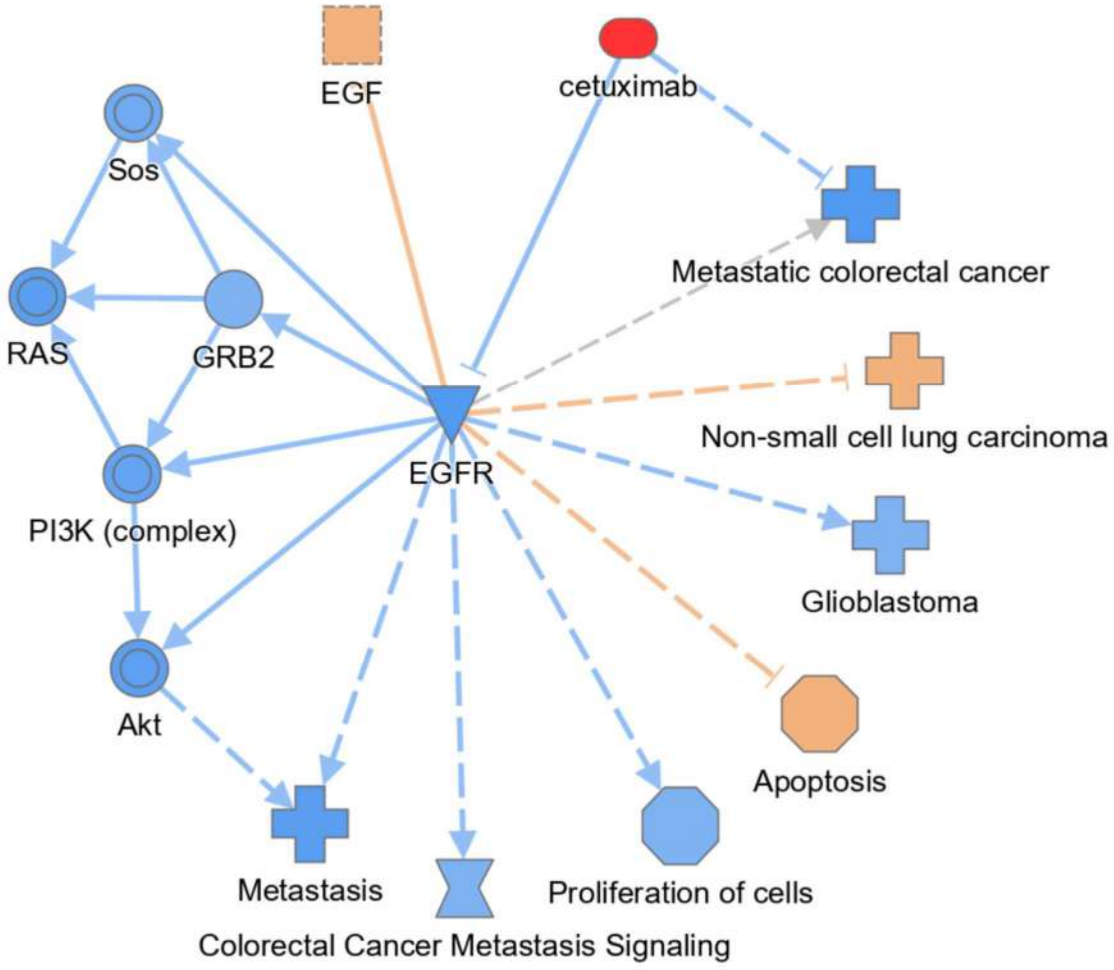
EGF – EGFR
[one of many]

Type: **activation**
Direction: **directional**
Effect: **increases**
Directness: **direct**
Tissue: **epithelial cells**
Location: **plasma membrane**
Source: **PMID: 17909010**

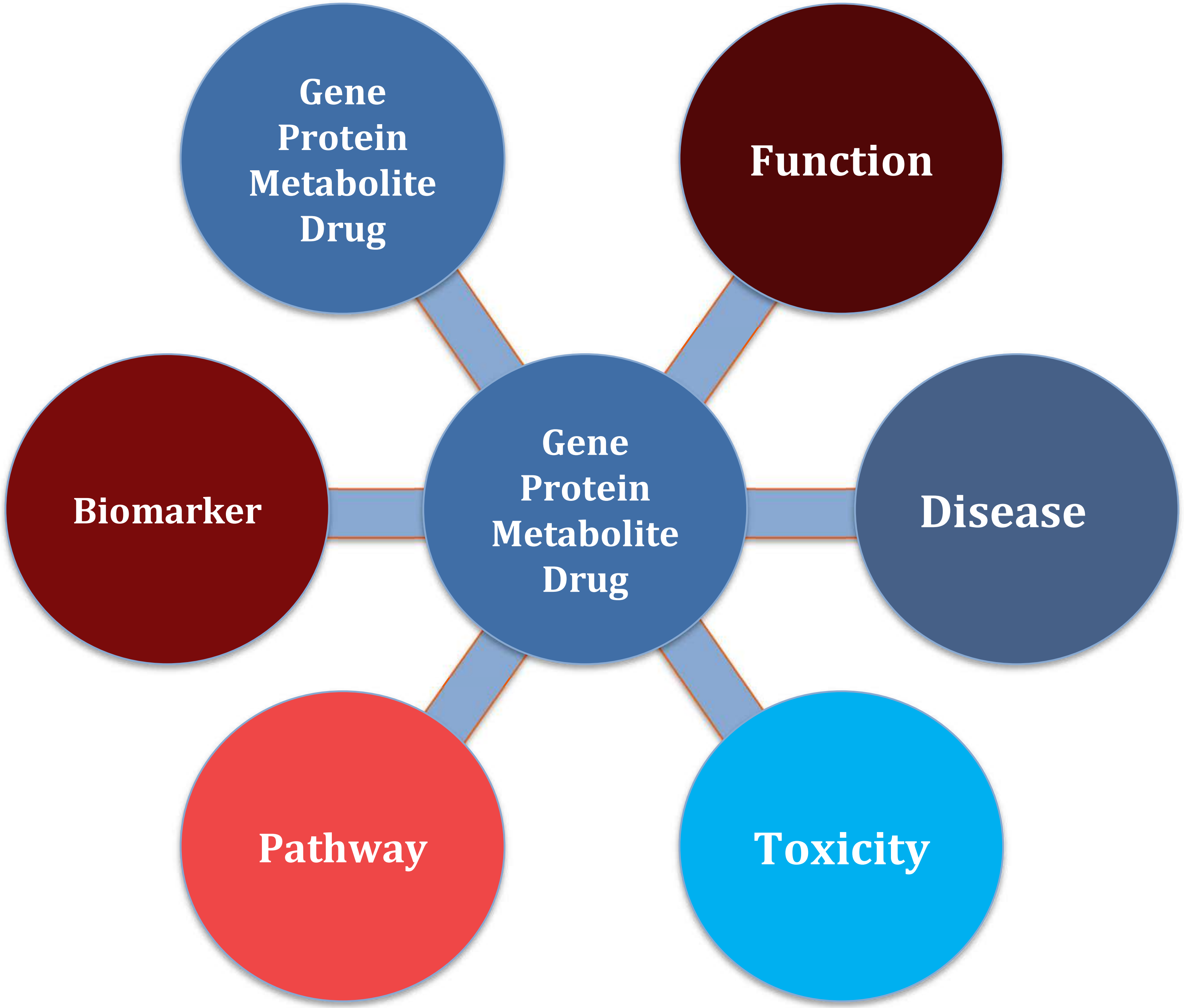
cetuximab – EGFR
[one of many]

Type: **phosphorylation**
Direction: **directional**
Effect: **decreases**
Cell line: **CaR1 cells**
Organism: **human**
Experiment: **immunoblot**
Source: **PMID: 23213241**

Decades of accumulated knowledge mapped in directional networks



Using IPA to Discover Relationships in Experimental Data



Gene
Protein
Metabolite
Drug

Function

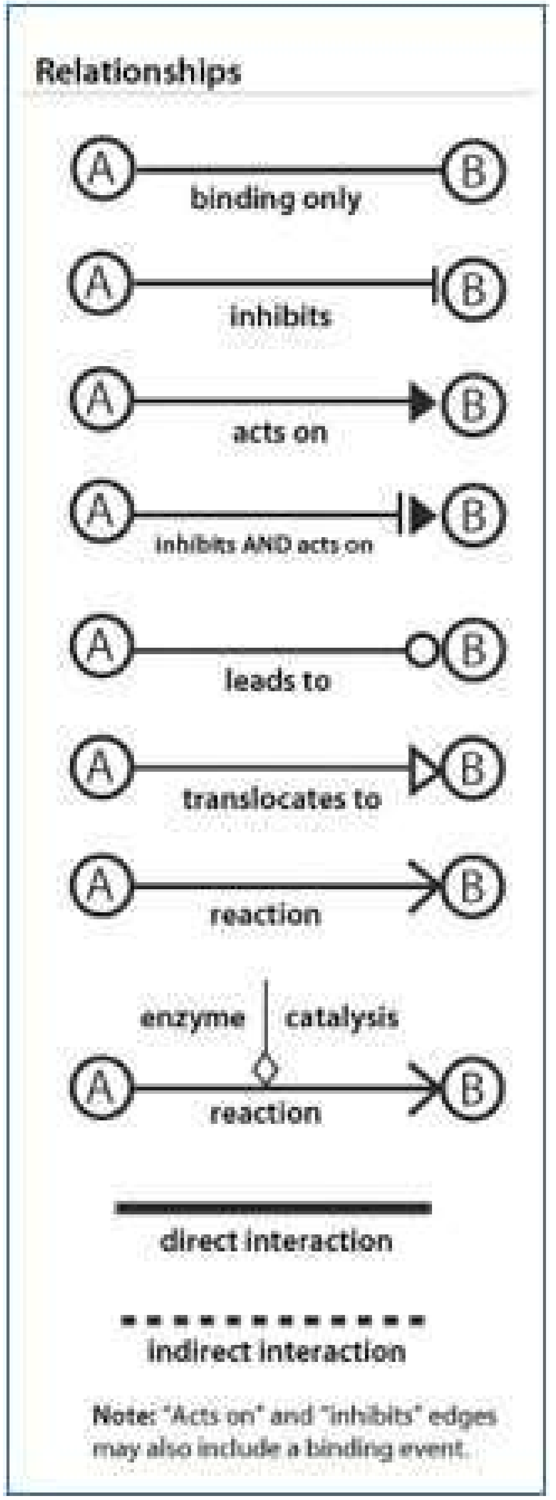
Biomarker

Gene
Protein
Metabolite
Drug

Disease

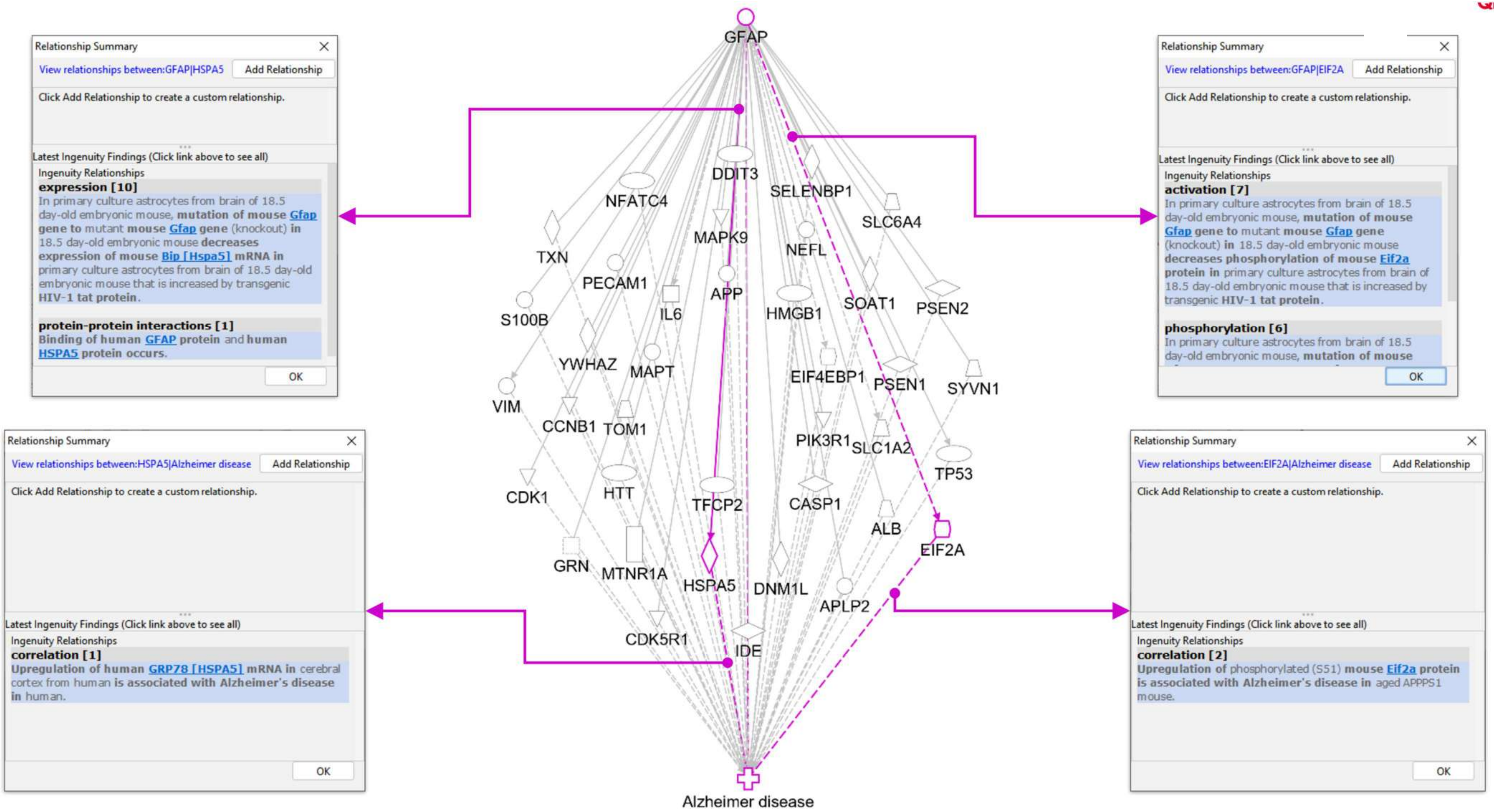
Pathway

Toxicity



Note: "Acts on" and "inhibits" edges may also include a binding event.

Every connection in IPA is backed by literature findings



View relationships between:GFAP|HSPA5

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

expression [10]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse Gfap gene to** mutant **mouse Gfap gene** (knockout) **in** 18.5 day-old embryonic mouse **decreases expression of mouse Bip [Hspa5] mRNA in** primary culture astrocytes from brain of 18.5 day-old embryonic mouse that is increased by transgenic **HIV-1 tat protein.**

protein-protein interactions [1]

Binding of human GFAP protein and **human HSPA5 protein occurs.**

View relationships between:GFAP|EIF2A

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

activation [7]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse Gfap gene to** mutant **mouse Gfap gene** (knockout) **in** 18.5 day-old embryonic mouse **decreases phosphorylation of mouse Eif2a protein in** primary culture astrocytes from brain of 18.5 day-old embryonic mouse that is increased by transgenic **HIV-1 tat protein.**

phosphorylation [6]

In primary culture astrocytes from brain of 18.5 day-old embryonic mouse, **mutation of mouse**

View relationships between:HSPA5|Alzheimer disease

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

correlation [1]

Upregulation of human GRP78 [HSPA5] mRNA in cerebral cortex from human **is associated with Alzheimer's disease in** human.

View relationships between:EIF2A|Alzheimer disease

Click Add Relationship to create a custom relationship.

Latest Ingenuity Findings (Click link above to see all)

Ingenuity Relationships

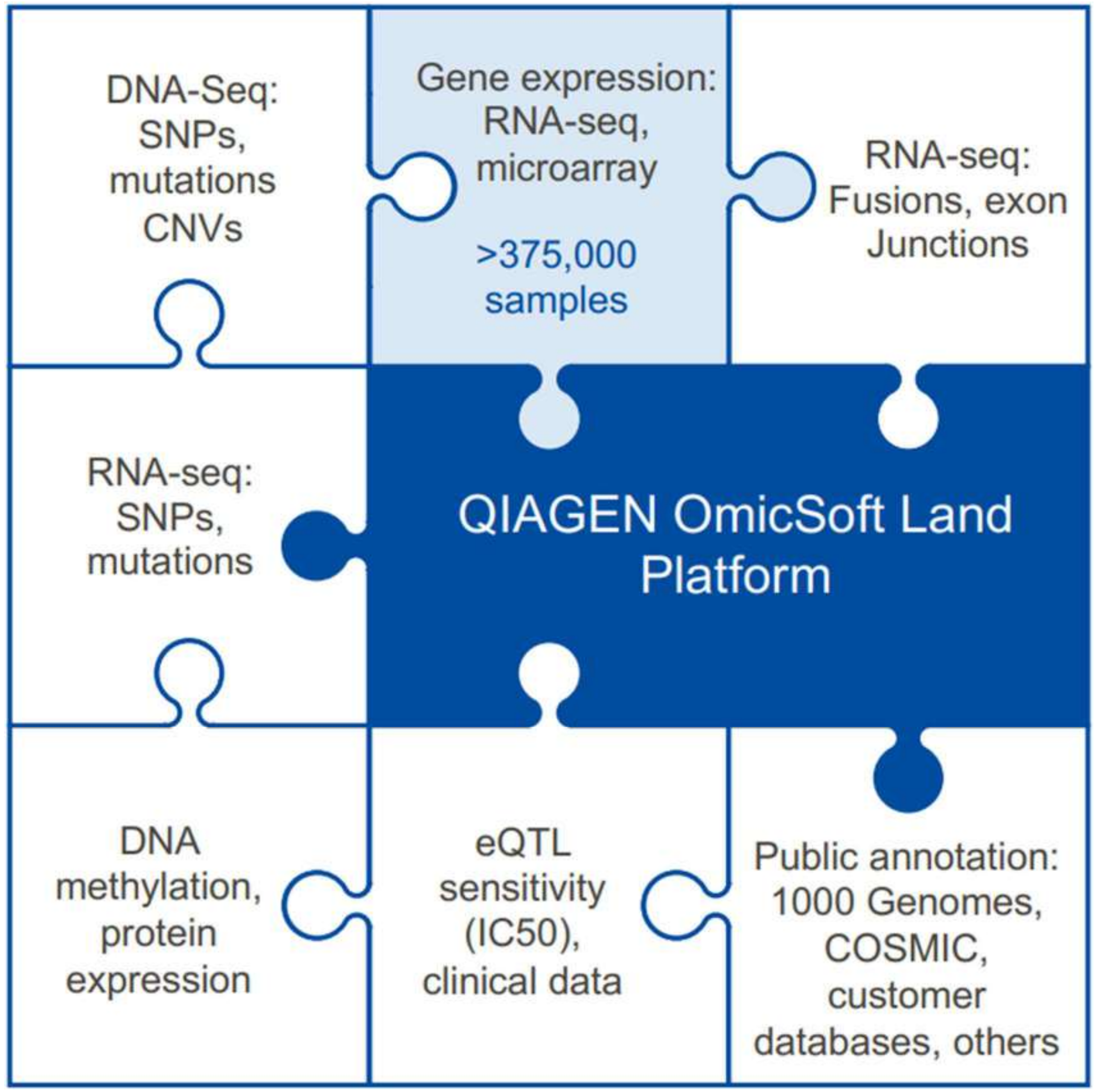
correlation [2]

Upregulation of phosphorylated (S51) **mouse Eif2a protein is associated with Alzheimer's disease in** aged APPPS1 mouse.

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



DNA-Seq: SNPs, mutations CNVs

Gene expression: RNA-seq, microarray

>375,000 samples

RNA-seq: Fusions, exon Junctions

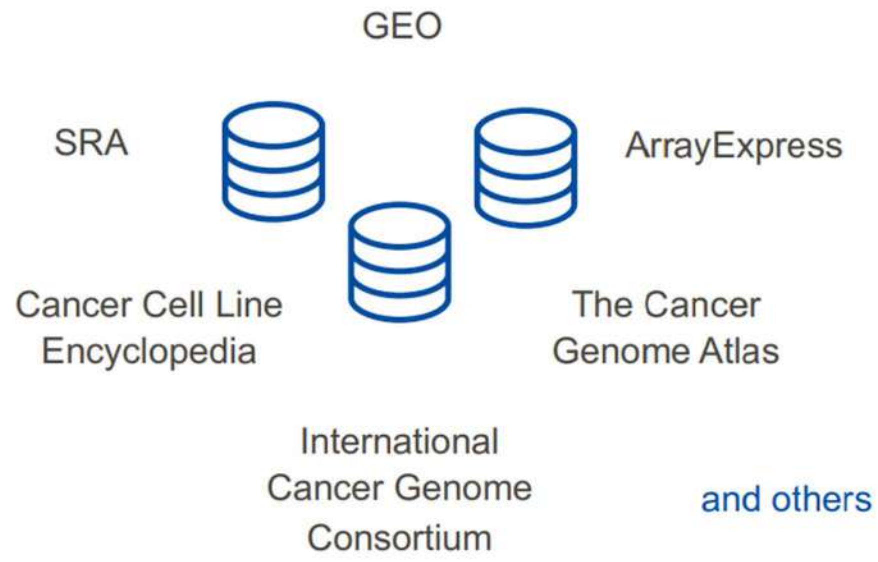
RNA-seq: SNPs, mutations

QIAGEN OmicSoft Land Platform

DNA methylation, protein expression

eQTL sensitivity (IC50), clinical data

Public annotation: 1000 Genomes, COSMIC, customer databases, others



GEO

SRA

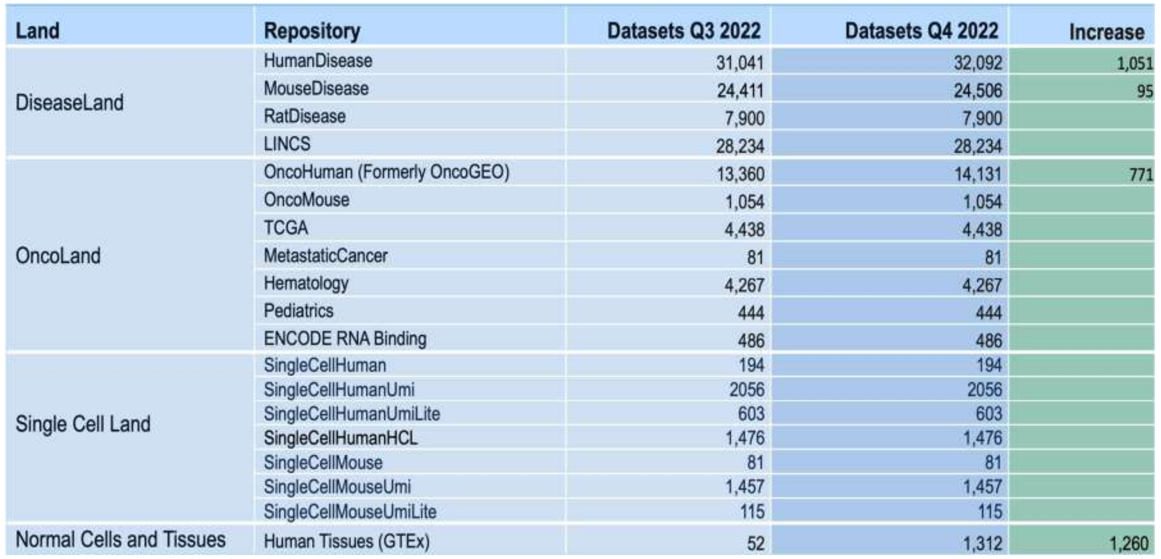
ArrayExpress

Cancer Cell Line Encyclopedia

The Cancer Genome Atlas

International Cancer Genome Consortium

and others



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

Species support within IPA

Fully supported:

Human

Mouse

Rat

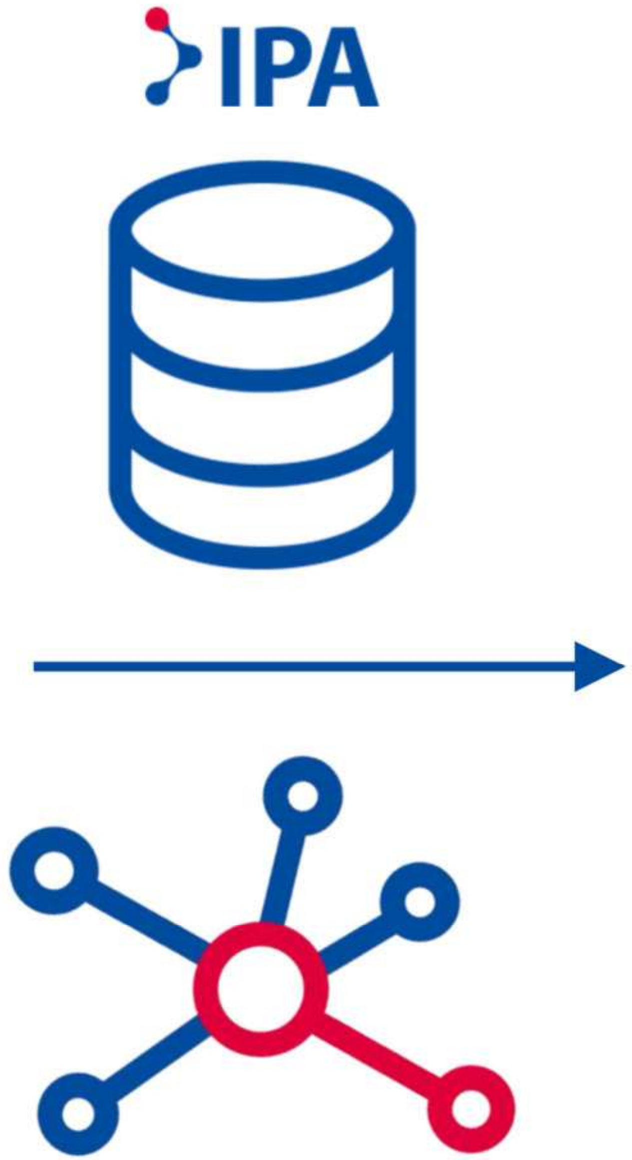
IPA can remap orthologous identifiers from the following species:

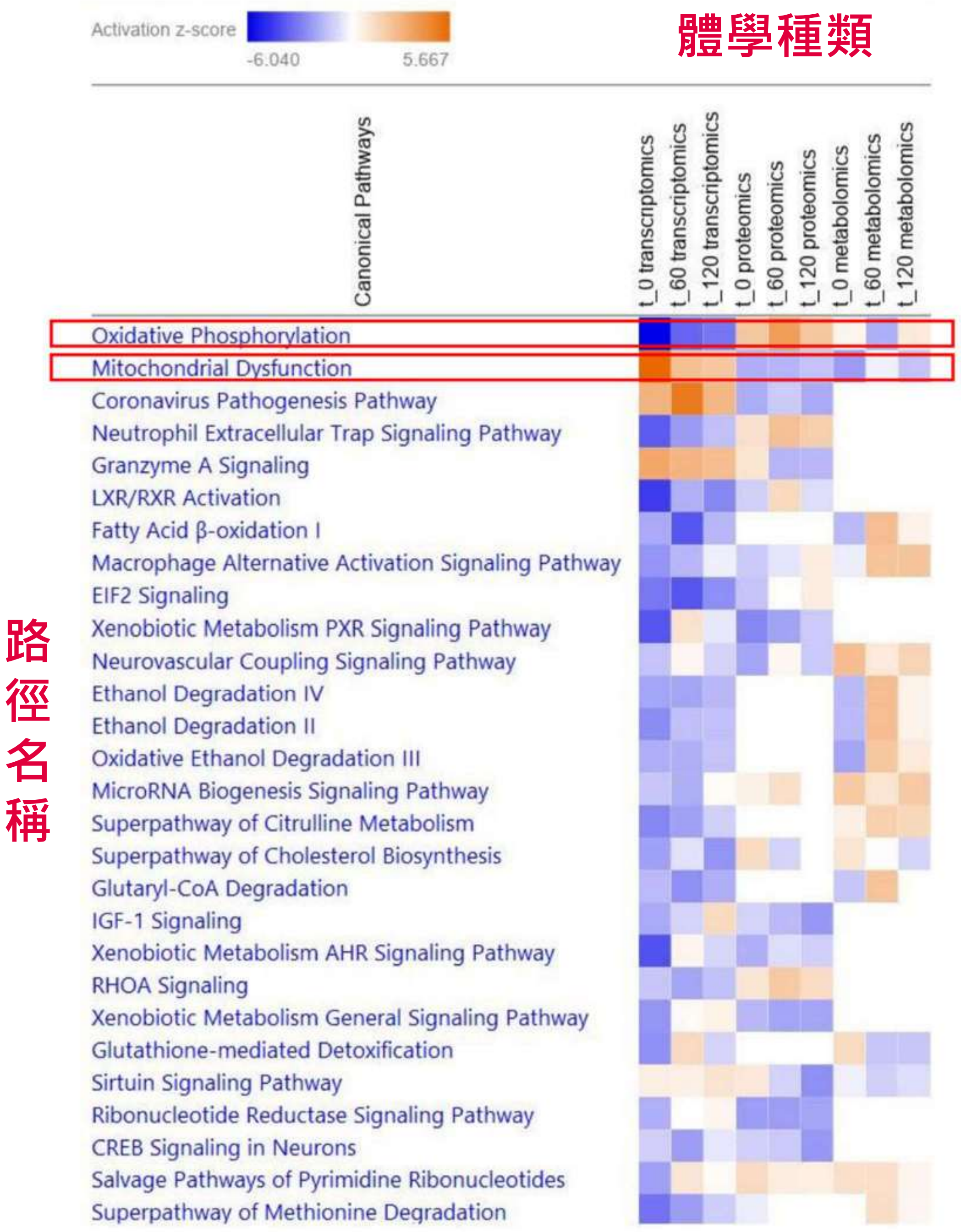
- Arabidopsis thaliana (*Thale cress*)
- Bat (*Rhinolophus ferrumequinum*)
- *Caenorhabditis elegans*
- Cat (domestic, *Felis catus*)
- Chicken (*Gallus gallus*)
- Chimpanzee (*Pan troglodytes*)
- Chinese hamster (*Cricetulus griseus*, CHO-K1)
- Cow (*Bos taurus*)
- Crab-eating macaque (*Macaca fascicularis*)
- Dog (*Canis lupus familiaris*)
- 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*)
- *Saccharomyces cerevisiae*
- *Schizosaccharomyces pombe*
- Western clawed frog (*Xenopus tropicalis*)
- Zebrafish (*Danio rerio*)

Multi-omics data analysis using QIAGEN IPA

Omics data type

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





體學種類

路徑名稱

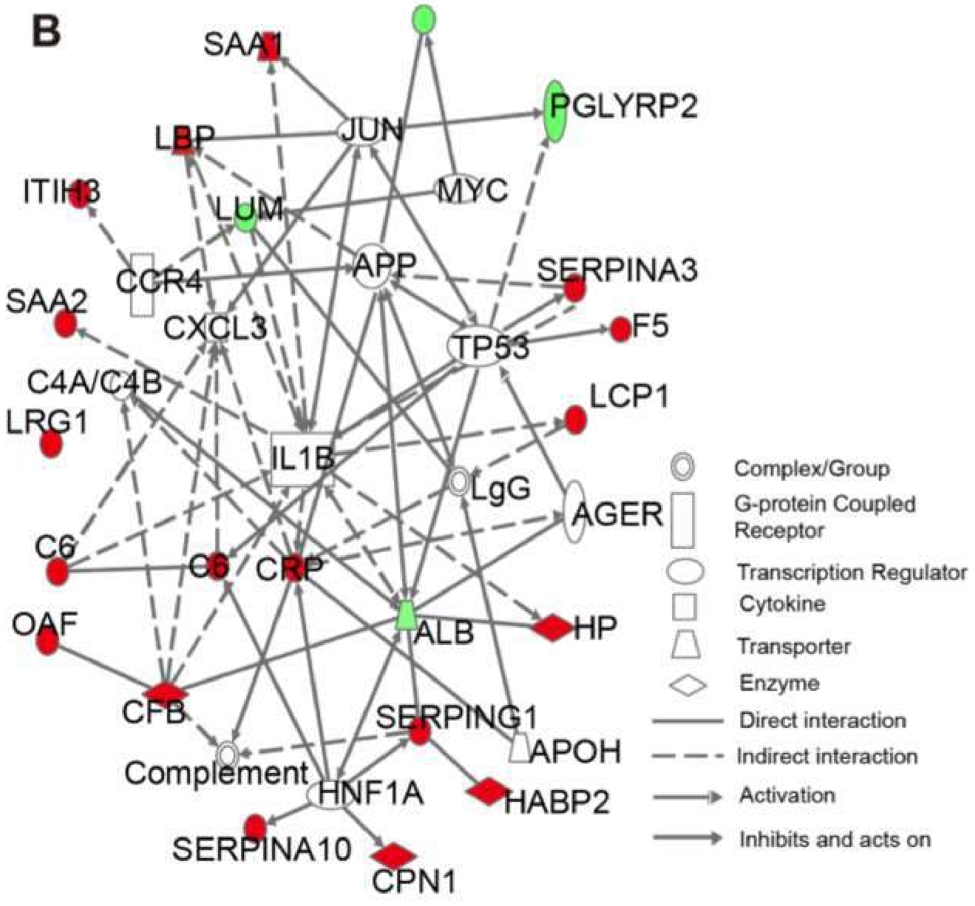
Supported Identifiers for Data Upload

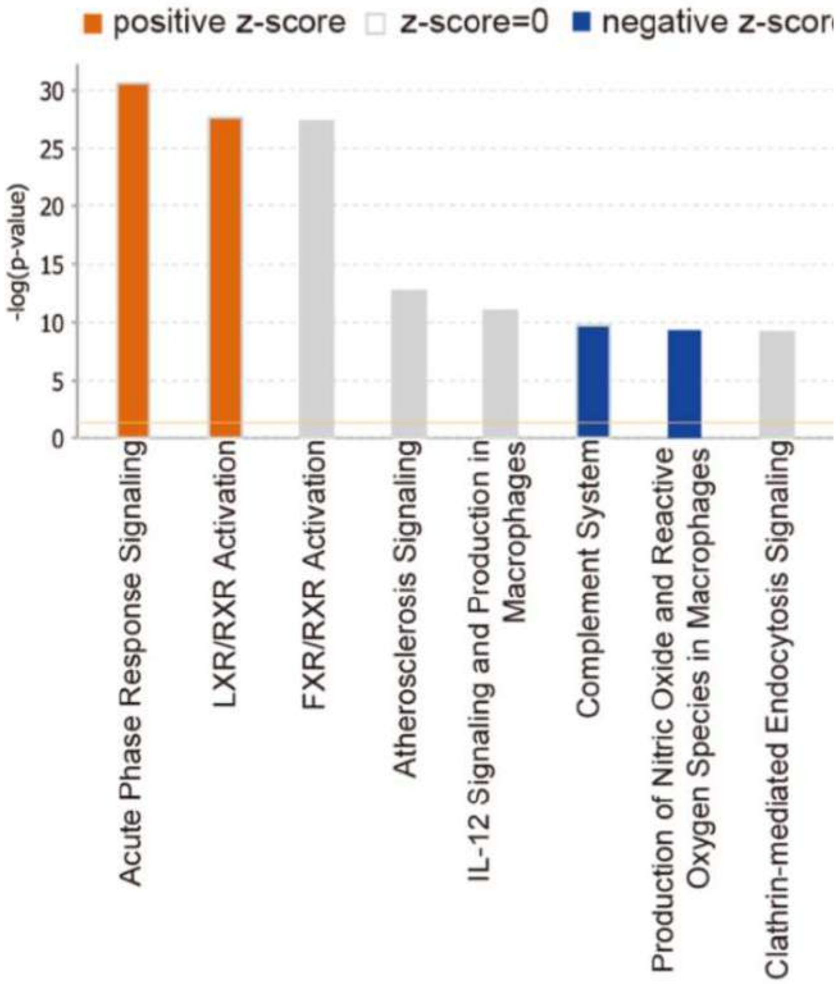
Get more complete mapping during dataset upload!

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					

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.



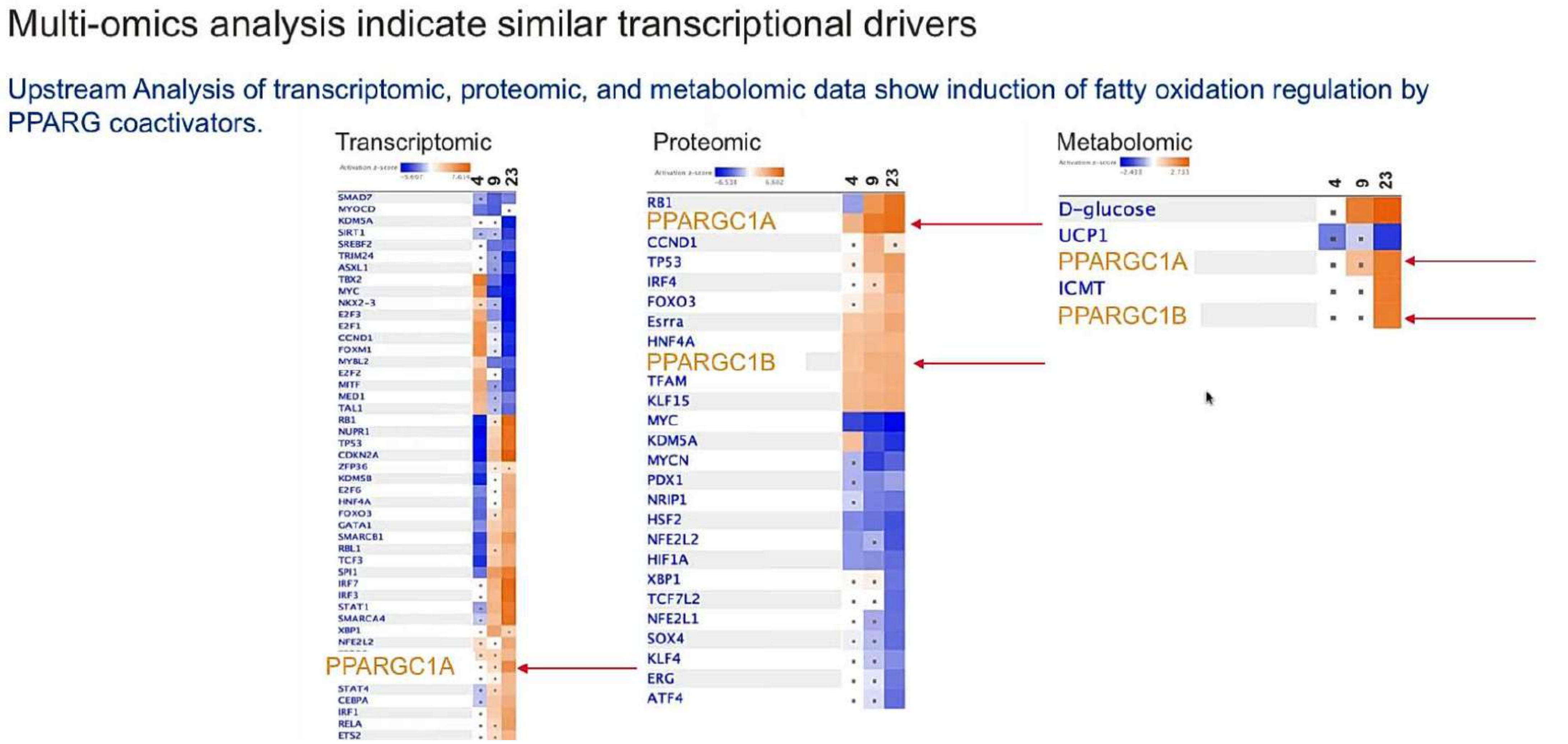


https://www.medrxiv.org/content/10.1101/2020.04.07.20054585v1

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

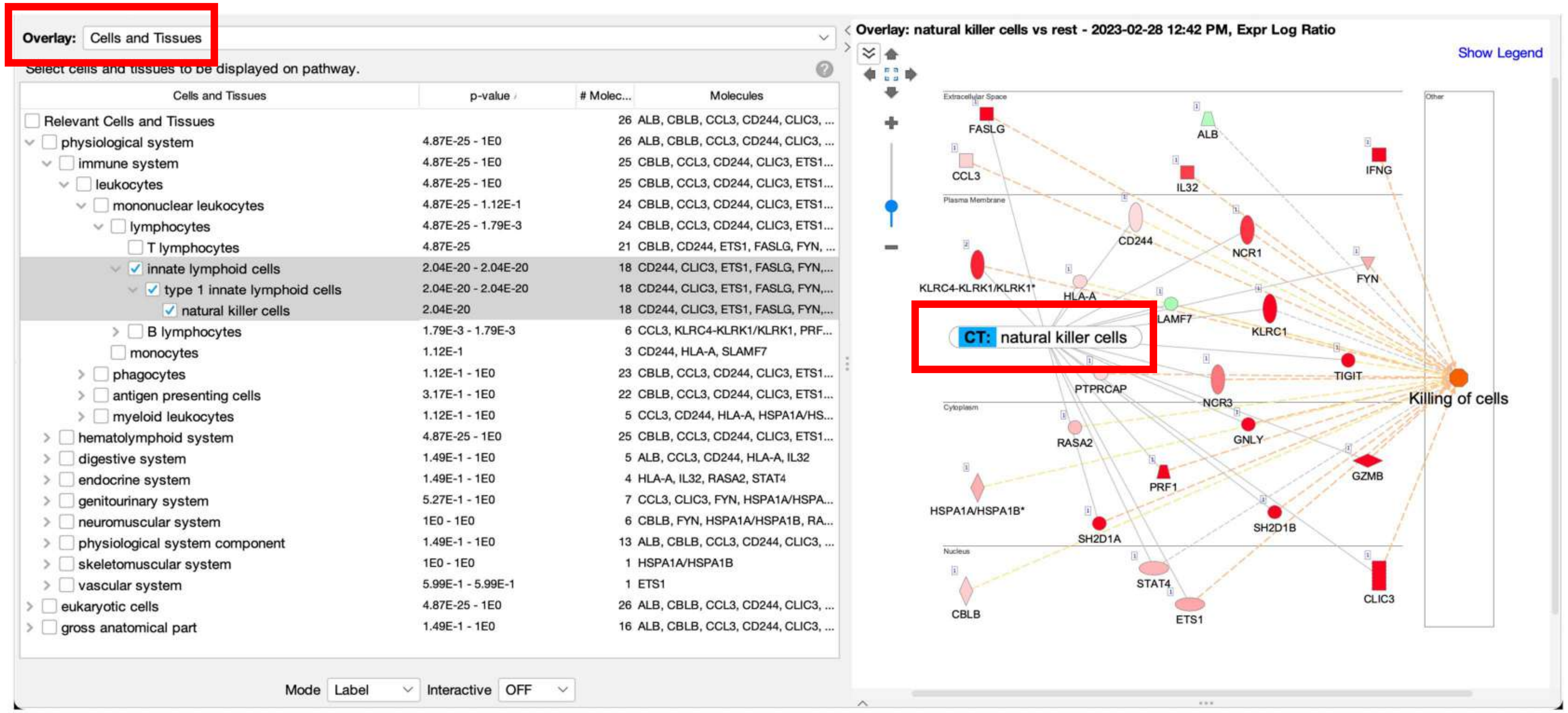
Upstream Analysis of transcriptomic, proteomic, and metabolomic data show induction of fatty oxidation regulation by PPARG coactivators.

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

Identify potential cell types based on the set of genes on networks and pathways

Overlay :Cell and Tissues

THE HUMAN PROTEIN ATLAS



Overlay: Cells and Tissues

Select cells and tissues to be displayed on pathway.

Cells and Tissues	p-value	# Molec...	Molecules
☐ Relevant Cells and Tissues		26	ALB, CBLB, CCL3, CD244, CLIC3, ...
☐ physiological system	4.87E-25 - 1E0	26	ALB, CBLB, CCL3, CD244, CLIC3, ...
☐ immune system	4.87E-25 - 1E0	25	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ leukocytes	4.87E-25 - 1E0	25	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ mononuclear leukocytes	4.87E-25 - 1.12E-1	24	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ lymphocytes	4.87E-25 - 1.79E-3	24	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ T lymphocytes	4.87E-25	21	CBLB, CD244, ETS1, FASLG, FYN, ...
☑ innate lymphoid cells	2.04E-20 - 2.04E-20	18	CD244, CLIC3, ETS1, FASLG, FYN,...
☑ type 1 innate lymphoid cells	2.04E-20 - 2.04E-20	18	CD244, CLIC3, ETS1, FASLG, FYN,...
☑ natural killer cells	2.04E-20	18	CD244, CLIC3, ETS1, FASLG, FYN,...
☐ B lymphocytes	1.79E-3 - 1.79E-3	6	CCL3, KLRC4-KLRK1/KLRK1, PRF...
☐ monocytes	1.12E-1	3	CD244, HLA-A, SLAMF7
☐ phagocytes	1.12E-1 - 1E0	23	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ antigen presenting cells	3.17E-1 - 1E0	22	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ myeloid leukocytes	1.12E-1 - 1E0	5	CCL3, CD244, HLA-A, HSPA1A/HS...
☐ hematolymphoid system	4.87E-25 - 1E0	25	CBLB, CCL3, CD244, CLIC3, ETS1...
☐ digestive system	1.49E-1 - 1E0	5	ALB, CCL3, CD244, HLA-A, IL32
☐ endocrine system	1.49E-1 - 1E0	4	HLA-A, IL32, RASA2, STAT4
☐ genitourinary system	5.27E-1 - 1E0	7	CCL3, CLIC3, FYN, HSPA1A/HSPA...
☐ neuromuscular system	1E0 - 1E0	6	CBLB, FYN, HSPA1A/HSPA1B, RA...
☐ physiological system component	1.49E-1 - 1E0	13	ALB, CBLB, CCL3, CD244, CLIC3, ...
☐ skeletomuscular system	1E0 - 1E0	1	HSPA1A/HSPA1B
☐ vascular system	5.99E-1 - 5.99E-1	1	ETS1
☐ eukaryotic cells	4.87E-25 - 1E0	26	ALB, CBLB, CCL3, CD244, CLIC3, ...
☐ gross anatomical part	1.49E-1 - 1E0	16	ALB, CBLB, CCL3, CD244, CLIC3, ...

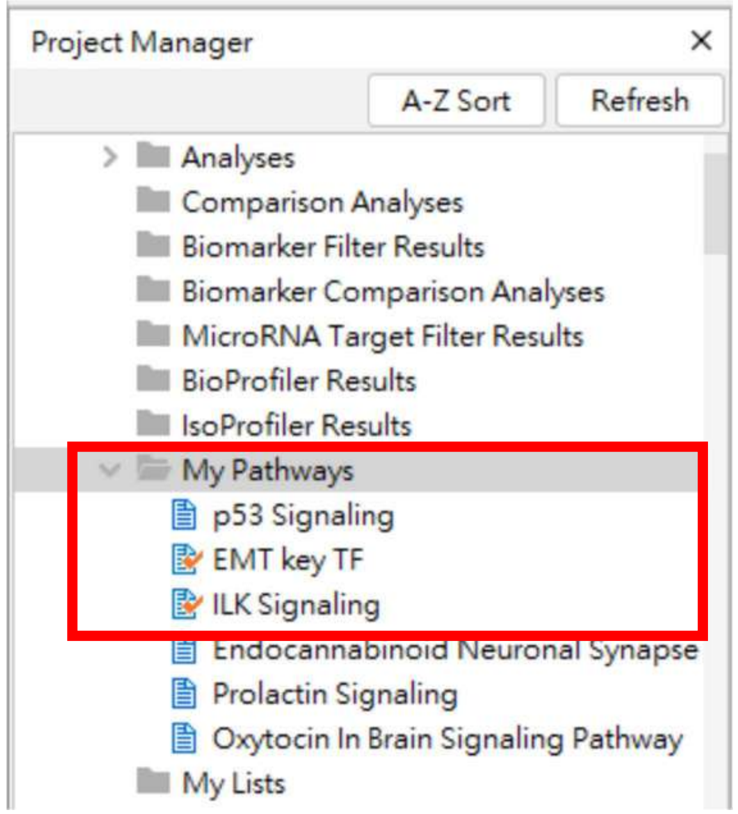
Mode: Label
Interactive: OFF

Overlay: natural killer cells vs rest - 2023-02-28 12:42 PM, Expr Log Ratio

Enrichment of natural killer enriched genes on a network.

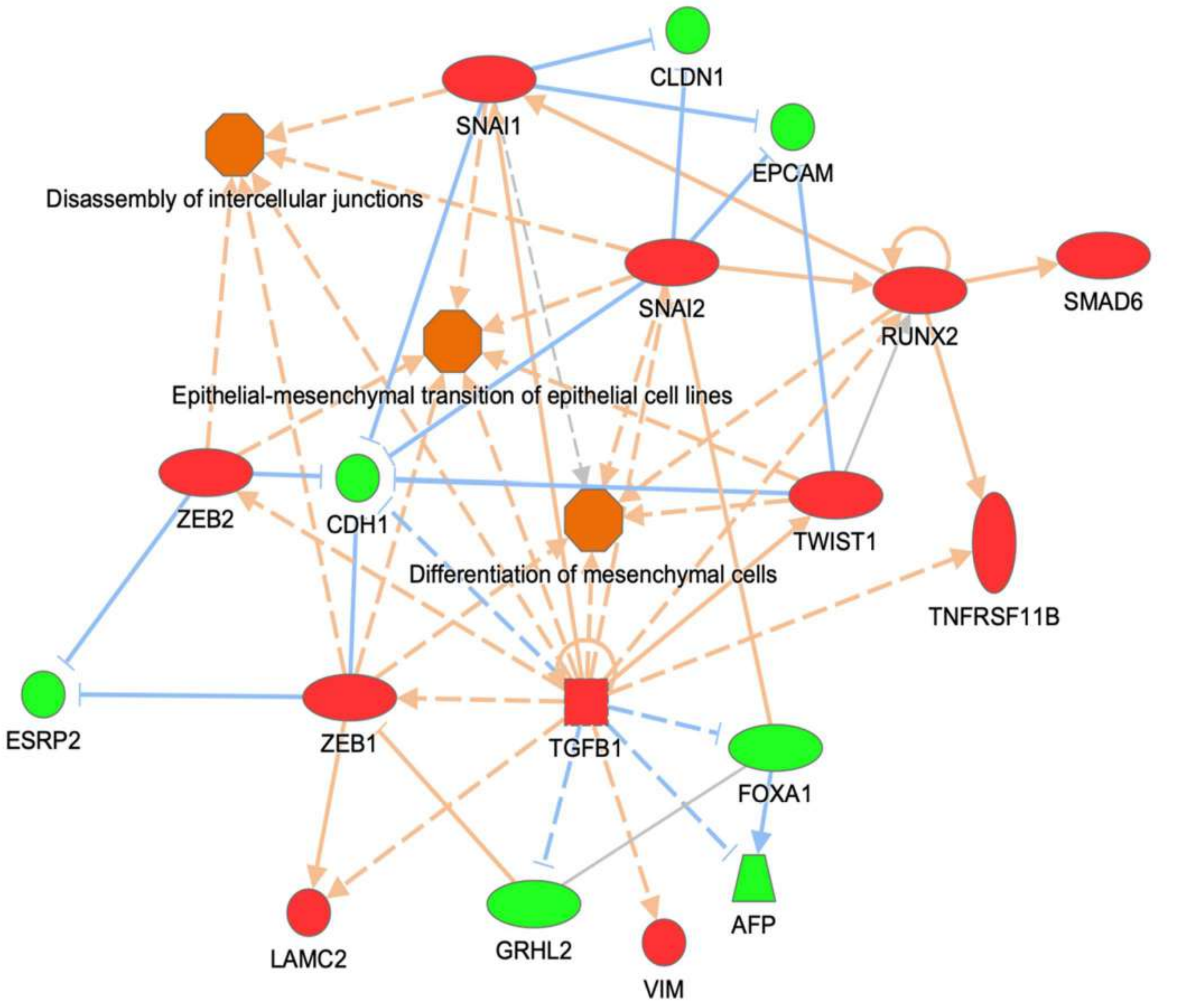
What’s new in the IPA spring release?

Causally score My Pathways in Core Analysis


Project Manager ×

A-Z Sort Refresh

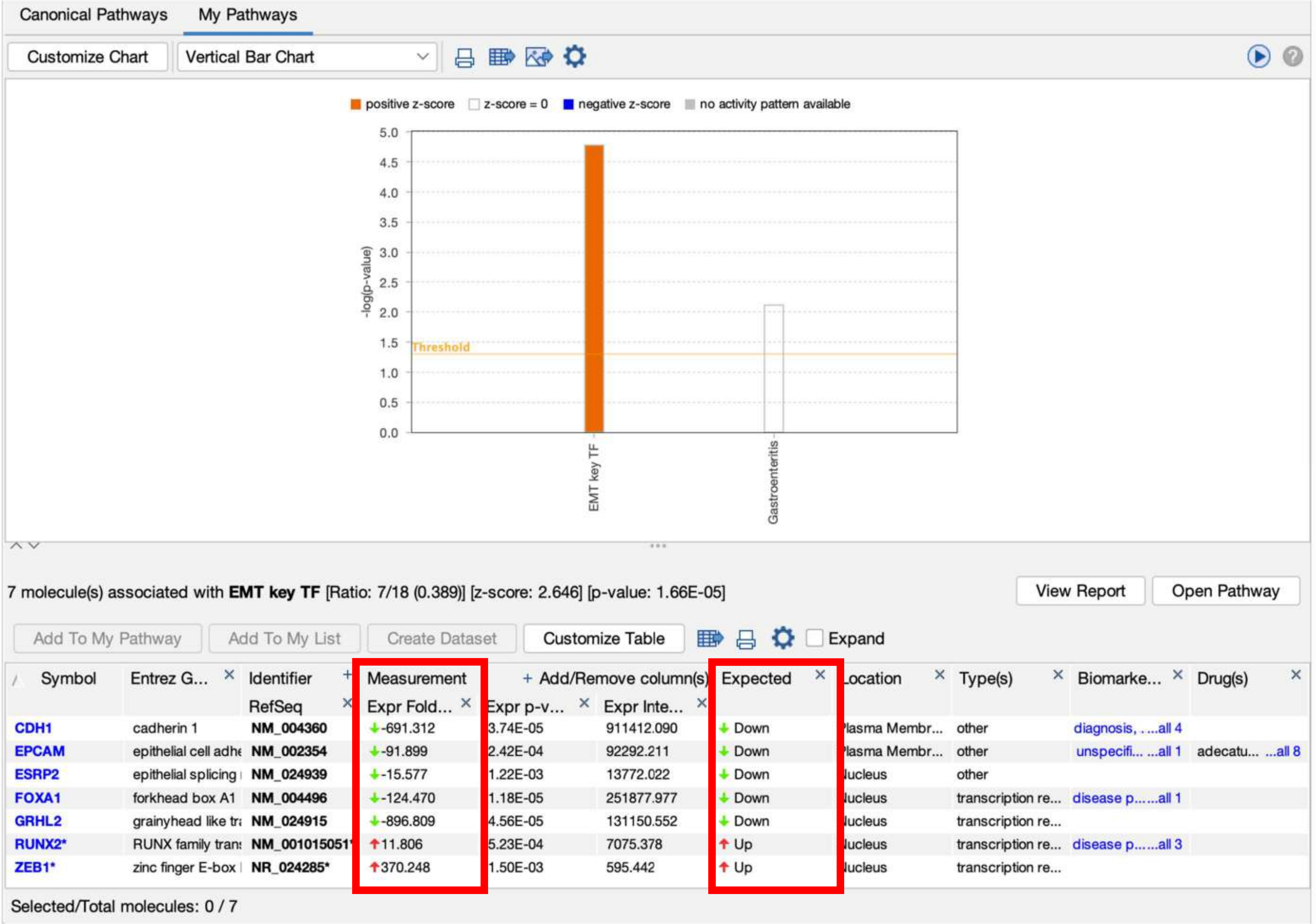
- Analyses
- Comparison Analyses
- Biomarker Filter Results
- Biomarker Comparison Analyses
- MicroRNA Target Filter Results
- BioProfiler Results
- IsoProfiler Results
- My Pathways
  - p53 Signaling
  - EMT key TF
  - ILK Signaling
  - Endocannabinoid Neuronal Synapse
  - Prolactin Signaling
  - Oxytocin In Brain Signaling Pathway
- My Lists



A custom My Pathway with nodes assigned by the user as activated (red) or green (inhibited).

What’s new in the IPA spring release?

Causally score My Pathways in Core Analysis



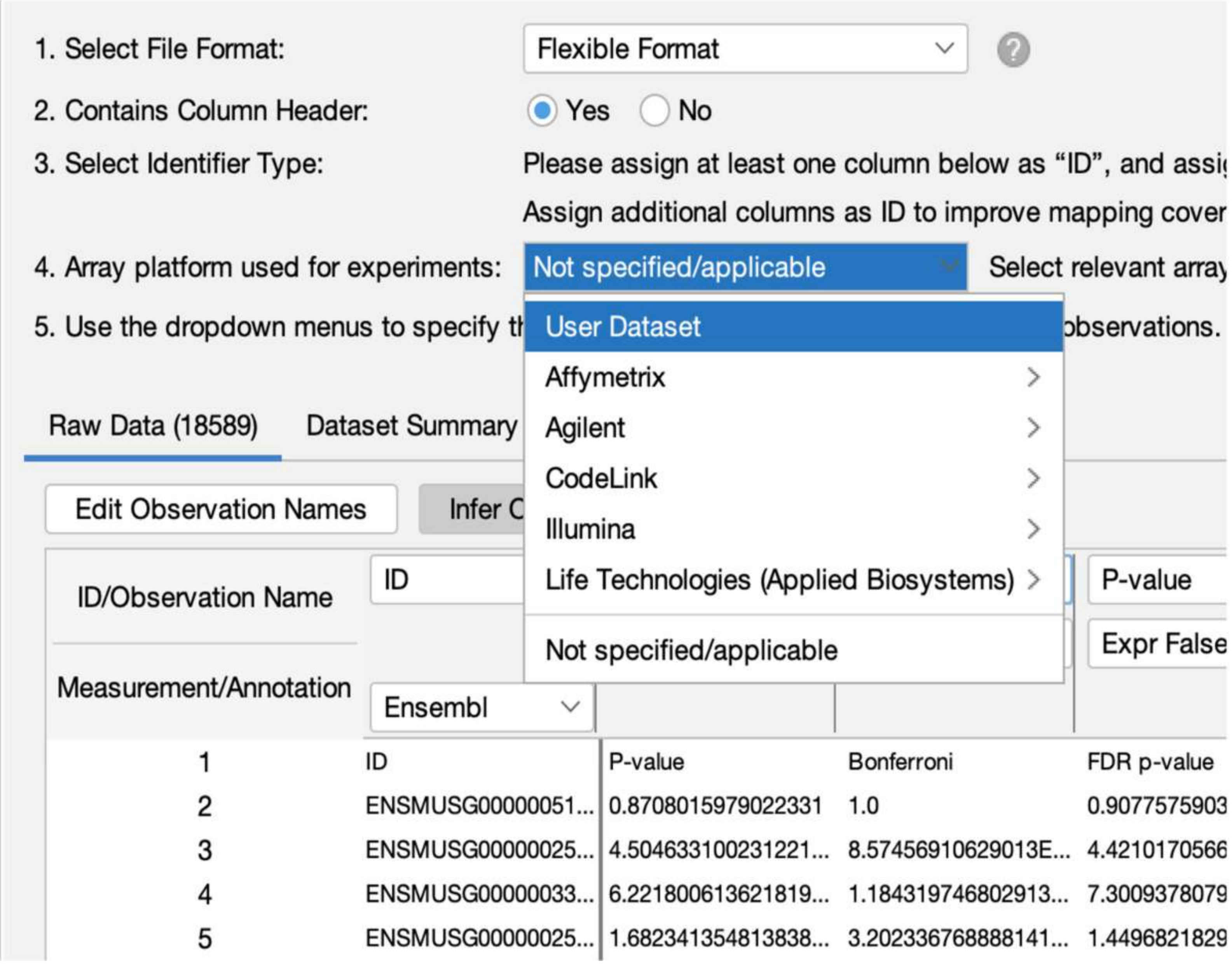
7 molecule(s) associated with **EMT key TF** [Ratio: 7/18 (0.389)] [z-score: 2.646] [p-value: 1.66E-05]

Symbol	Entrez G...	Identifier	Measurement			Expected	ocation	Type(s)	Biomarke...	Drug(s)
		RefSeq	Expr Fold...	xpr p-v...	Expr Inte...					
CDH1	cadherin 1	**NM_004360**	↓-691.312	3.74E-05	911412.090	↓ Down	lasma Membr...	other	diagnosis, ...all 4	
EPCAM	epithelial cell adhe	**NM_002354**	↓-91.899	2.42E-04	92292.211	↓ Down	lasma Membr...	other	unspecifi... ...all 1	adecatu... ...all 8
ESRP2	epithelial splicing	**NM_024939**	↓-15.577	1.22E-03	13772.022	↓ Down	ucleus	other		
FOXA1	forkhead box A1	**NM_004496**	↓-124.470	1.18E-05	251877.977	↓ Down	ucleus	transcription re...	disease p......all 1	
GRHL2	grainyhead like tr	**NM_024915**	↓-896.809	4.56E-05	131150.552	↓ Down	ucleus	transcription re...		
RUNX2*	RUNX family tran	**NM_001015051**	↑11.806	5.23E-04	7075.378	↑ Up	ucleus	transcription re...	disease p......all 3	
ZEB1*	zinc finger E-box	**NR_024285***	↑370.248	1.50E-03	595.442	↑ Up	ucleus	transcription re...		

Selected/Total molecules: 0 / 7

Causally scoring a My Pathway.

Set the “User Dataset” as the reference set when uploading a dataset



1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

3. Select Identifier Type: Please assign at least one column below as “ID”, and assi
Assign additional columns as ID to improve mapping cover

4. Array platform used for experiments: Not specified/applicable Select relevant array

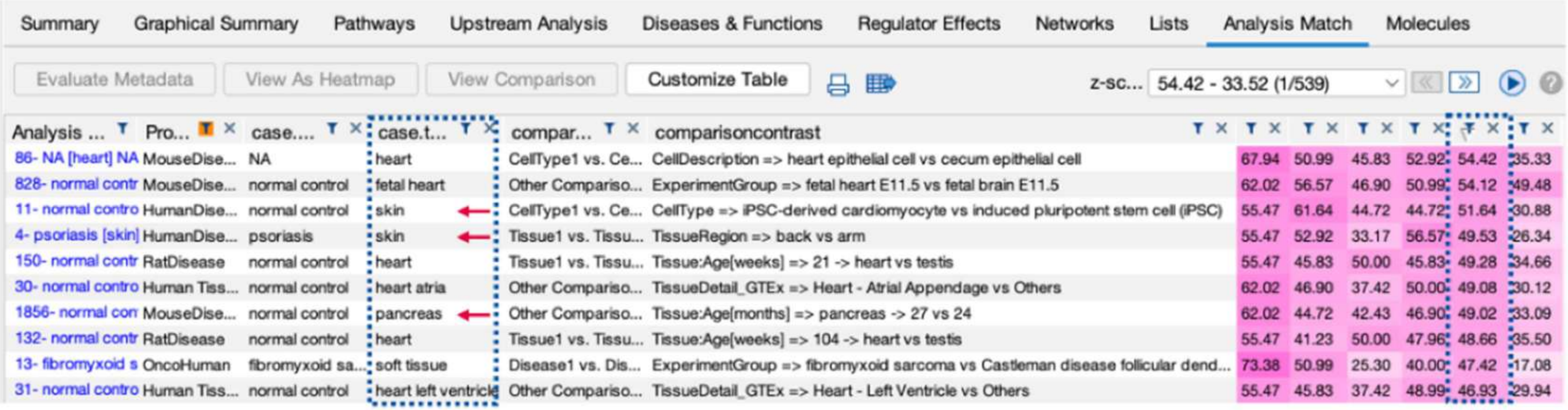
5. Use the dropdown menus to specify th observations.

1	ID	P-value	Bonferroni	FDR p-value
2	ENSMUSG00000051...	0.8708015979022331	1.0	0.9077575903
3	ENSMUSG00000025...	4.504633100231221...	8.57456910629013E...	4.4210170566
4	ENSMUSG00000033...	6.221800613621819...	1.184319746802913...	7.3009378079
5	ENSMUSG00000025...	1.682341354813838...	3.202336768888141...	1.4496821829

Setting the reference set to User Dataset reference during dataset upload.

What’s new in the IPA summer release?

Discover more precise matches in Analysis Match

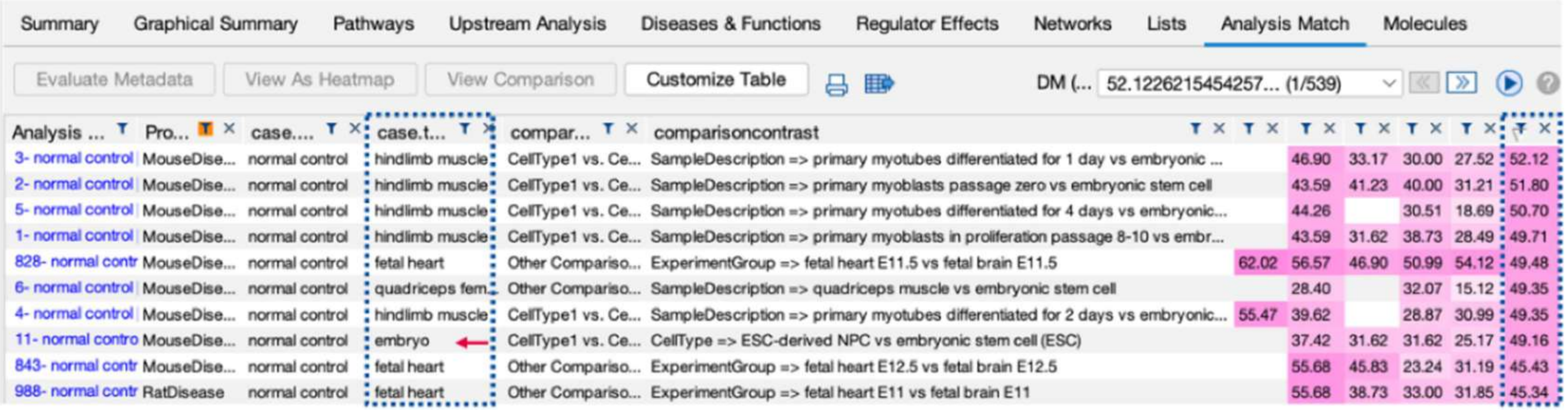


z-sc... 54.42 - 33.52 (1/539)

Analysis ...	Pro...	case....	case.t...	compar...	comparisoncontrast						
86- NA [heart] NA	MouseDise...	NA	heart	CellType1 vs. Ce...	CellDescription => heart epithelial cell vs cecum epithelial cell	67.94	50.99	45.83	52.92	54.42	35.33
828- normal contr	MouseDise...	normal control	fetal heart	Other Compariso...	ExperimentGroup => fetal heart E11.5 vs fetal brain E11.5	62.02	56.57	46.90	50.99	54.12	49.48
11- normal contro	HumanDise...	normal control	skin ←	CellType1 vs. Ce...	CellType => iPSC-derived cardiomyocyte vs induced pluripotent stem cell (iPSC)	55.47	61.64	44.72	44.72	51.64	30.88
4- psoriasis [skin]	HumanDise...	psoriasis	skin ←	Tissue1 vs. Tissu...	TissueRegion => back vs arm	55.47	52.92	33.17	56.57	49.53	26.34
150- normal contr	RatDisease	normal control	heart	Tissue1 vs. Tissu...	Tissue:Age[weeks] => 21 -> heart vs testis	55.47	45.83	50.00	45.83	49.28	34.66
30- normal contro	Human Tiss...	normal control	heart atria	Other Compariso...	TissueDetail_GTEx => Heart - Atrial Appendage vs Others	62.02	46.90	37.42	50.00	49.08	30.12
1856- normal con	MouseDise...	normal control	pancreas ←	Other Compariso...	Tissue:Age[months] => pancreas -> 27 vs 24	62.02	44.72	42.43	46.90	49.02	33.09
132- normal contr	RatDisease	normal control	heart	Tissue1 vs. Tissu...	Tissue:Age[weeks] => 104 -> heart vs testis	55.47	41.23	50.00	47.96	48.66	35.50
13- fibromyxoid s	OncoHuman	fibromyxoid sa...	soft tissue	Disease1 vs. Dis...	ExperimentGroup => fibromyxoid sarcoma vs Castleman disease follicular dend...	73.38	50.99	25.30	40.00	47.42	17.08
31- normal contro	Human Tiss...	normal control	heart left ventricle	Other Compariso...	TissueDetail_GTEx => Heart - Left Ventricle vs Others	55.47	45.83	37.42	48.99	46.93	29.94

Sorted by original overall z-score match

Matches to analyses from many tissue types, such as skin and pancreas



DM (... 52.1226215454257... (1/539)

Analysis ...	Pro...	case....	case.t...	compar...	comparisoncontrast						
3- normal control	MouseDise...	normal control	hindlimb muscle	CellType1 vs. Ce...	SampleDescription => primary myotubes differentiated for 1 day vs embryonic ...		46.90	33.17	30.00	27.52	52.12
2- normal control	MouseDise...	normal control	hindlimb muscle	CellType1 vs. Ce...	SampleDescription => primary myoblasts passage zero vs embryonic stem cell		43.59	41.23	40.00	31.21	51.80
5- normal control	MouseDise...	normal control	hindlimb muscle	CellType1 vs. Ce...	SampleDescription => primary myotubes differentiated for 4 days vs embryonic...		44.26		30.51	18.69	50.70
1- normal control	MouseDise...	normal control	hindlimb muscle	CellType1 vs. Ce...	SampleDescription => primary myoblasts in proliferation passage 8-10 vs embr...		43.59	31.62	38.73	28.49	49.71
828- normal contr	MouseDise...	normal control	fetal heart	Other Compariso...	ExperimentGroup => fetal heart E11.5 vs fetal brain E11.5	62.02	56.57	46.90	50.99	54.12	49.48
6- normal control	MouseDise...	normal control	quadriceps fem...	Other Compariso...	SampleDescription => quadriceps muscle vs embryonic stem cell		28.40		32.07	15.12	49.35
4- normal control	MouseDise...	normal control	hindlimb muscle	CellType1 vs. Ce...	SampleDescription => primary myotubes differentiated for 2 days vs embryonic...	55.47	39.62		28.87	30.99	49.35
11- normal contro	MouseDise...	normal control	embryo ←	CellType1 vs. Ce...	CellType => ESC-derived NPC vs embryonic stem cell (ESC)		37.42	31.62	31.62	25.17	49.16
843- normal contr	MouseDise...	normal control	fetal heart	Other Compariso...	ExperimentGroup => fetal heart E12.5 vs fetal brain E12.5		55.68	45.83	23.24	31.19	45.43
988- normal contr	RatDisease	normal control	fetal heart	Other Compariso...	ExperimentGroup => fetal heart E11 vs fetal brain E11		55.68	38.73	33.00	31.85	45.34

Sorted by new DM “dataset match” column

Results are more strictly heart or muscle cells vs embryonic cells

Analysis Match results sorted by the original score (top) and new score (bottom).

What's new in the IPA summer release?

Heatmap of the top forty matching analyses

Match Analyses Heatmap: Cardiomyocytes vs ESC - 891 genes

Settings/Legend

Measurement: Activation z-score -7.458 7.931

Sort Method: Hierarchical Clustering Visualize: z-score

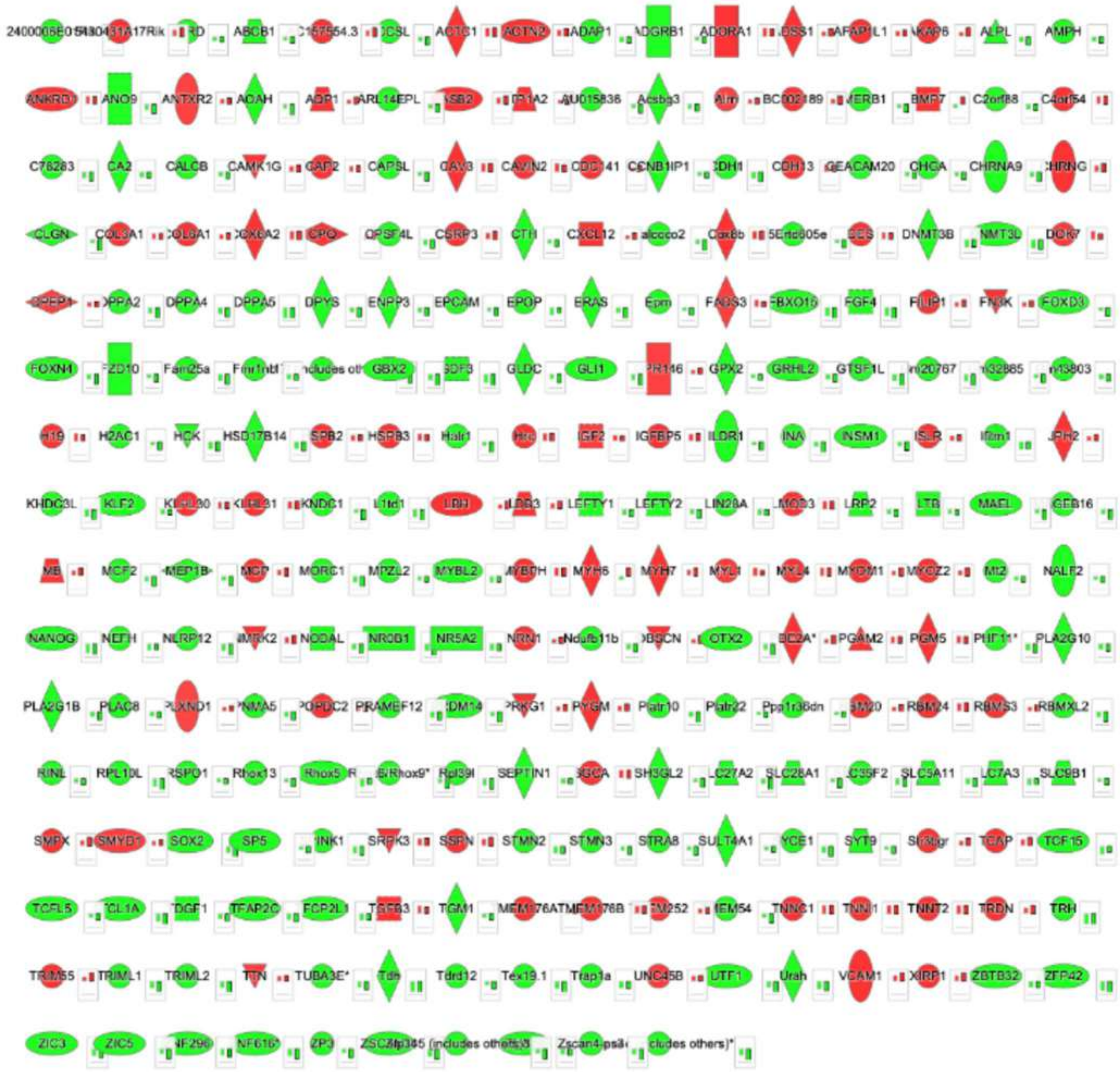
Insignificance Threshold: (absolute value)

Entity Type	Entity Name
DM	Analysis-ready genes
CN	GRIN3A
CN	BMP
CN	MEF2C
CN	Bvht
UR	Bvht
CN	FHOD1
CN	SRF
UR	SRF
CN	MYOCD
CN	GATA4
UR	GATA4
UR	MEF2C
UR	MYOCD
CN	TBX5
UR	TBX5
CN	HAND2
UR	HAND2
UR	TGFB1
UR	MYOD1
CN	MYOD1
UR	D-glucose
CN	GATA6
UR	AGT
CN	MEF2A
UR	MYD88
UR	EDN1
UR	ESRRA
CP	Oxytocin Signaling Pathway
CP	Cardiac Hypertrophy Signali...
UR	GATA6
UR	WNT11
CN	WNT11
UR	TEAD1
CN	YY2

Heatmap of the top forty matching analyses. Each orange-colored square in the top row of the heatmap represents the z-score for that analysis versus the query

What’s new in the IPA summer release?

Heatmap of the top forty matching analyses

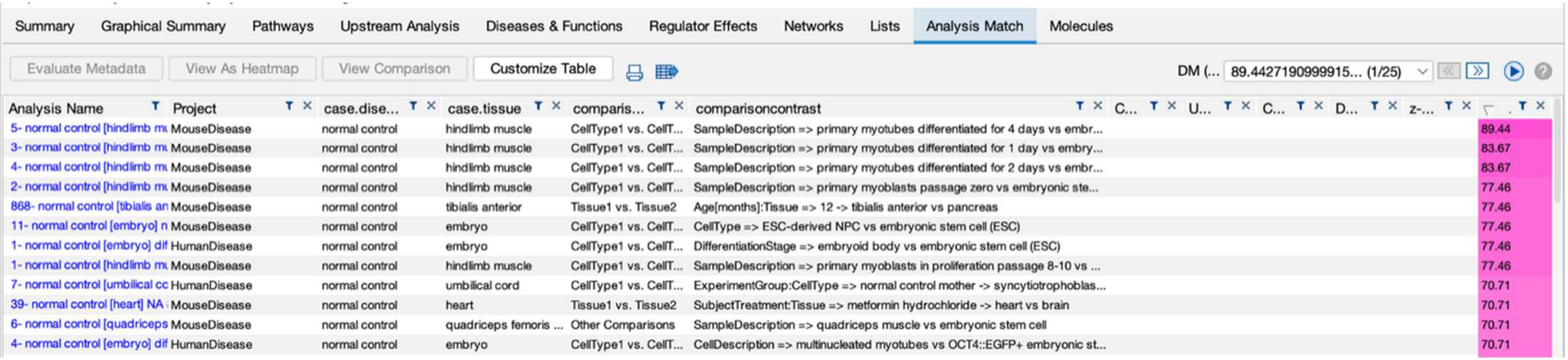


250 genes match between the cardiomyocyte analysis and its best matching analysis.

What’s new in the IPA summer release?

The new scoring method using a small dataset.

The new scoring method often works on small datasets, where there are typically too few genes to generate robust Upstream Regulator, Causal Network, Canonical Pathway, and Disease and Function signatures to match to other analyses.

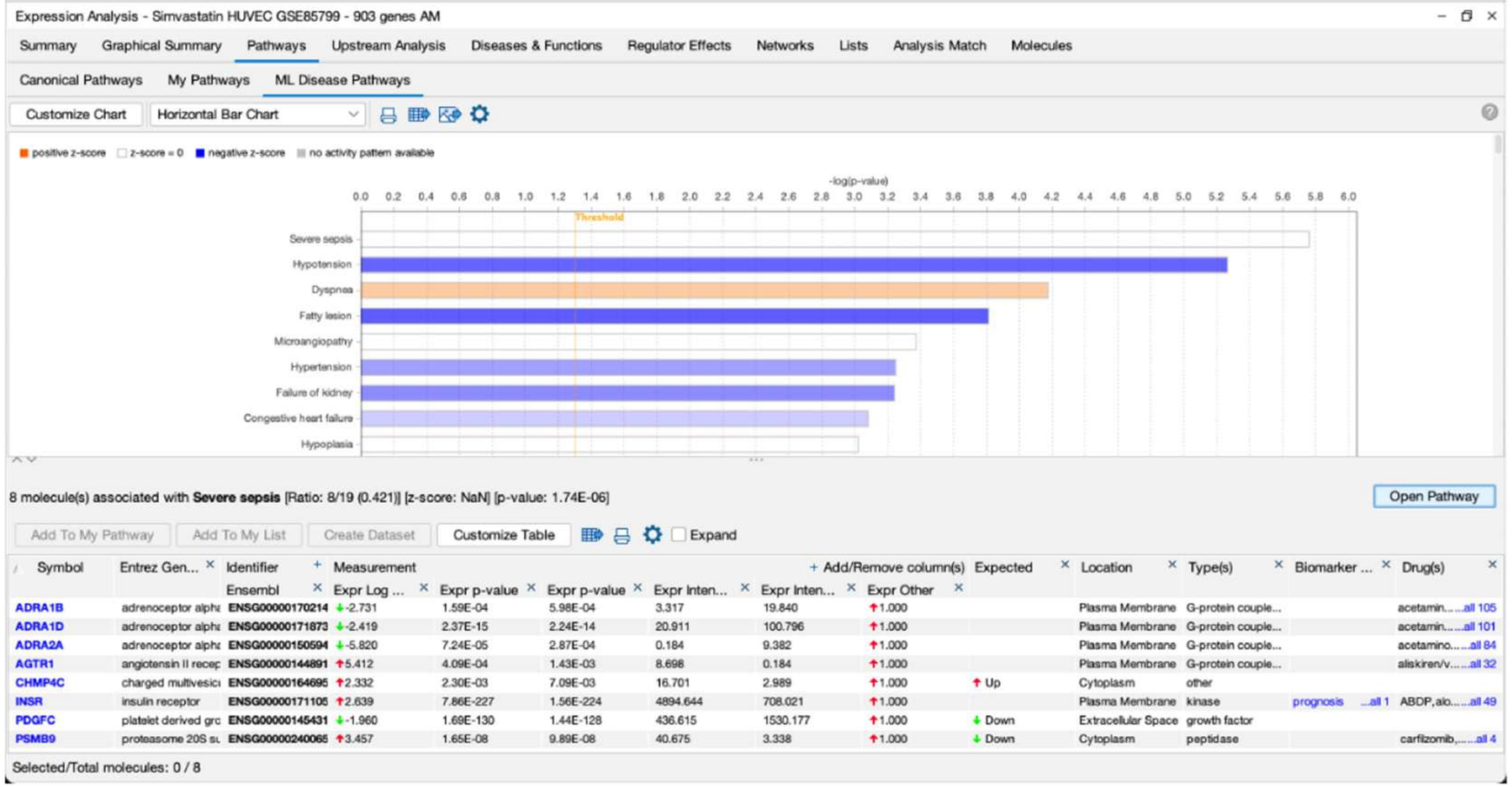


Analysis Name	Project	case.dise...	case.tissue	comparis...	comparisoncontrast	C...	U...	C...	D...	z-...	
5- normal control [hindlimb mu	MouseDisease	normal control	hindlimb muscle	CellType1 vs. CellT...	SampleDescription => primary myotubes differentiated for 4 days vs embr...						89.44
3- normal control [hindlimb mu	MouseDisease	normal control	hindlimb muscle	CellType1 vs. CellT...	SampleDescription => primary myotubes differentiated for 1 day vs embry...						83.67
4- normal control [hindlimb mu	MouseDisease	normal control	hindlimb muscle	CellType1 vs. CellT...	SampleDescription => primary myotubes differentiated for 2 days vs embr...						83.67
2- normal control [hindlimb mu	MouseDisease	normal control	hindlimb muscle	CellType1 vs. CellT...	SampleDescription => primary myoblasts passage zero vs embryonic ste...						77.46
868- normal control [tibialis an	MouseDisease	normal control	tibialis anterior	Tissue1 vs. Tissue2	Age[months]:Tissue => 12 -> tibialis anterior vs pancreas						77.46
11- normal control [embryo] n	MouseDisease	normal control	embryo	CellType1 vs. CellT...	CellType => ESC-derived NPC vs embryonic stem cell (ESC)						77.46
1- normal control [embryo] dif	HumanDisease	normal control	embryo	CellType1 vs. CellT...	DifferentiationStage => embryoid body vs embryonic stem cell (ESC)						77.46
1- normal control [hindlimb mu	MouseDisease	normal control	hindlimb muscle	CellType1 vs. CellT...	SampleDescription => primary myoblasts in proliferation passage 8-10 vs ...						77.46
7- normal control [umbilical cc	HumanDisease	normal control	umbilical cord	CellType1 vs. CellT...	ExperimentGroup:CellType => normal control mother -> syncytiotrophoblas...						70.71
39- normal control [heart] NA	MouseDisease	normal control	heart	Tissue1 vs. Tissue2	SubjectTreatment:Tissue => metformin hydrochloride -> heart vs brain						70.71
6- normal control [quadriceps	MouseDisease	normal control	quadriceps femoris ...	Other Comparisons	SampleDescription => quadriceps muscle vs embryonic stem cell						70.71
4- normal control [embryo] dif	HumanDisease	normal control	embryo	CellType1 vs. CellT...	CellDescription => multinucleated myotubes vs OCT4::EGFP+ embryonic st...						70.71

The analysis of a 10-gene dataset from the cardiomyocytes versus embryonic stem cells matches the expected types of analyses.

What’s new in the IPA summer release?

Find the unexpected with ML Disease Pathways in Core Analyses



8 molecule(s) associated with **Severe sepsis** [Ratio: 8/19 (0.421)] [z-score: NaN] [p-value: 1.74E-06]

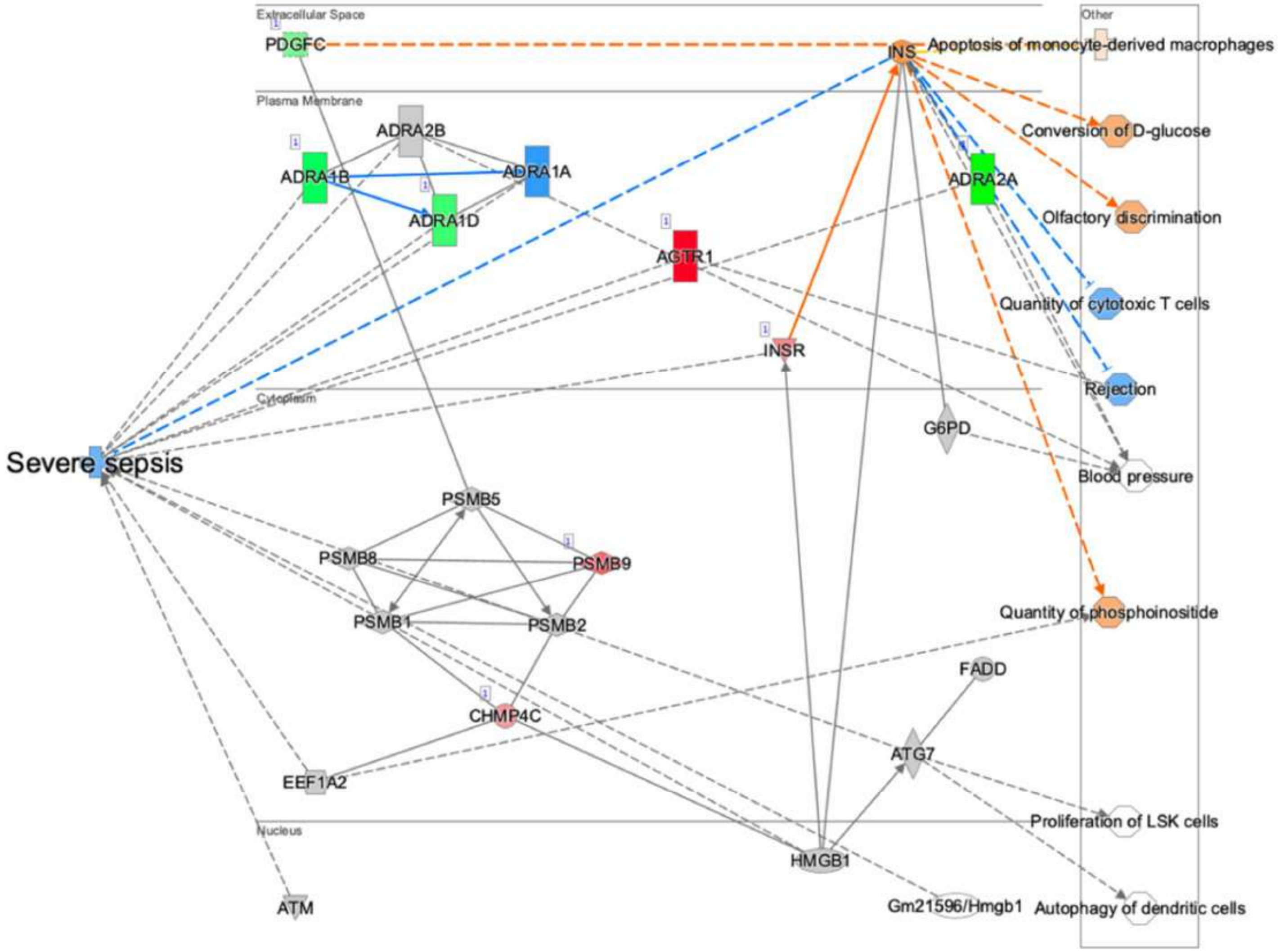
Symbol	Entrez Gen...	Identifier	Measurement						Expected	Location	Type(s)	Biomarker ...	Drug(s)
		Ensembl	Expr Log ...	Expr p-value	Expr p-value	Expr Inten...	Expr Inten...	Expr Other					
ADRA1B	adrenoceptor alph	ENSG00000170214	↓-2.731	1.59E-04	5.98E-04	3.317	19.840	↑1.000		Plasma Membrane	G-protein couple...		acetamin... ...all 105
ADRA1D	adrenoceptor alph	ENSG00000171873	↓-2.419	2.37E-15	2.24E-14	20.911	100.796	↑1.000		Plasma Membrane	G-protein couple...		acetamin... ...all 101
ADRA2A	adrenoceptor alph	ENSG00000150594	↓-5.820	7.24E-05	2.87E-04	0.184	9.382	↑1.000		Plasma Membrane	G-protein couple...		acetamino... ...all 84
AGTR1	angiotensin II recep	ENSG00000144891	↑5.412	4.09E-04	1.43E-03	8.698	0.184	↑1.000		Plasma Membrane	G-protein couple...		aliskiren/v... ...all 32
CHMP4C	charged multivesic	ENSG00000164695	↑2.332	2.30E-03	7.09E-03	16.701	2.989	↑1.000	↑ Up	Cytoplasm	other		
INSR	insulin receptor	ENSG00000171105	↑2.639	7.86E-227	1.56E-224	4894.644	708.021	↑1.000		Plasma Membrane	kinase	prognosis ...all 1	ABDP,alo... ...all 49
PDGFC	platelet derived grc	ENSG00000145431	↓-1.960	1.69E-130	1.44E-128	436.615	1530.177	↑1.000	↓ Down	Extracellular Space	growth factor		
PSMB9	proteasome 20S su	ENSG00000240065	↑3.457	1.65E-08	9.89E-08	40.675	3.338	↑1.000	↓ Down	Cytoplasm	peptidase		carfilzomib,... ...all 4

Selected/Total molecules: 0 / 8

ML Disease Pathways scored against simvastatin-treated rats (liver). The most significant result by Fisher’s Exact Test (right-tailed) is “Severe sepsis".

What’s new in the IPA summer release?

Find the unexpected with ML Disease Pathways in Core Analyses



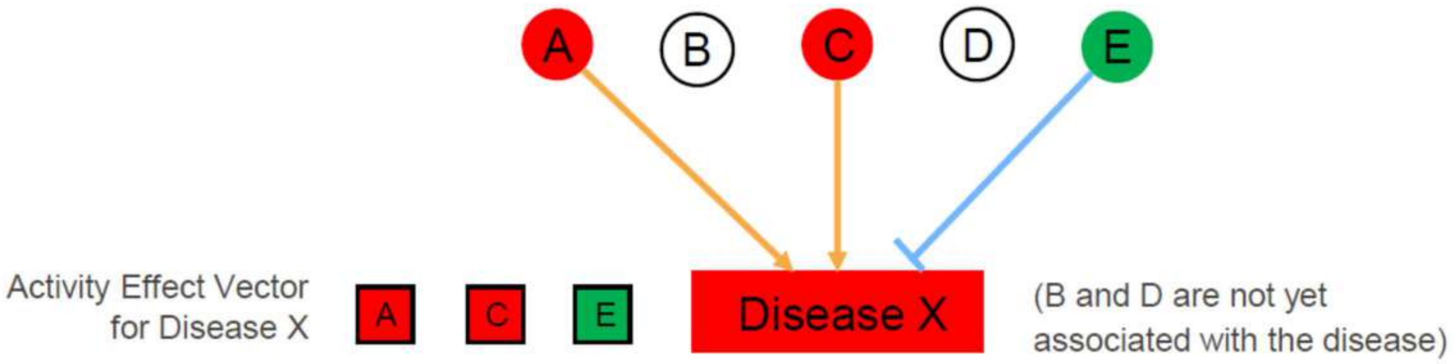
The severe sepsis ML pathway overlaid with simvastatin differential expression data. IPA predicts that simvastatin may decrease severe sepsis.

Explore previews of disease and phenotype networks

Enhancing the KB through Machine Learning

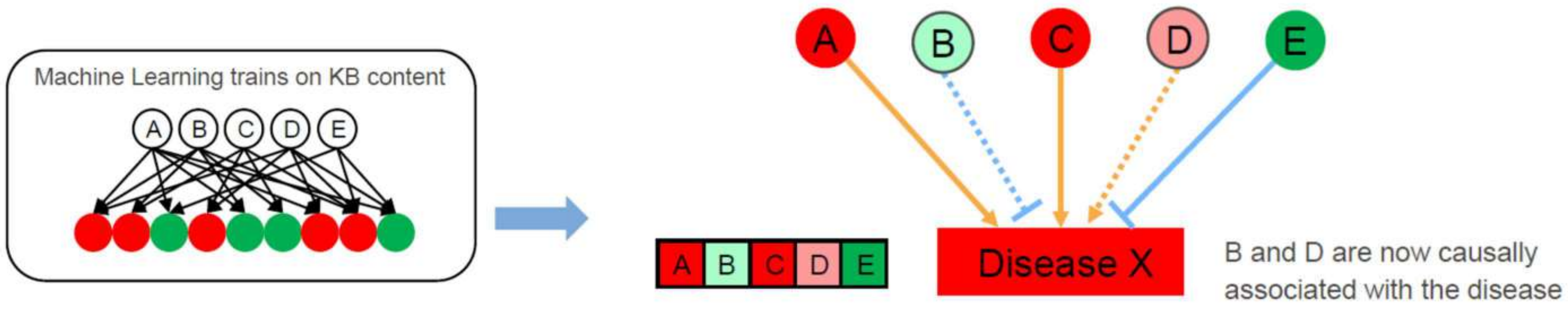
Standard KB

- Relationships between Disease X and neighboring genes can be described as an Activity Effect Vector built only from KB findings.



Enhanced KB

- Machine Learning builds richer Activity Effect Vectors by identifying molecules that have similar activity effects. Such vectors enable the inference of new associations and prioritization of relationships.
- In short, if two genes regulate the expression of a similar set of genes, but only one is associated with the disease, then the other likely has a similar biological impact as well.



Activity Effect Vectors consist of thousands of molecules in the KB. The approach has been validated by “rediscovering” known, curated findings in the KB.

What’s new in the IPA summer release?

Other software changes

- The speed to upload and save a dataset has been improved, most noticeably for datasets with many columns.
- “Reactome” appears as a content source in certain filters in the UI in this release, however, there is currently only a minor addition of Reactome content in IPA. As we prepare to add Reactome pathways in a future release, that source currently only refers to new groups and complexes that have added from Reactome.

What’s new in the IPA summer release?

New pathways

- Acetylcholine Receptor Signaling Pathway
- Adrenergic Receptor Signaling Pathway (Enhanced)
- Cachexia Signaling Pathway
- GABAergic Receptor Signaling Pathway (Enhanced)
- Glutaminergic Receptor Signaling Pathway (Enhanced)
- ISGylation Signaling Pathway
- Microautophagy Signaling Pathway
- NFKBIE Signaling Pathway
- Orexin Signaling Pathway
- Sertoli Cell Germ Cell Junction Signaling Pathway (Enhanced)

Existing pathways updated to include an activity pattern

- IL-17A Signaling in Fibroblasts
- Sertoli Cell-Sertoli Cell Junction Signaling
- TR/RXR Activation

What's new in the IPA summer release?

Addition of >400,000 new findings (bringing the total in IPA to over 12.6 million)

>29,000 protein-protein interaction findings from BioGrid
>407,000 cancer mutation findings from ClinVar
>1,800 target-to-disease findings from ClinicalTrials.gov
>1,700 drug-to-disease findings from ClinicalTrials.gov
>800 Gene Ontology findings
>220 mappable chemicals
> 3,800 Lipid Maps IDs

What’s new in the IPA summer release?

141,323 expression datasets (5,689 added)

Land	Repository	Datasets Q1 2023	Datasets Q2 2023	Increase
DiseaseLand	HumanDisease	32,680	33,672	992
	MouseDisease	25,070	25,253	183
	RatDisease	8,226	8,226	
	LINCS	28,234	28,234	
OncoLand	OncoHuman (Formerly OncoGEO)	15,147	17,125	1,978
	OncoMouse	1,054	1,054	
	TCGA	4,438	4,438	
	MetastaricCancer	81	81	
	Hematology	4,267	4,267	
	Pediatrics	444	444	
	ENCODE RNA Binding*	486	486	
Single Cell Land	SingleCellHuman	194	194	
	SingleCellHumanUmi	8,636	11,049	2,413
	SingleCellHumanUmiLite	603	603	
	SingleCellHumanHCL	1,476	1,469	**-7**
	SingleCellMouse	81	81	
	SingleCellMouseUmi	3,097	3,220	123
	SingleCellMouseUmiLite	115	115	
Normal Cell and Tissues	Human Tissues (GTEx)	1,312	1,312	

IPA與市售系統生物學分析工具比較

	IPA	Metacore	KEGG	Note
資料檢索				
基因、蛋白質	O	O	O	
藥物、毒物、代謝物	O	O	O	
疾病與生物功能	O	O	O	
Pathway	O	O	O	
miRNA	O	O	O	
調控作用關係	O	O	O	
Isoform	O	X	X	
Single Cell DB	O	X	X	
Patient Metadata	O	X	X	
Clinical data	O	X	X	
繪製Pathway功能				
互動式Pathway繪製工具	O	O	X(僅提供Mapping)	
Pattern Mapping	O	X	X	根據產生出來的Network以及實驗表現結果，搜尋資料庫疾病、Pathway是否有類似的表現趨勢以及路徑。
Path Tracer	O	X	X	在龐大的訊息路徑中，特別標示感興趣的訊息因子。
表現預測功能	O	O	X	根據實驗結果，預測上下游調控因子表現。

IPA與市售系統生物學分析工具比較

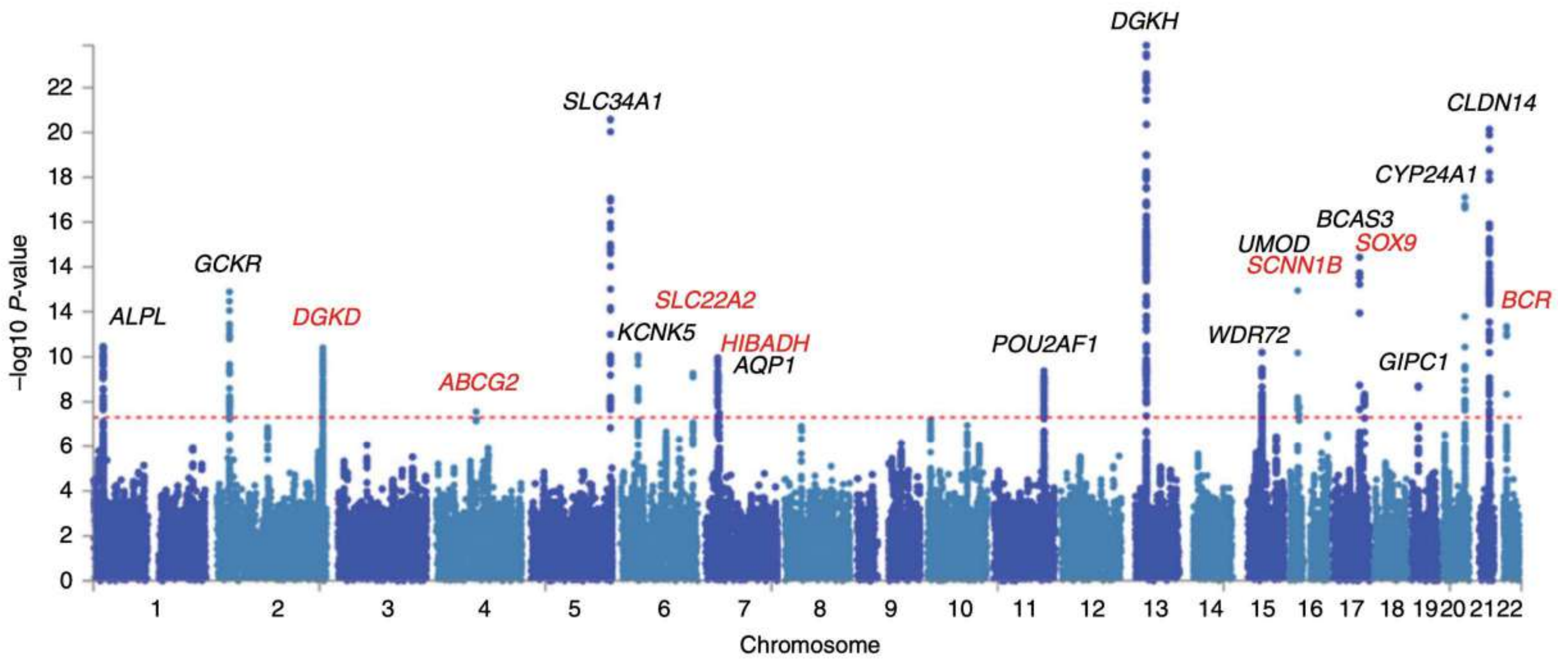
	IPA	Metacore	KEGG	Note
Enrichment Analysis				
基因體、蛋白質體表現分析	O	O	O	
代謝體	O	O	O	
毒物分析	O	O	O	
Enrichment Analysis結果視覺化表現	O	X	X	將各項Enrichment結果以不同的視覺化分析圖表呈現。
Enrichment Analysis Expression Pattern比較	O	X	X	將本次Enrichment結果與其他疾病、實驗的Dataset進行相似性比較。
因果網路分析	O	X	X	將Enrichment結果與感興趣的生物分子或者疾病、生物功能產生關連。
疾病熱圖	O	X	X	以Ontology分類，依據Enrichment分析p-value進行熱圖繪製，可找出較相關的生物功能以及疾病。
網絡關聯圖	O	X	X	將各項Enrichment結果依照重疊的訊息傳遞因子數量進行關聯統計。
泡泡圖分析	O	X	X	以泡泡圖進行三維分析數據結果解讀。可依照生物功能、疾病或者訊息路徑比對關聯性。
比較結果熱圖	O	X	X	以熱圖表示不同Enrichment結果差異，可用做Time or dosage – dependent的實驗比較。

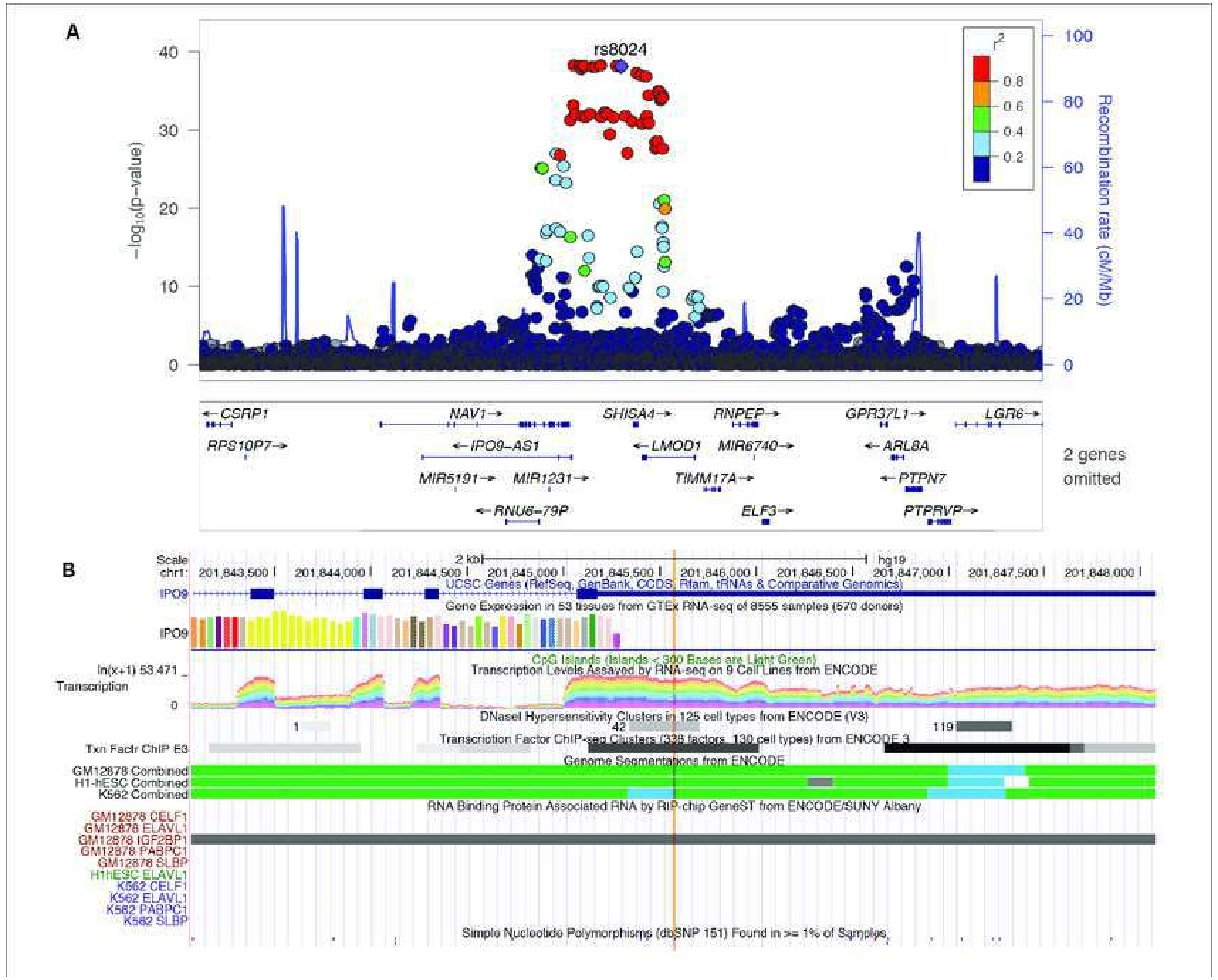
IPA與市售系統生物學分析工具比較

	IPA	Metacore	KEGG	Note
其他功能				
生物特性篩選	O	X	X	Bioprofiler，可篩選出具有相同生物特性的訊息傳遞因子。
Isoform篩選	O	X	X	Isoprofiler，可鑑別出同基因不同Isoform的生物表現結果。
基因於組織差異表現分析	O	X	X	GTEx Expression Pattern，用作於比較相同基因在不同組織的差異分析。
miRNA調控目標預測分析	O	X	X	miRNA Target filter，可進行miRNA與mRNA配對，進而比較出miRNA的作用方式。
磷酸化蛋白質體分析	O	X	X	用於確認不同位點的磷酸化蛋白質功能。
AI預測訊息路徑	O	O (僅有Drug)	X	透過機器學習方式，搜尋相似表現路徑的訊息傳遞因子，連結其相關影響疾病和生物功能。

Genome-wide association study

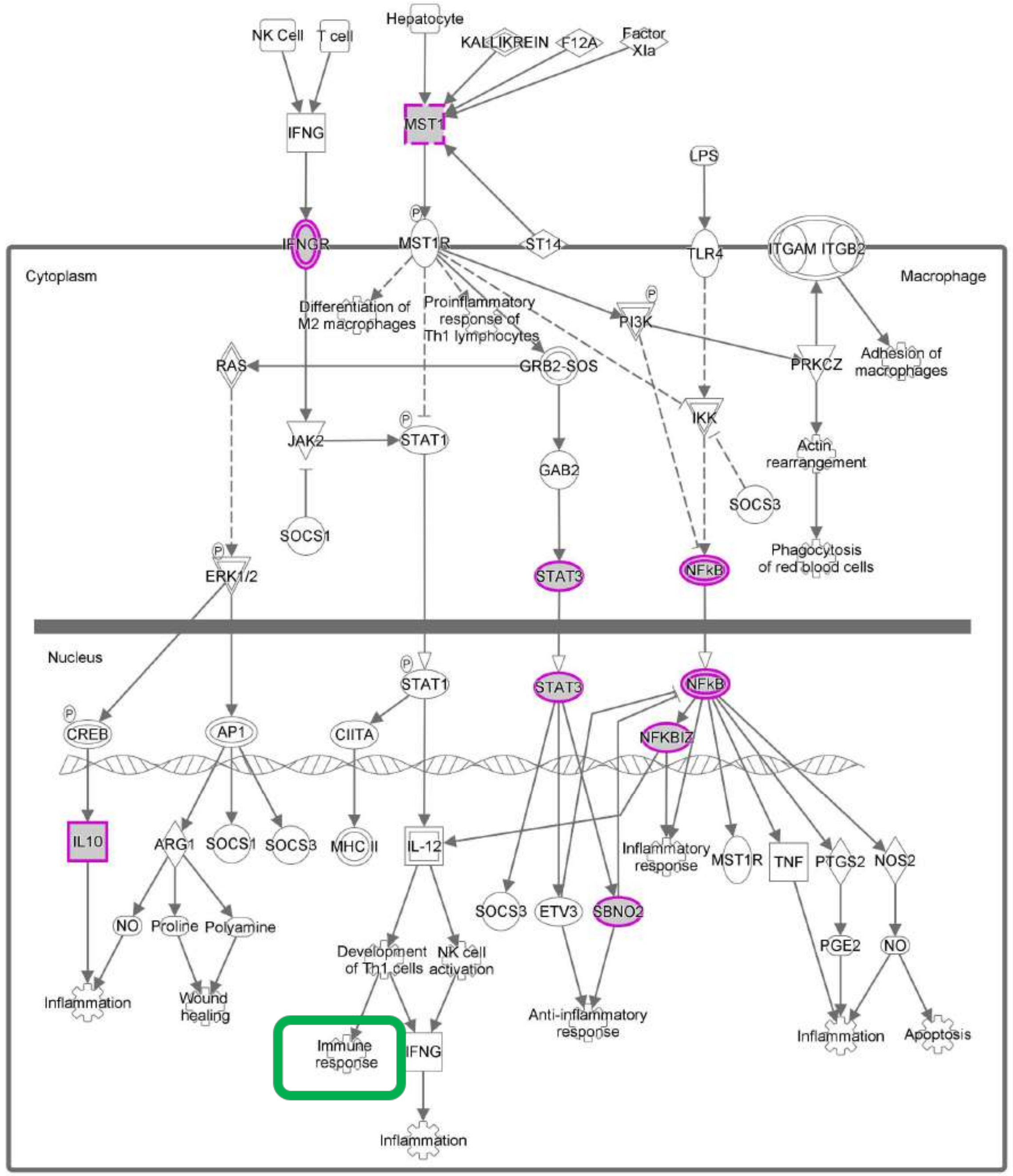
A genome-wide association study (GWA study, or GWAS), is an observational study of a genome-wide set of genetic variants in different individuals to see if any variant is associated with a trait. GWAS typically focus on associations between single-nucleotide polymorphisms (SNPs) and traits like major human diseases, but can equally be applied to any other genetic variants and any other organisms.



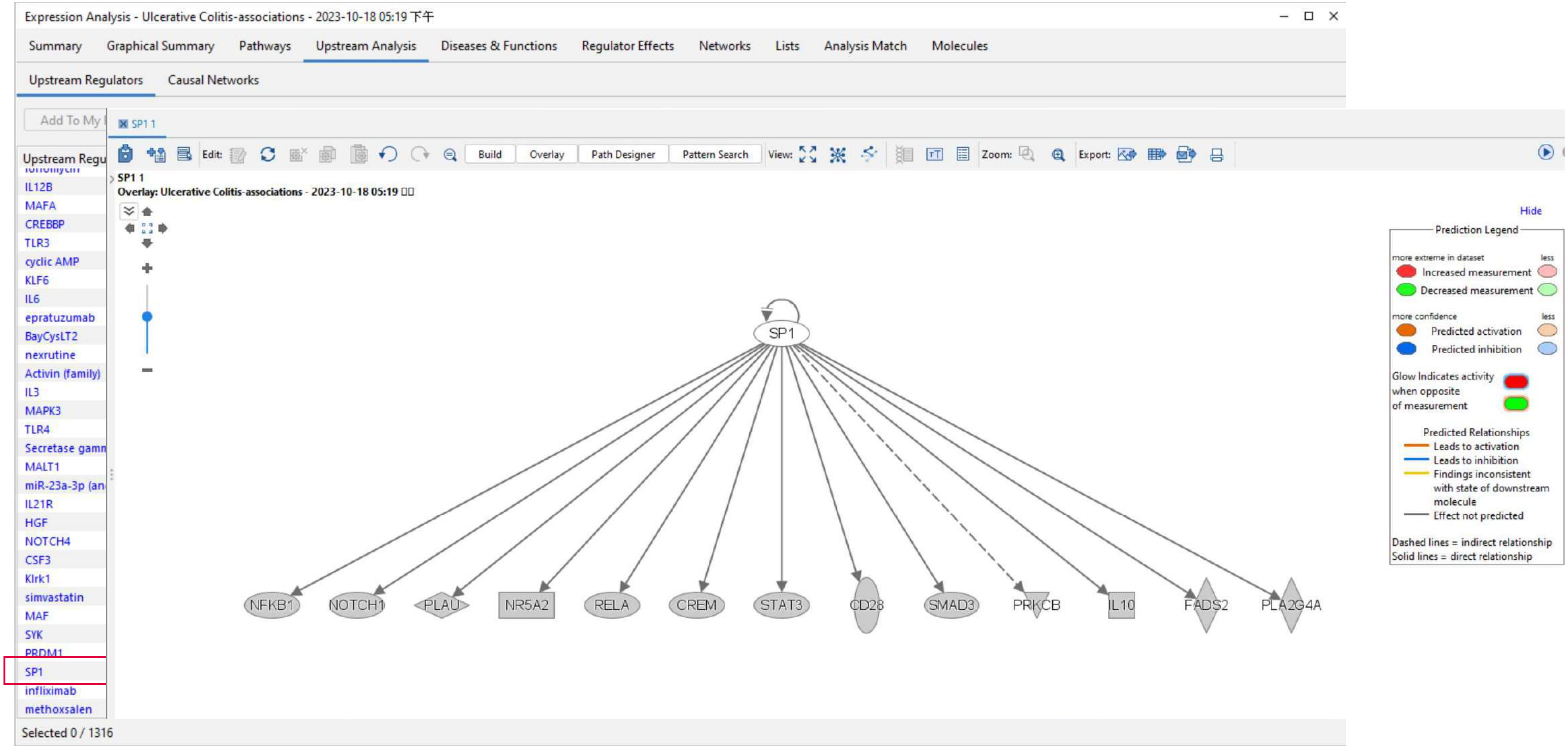


Analyze risk loci to identify enriched pathways

MSP-RON Signaling in Macrophages Pathway



Discover regulatory molecules influencing genes associated with risk loci

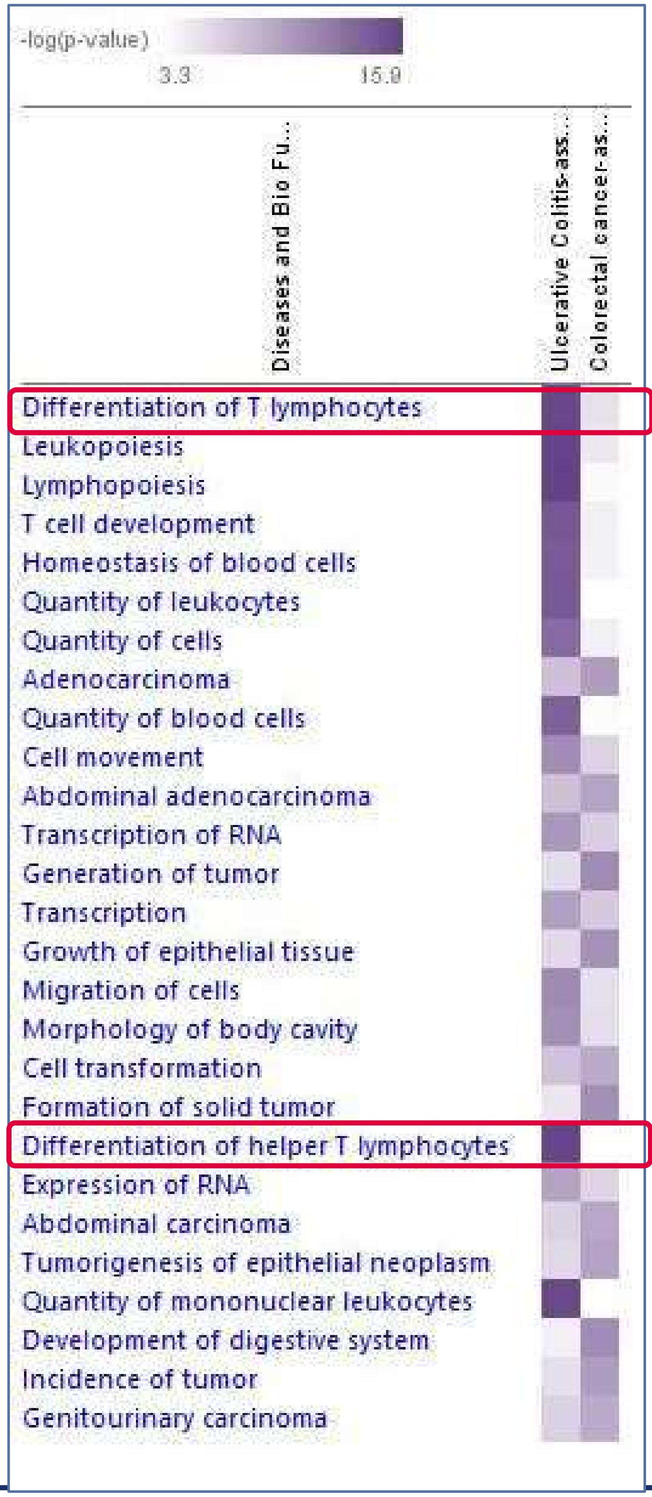


Compare multiple GWAS risk loci analysis using heatmaps

Canonical pathways

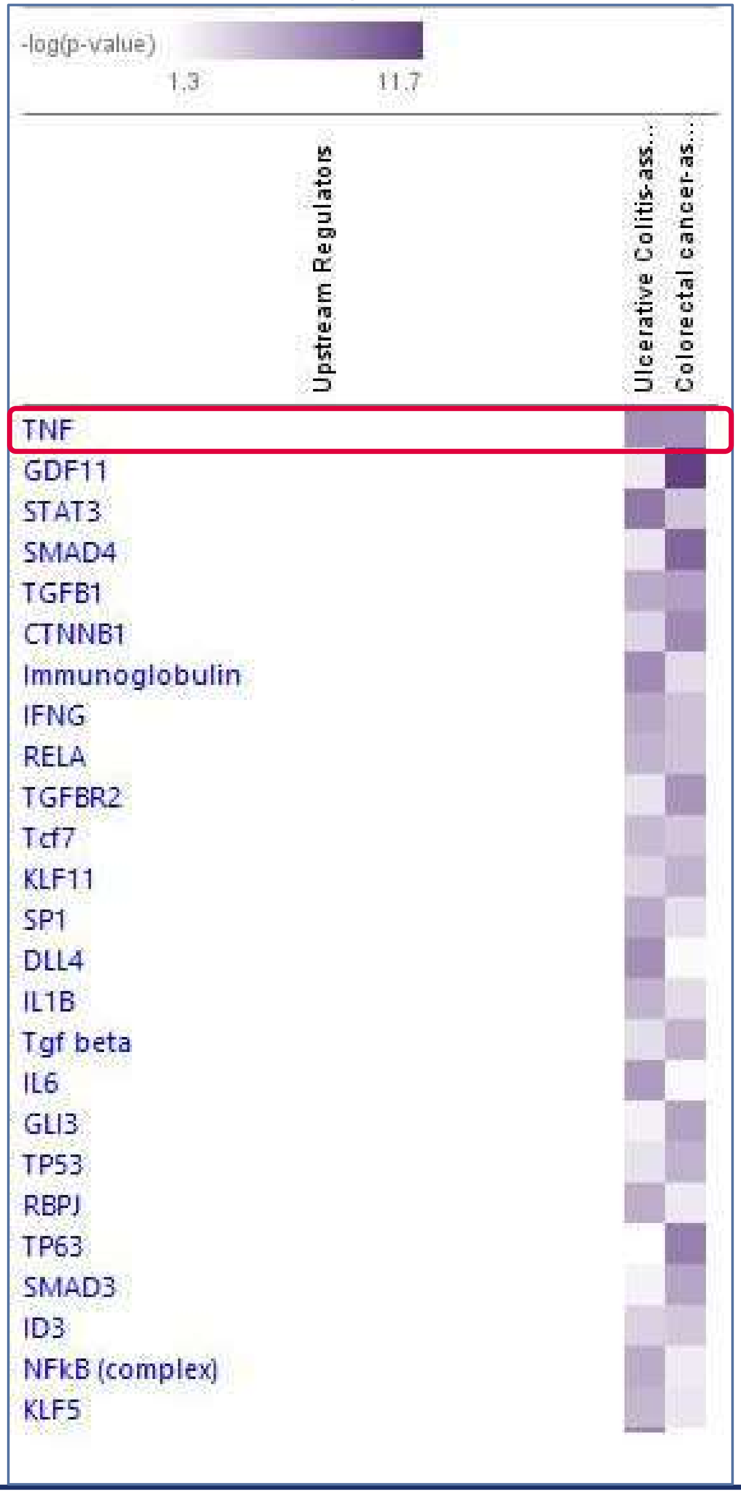
Human Embryonic Stem Cell Pluripotency
Myelination Signaling Pathway
Th1 Pathway
Pulmonary Fibrosis Idiopathic Signaling Pathway
IL-10 Signaling
Molecular Mechanisms of Cancer
Th1 and Th2 Activation Pathway
BMP signaling pathway
Pathogen Induced Cytokine Storm Signaling Pathway
Th2 Pathway
Axonal Guidance Signaling
IL-23 Signaling Pathway
TGF-β Signaling
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis
Chronic Myeloid Leukemia Signaling
Hepatic Fibrosis / Hepatic Stellate Cell Activation
Osteoarthritis Pathway
Basal Cell Carcinoma Signaling
S100 Family Signaling Pathway
CDX Gastrointestinal Cancer Signaling Pathway
Crosstalk between Dendritic Cells and Natural Killer Cells
Factors Promoting Cardiogenesis in Vertebrates
MSP-RON Signaling In Macrophages Pathway
Macrophage Classical Activation Signaling Pathway
Cardiomyocyte Differentiation via BMP Receptors
Hepatic Fibrosis Signaling Pathway
Regulation of the Epithelial-Mesenchymal Transition Pathway
Cardiac Hypertrophy Signaling (Enhanced)
Role Of Osteoblasts In Rheumatoid Arthritis Signaling Pathway

Disease and bio-functions



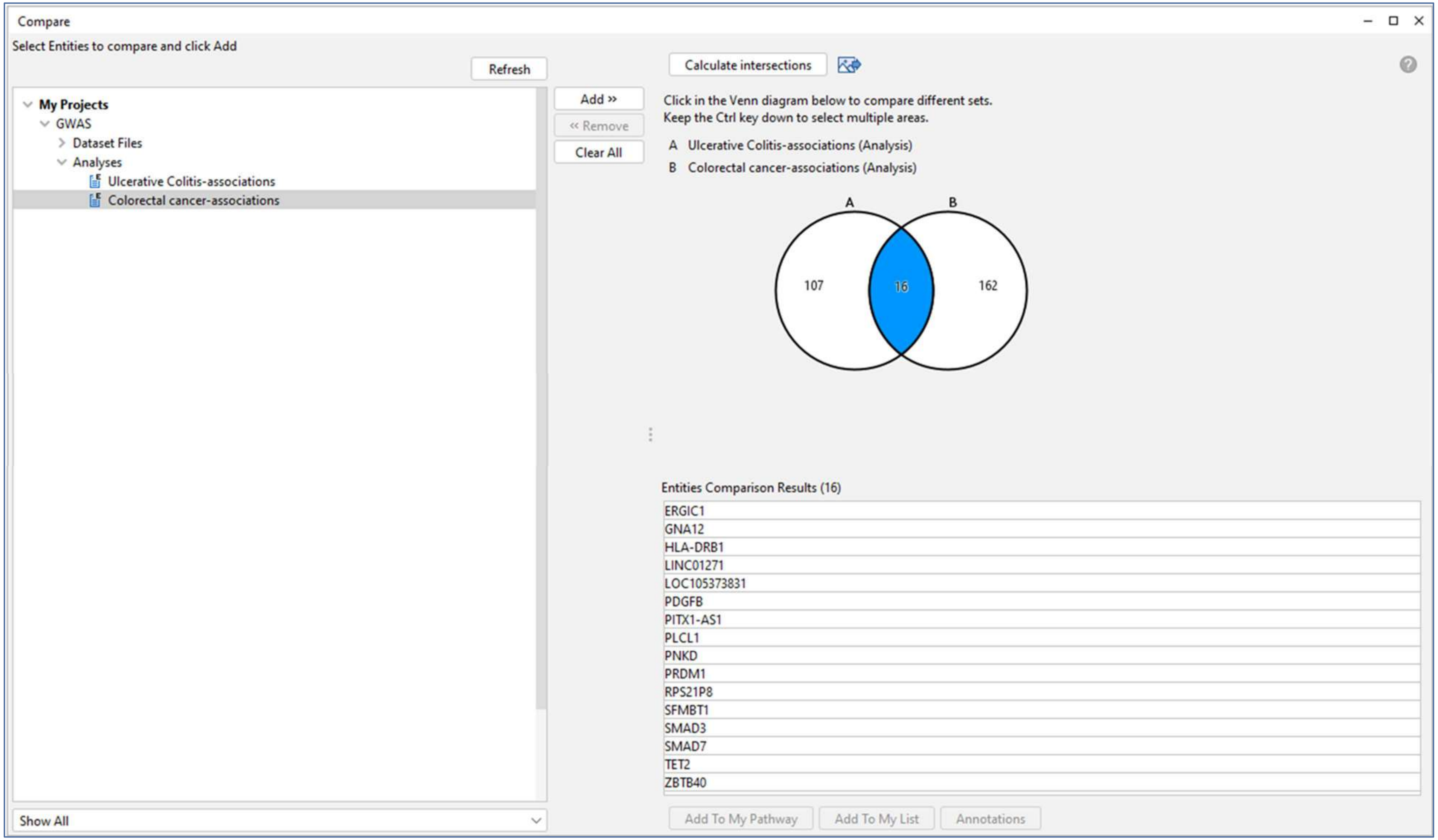
Differentiation of T lymphocytes
Leukopoiesis
Lymphopoiesis
T cell development
Homeostasis of blood cells
Quantity of leukocytes
Quantity of cells
Adenocarcinoma
Quantity of blood cells
Cell movement
Abdominal adenocarcinoma
Transcription of RNA
Generation of tumor
Transcription
Growth of epithelial tissue
Migration of cells
Morphology of body cavity
Cell transformation
Formation of solid tumor
Differentiation of helper T lymphocytes
Expression of RNA
Abdominal carcinoma
Tumorigenesis of epithelial neoplasm
Quantity of mononuclear leukocytes
Development of digestive system
Incidence of tumor
Genitourinary carcinoma

Upstream Regulators



TNF
GDF11
STAT3
SMAD4
TGFB1
CTNNB1
Immunoglobulin
IFNG
RELA
TGFBR2
Tcf7
KLF11
SP1
DLL4
IL1B
Tgf beta
IL6
GLI3
TP53
RBPJ
TP63
SMAD3
ID3
NFkB (complex)
KLF5

Compare and identify common molecules between risk loci list



Select Entities to compare and click Add

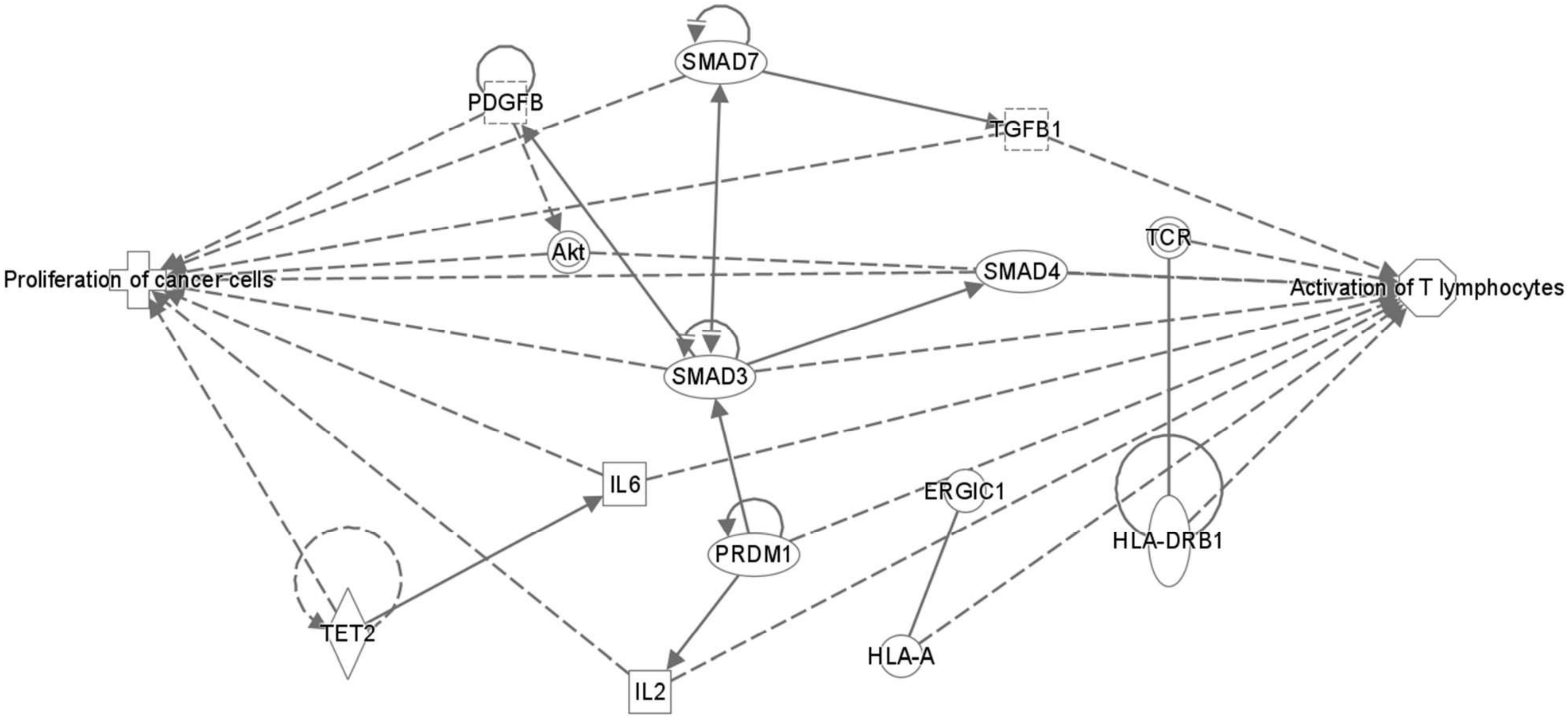
Click in the Venn diagram below to compare different sets.
Keep the Ctrl key down to select multiple areas.

A Ulcerative Colitis-associations (Analysis)
B Colorectal cancer-associations (Analysis)

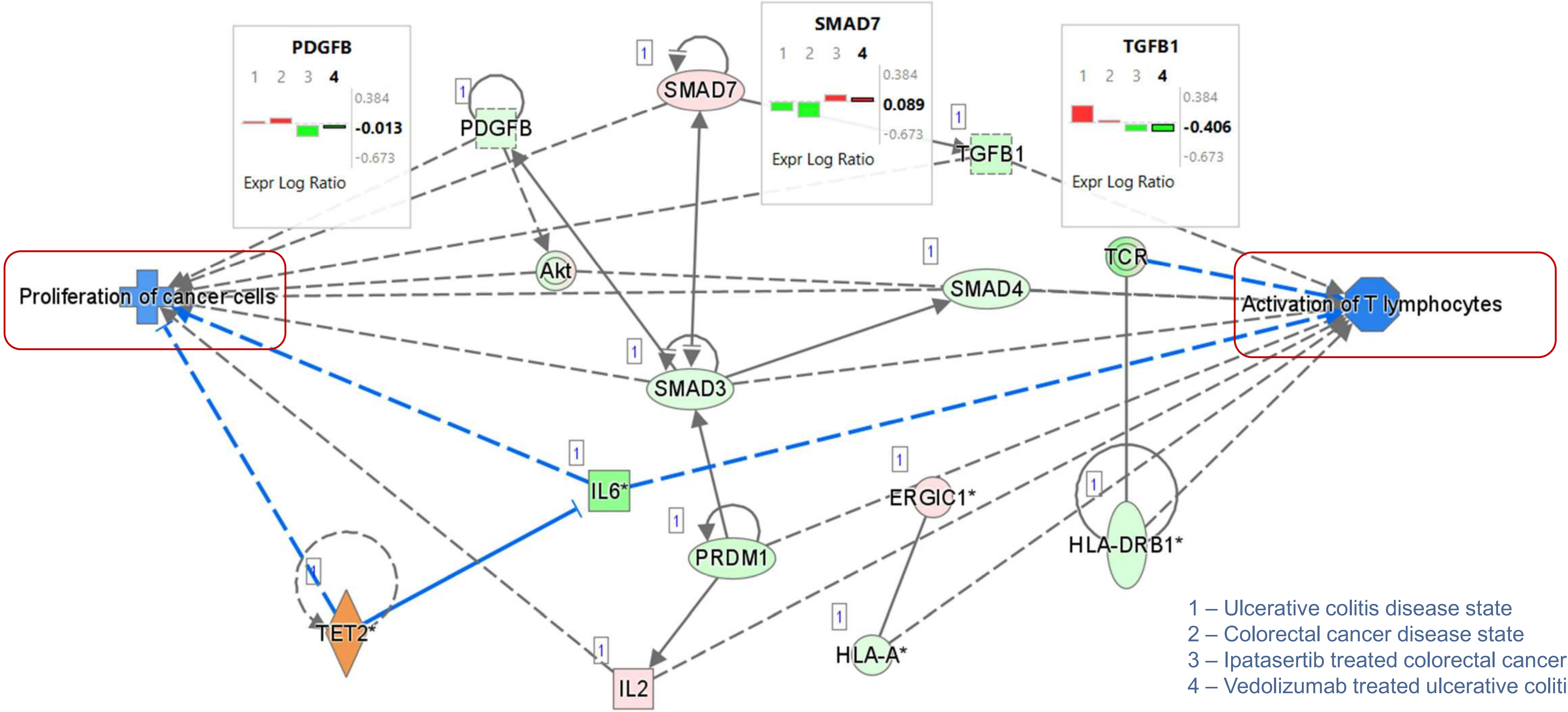
Entities Comparison Results (16)

ERGIC1
GNA12
HLA-DRB1
LINC01271
LOC105373831
PDGFB
PITX1-AS1
PLCL1
PNKD
PRDM1
RPS21P8
SFMBT1
SMAD3
SMAD7
TET2
ZBTB40

Construct a custom network using risk loci associated genes to discover relationships



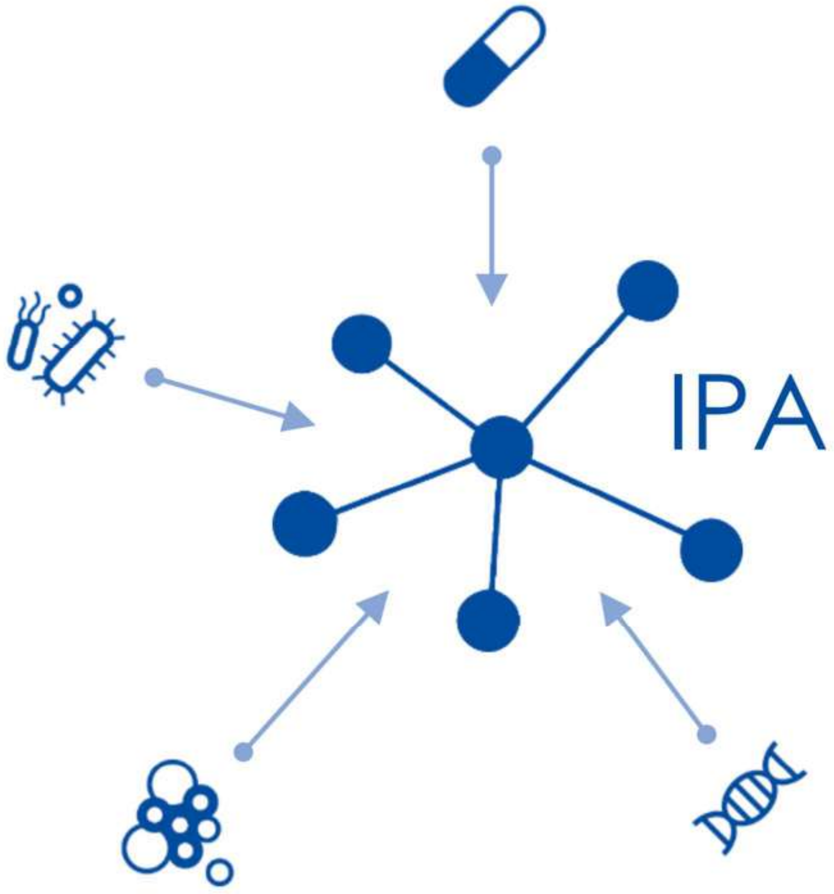
Contextualize a network using public omic data



1 – Ulcerative colitis disease state
2 – Colorectal cancer disease state
3 – Ipatasertib treated colorectal cancer
4 – Vedolizumab treated ulcerative colitis

IPA is powered by the QIAGEN Knowledge Base

Updated weekly with the latest clinical trials and manuscripts



12+ million findings curated using controlled vocabulary

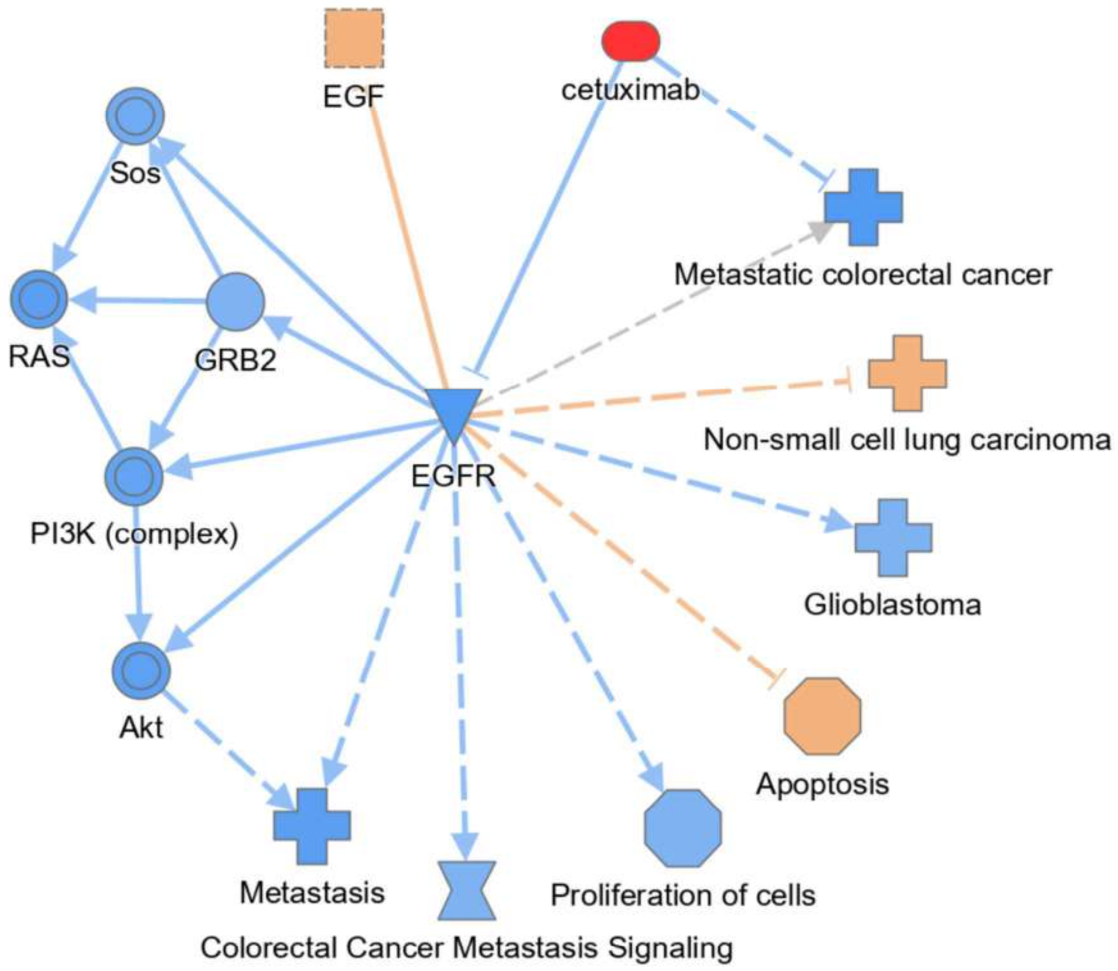
EGF – EGFR
[one of many]

Type:	**activation**
Direction:	**directional**
Effect:	**increases**
Directness:	**direct**
Tissue:	**epithelial cells**
Location:	**plasma membrane**
Source:	**PMID: 17909010**

cetuximab – EGFR
[one of many]

Type:	**phosphorylation**
Direction:	**directional**
Effect:	**decreases**
Cell line:	**CaR1 cells**
Organism:	**human**
Experiment:	**immunoblot**
Source:	**PMID: 23213241**

Decades of accumulated knowledge mapped in directional networks



Data format

	A
1	Risk loci
2	rs6012915
3	rs6095946
4	rs6091189
5	rs6014965
6	rs1741640
7	rs9983528
8	rs4616575
9	rs130651
10	rs5751474
11	rs34256596
12	rs9614460
13	rs9330814
14	rs2732875
15	rs174537
16	rs10751097
17	rs11236187
18	rs117042741
19	rs55864876
20	rs2155065
21	rs3087967
22	rs497916
23	rs10774214
24	rs3217810
25	rs3217874
26	rs10849432
27	rs10849434
28	rs77969132
29	rs2730985

Multiple ID columns

	A	B
1	Risk loci	Mapped gene
2	rs6012915	LINC01271
3	rs6095946	COX6CP2
4	rs6091189	RIPOR3
5	rs6014965	BMP7
6	rs1741640	LAMA5
7	rs9983528	PCNT
8	rs4616575	ZNRF3
9	rs130651	PDGFB
10	rs5751474	SCUBE1
11	rs34256596	LINC01639
12	rs9614460	SMC1B
13	rs9330814	WNT7B
14	rs2732875	SHROOM2
15	rs174537	MYRF
16	rs10751097	ANO1
17	rs11236187	POLD3
18	rs117042741	XRRA1

Accepted Files Formats

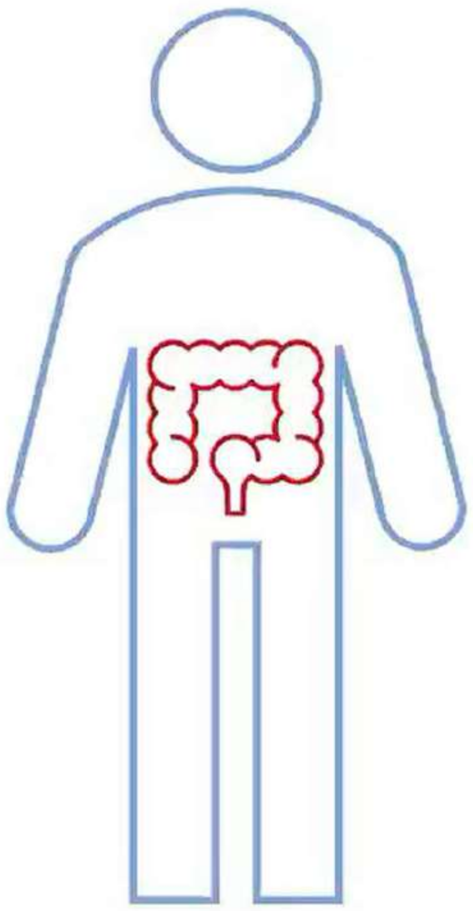
.txt (tab delimited text files)

.xls, .xlsx, .csv (excel files)

.diff (cuffdiff files)

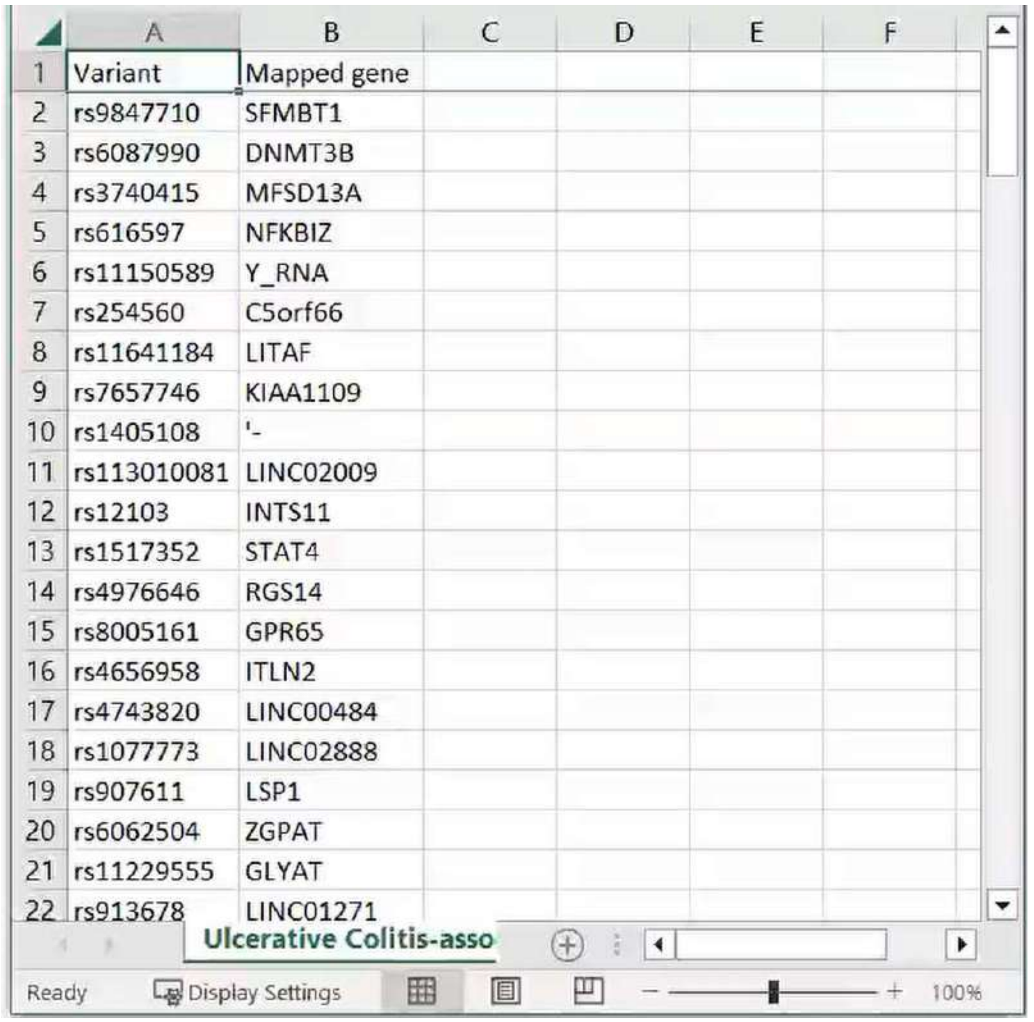
Use Case

Analysis of genetic loci list identified in genome-wide association study (GWAS)



Ulcerative Colitis

(PMID: 26192919)



Variant	Mapped gene
rs9847710	SFMBT1
rs6087990	DNMT3B
rs3740415	MFSD13A
rs616597	NFKBIZ
rs11150589	Y_RNA
rs254560	C5orf66
rs11641184	LITAF
rs7657746	KIAA1109
rs1405108	'-
rs113010081	LINC02009
rs12103	INTS11
rs1517352	STAT4
rs4976646	RGS14
rs8005161	GPR65
rs4656958	ITLN2
rs4743820	LINC00484
rs1077773	LINC02888
rs907611	LSP1
rs6062504	ZGPAT
rs11229555	GLYAT
rs913678	LINC01271

IPA Training Account & Demo Data

Account: ipaXX@ingenuity.com

(XX= 01~30)

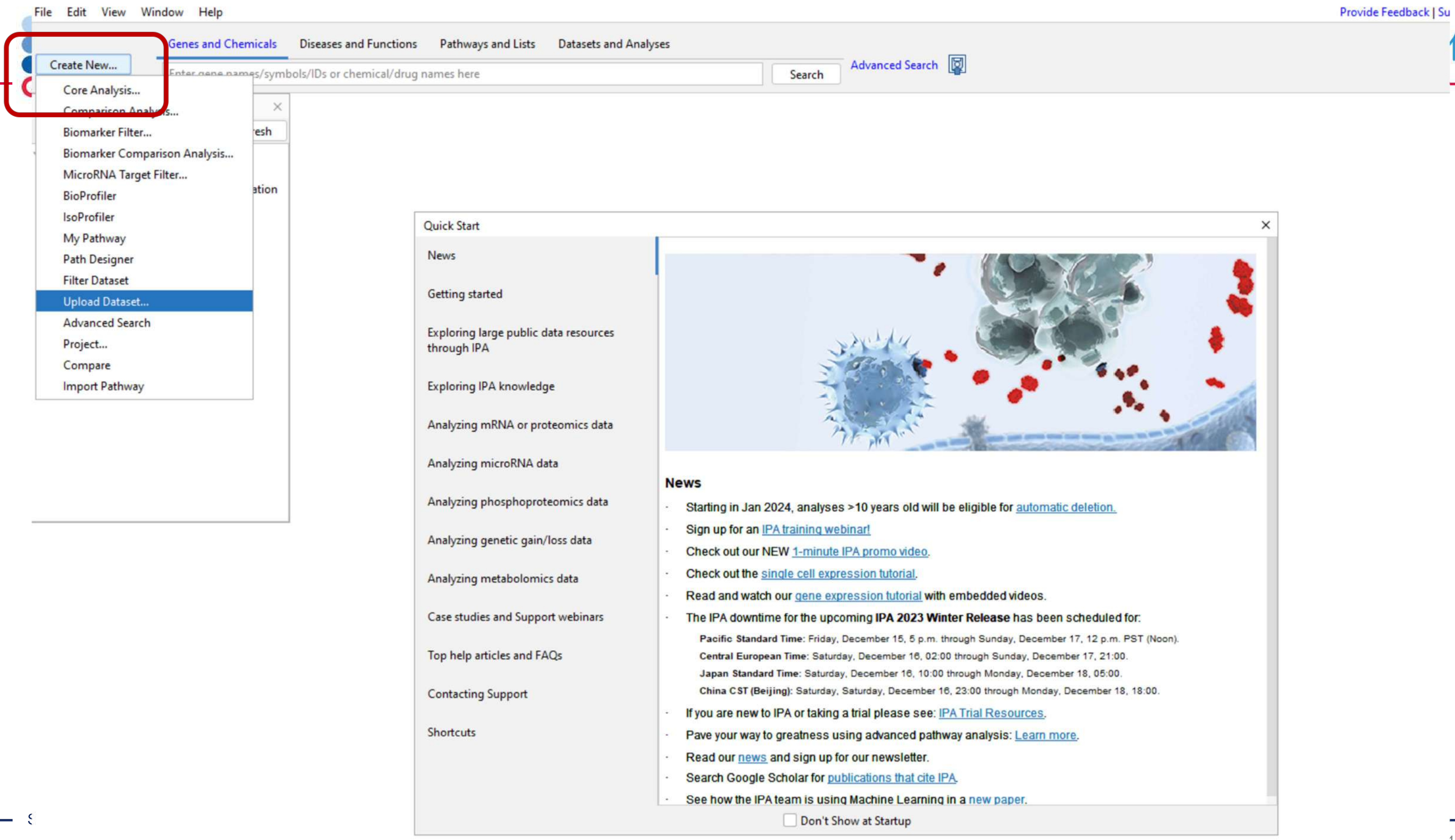
Password: **9-Str0ngP@&&IPA**

Expired until 10/20

Download website: https://tinyurl.com/**GGAIPA**

Dataset: https://tinyurl.com/**GGAdataset**

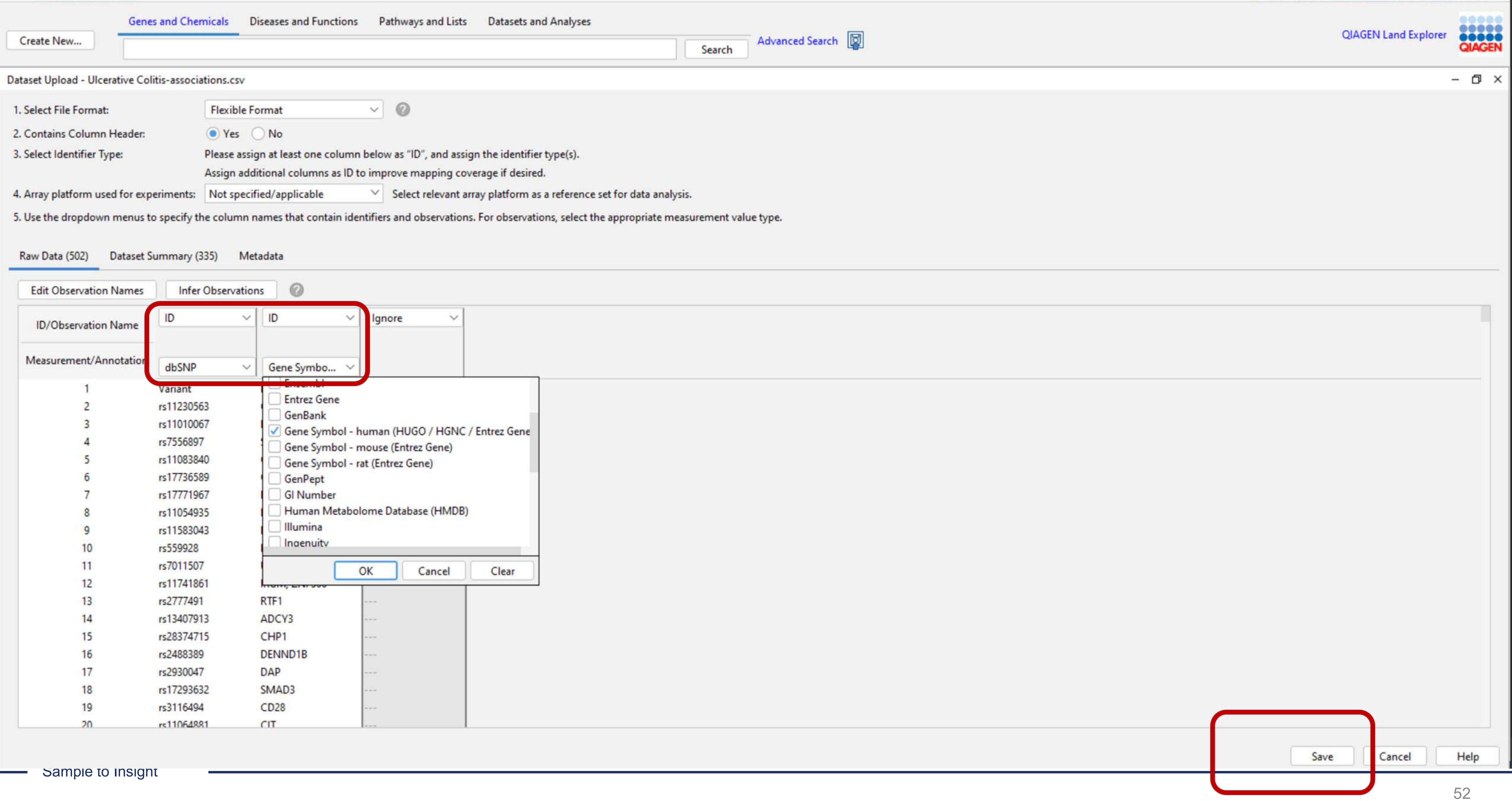
Client: (IPA Login)



News

- Starting in Jan 2024, analyses >10 years old will be eligible for automatic deletion.
- Sign up for an IPA training webinar!
- Check out our NEW 1-minute IPA promo video.
- Check out the single cell expression tutorial.
- Read and watch our gene expression tutorial with embedded videos.
- The IPA downtime for the upcoming **IPA 2023 Winter Release** has been scheduled for:
  - **Pacific Standard Time**: Friday, December 15, 5 p.m. through Sunday, December 17, 12 p.m. PST (Noon).
  - **Central European Time**: Saturday, December 16, 02:00 through Sunday, December 17, 21:00.
  - **Japan Standard Time**: Saturday, December 16, 10:00 through Monday, December 18, 05:00.
  - **China CST (Beijing)**: Saturday, Saturday, December 16, 23:00 through Monday, December 18, 18:00.
- If you are new to IPA or taking a trial please see: IPA Trial Resources.
- Pave your way to greatness using advanced pathway analysis: Learn more.
- Read our news and sign up for our newsletter.
- Search Google Scholar for publications that cite IPA.
- See how the IPA team is using Machine Learning in a new paper.

Titl



Dataset Upload - Ulcerative Colitis-associations.csv

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

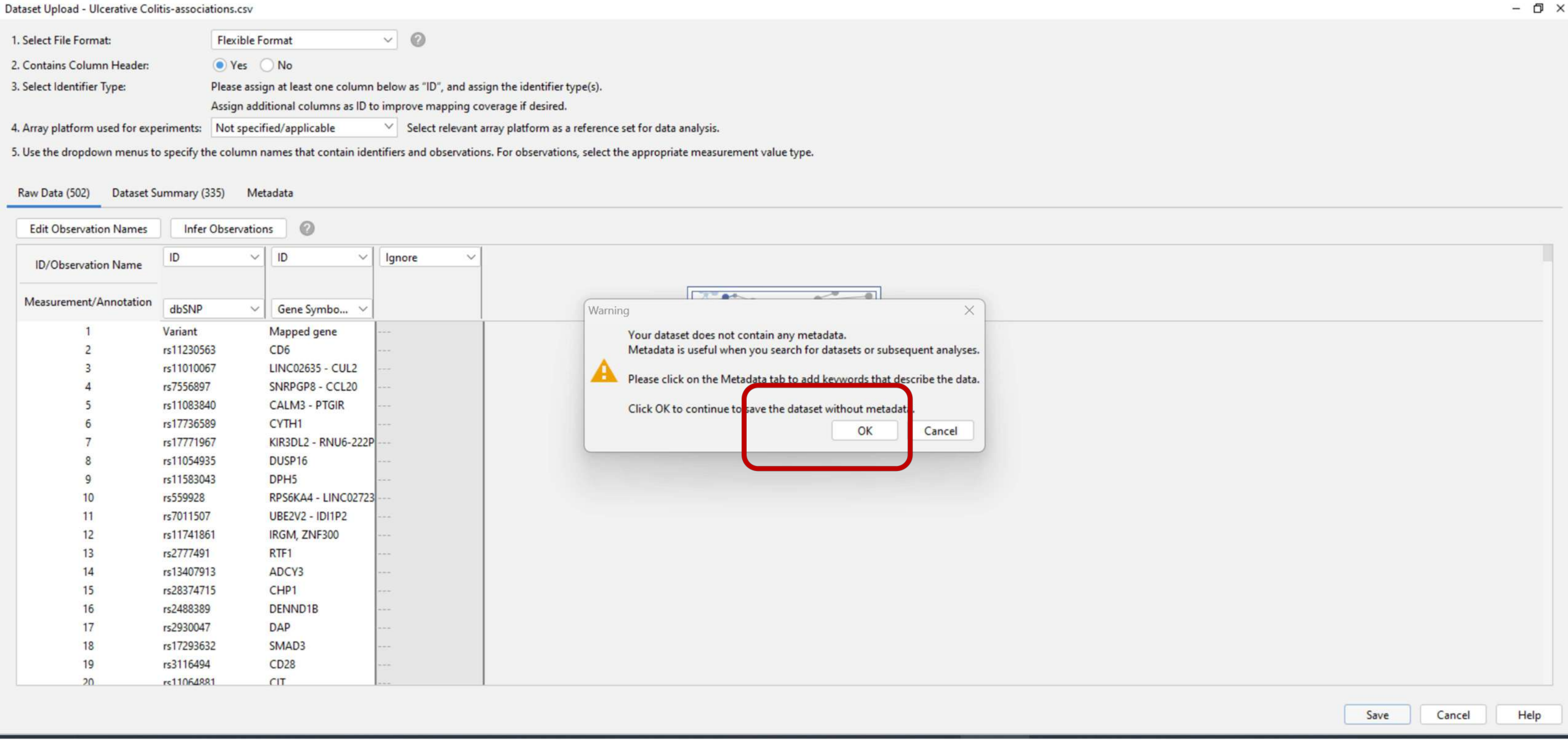
3. Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s).
Assign additional columns as ID to improve mapping coverage if desired.

4. Array platform used for experiments: Not specified/applicable Select relevant array platform as a reference set for data analysis.

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

ID/Observation Name	ID	ID	Ignore
Measurement/Annotation	dbSNP	Gene Symbo...	
1	Variant		
2	rs11230563		
3	rs11010067		
4	rs7556897		
5	rs11083840		
6	rs17736589		
7	rs17771967		
8	rs11054935		
9	rs11583043		
10	rs559928		
11	rs7011507		
12	rs11741861		
13	rs2777491	RTF1	---
14	rs13407913	ADCY3	---
15	rs28374715	CHP1	---
16	rs2488389	DENND1B	---
17	rs2930047	DAP	---
18	rs17293632	SMAD3	---
19	rs3116494	CD28	---
20	rs11064881	CIT	---

- ☐ Entrez Gene
- ☐ GenBank
- ☑ Gene Symbol - human (HUGO / HGNC / Entrez Gene
- ☐ Gene Symbol - mouse (Entrez Gene)
- ☐ Gene Symbol - rat (Entrez Gene)
- ☐ GenPept
- ☐ GI Number
- ☐ Human Metabolome Database (HMDB)
- ☐ Illumina
- ☐ Ingenuity



Dataset Upload - Ulcerative Colitis-associations.csv

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

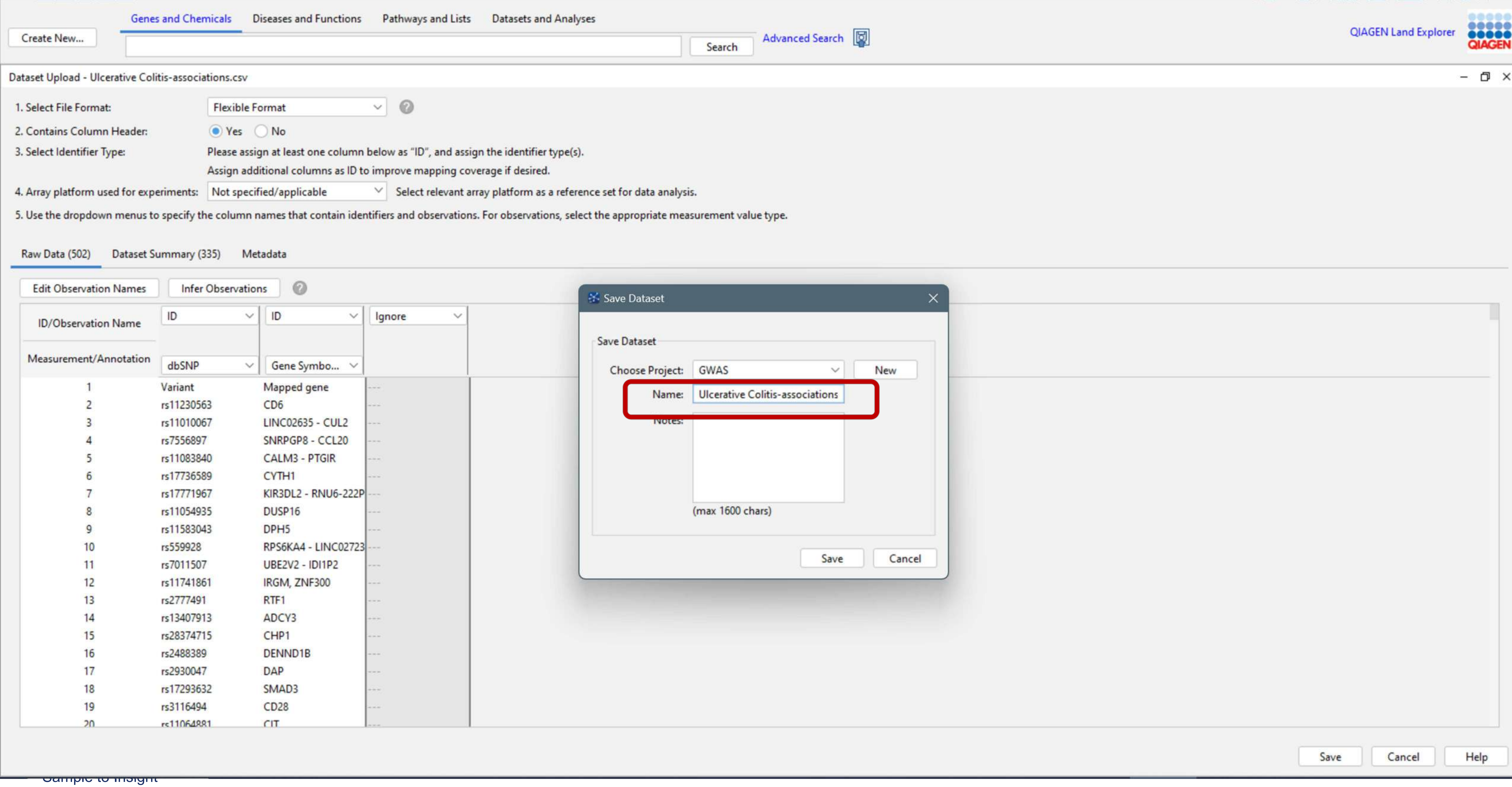
ID/Observation Name	ID	ID	Ignore
Measurement/Annotation	dbSNP	Gene Symbo...	
1	Variant	Mapped gene	---
2	rs11230563	CD6	---
3	rs11010067	LINC02635 - CUL2	---
4	rs7556897	SNRPGP8 - CCL20	---
5	rs11083840	CALM3 - PTGIR	---
6	rs17736589	CYTH1	---
7	rs17771967	KIR3DL2 - RNU6-222P	---
8	rs11054935	DUSP16	---
9	rs11583043	DPH5	---
10	rs559928	RPS6KA4 - LINC02723	---
11	rs7011507	UBE2V2 - IDI1P2	---
12	rs11741861	IRGM, ZNF300	---
13	rs2777491	RTF1	---
14	rs13407913	ADCY3	---
15	rs28374715	CHP1	---
16	rs2488389	DENND1B	---
17	rs2930047	DAP	---
18	rs17293632	SMAD3	---
19	rs3116494	CD28	---
20	rs11064881	CIT	---

Warning

Your dataset does not contain any metadata.
Metadata is useful when you search for datasets or subsequent analyses.

Please click on the Metadata tab to add keywords that describe the data.

Click OK to continue to save the dataset without metadata.



Dataset Upload - Ulcerative Colitis-associations.csv

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

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

4. Array platform used for experiments: Not specified/applicable — Select relevant array platform as a reference set for data analysis.

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

ID/Observation Name	ID	ID	Ignore
Measurement/Annotation	dbSNP	Gene Symbo...	
1	Variant	Mapped gene	---
2	rs11230563	CD6	---
3	rs11010067	LINC02635 - CUL2	---
4	rs7556897	SNRPGP8 - CCL20	---
5	rs11083840	CALM3 - PTGIR	---
6	rs17736589	CYTH1	---
7	rs17771967	KIR3DL2 - RNU6-222P	---
8	rs11054935	DUSP16	---
9	rs11583043	DPH5	---
10	rs559928	RPS6KA4 - LINC02723	---
11	rs7011507	UBE2V2 - IDI1P2	---
12	rs11741861	IRGM, ZNF300	---
13	rs2777491	RTF1	---
14	rs13407913	ADCY3	---
15	rs28374715	CHP1	---
16	rs2488389	DENND1B	---
17	rs2930047	DAP	---
18	rs17293632	SMAD3	---
19	rs3116494	CD28	---
20	rs11064881	CIT	---

Save Dataset

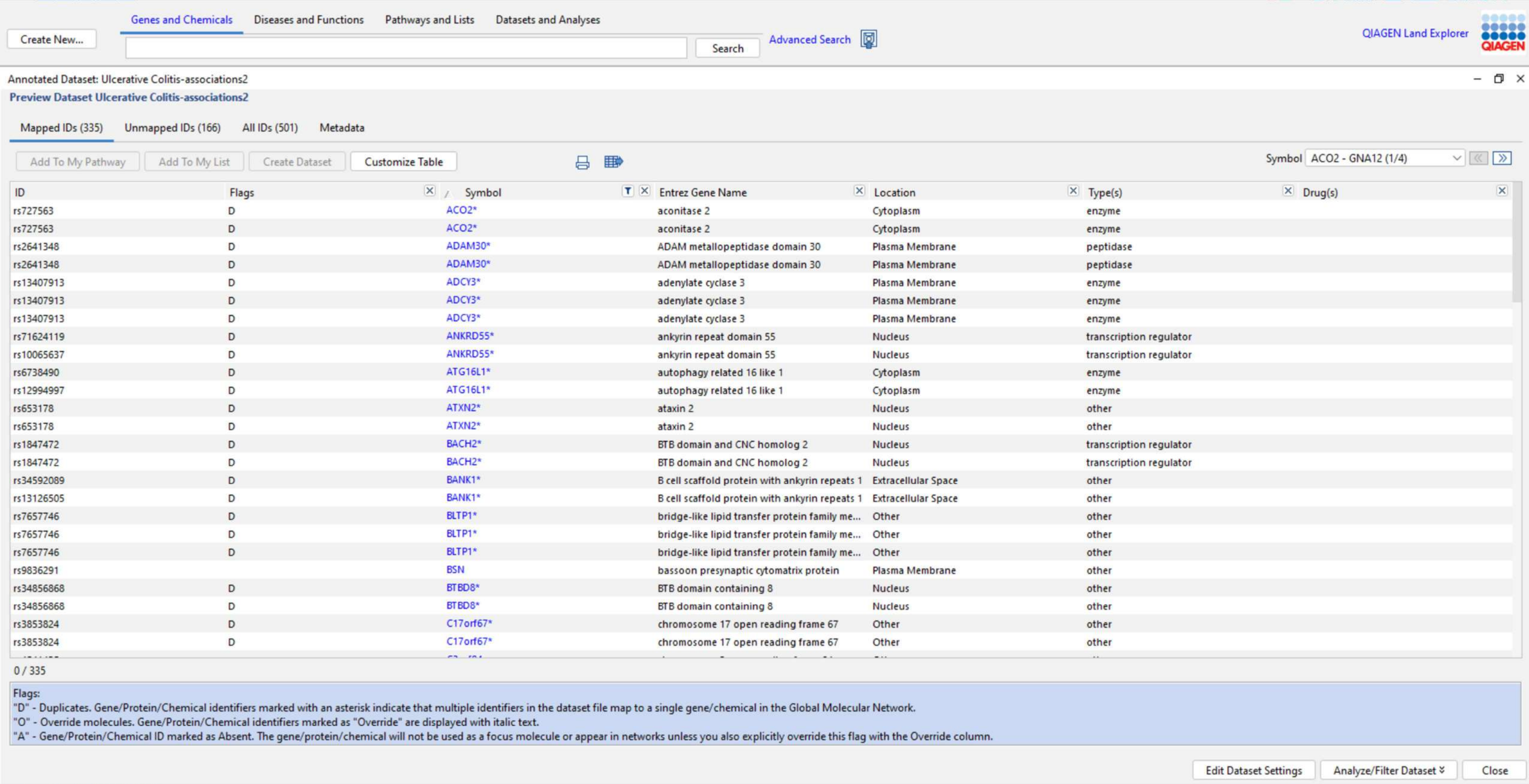
Save Dataset

Choose Project: GWAS

Name: Ulcerative Colitis-associations

Notes:

(max 1600 chars)



Annotated Dataset: Ulcerative Colitis-associations2

Preview Dataset Ulcerative Colitis-associations2

ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
rs727563	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
rs727563	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
rs2641348	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
rs2641348	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
rs13407913	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
rs13407913	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
rs13407913	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
rs71624119	D	ANKRD55*	ankyrin repeat domain 55	Nucleus	transcription regulator	
rs10065637	D	ANKRD55*	ankyrin repeat domain 55	Nucleus	transcription regulator	
rs6738490	D	ATG16L1*	autophagy related 16 like 1	Cytoplasm	enzyme	
rs12994997	D	ATG16L1*	autophagy related 16 like 1	Cytoplasm	enzyme	
rs653178	D	ATXN2*	ataxin 2	Nucleus	other	
rs653178	D	ATXN2*	ataxin 2	Nucleus	other	
rs1847472	D	BACH2*	BTB domain and CNC homolog 2	Nucleus	transcription regulator	
rs1847472	D	BACH2*	BTB domain and CNC homolog 2	Nucleus	transcription regulator	
rs34592089	D	BANK1*	B cell scaffold protein with ankyrin repeats 1	Extracellular Space	other	
rs13126505	D	BANK1*	B cell scaffold protein with ankyrin repeats 1	Extracellular Space	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs9836291		BSN	bassoon presynaptic cytomatrix protein	Plasma Membrane	other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	

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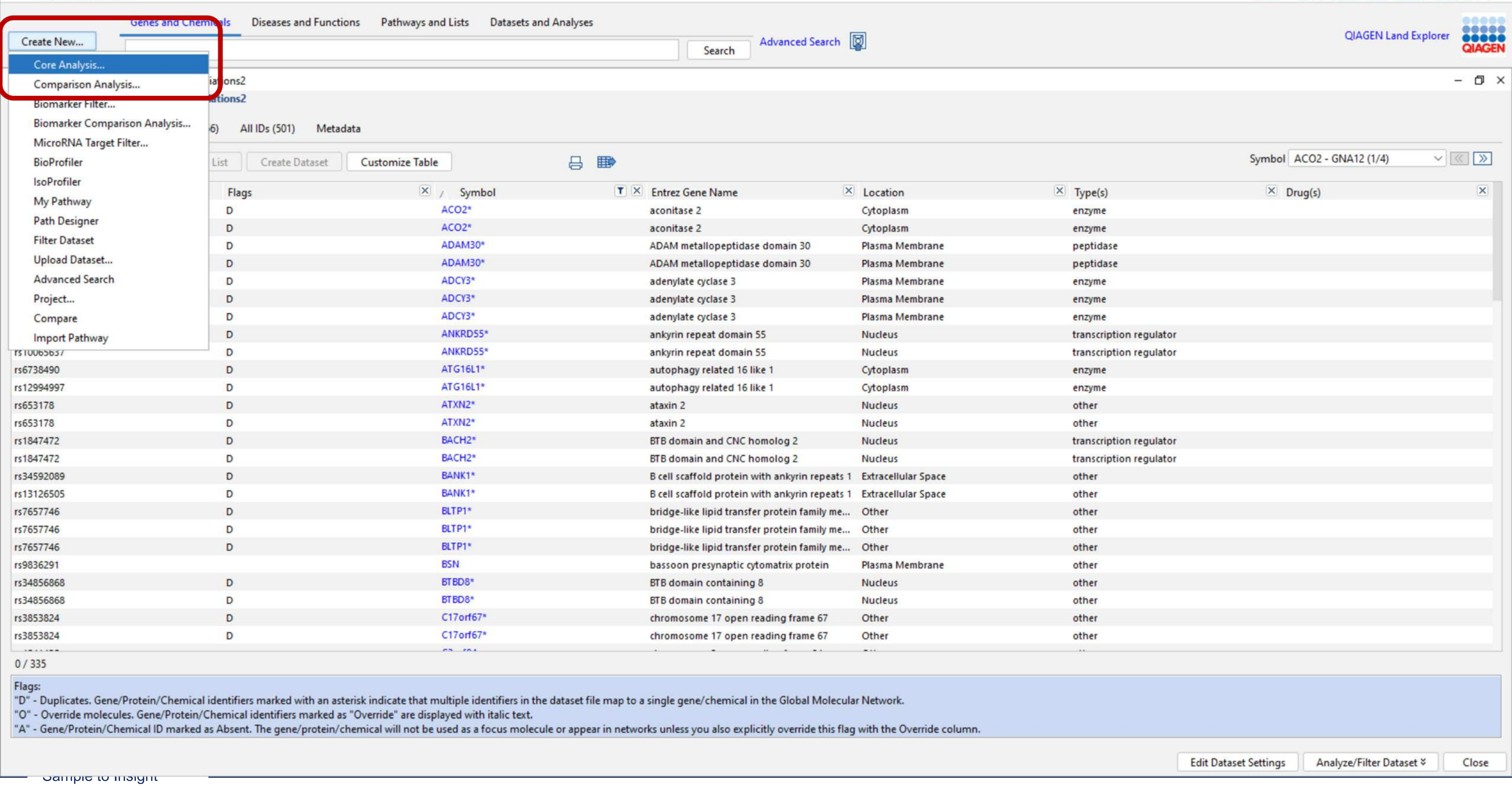
Flags:
"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.
"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with 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.



	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
	D	ADCY3*	adenylate cyclase 3	Plasma Membrane	enzyme	
	D	ANKRD55*	ankyrin repeat domain 55	Nucleus	transcription regulator	
rs10065637	D	ANKRD55*	ankyrin repeat domain 55	Nucleus	transcription regulator	
rs6738490	D	ATG16L1*	autophagy related 16 like 1	Cytoplasm	enzyme	
rs12994997	D	ATG16L1*	autophagy related 16 like 1	Cytoplasm	enzyme	
rs653178	D	ATXN2*	ataxin 2	Nucleus	other	
rs653178	D	ATXN2*	ataxin 2	Nucleus	other	
rs1847472	D	BACH2*	BTB domain and CNC homolog 2	Nucleus	transcription regulator	
rs1847472	D	BACH2*	BTB domain and CNC homolog 2	Nucleus	transcription regulator	
rs34592089	D	BANK1*	B cell scaffold protein with ankyrin repeats 1	Extracellular Space	other	
rs13126505	D	BANK1*	B cell scaffold protein with ankyrin repeats 1	Extracellular Space	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs7657746	D	BLTP1*	bridge-like lipid transfer protein family me...	Other	other	
rs9836291		BSN	bassoon presynaptic cytomatrix protein	Plasma Membrane	other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	

0 / 335

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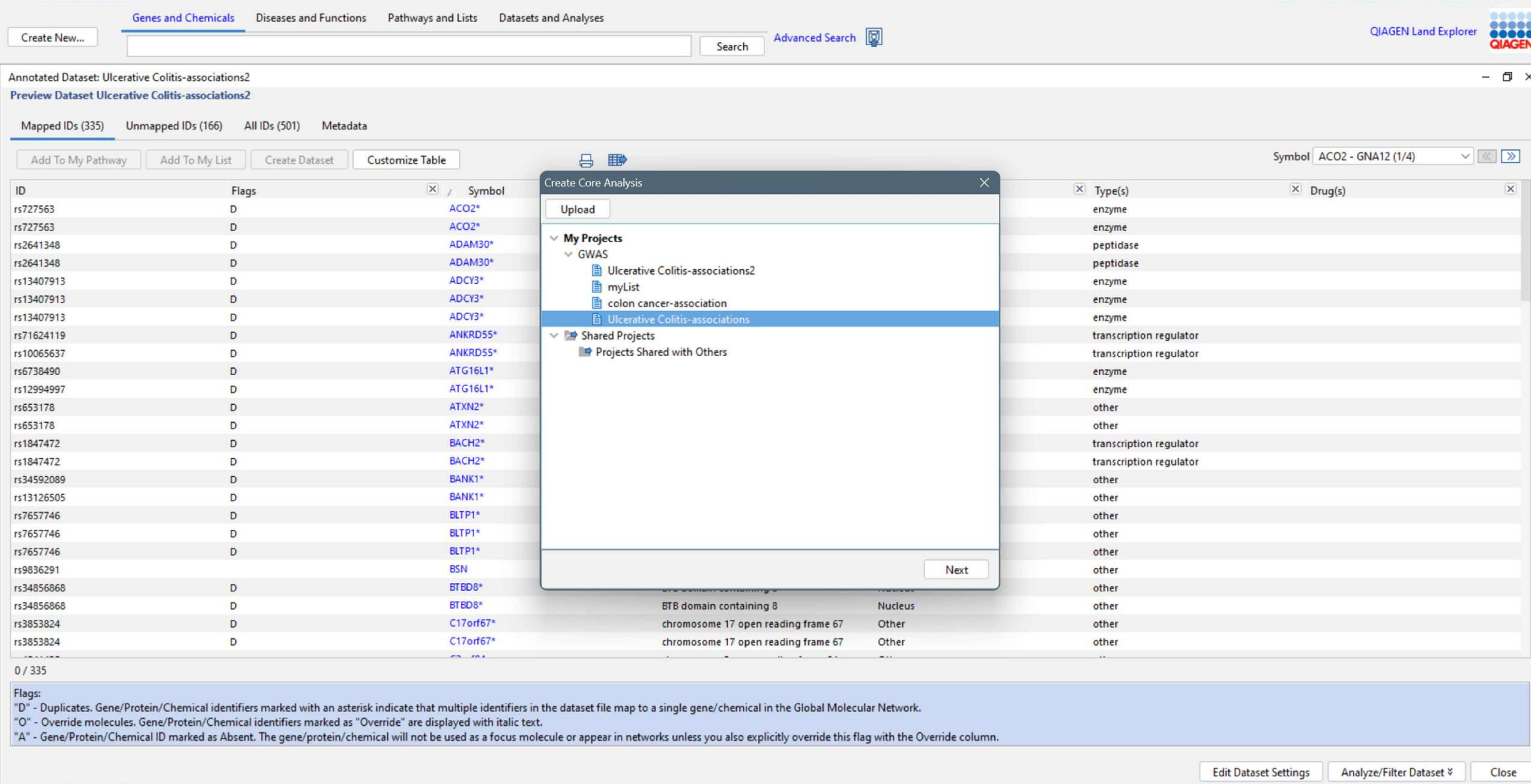

Annotated Dataset: Ulcerative Colitis-associations2

Preview Dataset Ulcerative Colitis-associations2

Symbol ACO2 - GNA12 (1/4)

ID	Flags	Symbol			Type(s)	Drug(s)
rs727563	D	ACO2*			enzyme	
rs727563	D	ACO2*			enzyme	
rs2641348	D	ADAM30*			peptidase	
rs2641348	D	ADAM30*			peptidase	
rs13407913	D	ADCY3*			enzyme	
rs13407913	D	ADCY3*			enzyme	
rs13407913	D	ADCY3*			enzyme	
rs71624119	D	ANKRD55*			transcription regulator	
rs10065637	D	ANKRD55*			transcription regulator	
rs6738490	D	ATG16L1*			enzyme	
rs12994997	D	ATG16L1*			enzyme	
rs653178	D	ATXN2*			other	
rs653178	D	ATXN2*			other	
rs1847472	D	BACH2*			transcription regulator	
rs1847472	D	BACH2*			transcription regulator	
rs34592089	D	BANK1*			other	
rs13126505	D	BANK1*			other	
rs7657746	D	BLTP1*			other	
rs7657746	D	BLTP1*			other	
rs7657746	D	BLTP1*			other	
rs9836291		BSN			other	
rs34856868	D	BTBD8*			other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	

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Create Core Analysis

- My Projects
  - GWAS
    - Ulcerative Colitis-associations2
    - myList
    - colon cancer-association
    - Ulcerative Colitis-associations
- Shared Projects
  - Projects Shared with Others

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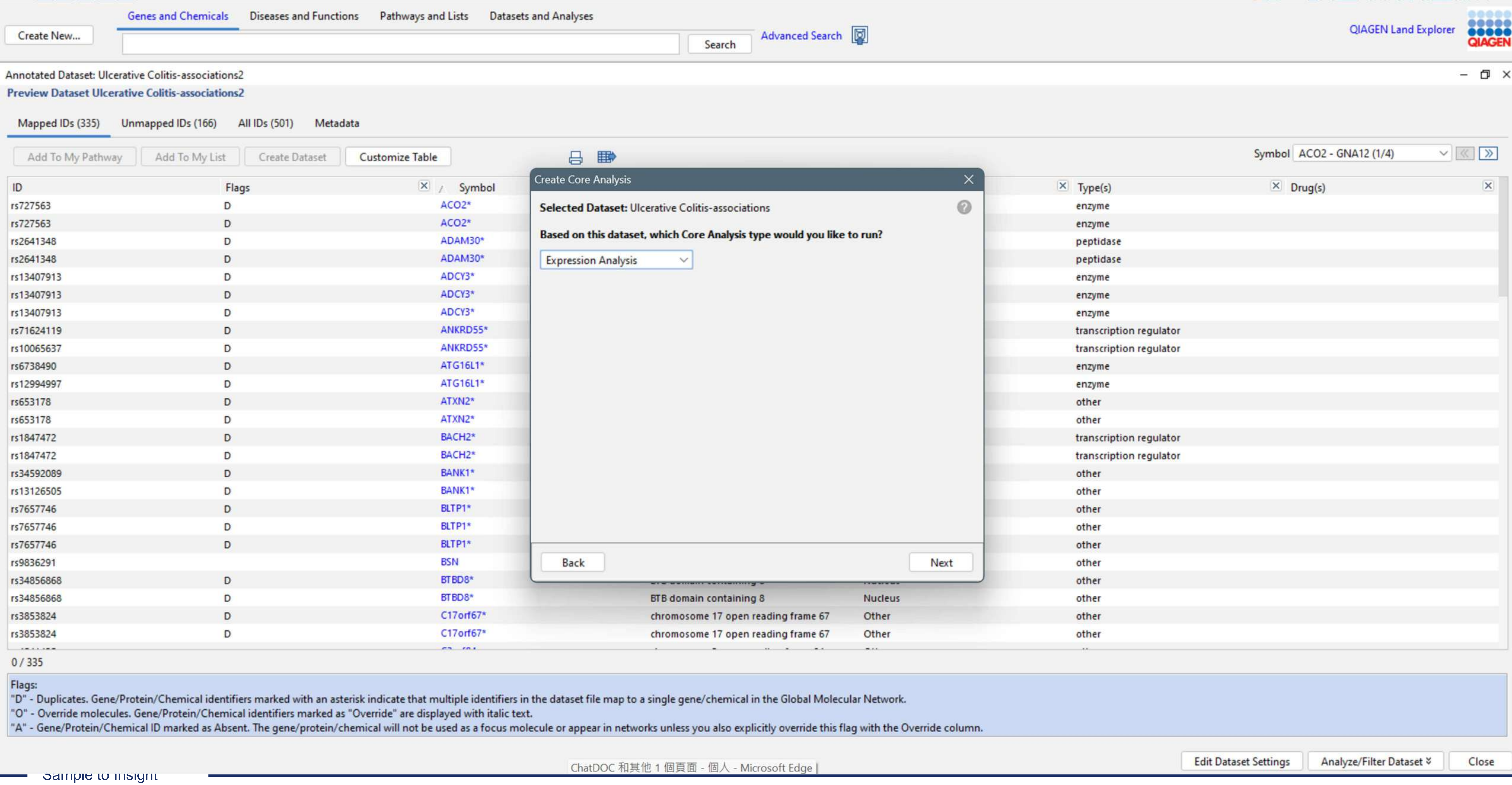
"A" - Gene/Protein/Chemical ID marked as Absent. The gene/protein/chemical will not be used as a focus molecule or appear in networks unless you also explicitly override this flag with the Override column.



Annotated Dataset: Ulcerative Colitis-associations2

Preview Dataset Ulcerative Colitis-associations2

Symbol: ACO2 - GNA12 (1/4)

Create Core Analysis

Selected Dataset: Ulcerative Colitis-associations

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

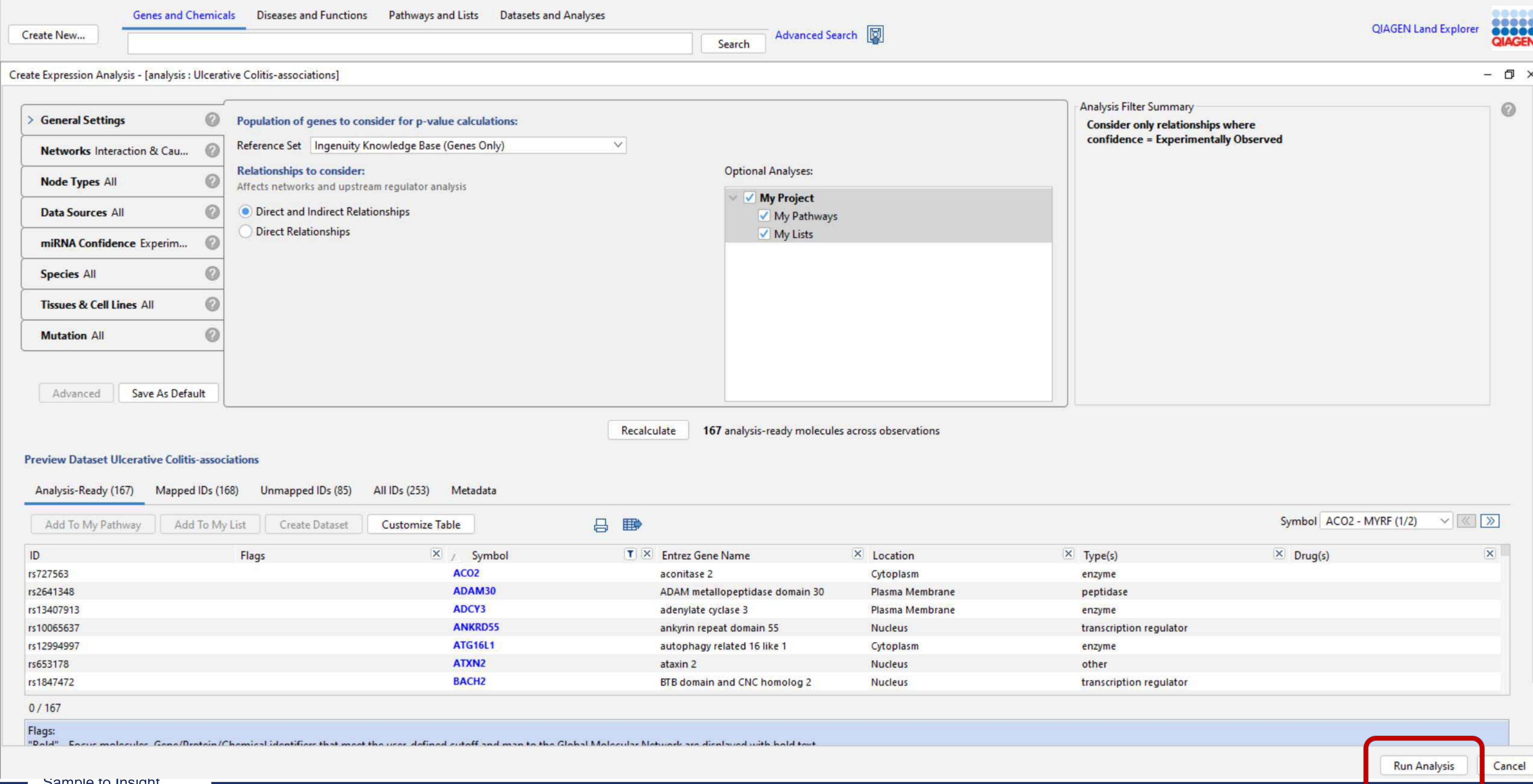
Expression Analysis

ID	Flags	Symbol			Type(s)	Drug(s)
rs727563	D	ACO2*			enzyme	
rs727563	D	ACO2*			enzyme	
rs2641348	D	ADAM30*			peptidase	
rs2641348	D	ADAM30*			peptidase	
rs13407913	D	ADCY3*			enzyme	
rs13407913	D	ADCY3*			enzyme	
rs13407913	D	ADCY3*			enzyme	
rs71624119	D	ANKRD55*			transcription regulator	
rs10065637	D	ANKRD55*			transcription regulator	
rs6738490	D	ATG16L1*			enzyme	
rs12994997	D	ATG16L1*			enzyme	
rs653178	D	ATXN2*			other	
rs653178	D	ATXN2*			other	
rs1847472	D	BACH2*			transcription regulator	
rs1847472	D	BACH2*			transcription regulator	
rs34592089	D	BANK1*			other	
rs13126505	D	BANK1*			other	
rs7657746	D	BLTP1*			other	
rs7657746	D	BLTP1*			other	
rs7657746	D	BLTP1*			other	
rs9836291		BSN			other	
rs34856868	D	BTBD8*			other	
rs34856868	D	BTBD8*	BTB domain containing 8	Nucleus	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	
rs3853824	D	C17orf67*	chromosome 17 open reading frame 67	Other	other	

0 / 335

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.

ChatDOC 和其他 1 個頁面 - 個人 - Microsoft Edge



Create Expression Analysis - [analysis : Ulcerative Colitis-associations]

- **General Settings**
- **Networks** Interaction & Cau...
- **Node Types** All
- **Data Sources** All
- **miRNA Confidence** Experim...
- **Species** All
- **Tissues & Cell Lines** All
- **Mutation** All

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

Optional Analyses:

- ☑ **My Project**
  - ☑ My Pathways
  - ☑ My Lists

Analysis Filter Summary

Consider only relationships where confidence = Experimentally Observed

167 analysis-ready molecules across observations

Preview Dataset Ulcerative Colitis-associations

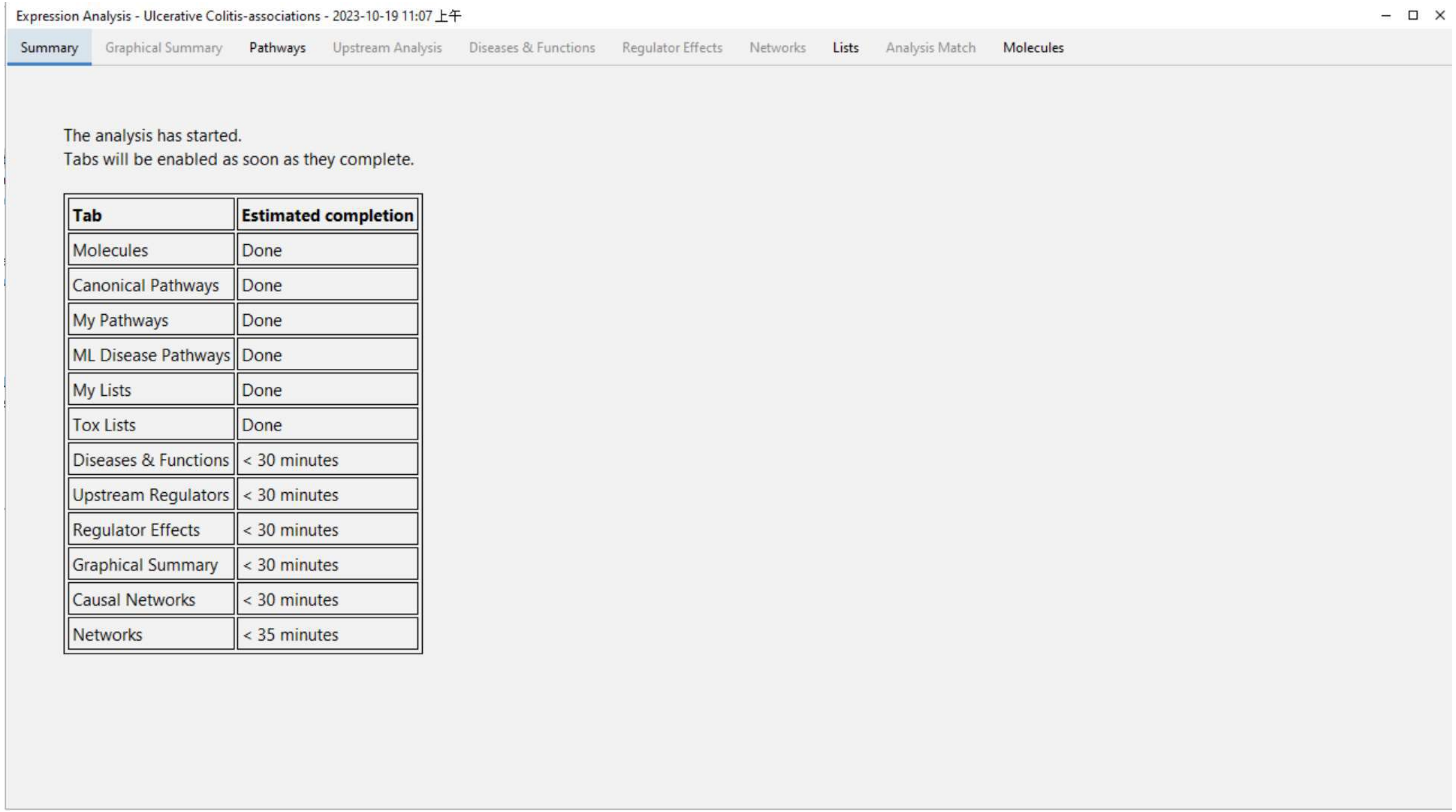
Symbol: ACO2 - MYRF (1/2)

ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
rs727563		ACO2	aconitase 2	Cytoplasm	enzyme	
rs2641348		ADAM30	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
rs13407913		ADCY3	adenylate cyclase 3	Plasma Membrane	enzyme	
rs10065637		ANKRD55	ankyrin repeat domain 55	Nucleus	transcription regulator	
rs12994997		ATG16L1	autophagy related 16 like 1	Cytoplasm	enzyme	
rs653178		ATXN2	ataxin 2	Nucleus	other	
rs1847472		BACH2	BTB domain and CNC homolog 2	Nucleus	transcription regulator	

0 / 167

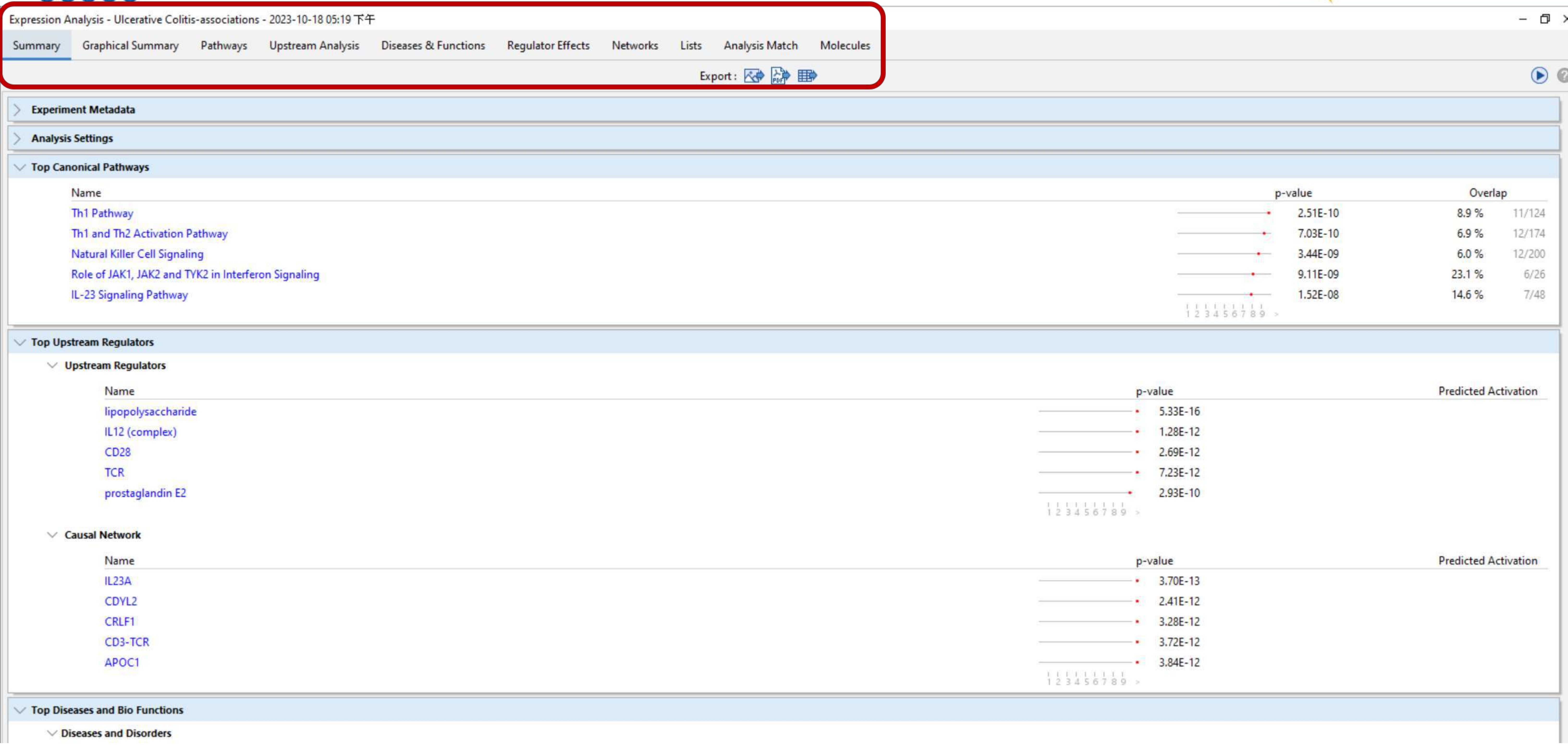
Flags:

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



The analysis has started.
Tabs will be enabled as soon as they complete.

Tab	Estimated completion
Molecules	Done
Canonical Pathways	Done
My Pathways	Done
ML Disease Pathways	Done
My Lists	Done
Tox Lists	Done
Diseases & Functions	< 30 minutes
Upstream Regulators	< 30 minutes
Regulator Effects	< 30 minutes
Graphical Summary	< 30 minutes
Causal Networks	< 30 minutes
Networks	< 35 minutes



Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

Experiment Metadata

Analysis Settings

Top Canonical Pathways

Name	p-value	Overlap	
Th1 Pathway	2.51E-10	8.9 %	11/124
Th1 and Th2 Activation Pathway	7.03E-10	6.9 %	12/174
Natural Killer Cell Signaling	3.44E-09	6.0 %	12/200
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	9.11E-09	23.1 %	6/26
IL-23 Signaling Pathway	1.52E-08	14.6 %	7/48

Top Upstream Regulators

Upstream Regulators

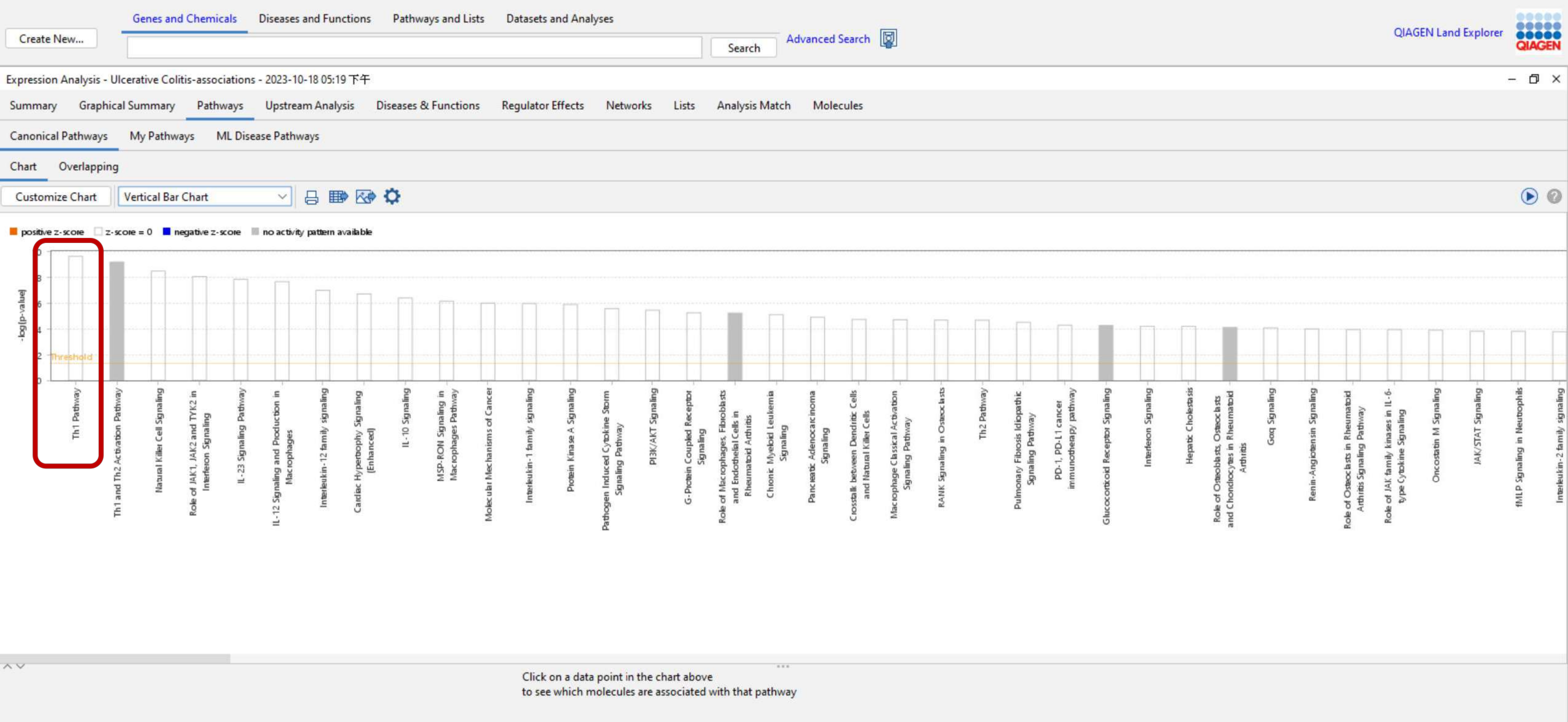
Name	p-value	Predicted Activation
lipopolysaccharide	5.33E-16	
IL12 (complex)	1.28E-12	
CD28	2.69E-12	
TCR	7.23E-12	
prostaglandin E2	2.93E-10	

Causal Network

Name	p-value	Predicted Activation
IL23A	3.70E-13	
CDYL2	2.41E-12	
CRLF1	3.28E-12	
CD3-TCR	3.72E-12	
APOC1	3.84E-12	

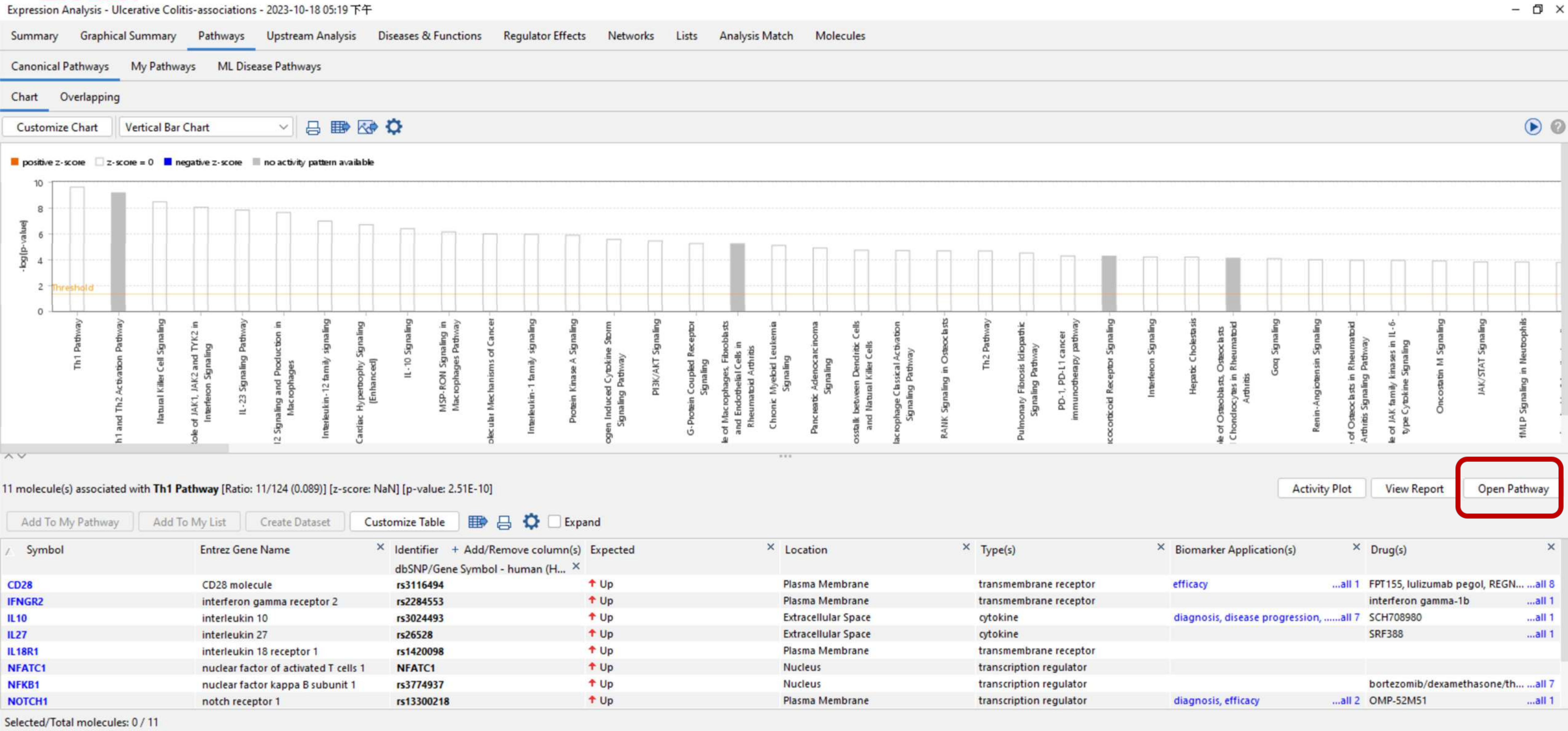
Top Diseases and Bio Functions

Diseases and Disorders



Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

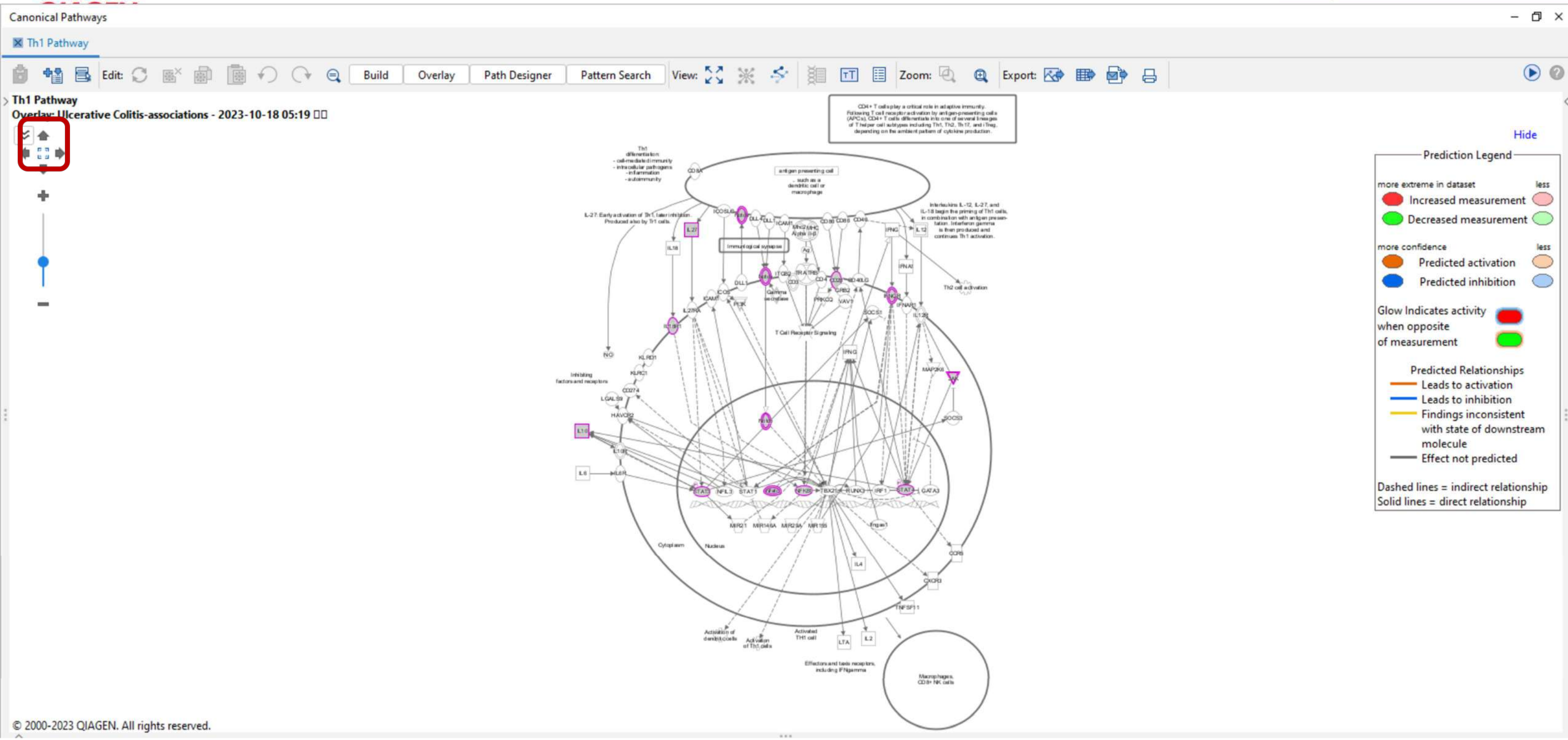
Click on a data point in the chart above
to see which molecules are associated with that pathway



11 molecule(s) associated with **Th1 Pathway** [Ratio: 11/124 (0.089)] [z-score: NaN] [p-value: 2.51E-10]

Symbol	Entrez Gene Name	Identifier + Add/Remove column(s) dbSNP/Gene Symbol - human (H...	Expected	Location	Type(s)	Biomarker Application(s)	Drug(s)
CD28	CD28 molecule	rs3116494	↑ Up	Plasma Membrane	transmembrane receptor	efficacy ...all 1	FPT155, lulizumab pegol, REGN... ...all 8
IFNGR2	interferon gamma receptor 2	rs2284553	↑ Up	Plasma Membrane	transmembrane receptor		interferon gamma-1b ...all 1
IL10	interleukin 10	rs3024493	↑ Up	Extracellular Space	cytokine	diagnosis, disease progression, ...all 7	SCH708980 ...all 1
IL27	interleukin 27	rs26528	↑ Up	Extracellular Space	cytokine		SRF388 ...all 1
IL18R1	interleukin 18 receptor 1	rs1420098	↑ Up	Plasma Membrane	transmembrane receptor		
NFATC1	nuclear factor of activated T cells 1	NFATC1	↑ Up	Nucleus	transcription regulator		
NFKB1	nuclear factor kappa B subunit 1	rs3774937	↑ Up	Nucleus	transcription regulator		bortezomib/dexamethasone/th... ...all 7
NOTCH1	notch receptor 1	rs13300218	↑ Up	Plasma Membrane	transcription regulator	diagnosis, efficacy ...all 2	OMP-52M51 ...all 1

Selected/Total molecules: 0 / 11



Th1 Pathway

Overlay: Ulcerative Colitis-associations - 2023-10-18 05:19

CD4+ T cells play a critical role in adaptive immunity. Following T cell receptor activation by antigen-presenting cells (APCs), CD4+ T cells differentiate into one of several lineages of T helper cell subtypes including Th1, Th2, Th17, and iTreg, depending on the ambient pattern of cytokine production.

Prediction Legend

more extreme in dataset	less
● Increased measurement	●
● Decreased measurement	●

more confidence	less
● Predicted activation	●
● Predicted inhibition	●

Glow Indicates activity when opposite of measurement

Predicted Relationships
- Leads to activation
- Leads to inhibition
- Findings inconsistent with state of downstream molecule
- Effect not predicted

Dashed lines = indirect relationship
Solid lines = direct relationship

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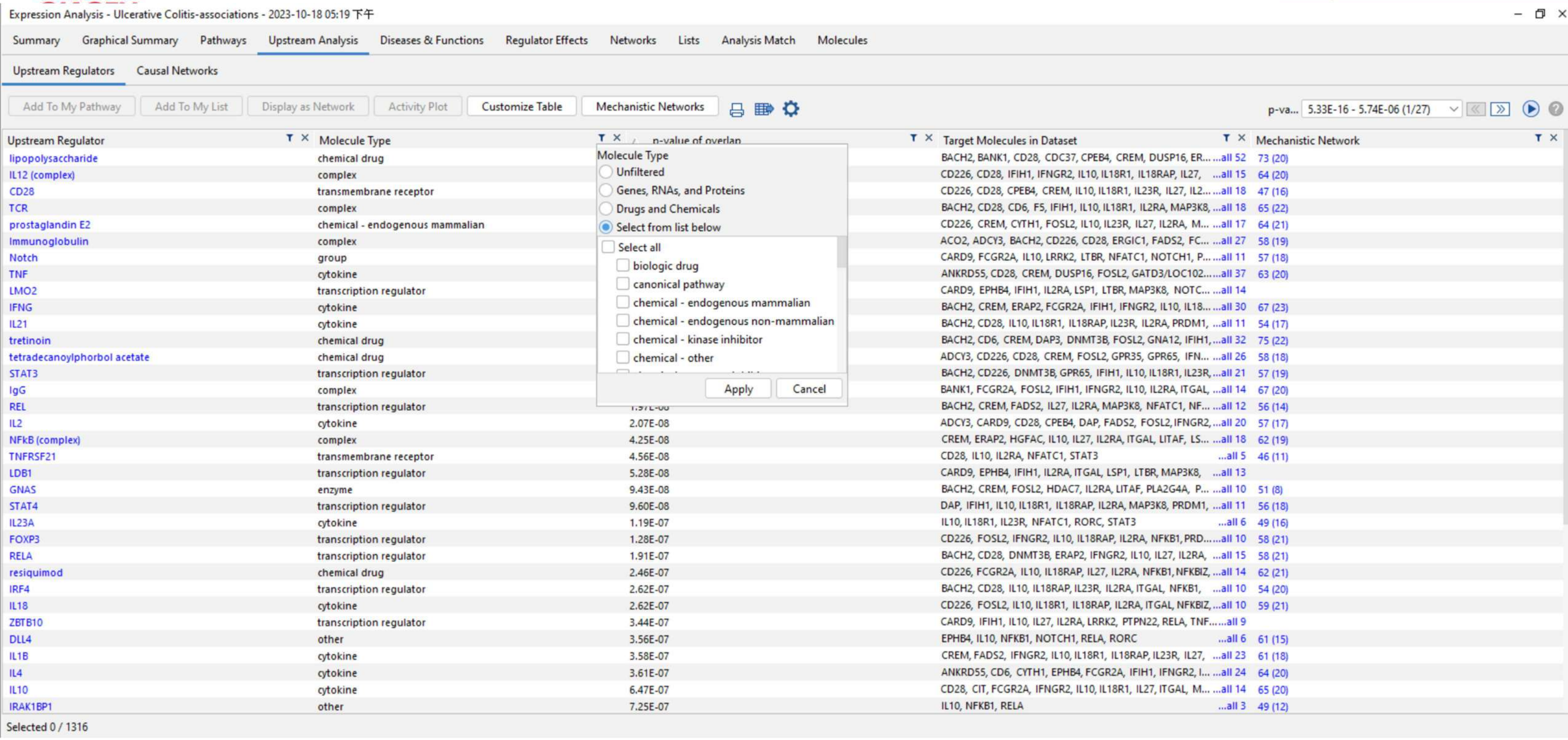

Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

p-va... 5.33E-16 - 5.74E-06 (1/27)

Molecule Type
○ Unfiltered
○ Genes, RNAs, and Proteins
○ Drugs and Chemicals
● Select from list below

☐ Select all
☐ biologic drug
☐ canonical pathway
☐ chemical - endogenous mammalian
☐ chemical - endogenous non-mammalian
☐ chemical - kinase inhibitor
☐ chemical - other

Upstream Regulator	Molecule Type	p-value of overlap	Target Molecules in Dataset		Mechanistic Network
lipopolysaccharide	chemical drug		BACH2, BANK1, CD28, CDC37, CPEB4, CREM, DUSP16, ER...	...all 52	73 (20)
IL12 (complex)	complex		CD226, CD28, IFIH1, IFNGR2, IL10, IL18R1, IL18RAP, IL27,	...all 15	64 (20)
CD28	transmembrane receptor		CD226, CD28, CPEB4, CREM, IL10, IL18R1, IL23R, IL27, IL2...	...all 18	47 (16)
TCR	complex		BACH2, CD28, CD6, F5, IFIH1, IL10, IL18R1, IL2RA, MAP3K8,	...all 18	65 (22)
prostaglandin E2	chemical - endogenous mammalian		CD226, CREM, CYTH1, FOSL2, IL10, IL23R, IL27, IL2RA, M...	...all 17	64 (21)
Immunoglobulin	complex		ACO2, ADCY3, BACH2, CD226, CD28, ERGIC1, FADS2, FC...	...all 27	58 (19)
Notch	group		CARD9, FCGR2A, IL10, LRRK2, LTBR, NFATC1, NOTCH1, P...	...all 11	57 (18)
TNF	cytokine		ANKRD55, CD28, CREM, DUSP16, FOSL2, GATD3/LOC102...	...all 37	63 (20)
LMO2	transcription regulator		CARD9, EPHB4, IFIH1, IL2RA, LSP1, LTBR, MAP3K8, NOTC...	...all 14	
IFNG	cytokine		BACH2, CREM, ERAP2, FCGR2A, IFIH1, IFNGR2, IL10, IL18...	...all 30	67 (23)
IL21	cytokine		BACH2, CD28, IL10, IL18R1, IL18RAP, IL23R, IL2RA, PRDM1,	...all 11	54 (17)
tretinoin	chemical drug		BACH2, CD6, CREM, DAP3, DNMT3B, FOSL2, GNA12, IFIH1,	...all 32	75 (22)
tetradecanoylphorbol acetate	chemical drug		ADCY3, CD226, CD28, CREM, FOSL2, GPR35, GPR65, IFN...	...all 26	58 (18)
STAT3	transcription regulator		BACH2, CD226, DNMT3B, GPR65, IFIH1, IL10, IL18R1, IL23R,	...all 21	57 (19)
IgG	complex		BANK1, FCGR2A, FOSL2, IFIH1, IFNGR2, IL10, IL2RA, ITGAL,	...all 14	67 (20)
REL	transcription regulator	1.97E-08	BACH2, CREM, FADS2, IL27, IL2RA, MAP3K8, NFATC1, NF...	...all 12	56 (14)
IL2	cytokine	2.07E-08	ADCY3, CARD9, CD28, CPEB4, DAP, FADS2, FOSL2, IFNGR2,	...all 20	57 (17)
NFkB (complex)	complex	4.25E-08	CREM, ERAP2, HGFAC, IL10, IL27, IL2RA, ITGAL, LITAF, LS...	...all 18	62 (19)
TNFRSF21	transmembrane receptor	4.56E-08	CD28, IL10, IL2RA, NFATC1, STAT3	...all 5	46 (11)
LDB1	transcription regulator	5.28E-08	CARD9, EPHB4, IFIH1, IL2RA, ITGAL, LSP1, LTBR, MAP3K8,	...all 13	
GNAS	enzyme	9.43E-08	BACH2, CREM, FOSL2, HDAC7, IL2RA, LITAF, PLA2G4A, P...	...all 10	51 (8)
STAT4	transcription regulator	9.60E-08	DAP, IFIH1, IL10, IL18R1, IL18RAP, IL2RA, MAP3K8, PRDM1,	...all 11	56 (18)
IL23A	cytokine	1.19E-07	IL10, IL18R1, IL23R, NFATC1, RORC, STAT3	...all 6	49 (16)
FOXP3	transcription regulator	1.28E-07	CD226, FOSL2, IFNGR2, IL10, IL18RAP, IL2RA, NFKB1, PRD...	...all 10	58 (21)
RELA	transcription regulator	1.91E-07	BACH2, CD28, DNMT3B, ERAP2, IFNGR2, IL10, IL27, IL2RA,	...all 15	58 (21)
resiquimod	chemical drug	2.46E-07	CD226, FCGR2A, IL10, IL18RAP, IL27, IL2RA, NFKB1, NFKBIZ,	...all 14	62 (21)
IRF4	transcription regulator	2.62E-07	BACH2, CD28, IL10, IL18RAP, IL23R, IL2RA, ITGAL, NFKB1,	...all 10	54 (20)
IL18	cytokine	2.62E-07	CD226, FOSL2, IL10, IL18R1, IL18RAP, IL2RA, ITGAL, NFKBIZ,	...all 10	59 (21)
ZBTB10	transcription regulator	3.44E-07	CARD9, IFIH1, IL10, IL27, IL2RA, LRRK2, PTPN22, RELA, TNF...	...all 9	
DLL4	other	3.56E-07	EPHB4, IL10, NFKB1, NOTCH1, RELA, RORC	...all 6	61 (15)
IL1B	cytokine	3.58E-07	CREM, FADS2, IFNGR2, IL10, IL18R1, IL18RAP, IL23R, IL27,	...all 23	61 (18)
IL4	cytokine	3.61E-07	ANKRD55, CD6, CYTH1, EPHB4, FCGR2A, IFIH1, IFNGR2, I...	...all 24	64 (20)
IL10	cytokine	6.47E-07	CD28, CIT, FCGR2A, IFNGR2, IL10, IL18R1, IL27, ITGAL, M...	...all 14	65 (20)
IRAK1BP1	other	7.25E-07	IL10, NFKB1, RELA	...all 3	49 (12)

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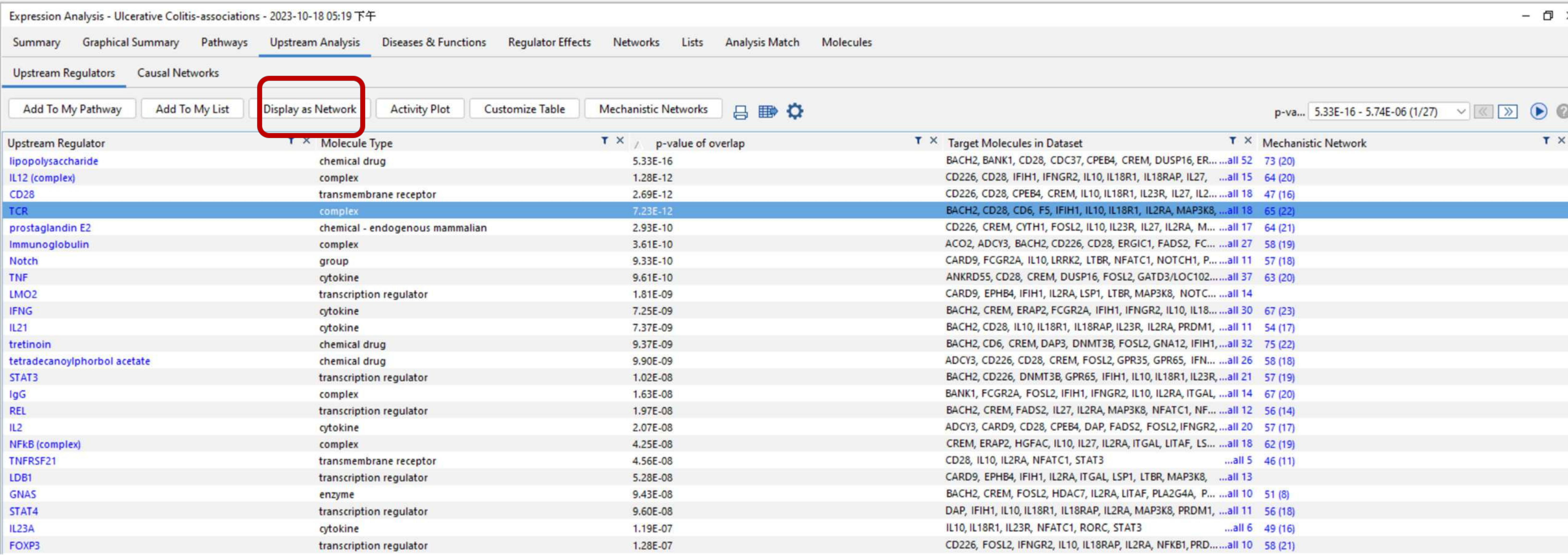
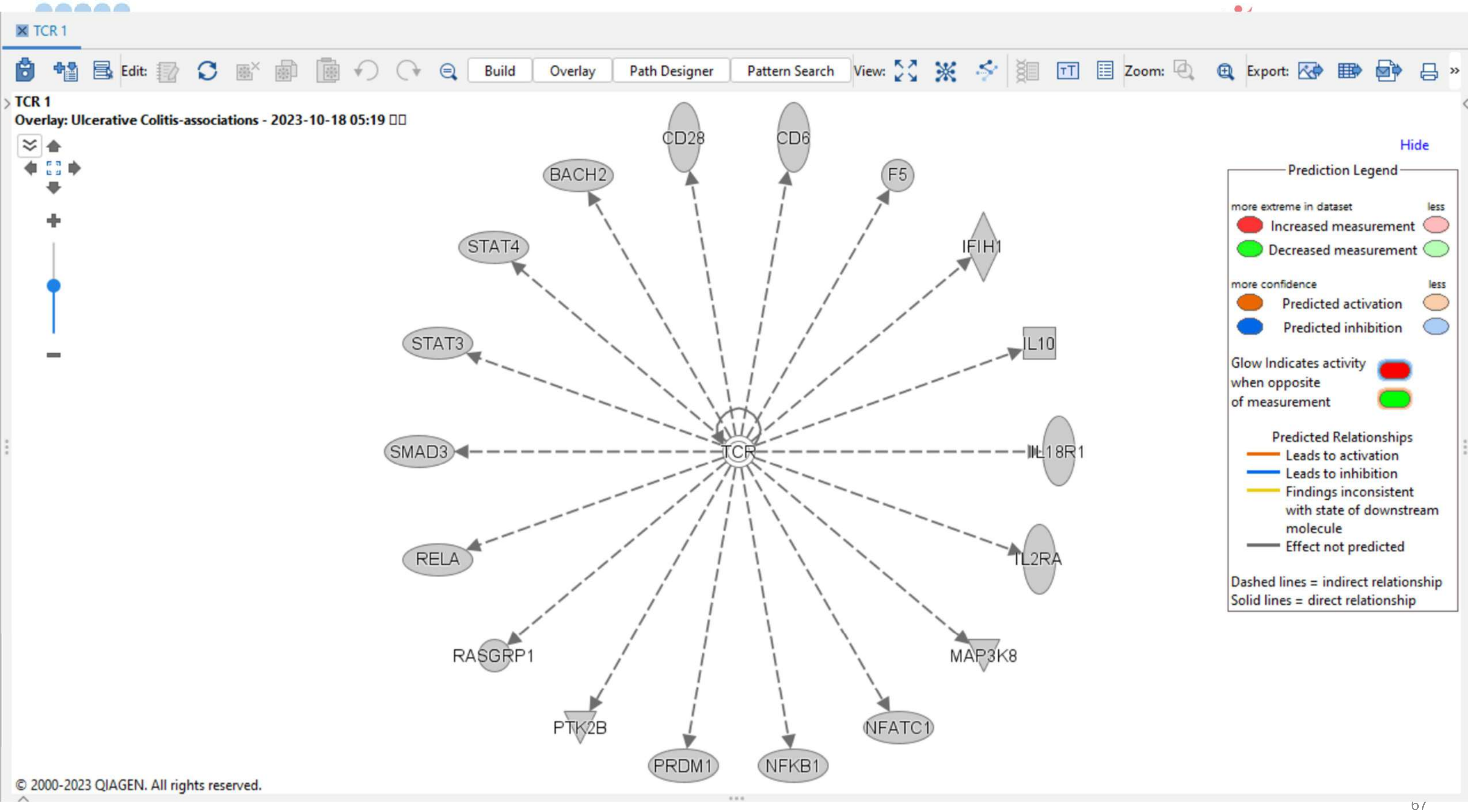


Upstream Regulator	Molecule Type	p-value of overlap	Target Molecules in Dataset	Mechanistic Network
lipopolysaccharide	chemical drug	5.33E-16	BACH2, BANK1, CD28, CDC37, CPEB4, CREM, DUSP16, ER... ...all 52	73 (20)
IL12 (complex)	complex	1.28E-12	CD226, CD28, IFIH1, IFNGR2, IL10, IL18R1, IL18RAP, IL27, ...all 15	64 (20)
CD28	transmembrane receptor	2.69E-12	CD226, CD28, CPEB4, CREM, IL10, IL18R1, IL23R, IL27, IL2... ...all 18	47 (16)
TCR	complex	7.23E-12	BACH2, CD28, CD6, F5, IFIH1, IL10, IL18R1, IL2RA, MAP3K8, ...all 18	65 (22)
prostaglandin E2	chemical - endogenous mammalian	2.93E-10	CD226, CREM, CYTH1, FOSL2, IL10, IL23R, IL27, IL2RA, M... ...all 17	64 (21)
Immunoglobulin	complex	3.61E-10	ACO2, ADCY3, BACH2, CD226, CD28, ERGIC1, FADS2, FC... ...all 27	58 (19)
Notch	group	9.33E-10	CARD9, FCGR2A, IL10, LRRK2, LTBR, NFATC1, NOTCH1, P... ...all 11	57 (18)
TNF	cytokine	9.61E-10	ANKRD55, CD28, CREM, DUSP16, FOSL2, GATD3/LOC102... ...all 37	63 (20)
LMO2	transcription regulator	1.81E-09	CARD9, EPHB4, IFIH1, IL2RA, LSP1, LTBR, MAP3K8, NOTC... ...all 14	
IFNG	cytokine	7.25E-09	BACH2, CREM, ERAP2, FCGR2A, IFIH1, IFNGR2, IL10, IL18... ...all 30	67 (23)
IL21	cytokine	7.37E-09	BACH2, CD28, IL10, IL18R1, IL18RAP, IL23R, IL2RA, PRDM1, ...all 11	54 (17)
tretinoin	chemical drug	9.37E-09	BACH2, CD6, CREM, DAP3, DNMT3B, FOSL2, GNA12, IFIH1, ...all 32	75 (22)
tetradecanoylphorbol acetate	chemical drug	9.90E-09	ADCY3, CD226, CD28, CREM, FOSL2, GPR35, GPR65, IFN... ...all 26	58 (18)
STAT3	transcription regulator	1.02E-08	BACH2, CD226, DNMT3B, GPR65, IFIH1, IL10, IL18R1, IL23R, ...all 21	57 (19)
IgG	complex	1.63E-08	BANK1, FCGR2A, FOSL2, IFIH1, IFNGR2, IL10, IL2RA, ITGAL, ...all 14	67 (20)
REL	transcription regulator	1.97E-08	BACH2, CREM, FADS2, IL27, IL2RA, MAP3K8, NFATC1, NF... ...all 12	56 (14)
IL2	cytokine	2.07E-08	ADCY3, CARD9, CD28, CPEB4, DAP, FADS2, FOSL2, IFNGR2, ...all 20	57 (17)
NFkB (complex)	complex	4.25E-08	CREM, ERAP2, HGFAC, IL10, IL27, IL2RA, ITGAL, LITAF, LS... ...all 18	62 (19)
TNFRSF21	transmembrane receptor	4.56E-08	CD28, IL10, IL2RA, NFATC1, STAT3 ...all 5	46 (11)
LDB1	transcription regulator	5.28E-08	CARD9, EPHB4, IFIH1, IL2RA, ITGAL, LSP1, LTBR, MAP3K8, ...all 13	
GNAS	enzyme	9.43E-08	BACH2, CREM, FOSL2, HDAC7, IL2RA, LITAF, PLA2G4A, P... ...all 10	51 (8)
STAT4	transcription regulator	9.60E-08	DAP, IFIH1, IL10, IL18R1, IL18RAP, IL2RA, MAP3K8, PRDM1, ...all 11	56 (18)
IL23A	cytokine	1.19E-07	IL10, IL18R1, IL23R, NFATC1, RORC, STAT3 ...all 6	49 (16)
FOXP3	transcription regulator	1.28E-07	CD226, FOSL2, IFNGR2, IL10, IL18RAP, IL2RA, NFKB1, PRD... ...all 10	58 (21)



TCR 1

Overlay: Ulcerative Colitis-associations - 2023-10-18 05:19

Prediction Legend

more extreme in dataset — less

- 🟥 Increased measurement
- 🟩 Decreased measurement

more confidence — less

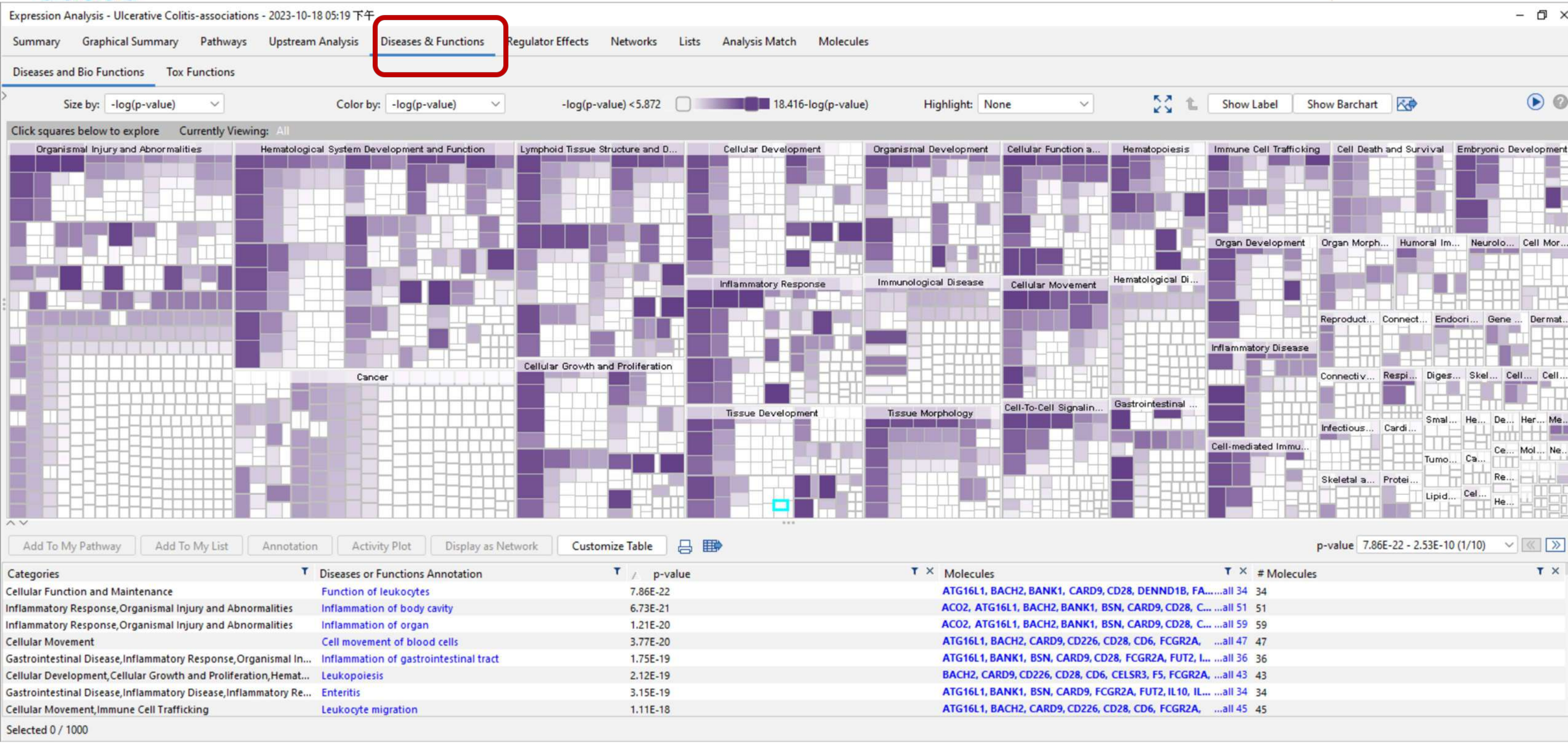
- 🟧 Predicted activation
- 🟦 Predicted inhibition

Glow Indicates activity when opposite of measurement

Predicted Relationships

- Leads to activation
- Leads to inhibition
- Findings inconsistent with state of downstream molecule
- Effect not predicted

Dashed lines = indirect relationship
Solid lines = direct relationship



Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

Size by: -log(p-value)

Color by: -log(p-value)

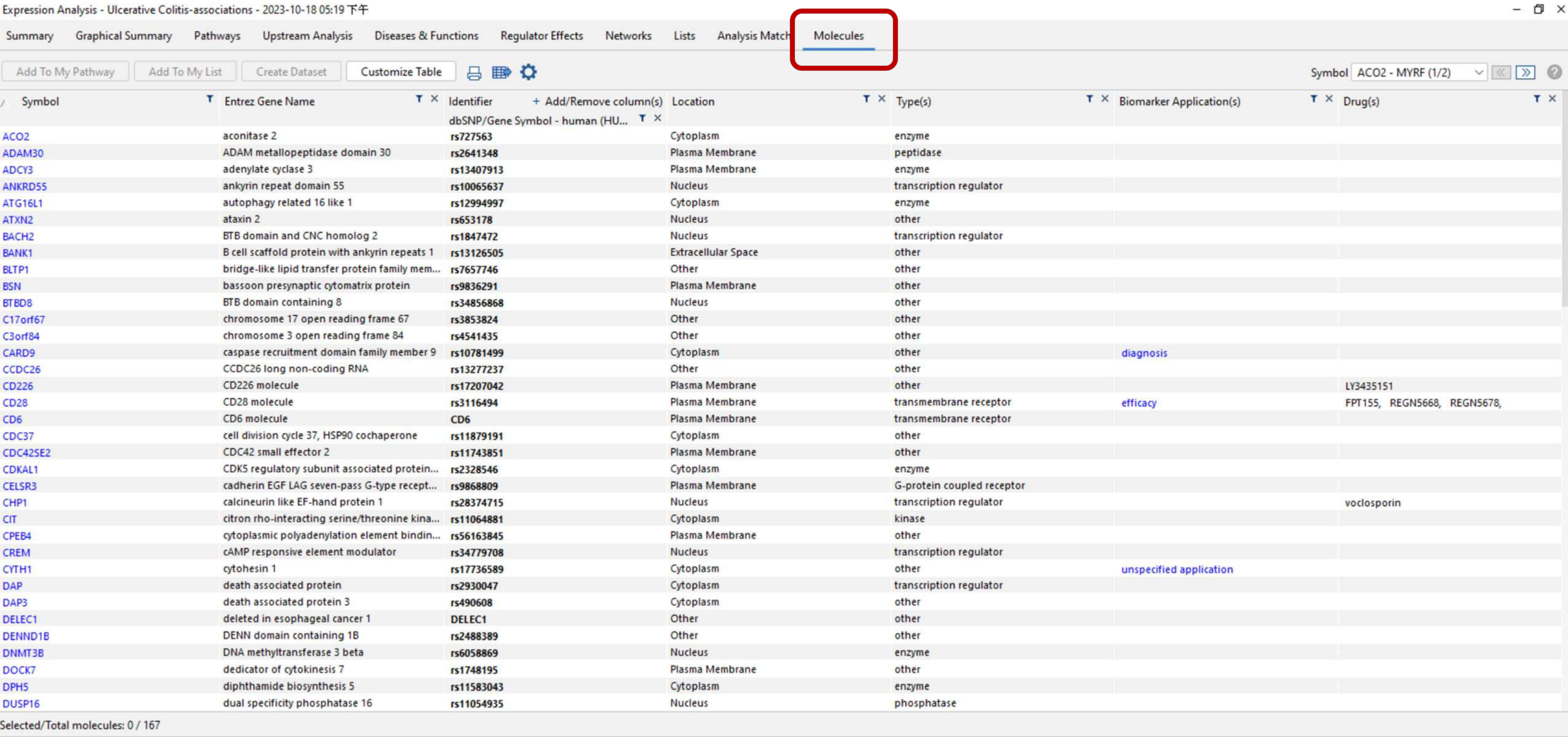
-log(p-value) <5.872 ☐ 18.416-log(p-value)

Highlight: None

p-value 7.86E-22 - 2.53E-10 (1/10)

Categories	Diseases or Functions Annotation	p-value	Molecules	# Molecules
Cellular Function and Maintenance	Function of leukocytes	7.86E-22	ATG16L1, BACH2, BANK1, CARD9, CD28, DENND1B, FA... ...all 34	34
Inflammatory Response,Organismal Injury and Abnormalities	Inflammation of body cavity	6.73E-21	ACO2, ATG16L1, BACH2, BANK1, BSN, CARD9, CD28, C... ...all 51	51
Inflammatory Response,Organismal Injury and Abnormalities	Inflammation of organ	1.21E-20	ACO2, ATG16L1, BACH2, BANK1, BSN, CARD9, CD28, C... ...all 59	59
Cellular Movement	Cell movement of blood cells	3.77E-20	ATG16L1, BACH2, CARD9, CD226, CD28, CD6, FCGR2A, ...all 47	47
Gastrointestinal Disease,Inflammatory Response,Organismal In...	Inflammation of gastrointestinal tract	1.75E-19	ATG16L1, BANK1, BSN, CARD9, CD28, FCGR2A, FUT2, I... ...all 36	36
Cellular Development,Cellular Growth and Proliferation,Hemat...	Leukopoiesis	2.12E-19	BACH2, CARD9, CD226, CD28, CD6, CELSR3, F5, FCGR2A, ...all 43	43
Gastrointestinal Disease,Inflammatory Disease,Inflammatory Re...	Enteritis	3.15E-19	ATG16L1, BANK1, BSN, CARD9, FCGR2A, FUT2, IL10, IL... ...all 34	34
Cellular Movement,Immune Cell Trafficking	Leukocyte migration	1.11E-18	ATG16L1, BACH2, CARD9, CD226, CD28, CD6, FCGR2A, ...all 45	45

Selected 0 / 1000



Symbol	Entrez Gene Name	Identifier dbSNP/Gene Symbol - human (HU...	Location	Type(s)	Biomarker Application(s)	Drug(s)
ACO2	aconitase 2	rs727563	Cytoplasm	enzyme		
ADAM30	ADAM metallopeptidase domain 30	rs2641348	Plasma Membrane	peptidase		
ADCY3	adenylate cyclase 3	rs13407913	Plasma Membrane	enzyme		
ANKRD55	ankyrin repeat domain 55	rs10065637	Nucleus	transcription regulator		
ATG16L1	autophagy related 16 like 1	rs12994997	Cytoplasm	enzyme		
ATXN2	ataxin 2	rs653178	Nucleus	other		
BACH2	BTB domain and CNC homolog 2	rs1847472	Nucleus	transcription regulator		
BANK1	B cell scaffold protein with ankyrin repeats 1	rs13126505	Extracellular Space	other		
BLTP1	bridge-like lipid transfer protein family mem...	rs7657746	Other	other		
BSN	bassoon presynaptic cytomatrix protein	rs9836291	Plasma Membrane	other		
BTBD8	BTB domain containing 8	rs34856868	Nucleus	other		
C17orf67	chromosome 17 open reading frame 67	rs3853824	Other	other		
C3orf84	chromosome 3 open reading frame 84	rs4541435	Other	other		
CARD9	caspase recruitment domain family member 9	rs10781499	Cytoplasm	other	diagnosis	
CCDC26	CCDC26 long non-coding RNA	rs13277237	Other	other		
CD226	CD226 molecule	rs17207042	Plasma Membrane	other		LY3435151
CD28	CD28 molecule	rs3116494	Plasma Membrane	transmembrane receptor	efficacy	FPT155, REGN5668, REGN5678,
CD6	CD6 molecule	CD6	Plasma Membrane	transmembrane receptor		
CDC37	cell division cycle 37, HSP90 cochaperone	rs11879191	Cytoplasm	other		
CDC42SE2	CDC42 small effector 2	rs11743851	Plasma Membrane	other		
CDKAL1	CDK5 regulatory subunit associated protein...	rs2328546	Cytoplasm	enzyme		
CELSR3	cadherin EGF LAG seven-pass G-type recept...	rs9868809	Plasma Membrane	G-protein coupled receptor		
CHP1	calcineurin like EF-hand protein 1	rs28374715	Nucleus	transcription regulator		voclosporin
CIT	citron rho-interacting serine/threonine kina...	rs11064881	Cytoplasm	kinase		
CPEB4	cytoplasmic polyadenylation element bindin...	rs56163845	Plasma Membrane	other		
CREM	cAMP responsive element modulator	rs34779708	Nucleus	transcription regulator		
CYTH1	cytohesin 1	rs17736589	Cytoplasm	other	unspecified application	
DAP	death associated protein	rs2930047	Cytoplasm	transcription regulator		
DAP3	death associated protein 3	rs490608	Cytoplasm	other		
DELEC1	deleted in esophageal cancer 1	DELEC1	Other	other		
DENND1B	DENN domain containing 1B	rs2488389	Other	other		
DNMT3B	DNA methyltransferase 3 beta	rs6058869	Nucleus	enzyme		
DOCK7	dedicator of cytokinesis 7	rs1748195	Plasma Membrane	other		
DPH5	diphthamide biosynthesis 5	rs11583043	Cytoplasm	enzyme		
DUSP16	dual specificity phosphatase 16	rs11054935	Nucleus	phosphatase		

Selected/Total molecules: 0 / 167

Use Case

Secondary **colon cancer** in patients with **ulcerative colitis**: a systemmtic review and meta-analysis.

Zhang L. Gan H.

J Gastrointest Oncol. 2021 Dec:12(6):2882-2890. doi: 10.21037/jgo-21-800.

A young woman who developed ascending **colon cancer** 2 years after the onset of **ulcerative colitis**.

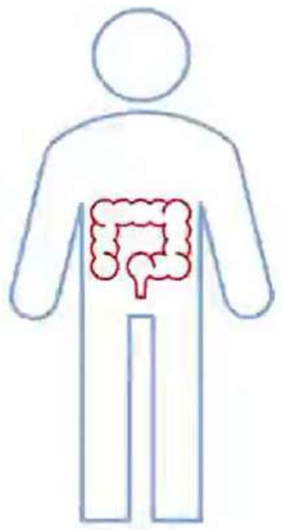
Matsuda K, Hashiguchi Y, Asako K, Okada Y, Ohno K, Tsukamoto M, Fukushima Y, Shimada R, Ozawa T, Hayama T, Nozawa K, Fukagawa T, Kikuchi Y, Sasajima Y.

Clin J Gastroenterol. 2020 Dec: 13(6):1189-1195

Risk of **Colon Cancer** and Recommended Surveillance Strategies in Patients with **Ulcerative Colitis**.

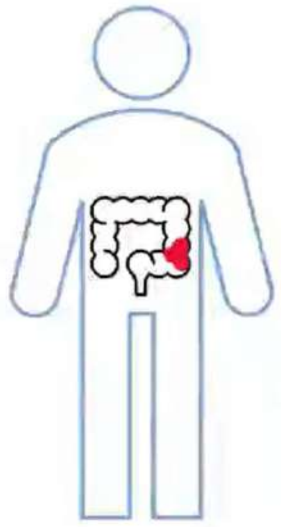
Rabbenou W, Ullman TA.

Gastroenterol Clin North Am. 2020 Dec:49(4):791-807



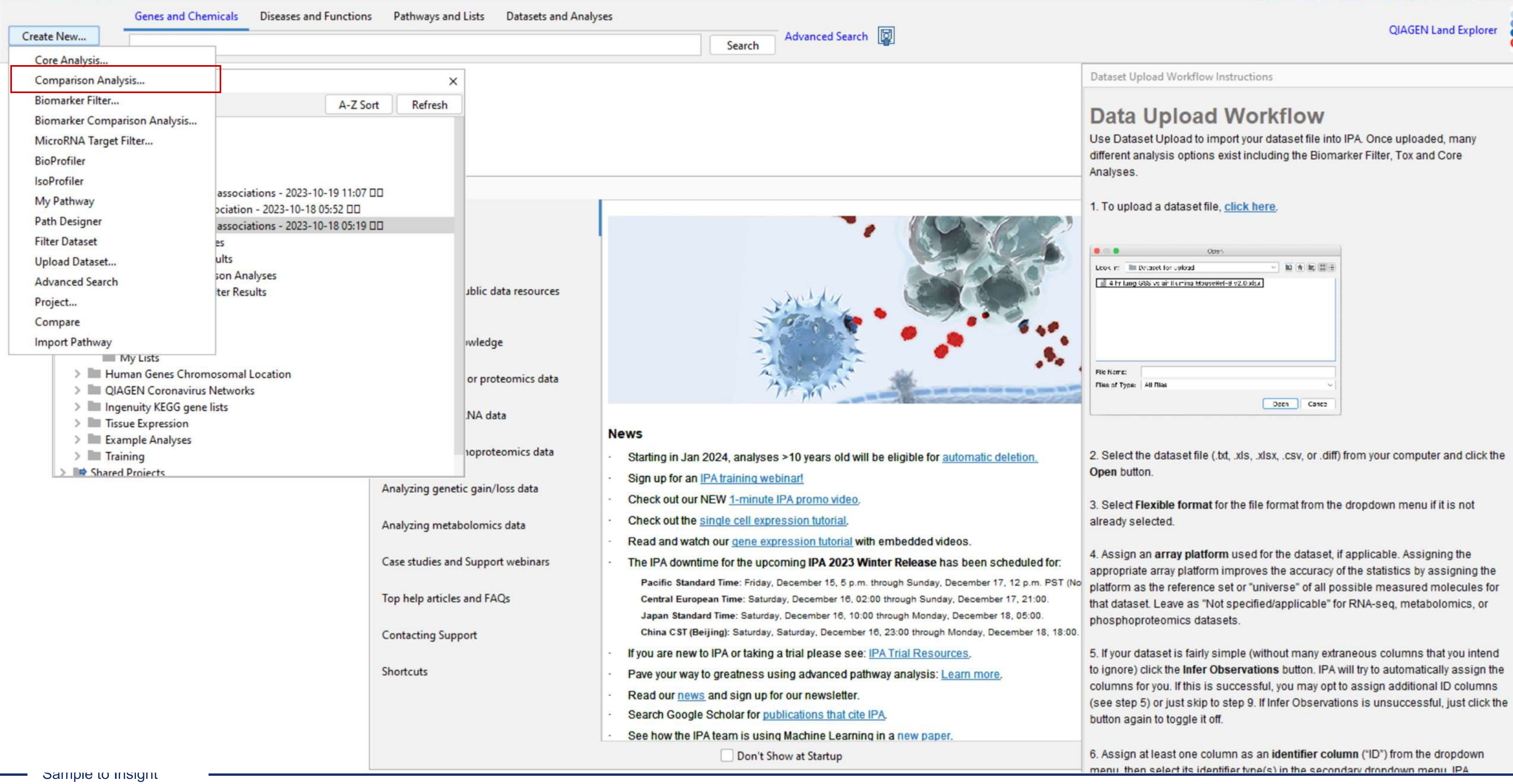
Ulcerative Colitis GWAS

(PMID: 26192919)



Colorectal Cancer GWAS

(PMID: 36539618)



News

- Starting in Jan 2024, analyses >10 years old will be eligible for automatic deletion.
- Sign up for an IPA training webinar!
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Data Upload Workflow

Use Dataset Upload to import your dataset file into IPA. Once uploaded, many different analysis options exist including the Biomarker Filter, Tox and Core Analyses.

1. To upload a dataset file, click here.

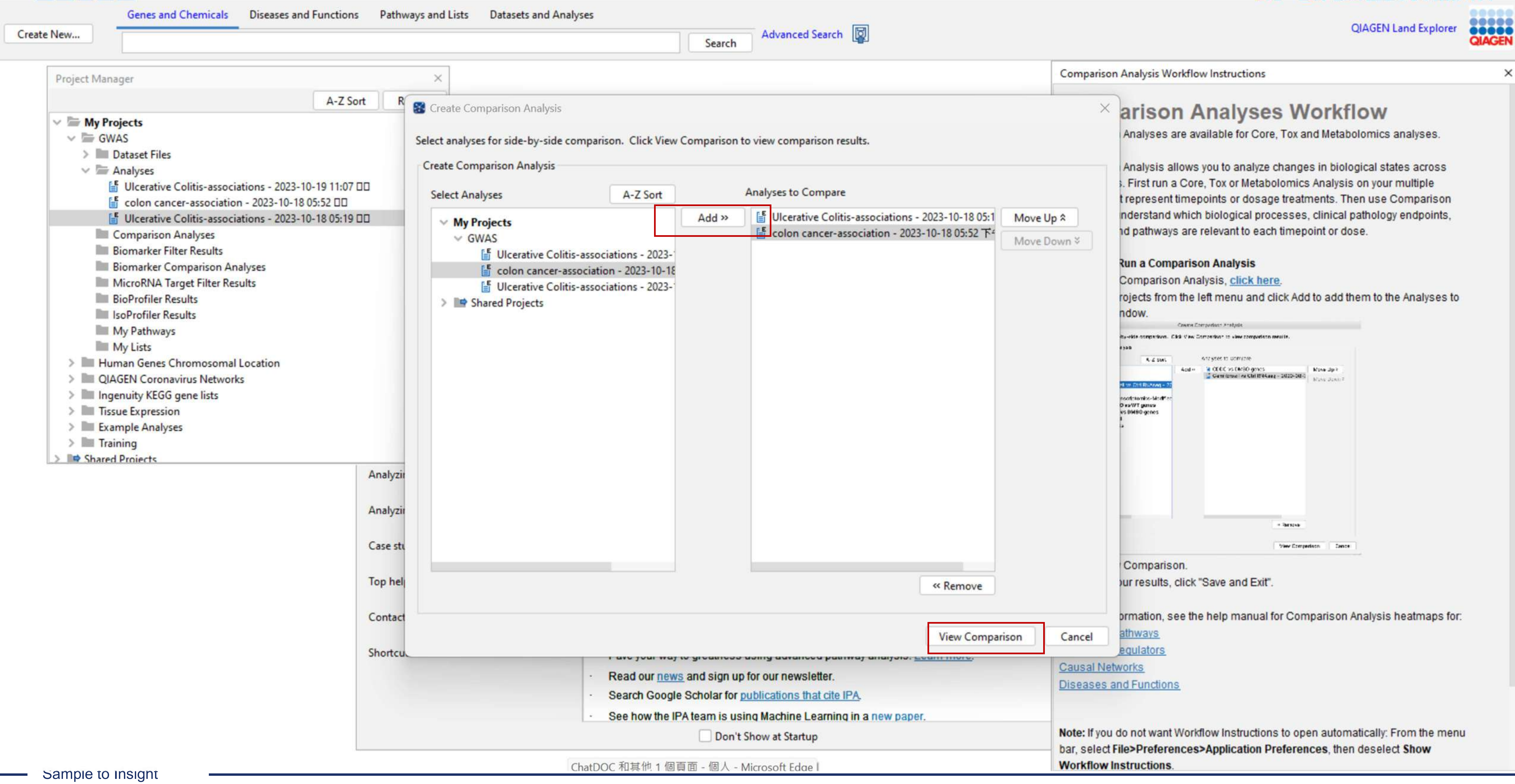
2. Select the dataset file (.txt, .xls, .xlsx, .csv, or .diff) from your computer and click the **Open** button.

3. Select **Flexible format** for the file format from the dropdown menu if it is not already selected.

4. Assign an **array platform** used for the dataset, if applicable. Assigning the appropriate array platform improves the accuracy of the statistics by assigning the platform as the reference set or "universe" of all possible measured molecules for that dataset. Leave as "Not specified/applicable" for RNA-seq, metabolomics, or phosphoproteomics datasets.

5. If your dataset is fairly simple (without many extraneous columns that you intend to ignore) click the **Infer Observations** button. IPA will try to automatically assign the columns for you. If this is successful, you may opt to assign additional ID columns (see step 5) or just skip to step 9. If Infer Observations is unsuccessful, just click the button again to toggle it off.

6. Assign at least one column as an **identifier column** ("ID") from the dropdown menu, then select its identifier type(s) in the secondary dropdown menu. IPA



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

Analyses to Compare:
- Ulcerative Colitis-associations - 2023-10-18 05:1
- colon cancer-association - 2023-10-18 05:52 下

arison Analyses Workflow

Analyses are available for Core, Tox and Metabolomics analyses.

Analysis allows you to analyze changes in biological states across . First run a Core, Tox or Metabolomics Analysis on your multiple t represent timepoints or dosage treatments. Then use Comparison nderstand which biological processes, clinical pathology endpoints, nd pathways are relevant to each timepoint or dose.

Run a Comparison Analysis

Comparison Analysis, click here.

rojects from the left menu and click Add to add them to the Analyses to ndow.

Comparison.

ur results, click "Save and Exit".

ormation, see the help manual for Comparison Analysis heatmaps for:

athways

egulators

Causal Networks

Diseases and Functions

Note: If you do not want Workflow Instructions to open automatically: From the menu bar, select **File>Preferences>Application Preferences**, then deselect **Show Workflow Instructions**.

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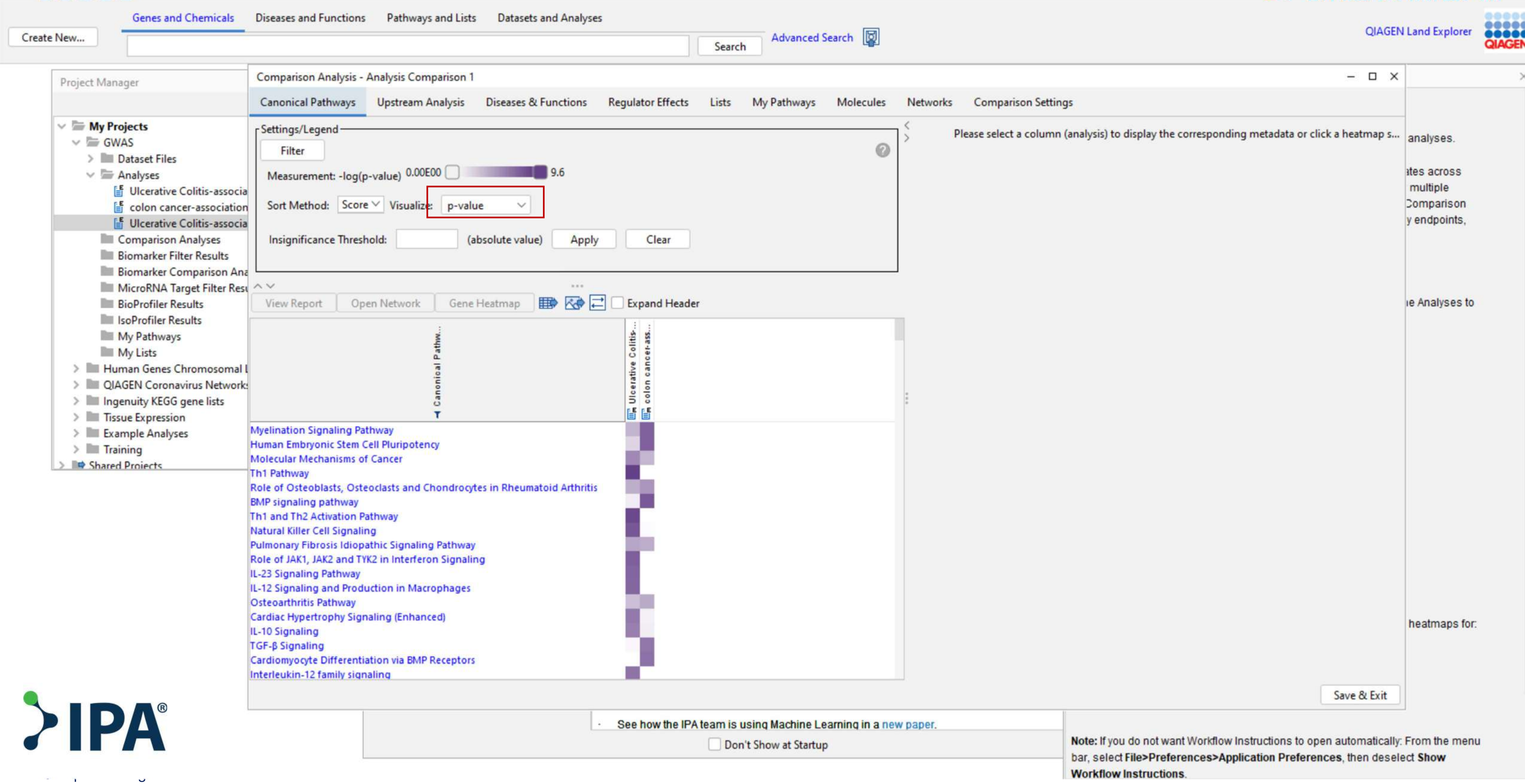
Comparison Analysis – P-value



Measurement: -log(p-value) 0.00E00 ☐ 9.6

Sort Method: Score

Visualize: p-value

Insignificance Threshold: (absolute value)

☐ Expand Header

Please select a column (analysis) to display the corresponding metadata or click a heatmap s...

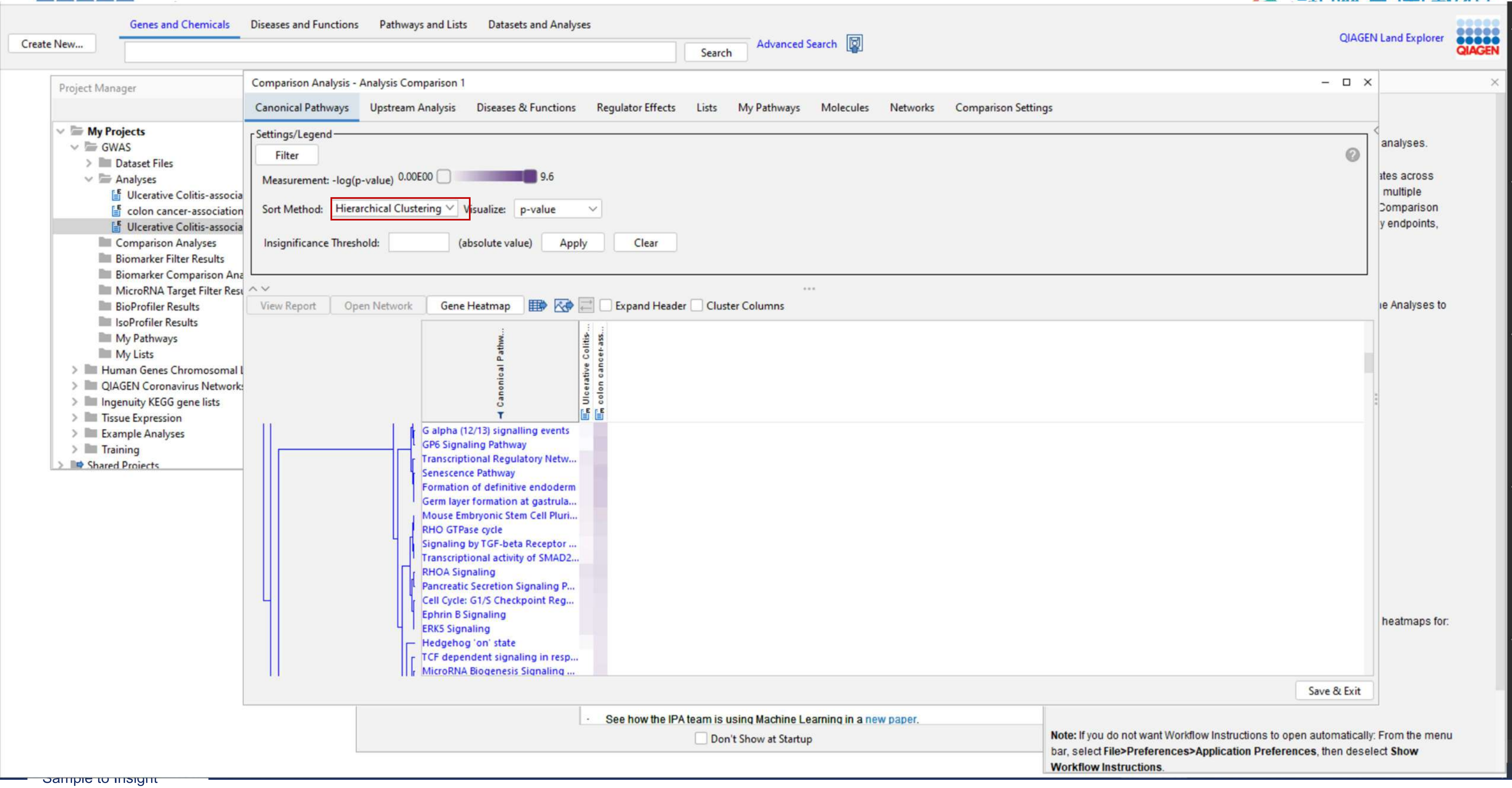
Myelination Signaling Pathway
Human Embryonic Stem Cell Pluripotency
Molecular Mechanisms of Cancer
Th1 Pathway
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis
BMP signaling pathway
Th1 and Th2 Activation Pathway
Natural Killer Cell Signaling
Pulmonary Fibrosis Idiopathic Signaling Pathway
Role of JAK1, JAK2 and TYK2 in Interferon Signaling
IL-23 Signaling Pathway
IL-12 Signaling and Production in Macrophages
Osteoarthritis Pathway
Cardiac Hypertrophy Signaling (Enhanced)
IL-10 Signaling
TGF-β Signaling
Cardiomyocyte Differentiation via BMP Receptors
Interleukin-12 family signaling

See how the IPA team is using Machine Learning in a new paper.

☐ Don't Show at Startup

Note: If you do not want Workflow Instructions to open automatically: From the menu bar, select **File>Preferences>Application Preferences**, then deselect **Show Workflow Instructions**.

https://qiagen.my.salesforce-sites.com/KnowledgeBase/KnowledgeNavigatorPage?id=kA41i000000L5nQCAS&categoryName=BioX



Measurement: -log(p-value) 0.00E00 9.6

Sort Method: Hierarchical Clustering

Visualize: p-value

Insignificance Threshold: (absolute value)

G alpha (12/13) signalling events
GP6 Signaling Pathway
Transcriptional Regulatory Netw...
Senescence Pathway
Formation of definitive endoderm
Germ layer formation at gastrula...
Mouse Embryonic Stem Cell Pluri...
RHO GTPase cycle
Signaling by TGF-beta Receptor ...
Transcriptional activity of SMAD2...
RHOA Signaling
Pancreatic Secretion Signaling P...
Cell Cycle: G1/S Checkpoint Reg...
Ephrin B Signaling
ERK5 Signaling
Hedgehog 'on' state
TCF dependent signaling in resp...
MicroRNA Biogenesis Signaling ...

analyses.

ates across
multiple
Comparison
y endpoints,

e Analyses to

heatmaps for:

See how the IPA team is using Machine Learning in a new paper.

☐ Don't Show at Startup

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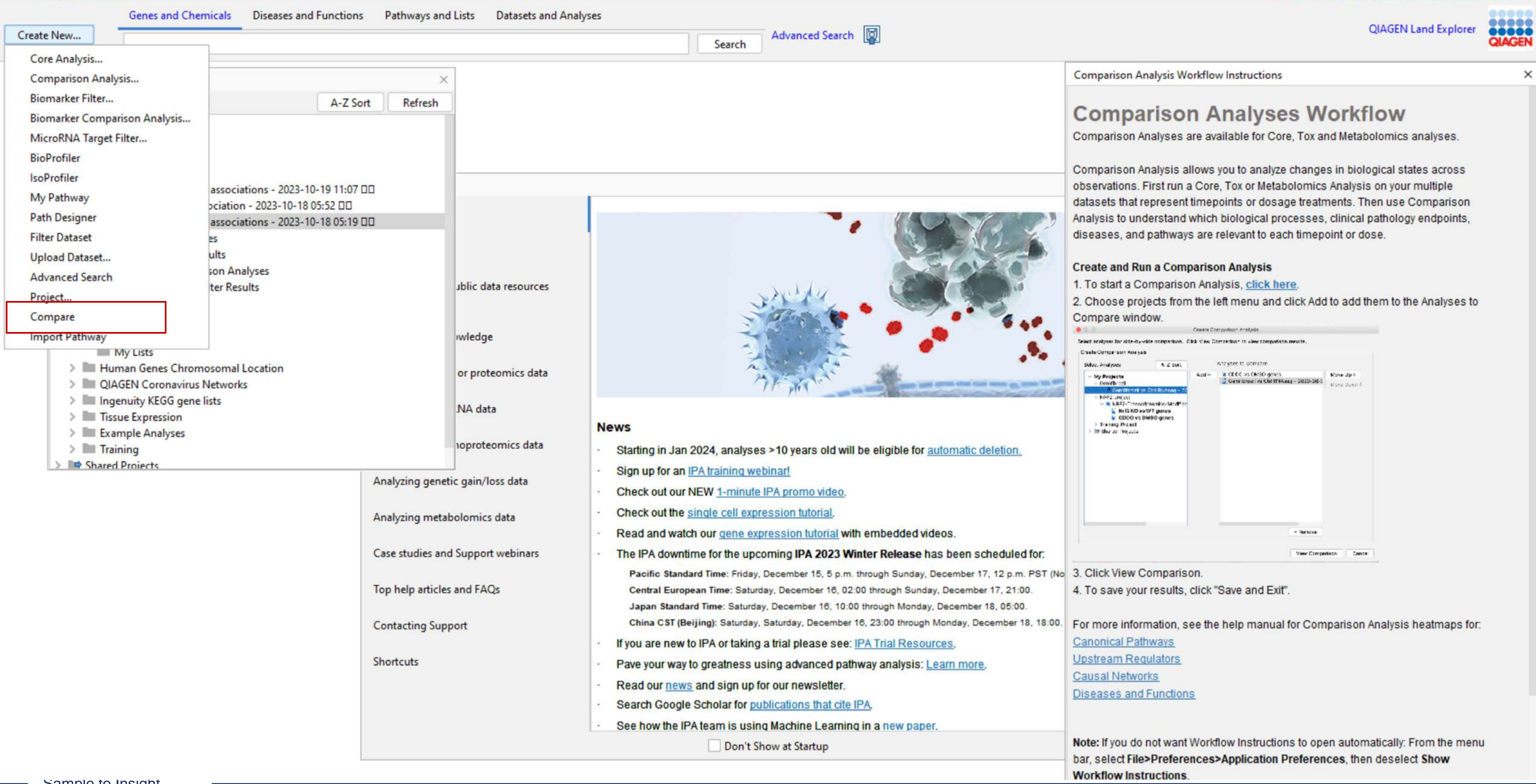

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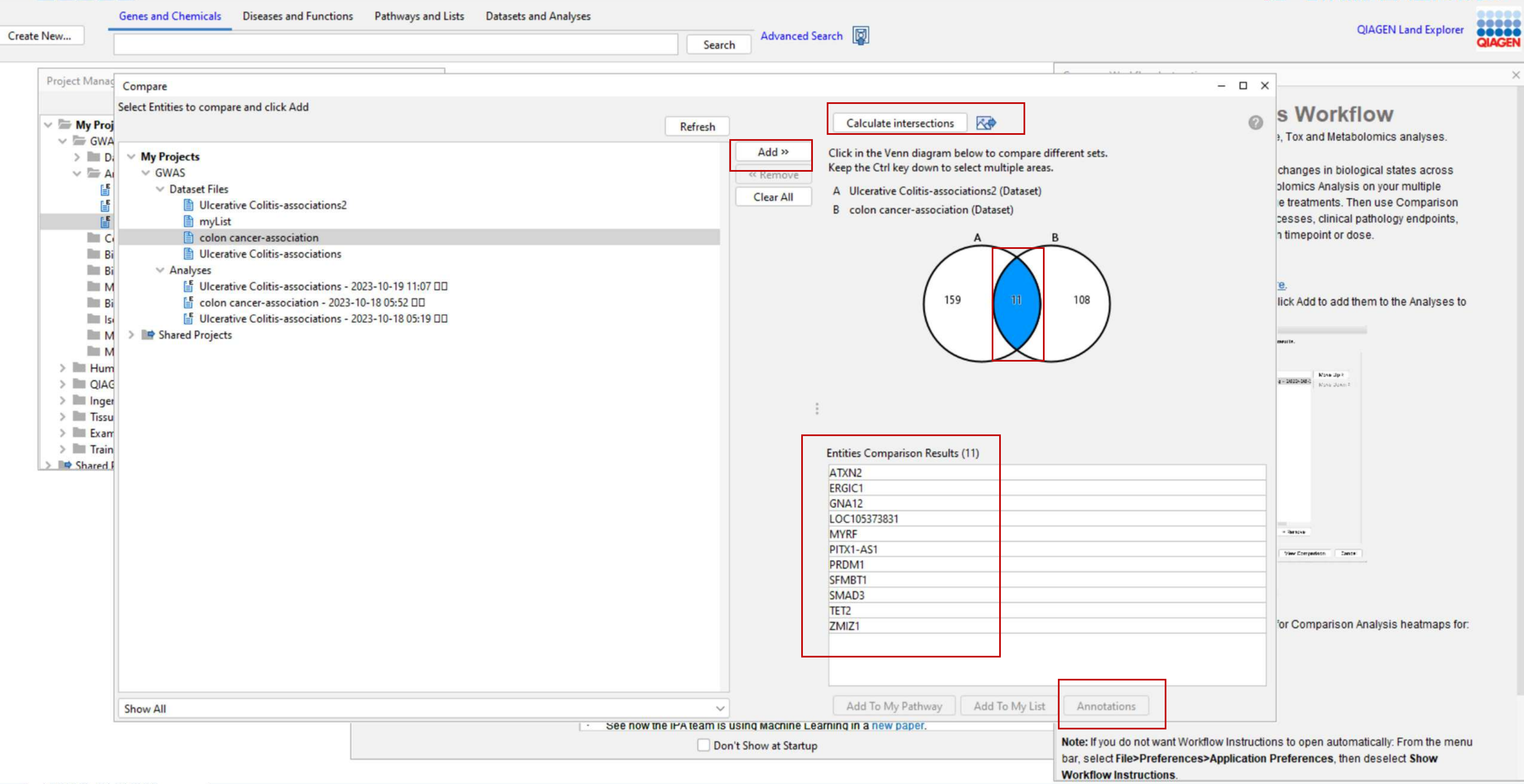
Create and Run a Comparison Analysis

1. To start a Comparison Analysis, click here.
2. Choose projects from the left menu and click Add to add them to the Analyses to Compare window.
3. Click View Comparison.
4. To save your results, click "Save and Exit".

For more information, see the help manual for Comparison Analysis heatmaps for:

Canonical Pathways
Upstream Regulators
Causal Networks
Diseases and Functions

Note: If you do not want Workflow Instructions to open automatically: From the menu bar, select **File>Preferences>Application Preferences**, then deselect **Show Workflow Instructions**.



Select Entities to compare and click Add

- My Projects
  - GWAS
    - Dataset Files
      - Ulcerative Colitis-associations2
      - myList
      - colon cancer-association
      - Ulcerative Colitis-associations
    - Analyses
      - Ulcerative Colitis-associations - 2023-10-19 11:07 □□
      - colon cancer-association - 2023-10-18 05:52 □□
      - Ulcerative Colitis-associations - 2023-10-18 05:19 □□
- Shared Projects

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

A Ulcerative Colitis-associations2 (Dataset)
B colon cancer-association (Dataset)

Entities Comparison Results (11)

ATXN2
ERGIC1
GNA12
LOC105373831
MYRF
PITX1-AS1
PRDM1
SFMBT1
SMAD3
TET2
ZMIZ1

s Workflow

, Tox and Metabolomics analyses.

changes in biological states across
olomics Analysis on your multiple
e treatments. Then use Comparison
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timepoint or dose.

lick Add to add them to the Analyses to

or Comparison Analysis heatmaps for:

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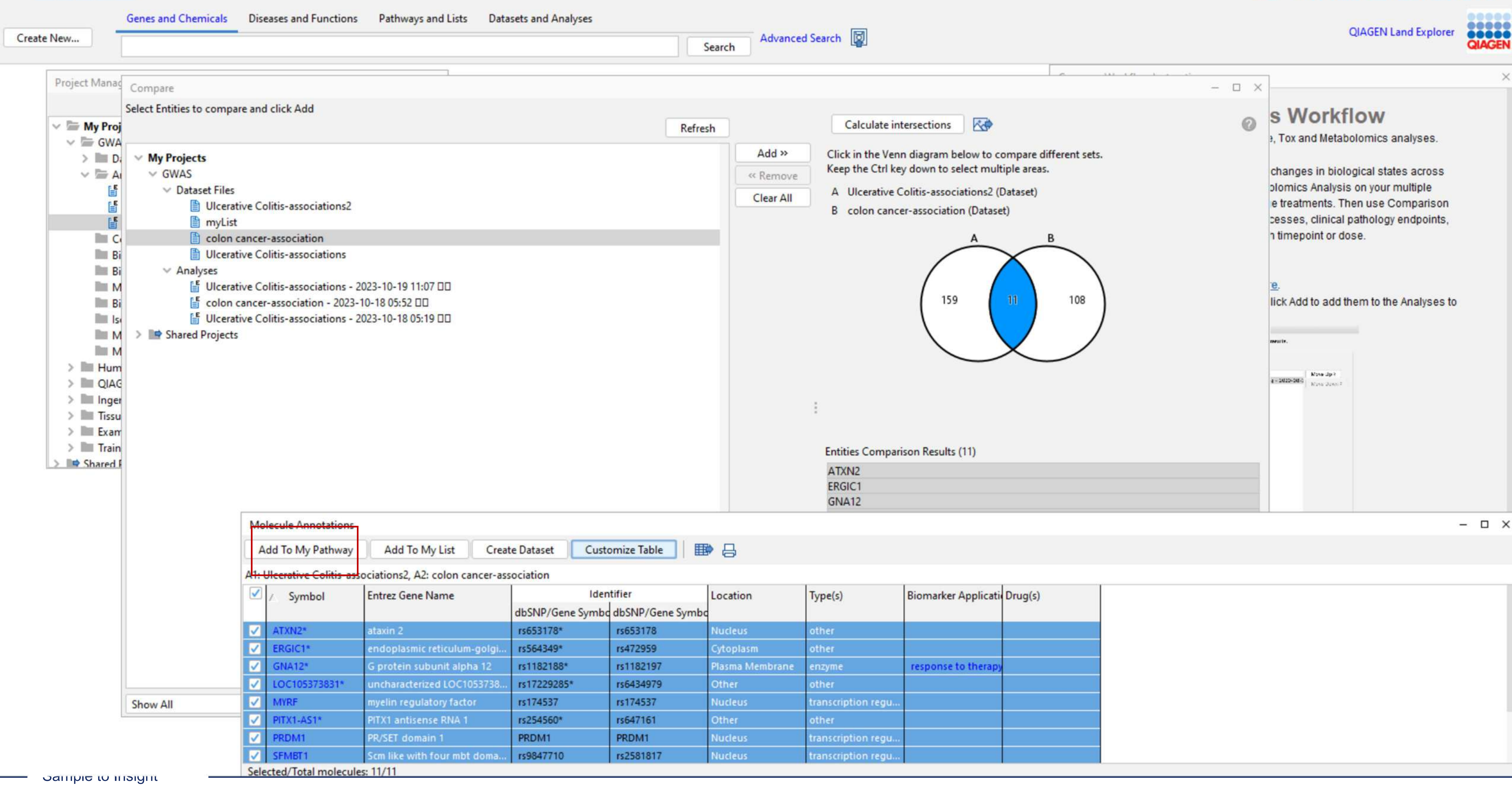

Select Entities to compare and click Add

- My Projects
  - GWAS
    - Dataset Files
      - Ulcerative Colitis-associations2
      - myList
      - colon cancer-association
      - Ulcerative Colitis-associations
    - Analyses
      - Ulcerative Colitis-associations - 2023-10-19 11:07 □□
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      - Ulcerative Colitis-associations - 2023-10-18 05:19 □□
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A Ulcerative Colitis-associations2 (Dataset)
B colon cancer-association (Dataset)

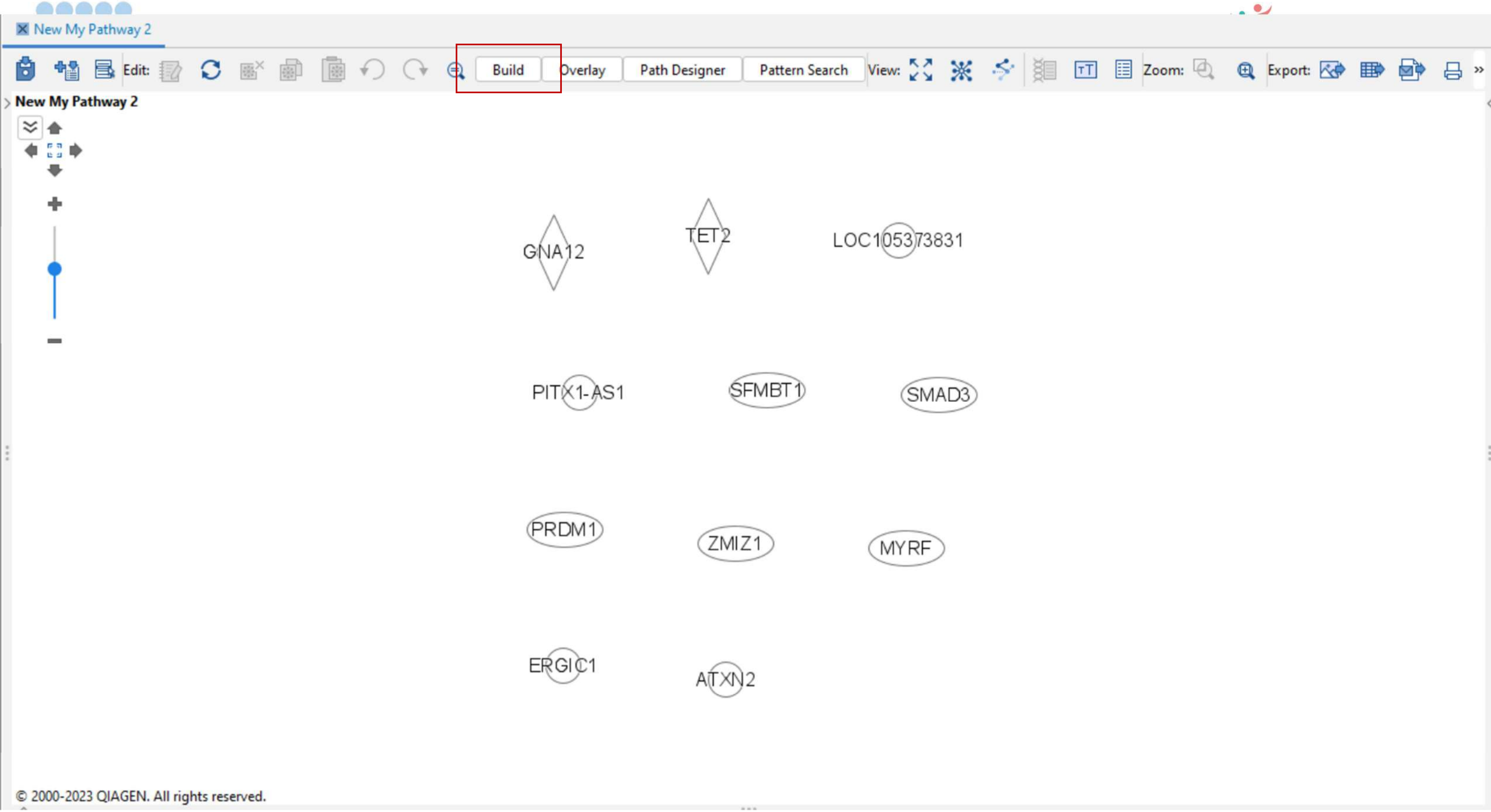
Entities Comparison Results (11)

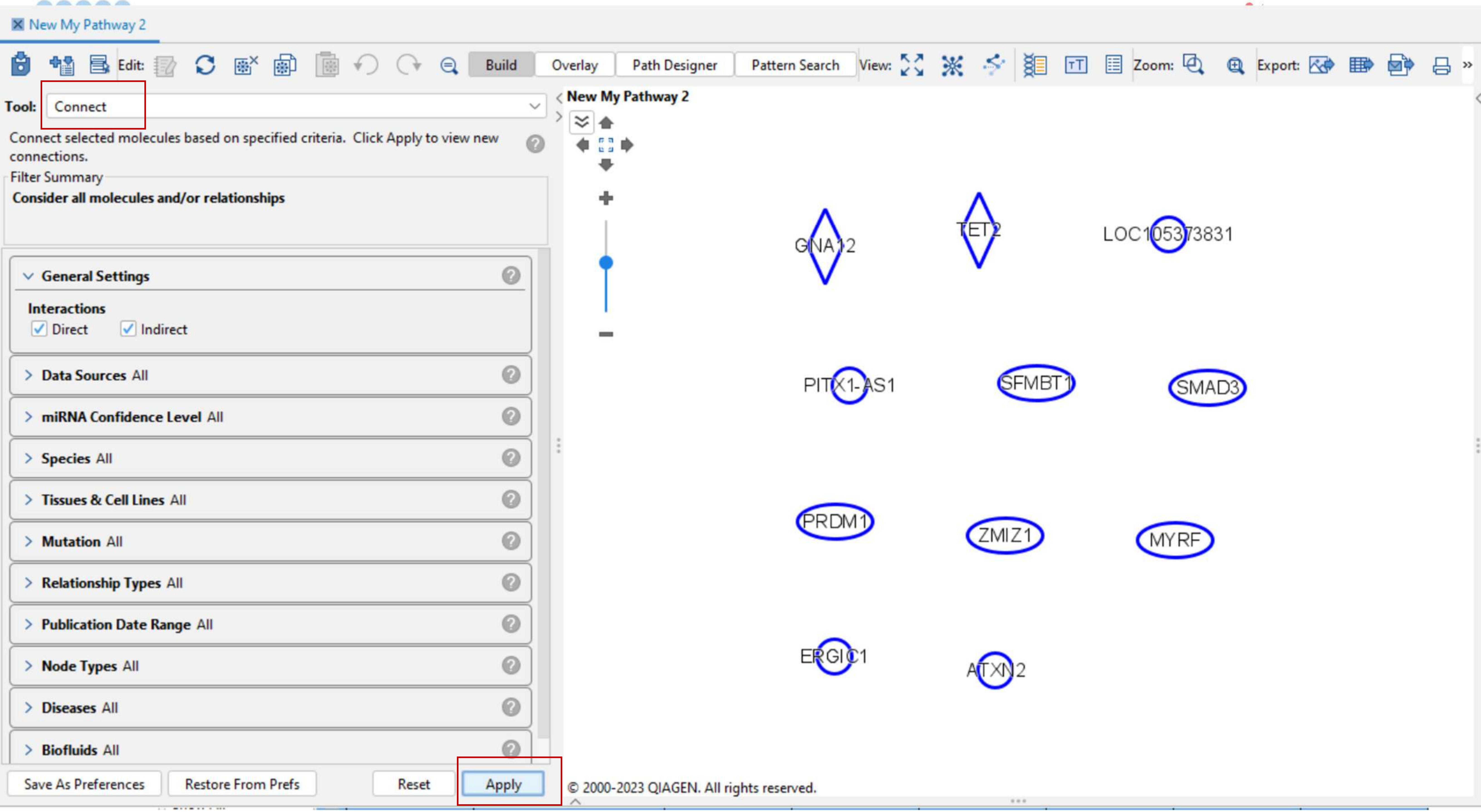
ATXN2
ERGIC1
GNA12

A1: Ulcerative Colitis-associations2, A2: colon cancer-association

☑	Symbol	Entrez Gene Name	Identifier		Location	Type(s)	Biomarker Applicati	Drug(s)
			dbSNP/Gene Symbo	dbSNP/Gene Symbo				
☑	ATXN2*	ataxin 2	rs653178*	rs653178	Nucleus	other		
☑	ERGIC1*	endoplasmic reticulum-golgi...	rs564349*	rs472959	Cytoplasm	other		
☑	GNA12*	G protein subunit alpha 12	rs1182188*	rs1182197	Plasma Membrane	enzyme	response to therapy	
☑	LOC105373831*	uncharacterized LOC1053738...	rs17229285*	rs6434979	Other	other		
☑	MYRF	myelin regulatory factor	rs174537	rs174537	Nucleus	transcription regu...		
☑	PITX1-AS1*	PITX1 antisense RNA 1	rs254560*	rs647161	Other	other		
☑	PRDM1	PR/SET domain 1	PRDM1	PRDM1	Nucleus	transcription regu...		
☑	SFMBT1	Scm like with four mbt doma...	rs9847710	rs2581817	Nucleus	transcription regu...		

Selected/Total molecules: 11/11


New My Pathway 2
Edit:
Build
Overlay
Path Designer
Pattern Search
View:
Zoom:
Export:
New My Pathway 2
GNA12
TET2
LOC105373831
PITX1-AS1
SFMBT1
SMAD3
PRDM1
ZMIZ1
MYRF
ERGIC1
ATXN2



New My Pathway 2

Tool: Connect

Connect selected molecules based on specified criteria. Click Apply to view new connections.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Data Sources All

miRNA Confidence Level All

Species All

Tissues & Cell Lines All

Mutation All

Relationship Types All

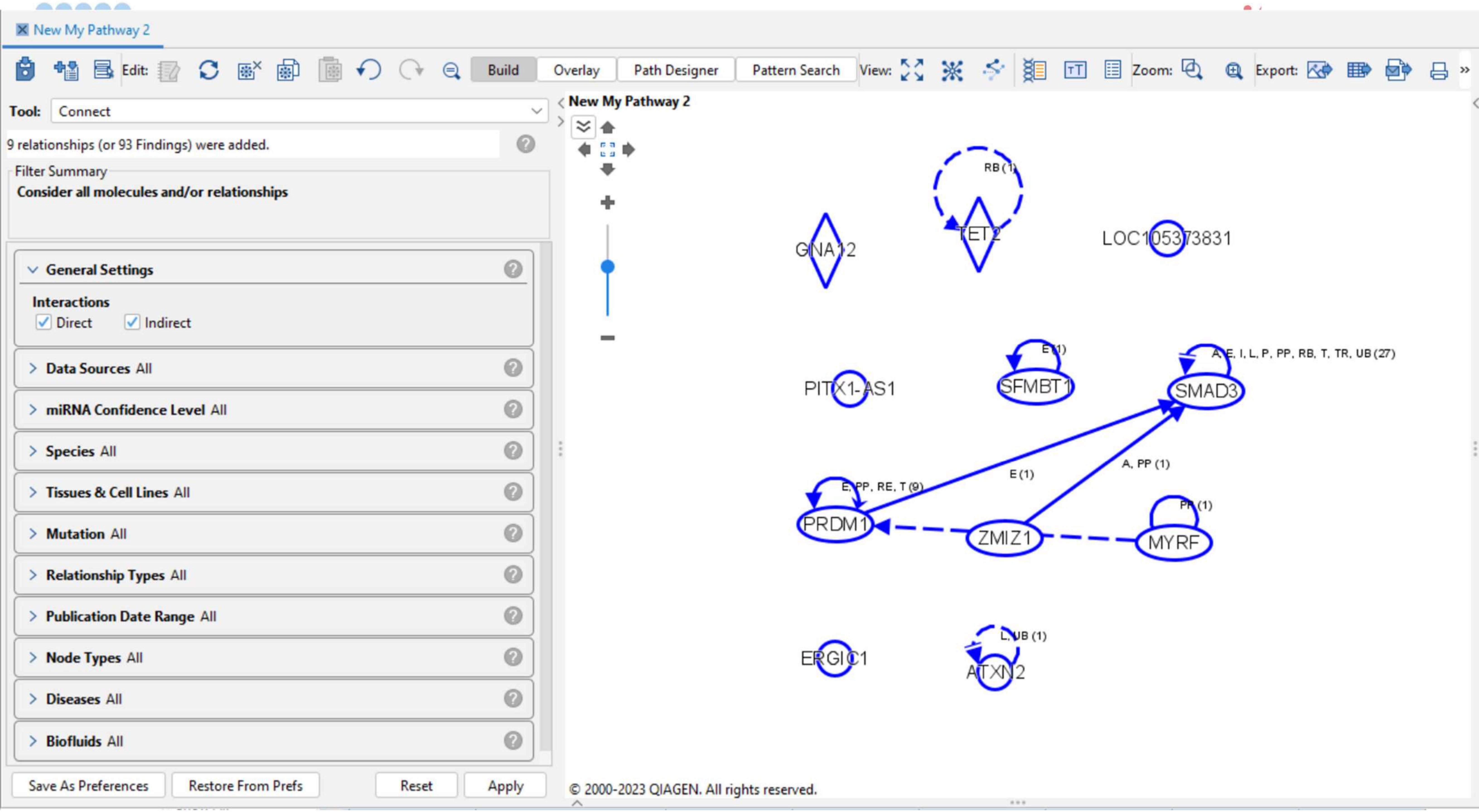
Publication Date Range All

Node Types All

Diseases All

Biofluids All

New My Pathway 2



Tool: Connect

9 relationships (or 93 Findings) were added.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Data Sources All

miRNA Confidence Level All

Species All

Tissues & Cell Lines All

Mutation All

Relationship Types All

Publication Date Range All

Node Types All

Diseases All

Biofluids All

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Construct a custom network to discover relationships

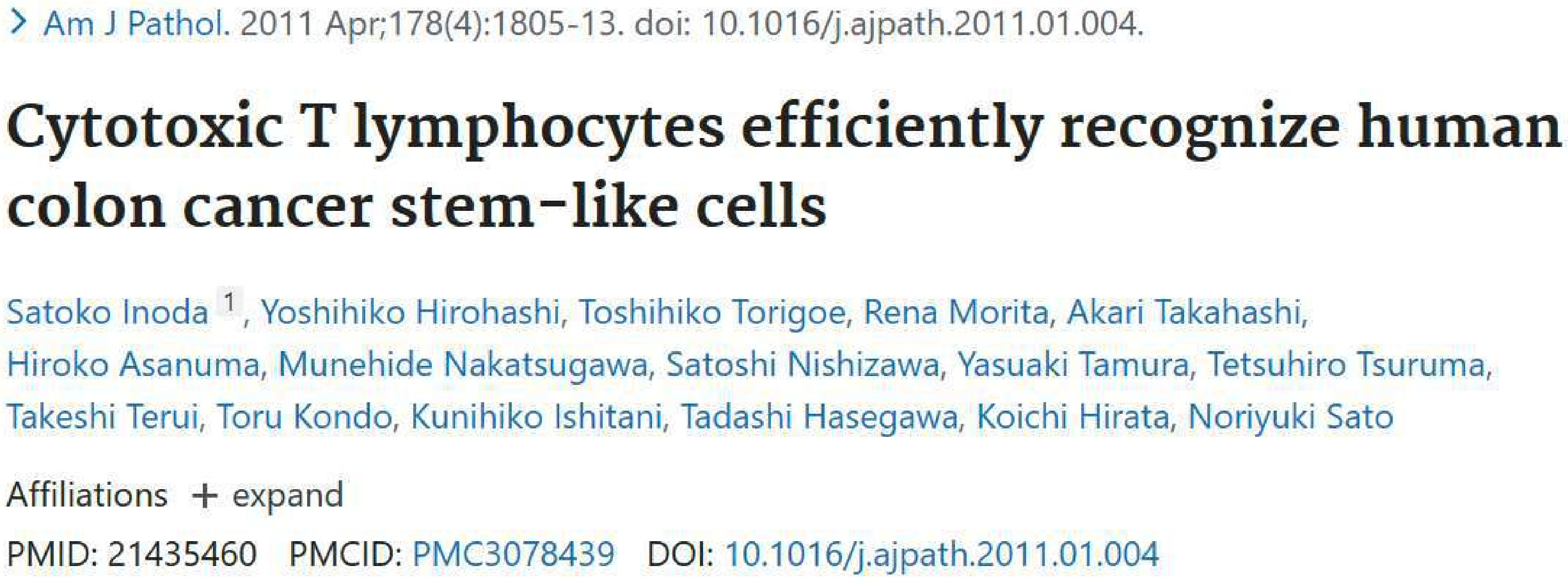
> BMC Gastroenterol. 2023 Apr 27;23(1):136. doi: 10.1186/s12876-023-02769-5.

Peripheral blood T-lymphocyte subsets are potential biomarkers of disease severity and clinical outcomes in patients with ulcerative colitis: a retrospective study

Bailu Geng[1], Xueli Ding[1], Xiaoyu Li[1], Hua Liu[1], Wenjun Zhao[1], Haihong Gong[2], Zibin Tian[3], Jing Guo[4]

Affiliations + expand

PMID: 37106335 PMCID: PMC10134527 DOI: 10.1186/s12876-023-02769-5



> Am J Pathol. 2011 Apr;178(4):1805-13. doi: 10.1016/j.ajpath.2011.01.004.

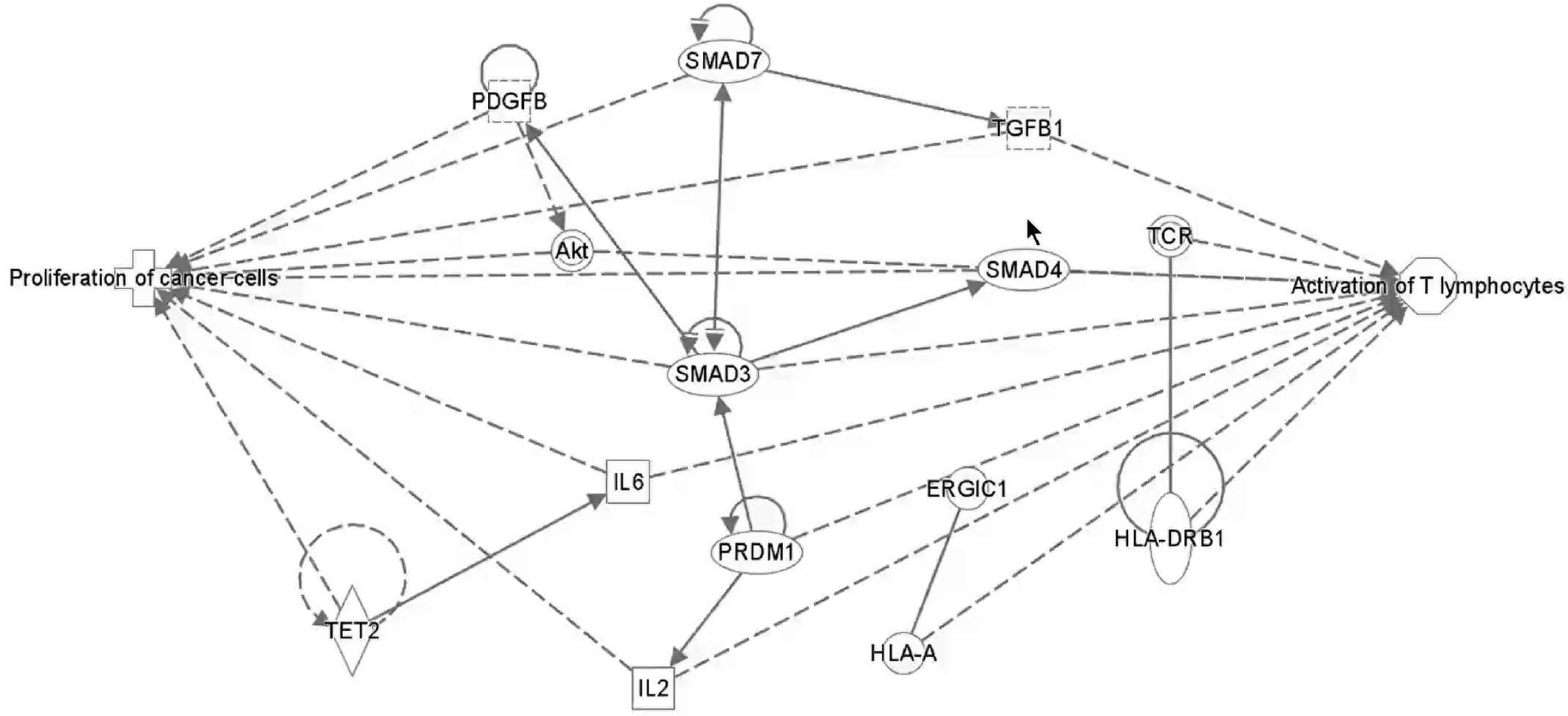
Cytotoxic T lymphocytes efficiently recognize human colon cancer stem-like cells

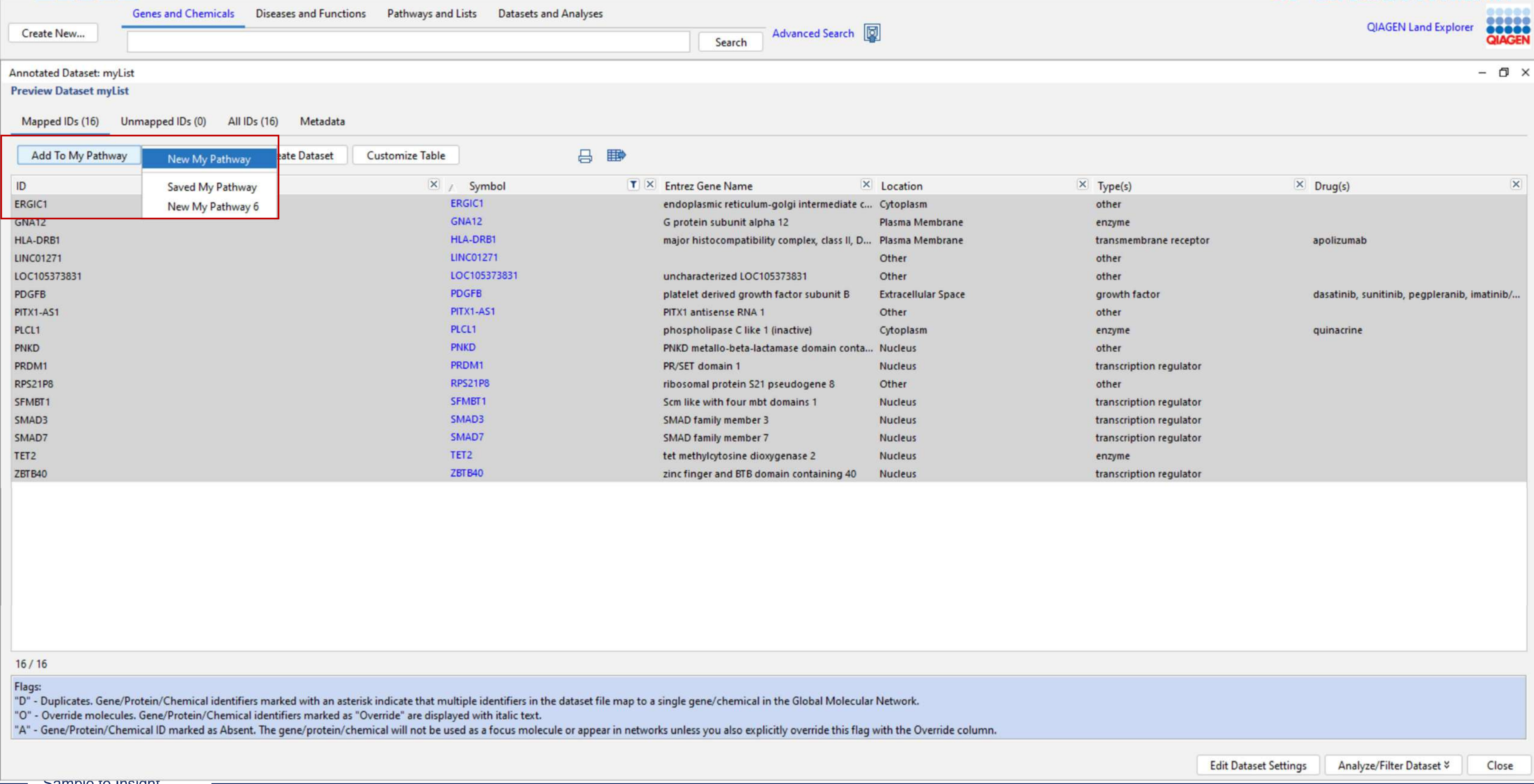
Satoko Inoda[1], Yoshihiko Hirohashi, Toshihiko Torigoe, Rena Morita, Akari Takahashi, Hiroko Asanuma, Munehide Nakatsugawa, Satoshi Nishizawa, Yasuaki Tamura, Tetsuhiro Tsuruma, Takeshi Terui, Toru Kondo, Kunihiko Ishitani, Tadashi Hasegawa, Koichi Hirata, Noriyuki Sato

Affiliations + expand

PMID: 21435460 PMCID: PMC3078439 DOI: 10.1016/j.ajpath.2011.01.004

Construct a custom network to discover relationships

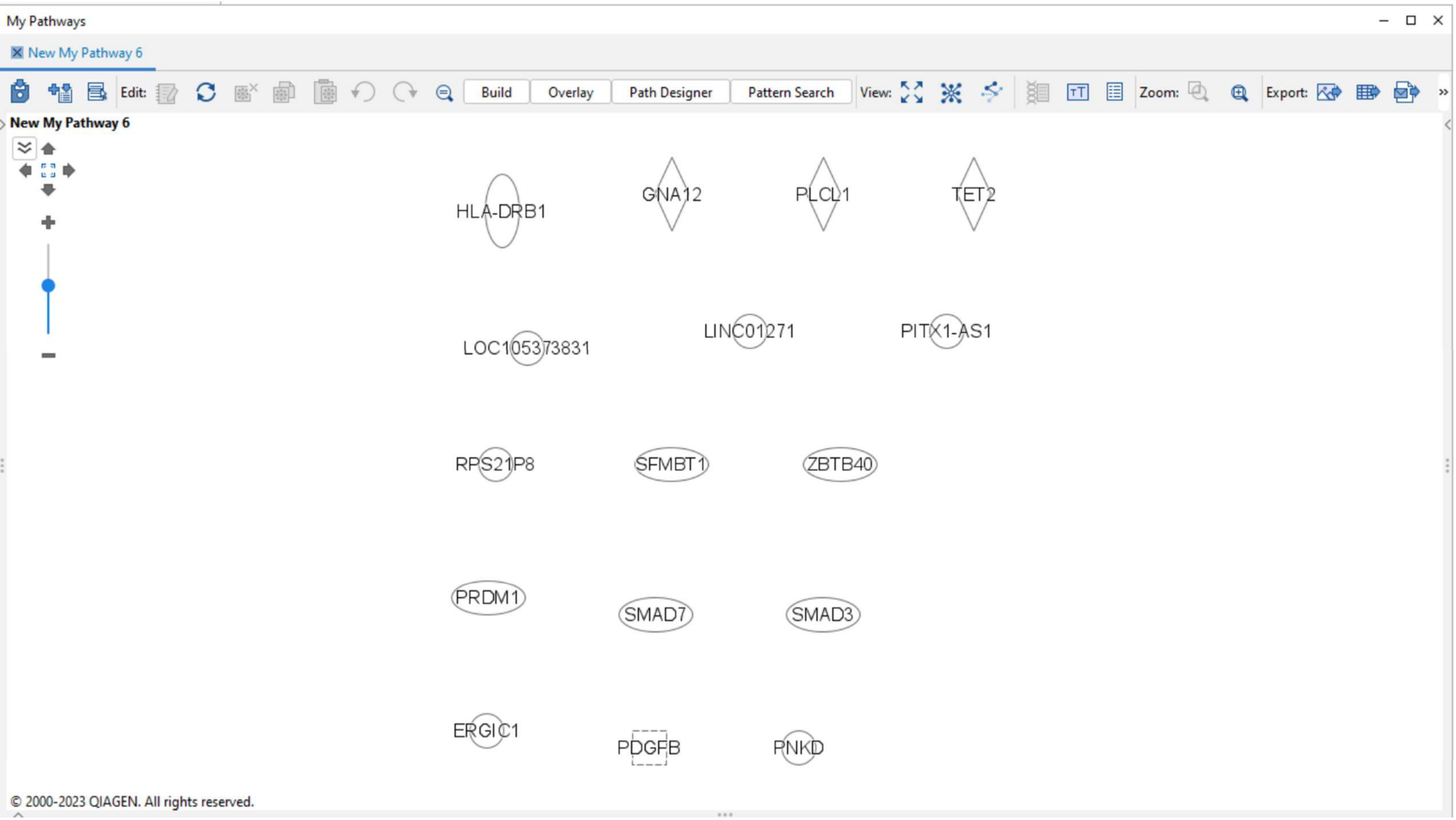




ID	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
ERGIC1	ERGIC1	endoplasmic reticulum-golgi intermediate c...	Cytoplasm	other	
GNA12	GNA12	G protein subunit alpha 12	Plasma Membrane	enzyme	
HLA-DRB1	HLA-DRB1	major histocompatibility complex, class II, D...	Plasma Membrane	transmembrane receptor	apolizumab
LINC01271	LINC01271		Other	other	
LOC105373831	LOC105373831	uncharacterized LOC105373831	Other	other	
PDGFB	PDGFB	platelet derived growth factor subunit B	Extracellular Space	growth factor	dasatinib, sunitinib, pegpleranib, imatinib/...
PITX1-AS1	PITX1-AS1	PITX1 antisense RNA 1	Other	other	
PLCL1	PLCL1	phospholipase C like 1 (inactive)	Cytoplasm	enzyme	quinacrine
PNKD	PNKD	PNKD metallo-beta-lactamase domain conta...	Nucleus	other	
PRDM1	PRDM1	PR/SET domain 1	Nucleus	transcription regulator	
RPS21P8	RPS21P8	ribosomal protein S21 pseudogene 8	Other	other	
SFMBT1	SFMBT1	Scm like with four mbt domains 1	Nucleus	transcription regulator	
SMAD3	SMAD3	SMAD family member 3	Nucleus	transcription regulator	
SMAD7	SMAD7	SMAD family member 7	Nucleus	transcription regulator	
TET2	TET2	tet methylcytosine dioxygenase 2	Nucleus	enzyme	
ZBTB40	ZBTB40	zinc finger and BTB domain containing 40	Nucleus	transcription regulator	

16 / 16

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.


My Pathways
New My Pathway 6
Edit:
Build
Overlay
Path Designer
Pattern Search
View:
Zoom:
Export:
New My Pathway 6
HLA-DRB1
GNA12
PLCL1
TET2
LOC105373831
LINC01271
PITX1-AS1
RPS21P8
SFMBT1
ZBTB40
PRDM1
SMAD7
SMAD3
ERGIC1
PDGFB
PNKD
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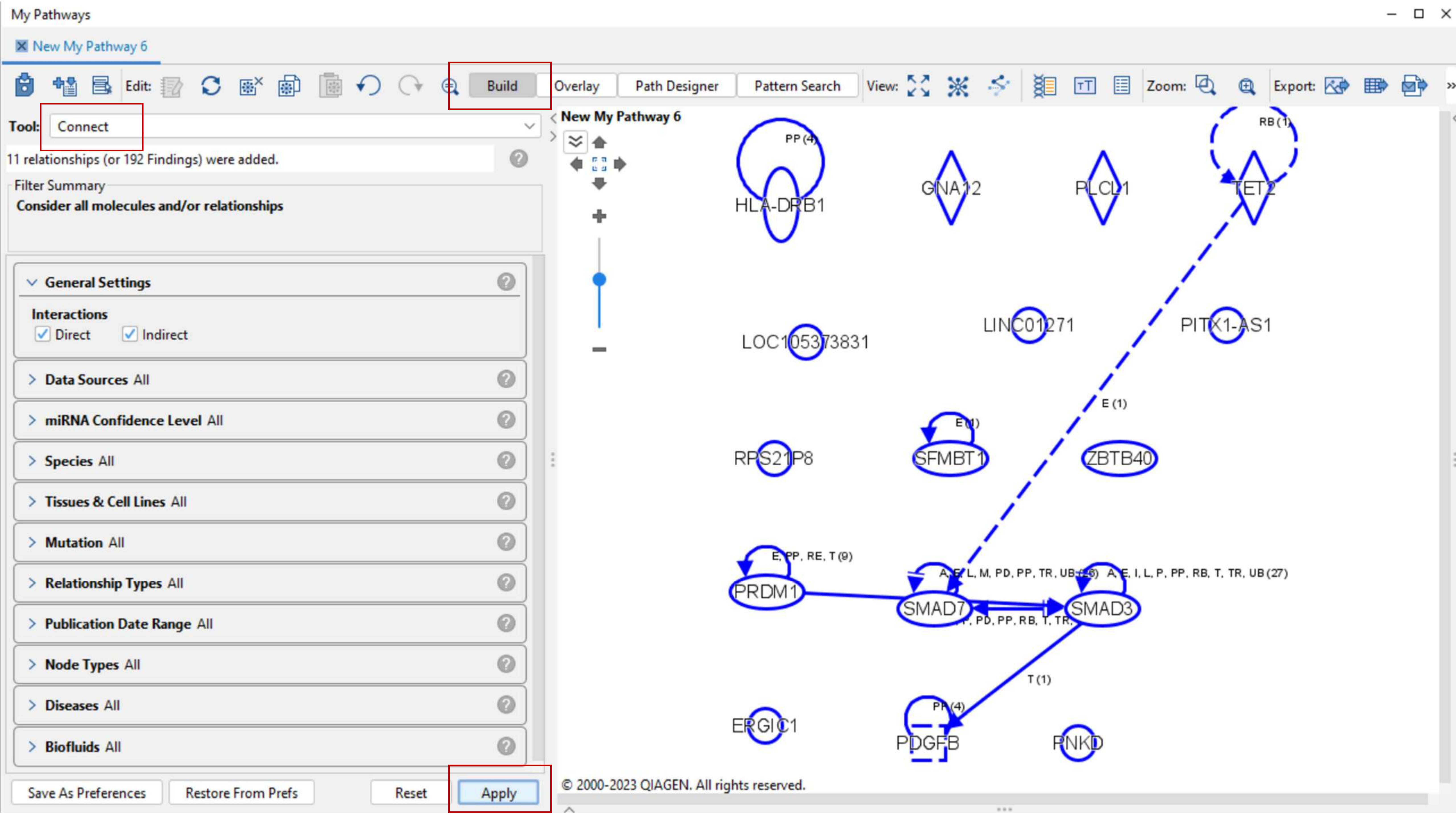

Tool: Connect

11 relationships (or 192 Findings) were added.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Data Sources All

miRNA Confidence Level All

Species All

Tissues & Cell Lines All

Mutation All

Relationship Types All

Publication Date Range All

Node Types All

Diseases All

Biofluids All

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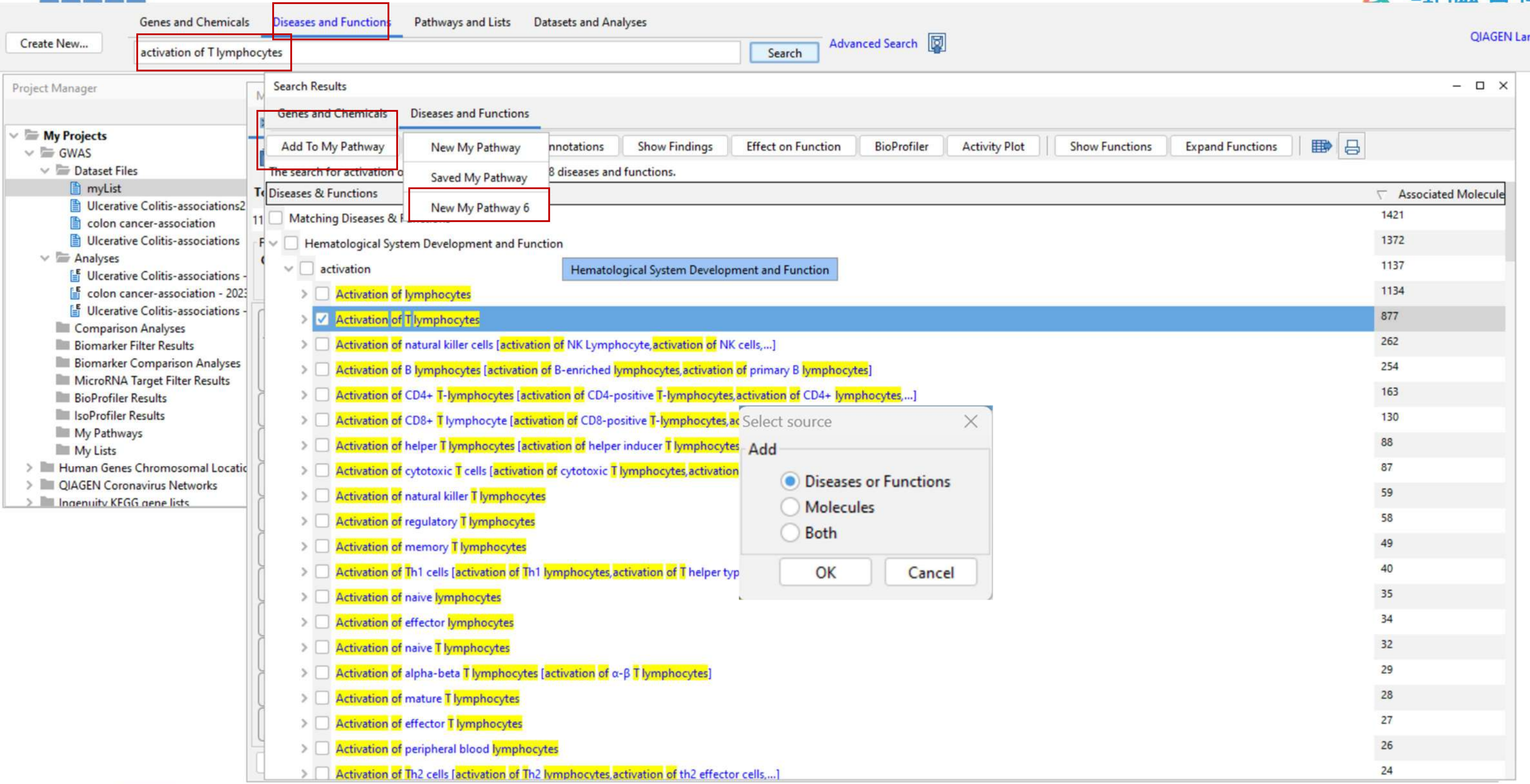


activation of T lymphocytes

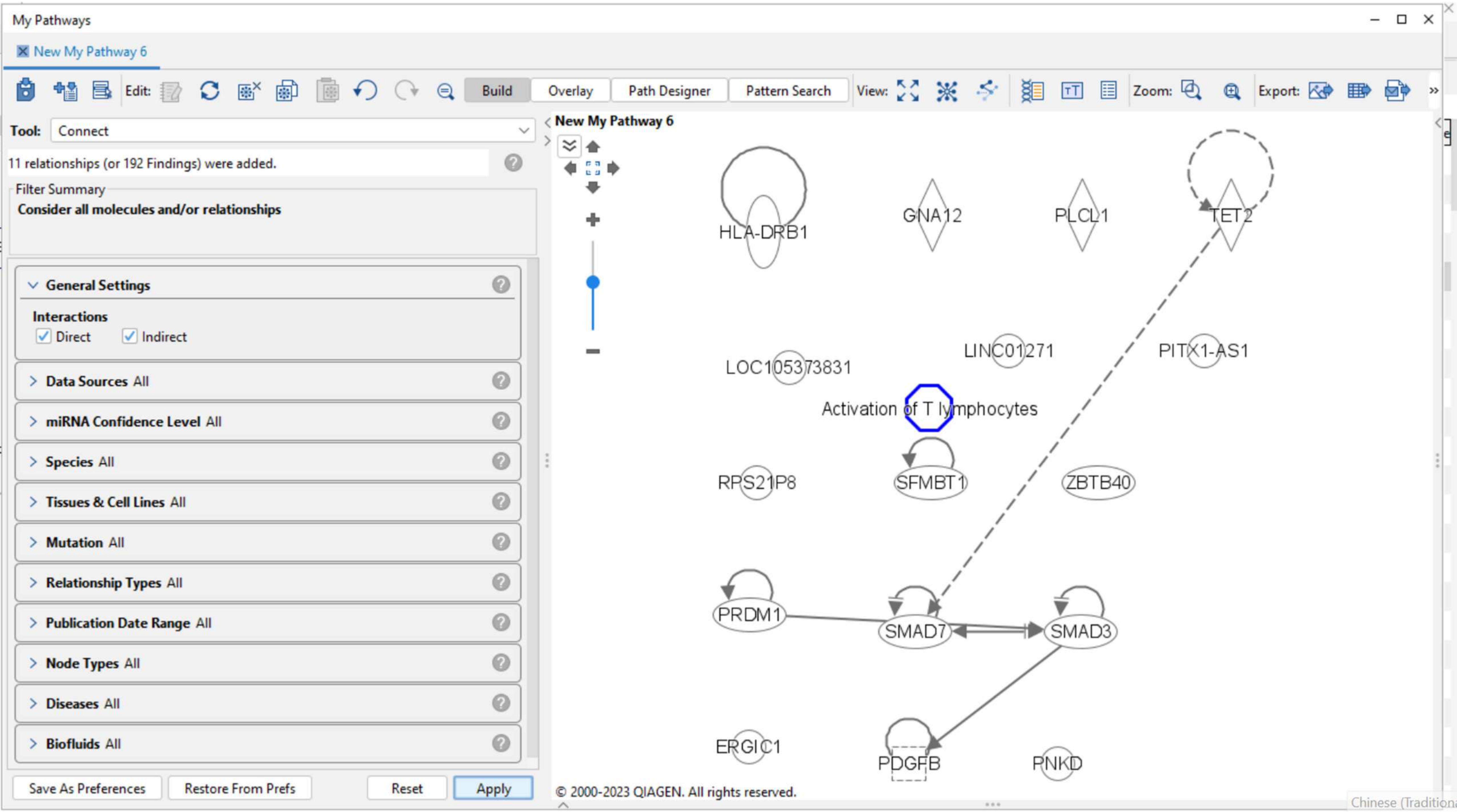
The search for activation o… 8 diseases and functions.

Diseases & Functions	Associated Molecule
☐ Matching Diseases & F…	1421
☐ Hematological System Development and Function	1372
☐ activation	1137
☐ Activation of lymphocytes	1134
☑ Activation of T lymphocytes	877
☐ Activation of natural killer cells [activation of NK Lymphocyte,activation of NK cells,...]	262
☐ Activation of B lymphocytes [activation of B-enriched lymphocytes,activation of primary B lymphocytes]	254
☐ Activation of CD4+ T-lymphocytes [activation of CD4-positive T-lymphocytes,activation of CD4+ lymphocytes,...]	163
☐ Activation of CD8+ T lymphocyte [activation of CD8-positive T-lymphocytes,ac	130
☐ Activation of helper T lymphocytes [activation of helper inducer T lymphocytes	88
☐ Activation of cytotoxic T cells [activation of cytotoxic T lymphocytes,activation	87
☐ Activation of natural killer T lymphocytes	59
☐ Activation of regulatory T lymphocytes	58
☐ Activation of memory T lymphocytes	49
☐ Activation of Th1 cells [activation of Th1 lymphocytes,activation of T helper typ	40
☐ Activation of naive lymphocytes	35
☐ Activation of effector lymphocytes	34
☐ Activation of naive T lymphocytes	32
☐ Activation of alpha-beta T lymphocytes [activation of α-β T lymphocytes]	29
☐ Activation of mature T lymphocytes	28
☐ Activation of effector T lymphocytes	27
☐ Activation of peripheral blood lymphocytes	26
☐ Activation of Th2 cells [activation of Th2 lymphocytes,activation of th2 effector cells,...]	24

Select source

Add

● Diseases or Functions
○ Molecules
○ Both



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Relationship Types All

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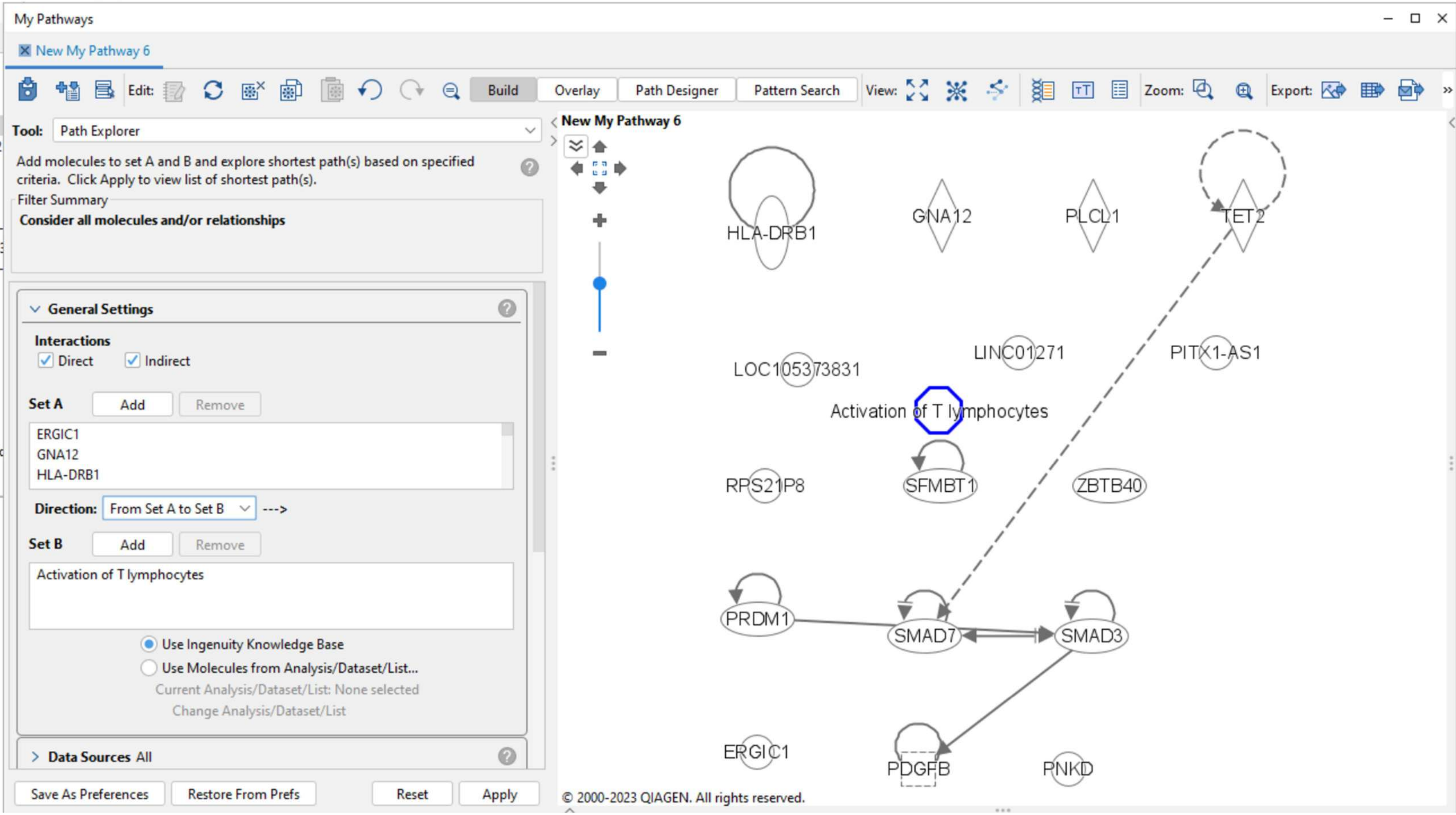
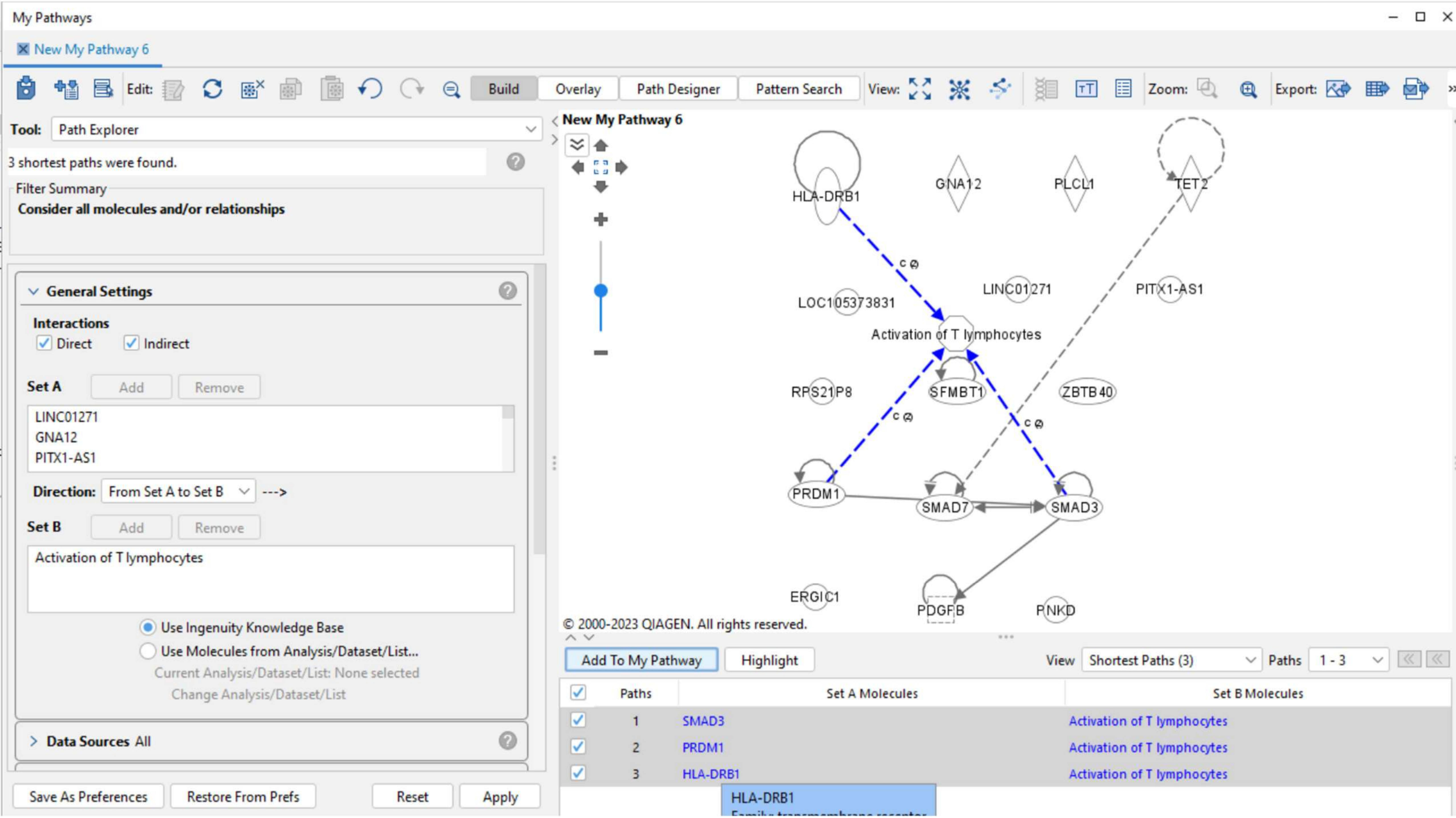
Diseases All

Biofluids All





Tool: Path Explorer

3 shortest paths were found.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Set A Add Remove

LINC01271
GNA12
PITX1-AS1

Direction: From Set A to Set B --->

Set B Add Remove

Activation of T lymphocytes

● Use Ingenuity Knowledge Base

○ Use Molecules from Analysis/Dataset/List...

Current Analysis/Dataset/List: None selected

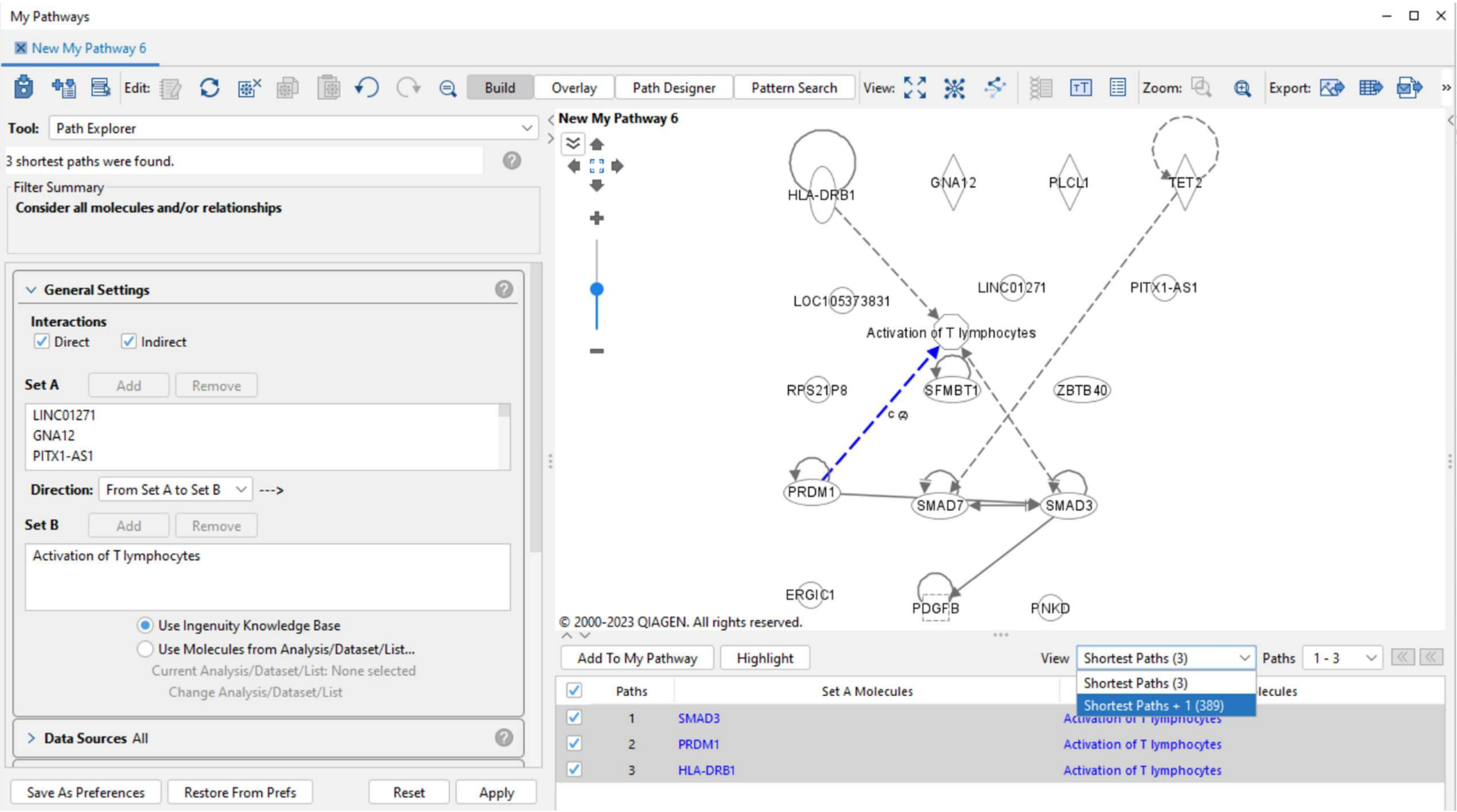
Change Analysis/Dataset/List

Data Sources All

View: Shortest Paths (3) Paths: 1 - 3

☑	Paths	Set A Molecules	Set B Molecules
☑	1	SMAD3	Activation of T lymphocytes
☑	2	PRDM1	Activation of T lymphocytes
☑	3	HLA-DRB1	Activation of T lymphocytes

HLA-DRB1



Tool: Path Explorer

3 shortest paths were found.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Set A

LINC01271
GNA12
PITX1-AS1

Direction: From Set A to Set B --->

Set B

Activation of T lymphocytes

● Use Ingenuity Knowledge Base

○ Use Molecules from Analysis/Dataset/List...

Current Analysis/Dataset/List: None selected

Change Analysis/Dataset/List

Data Sources All

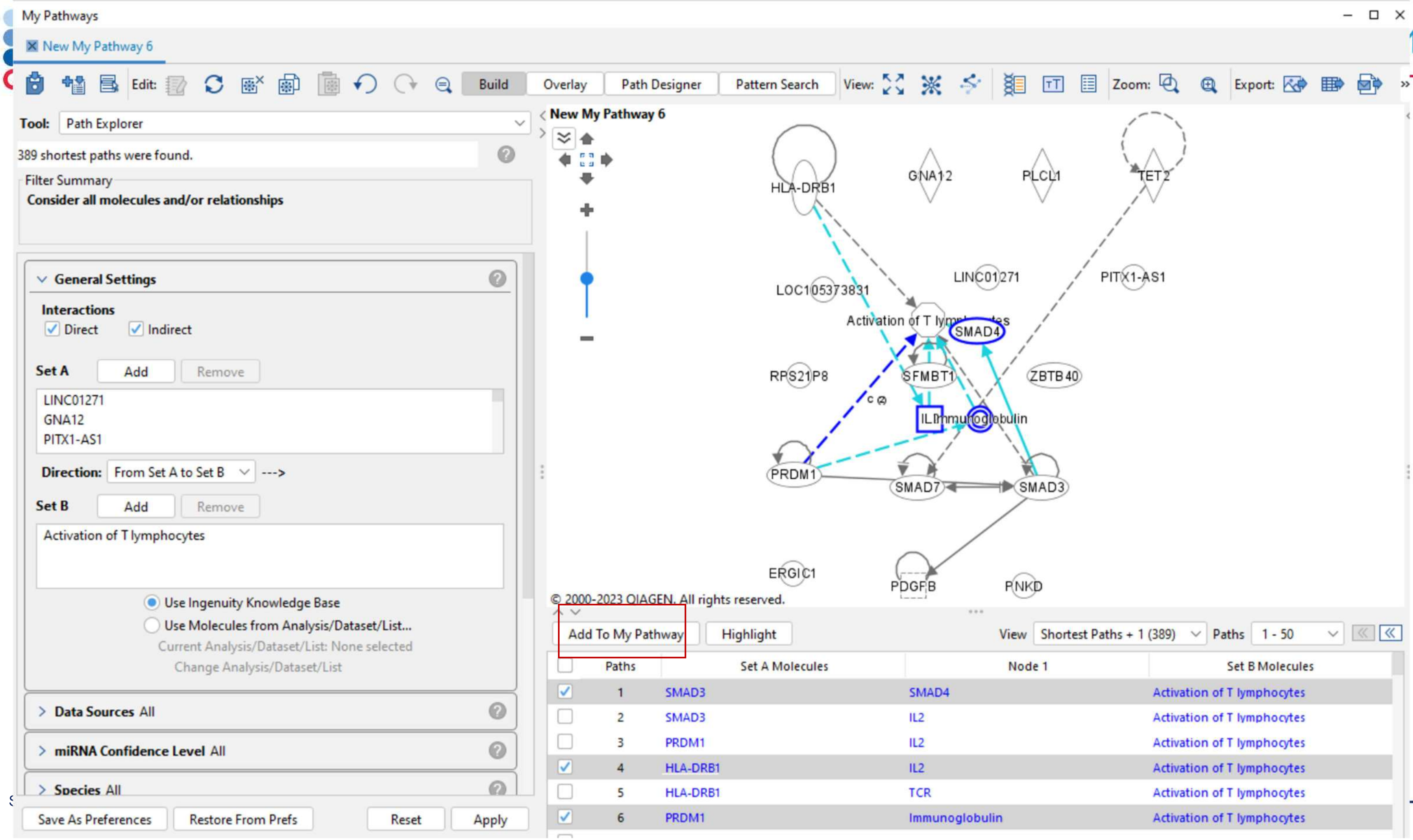
View: Shortest Paths (3)

- Shortest Paths (3)
- Shortest Paths + 1 (389)

Paths: 1 - 3

☑	Paths	Set A Molecules	lecules
☑	1	SMAD3	Activation of T lymphocytes
☑	2	PRDM1	Activation of T lymphocytes
☑	3	HLA-DRB1	Activation of T lymphocytes
)

位



Tool: Path Explorer

389 shortest paths were found.

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

☑ Direct ☑ Indirect

Set A Add Remove

LINC01271
GNA12
PITX1-AS1

Direction: From Set A to Set B --->

Set B Add Remove

Activation of T lymphocytes

● Use Ingenuity Knowledge Base
○ Use Molecules from Analysis/Dataset/List...

Current Analysis/Dataset/List: None selected

Change Analysis/Dataset/List

Data Sources All

miRNA Confidence Level All

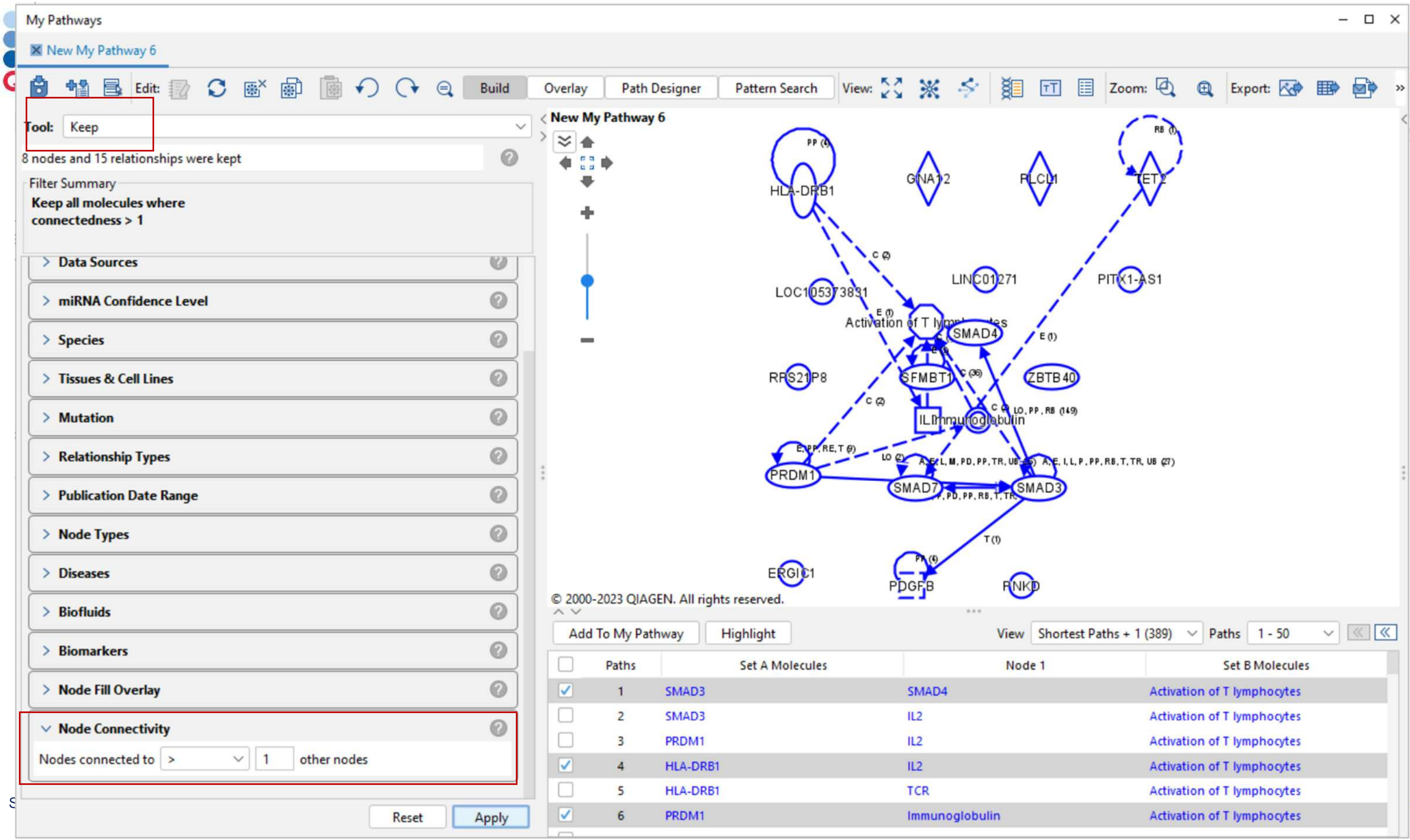
Species All

Save As Preferences | Restore From Prefs | Reset | Apply

View: Shortest Paths + 1 (389) Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

位



Tool: Keep

8 nodes and 15 relationships were kept

Filter Summary

Keep all molecules where connectedness > 1

Node Connectivity

Nodes connected to > 1 other nodes

New My Pathway 6

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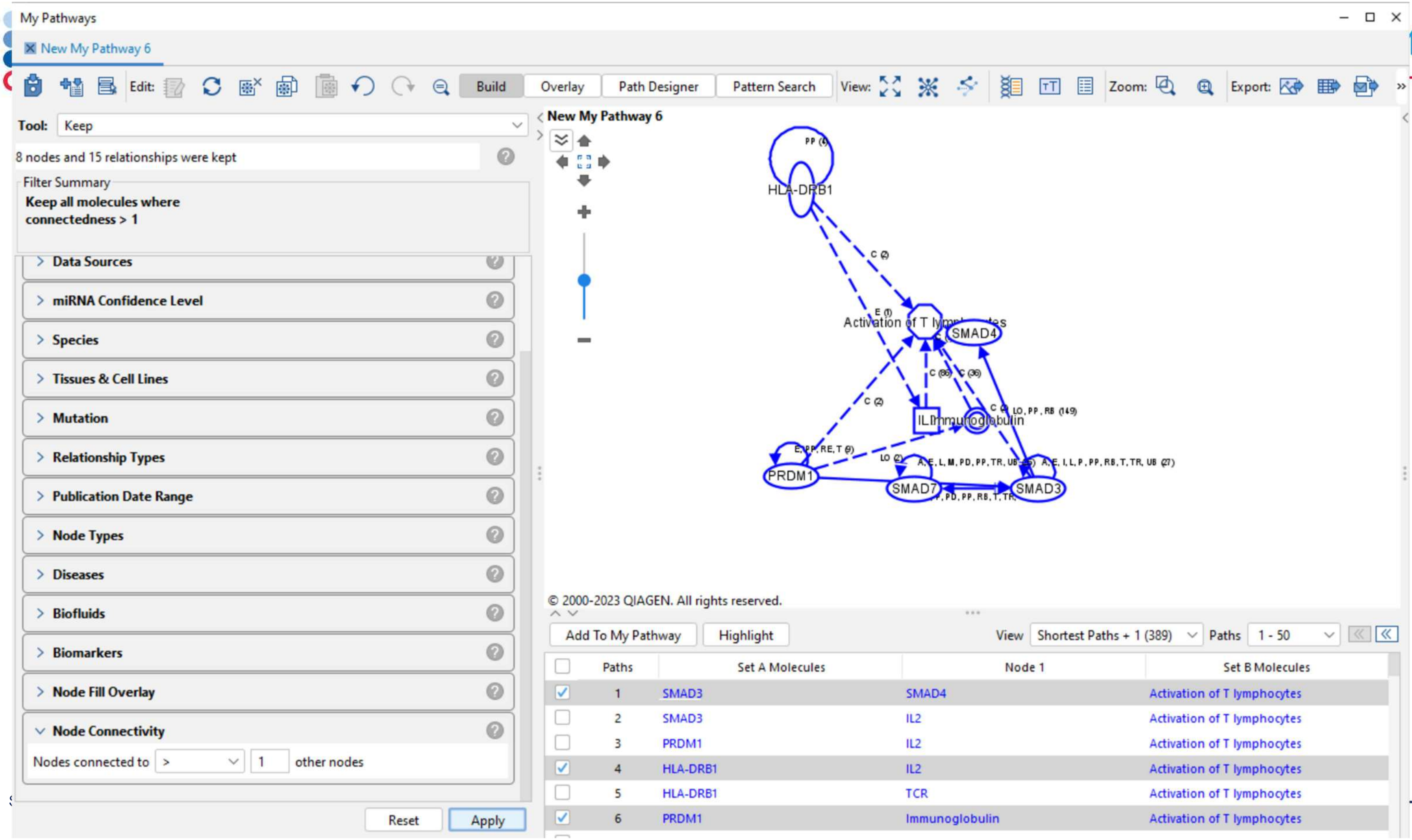
View: Shortest Paths + 1 (389)   Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes



Tool: Keep

8 nodes and 15 relationships were kept

Filter Summary

Keep all molecules where connectedness > 1

- Data Sources
- miRNA Confidence Level
- Species
- Tissues & Cell Lines
- Mutation
- Relationship Types
- Publication Date Range
- Node Types
- Diseases
- Biofluids
- Biomarkers
- Node Fill Overlay
- Node Connectivity

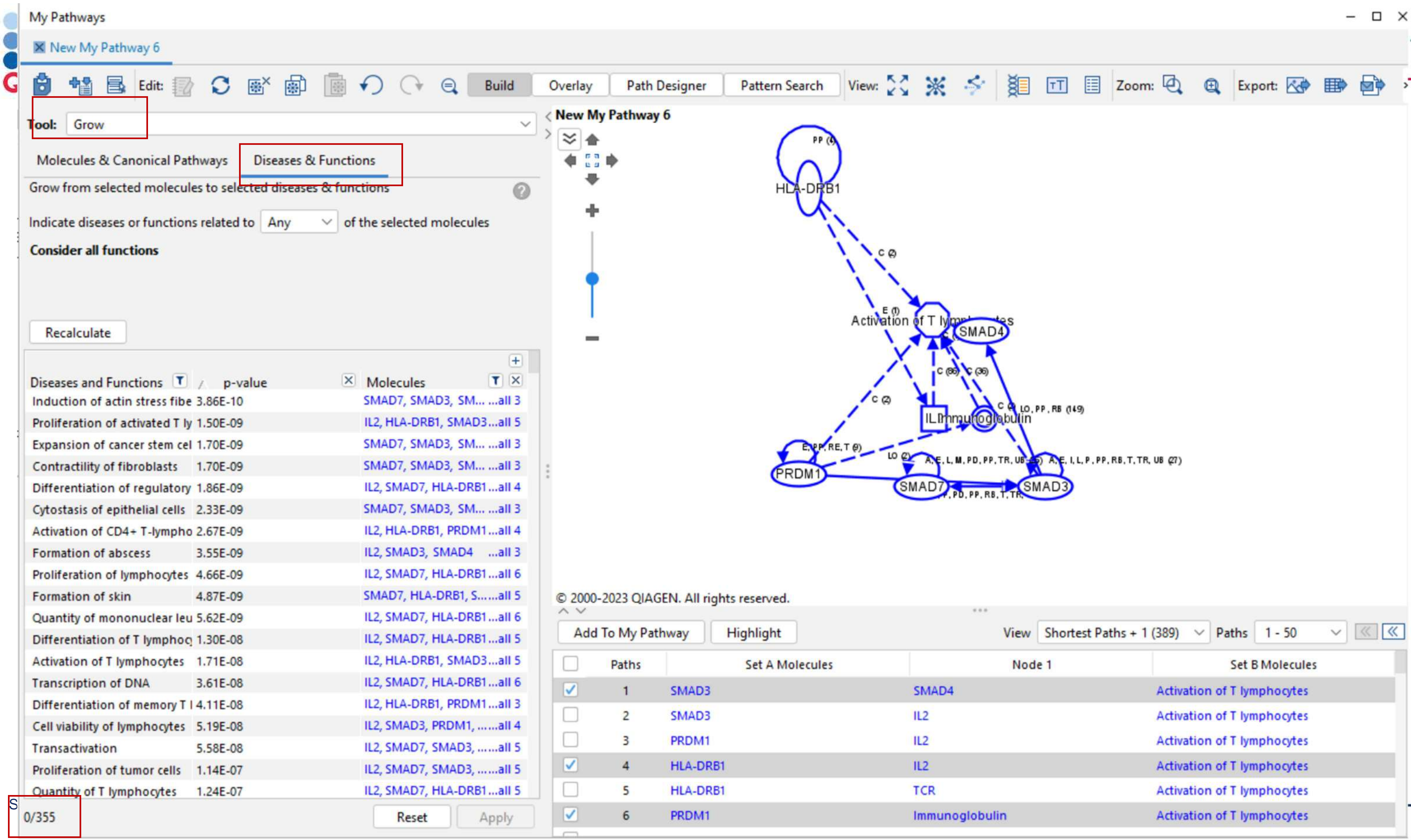
Nodes connected to > 1 other nodes

View: Shortest Paths + 1 (389)   Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

位

位



Tool: Grow

Molecules & Canonical Pathways | Diseases & Functions

Grow from selected molecules to selected diseases & functions

Indicate diseases or functions related to Any of the selected molecules

Consider all functions

Diseases and Functions	p-value	Molecules
Induction of actin stress fibe	3.86E-10	SMAD7, SMAD3, SM... ...all 3
Proliferation of activated T ly	1.50E-09	IL2, HLA-DRB1, SMAD3...all 5
Expansion of cancer stem cel	1.70E-09	SMAD7, SMAD3, SM... ...all 3
Contractility of fibroblasts	1.70E-09	SMAD7, SMAD3, SM... ...all 3
Differentiation of regulatory	1.86E-09	IL2, SMAD7, HLA-DRB1...all 4
Cytostasis of epithelial cells	2.33E-09	SMAD7, SMAD3, SM... ...all 3
Activation of CD4+ T-lympho	2.67E-09	IL2, HLA-DRB1, PRDM1...all 4
Formation of abscess	3.55E-09	IL2, SMAD3, SMAD4 ...all 3
Proliferation of lymphocytes	4.66E-09	IL2, SMAD7, HLA-DRB1...all 6
Formation of skin	4.87E-09	SMAD7, HLA-DRB1, S......all 5
Quantity of mononuclear leu	5.62E-09	IL2, SMAD7, HLA-DRB1...all 6
Differentiation of T lymphoc	1.30E-08	IL2, SMAD7, HLA-DRB1...all 5
Activation of T lymphocytes	1.71E-08	IL2, HLA-DRB1, SMAD3...all 5
Transcription of DNA	3.61E-08	IL2, SMAD7, HLA-DRB1...all 6
Differentiation of memory T l	4.11E-08	IL2, HLA-DRB1, PRDM1...all 3
Cell viability of lymphocytes	5.19E-08	IL2, SMAD3, PRDM1, ...all 4
Transactivation	5.58E-08	IL2, SMAD7, SMAD3, ...all 5
Proliferation of tumor cells	1.14E-07	IL2, SMAD7, SMAD3, ...all 5
Quantity of T lymphocytes	1.24E-07	IL2, SMAD7, HLA-DRB1...all 5

0/355

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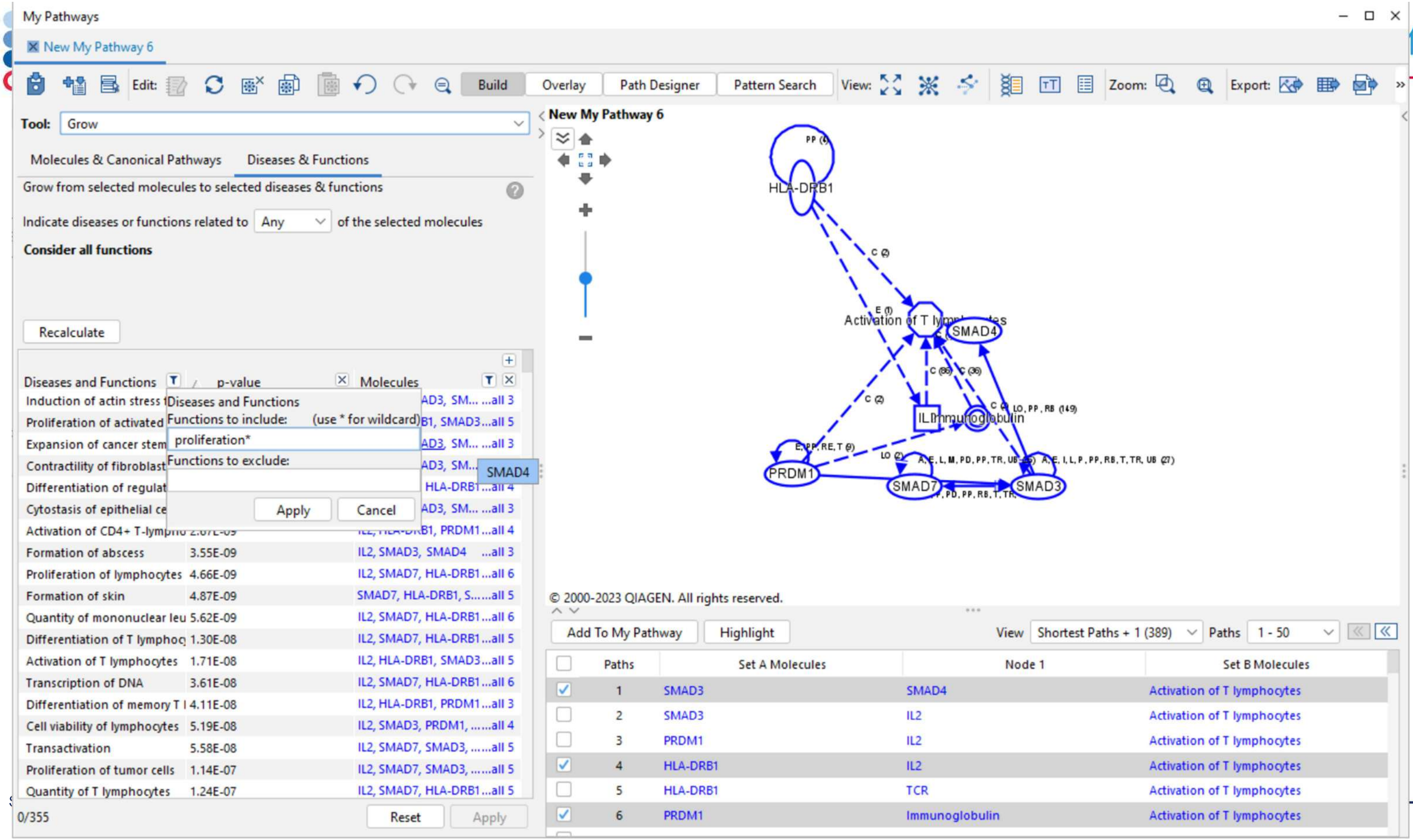
View: Shortest Paths + 1 (389)   Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

位



Tool: Grow

Grow from selected molecules to selected diseases & functions

Indicate diseases or functions related to Any of the selected molecules

Consider all functions

Diseases and Functions

Functions to include: (use * for wildcard) proliferation*

Functions to exclude:

Diseases and Functions	p-value	Molecules
Induction of actin stress f		AD3, SM... ...all 3
Proliferation of activated		B1, SMAD3...all 5
Expansion of cancer stem		AD3, SM... ...all 3
Contractility of fibroblast		AD3, SM... SMAD4
Differentiation of regulat		HLA-DRB1...all 4
Cytostasis of epithelial ce		AD3, SM... ...all 3
Activation of CD4+ T-lympho		B1, PRDM1...all 4
Formation of abscess	3.55E-09	IL2, SMAD3, SMAD4 ...all 3
Proliferation of lymphocytes	4.66E-09	IL2, SMAD7, HLA-DRB1...all 6
Formation of skin	4.87E-09	SMAD7, HLA-DRB1, S... ...all 5
Quantity of mononuclear leu	5.62E-09	IL2, SMAD7, HLA-DRB1...all 6
Differentiation of T lymphoc	1.30E-08	IL2, SMAD7, HLA-DRB1...all 5
Activation of T lymphocytes	1.71E-08	IL2, HLA-DRB1, SMAD3...all 5
Transcription of DNA	3.61E-08	IL2, SMAD7, HLA-DRB1...all 6
Differentiation of memory T l	4.11E-08	IL2, HLA-DRB1, PRDM1...all 3
Cell viability of lymphocytes	5.19E-08	IL2, SMAD3, PRDM1, ...all 4
Transactivation	5.58E-08	IL2, SMAD7, SMAD3, ...all 5
Proliferation of tumor cells	1.14E-07	IL2, SMAD7, SMAD3, ...all 5
Quantity of T lymphocytes	1.24E-07	IL2, SMAD7, HLA-DRB1...all 5

0/355

New My Pathway 6

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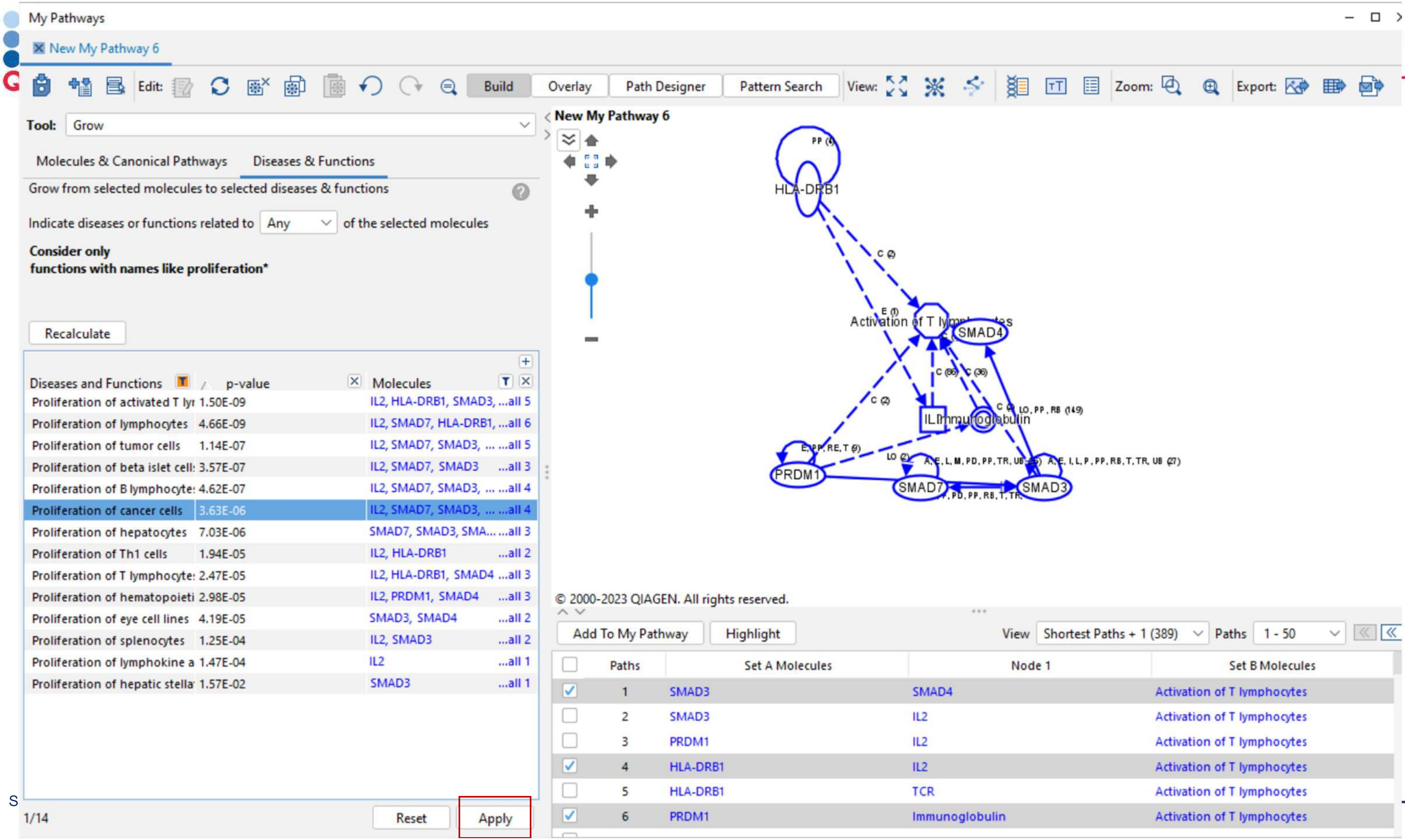
View Shortest Paths + 1 (389) Paths 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes



Tool: Grow

Molecules & Canonical Pathways | Diseases & Functions

Grow from selected molecules to selected diseases & functions

Indicate diseases or functions related to Any of the selected molecules

Consider only
functions with names like proliferation*

Diseases and Functions	p-value	Molecules
Proliferation of activated T lyı	1.50E-09	IL2, HLA-DRB1, SMAD3, ...all 5
Proliferation of lymphocytes	4.66E-09	IL2, SMAD7, HLA-DRB1, ...all 6
Proliferation of tumor cells	1.14E-07	IL2, SMAD7, SMAD3, ...all 5
Proliferation of beta islet cell:	3.57E-07	IL2, SMAD7, SMAD3 ...all 3
Proliferation of B lymphocyte:	4.62E-07	IL2, SMAD7, SMAD3, ...all 4
Proliferation of cancer cells	3.63E-06	IL2, SMAD7, SMAD3, ...all 4
Proliferation of hepatocytes	7.03E-06	SMAD7, SMAD3, SMA... ...all 3
Proliferation of Th1 cells	1.94E-05	IL2, HLA-DRB1 ...all 2
Proliferation of T lymphocyte:	2.47E-05	IL2, HLA-DRB1, SMAD4 ...all 3
Proliferation of hematopoieti	2.98E-05	IL2, PRDM1, SMAD4 ...all 3
Proliferation of eye cell lines	4.19E-05	SMAD3, SMAD4 ...all 2
Proliferation of splenocytes	1.25E-04	IL2, SMAD3 ...all 2
Proliferation of lymphokine a	1.47E-04	IL2 ...all 1
Proliferation of hepatic stella	1.57E-02	SMAD3 ...all 1

1/14

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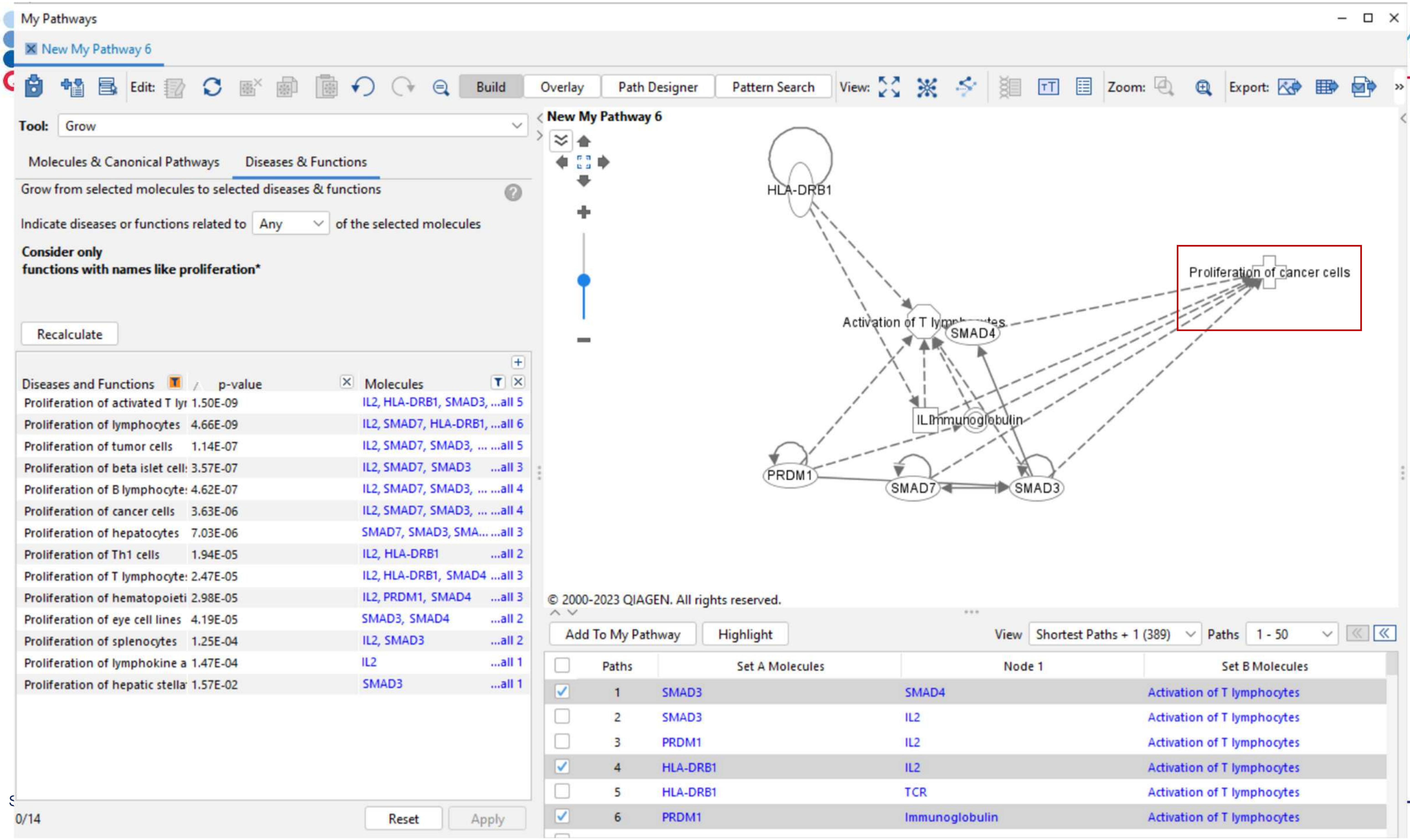
View Shortest Paths + 1 (389) Paths 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

位



Tool: Grow

Grow from selected molecules to selected diseases & functions

Indicate diseases or functions related to Any of the selected molecules

Consider only
functions with names like proliferation*

Diseases and Functions	p-value	Molecules	
Proliferation of activated T lyr	1.50E-09	IL2, HLA-DRB1, SMAD3, ...	...all 5
Proliferation of lymphocytes	4.66E-09	IL2, SMAD7, HLA-DRB1, ...	...all 6
Proliferation of tumor cells	1.14E-07	IL2, SMAD7, SMAD3, ...	...all 5
Proliferation of beta islet cell:	3.57E-07	IL2, SMAD7, SMAD3	...all 3
Proliferation of B lymphocyte:	4.62E-07	IL2, SMAD7, SMAD3, ...	...all 4
Proliferation of cancer cells	3.63E-06	IL2, SMAD7, SMAD3, ...	...all 4
Proliferation of hepatocytes	7.03E-06	SMAD7, SMAD3, SMA...	...all 3
Proliferation of Th1 cells	1.94E-05	IL2, HLA-DRB1	...all 2
Proliferation of T lymphocyte:	2.47E-05	IL2, HLA-DRB1, SMAD4	...all 3
Proliferation of hematopoieti	2.98E-05	IL2, PRDM1, SMAD4	...all 3
Proliferation of eye cell lines	4.19E-05	SMAD3, SMAD4	...all 2
Proliferation of splenocytes	1.25E-04	IL2, SMAD3	...all 2
Proliferation of lymphokine a	1.47E-04	IL2	...all 1
Proliferation of hepatic stella	1.57E-02	SMAD3	...all 1

0/14

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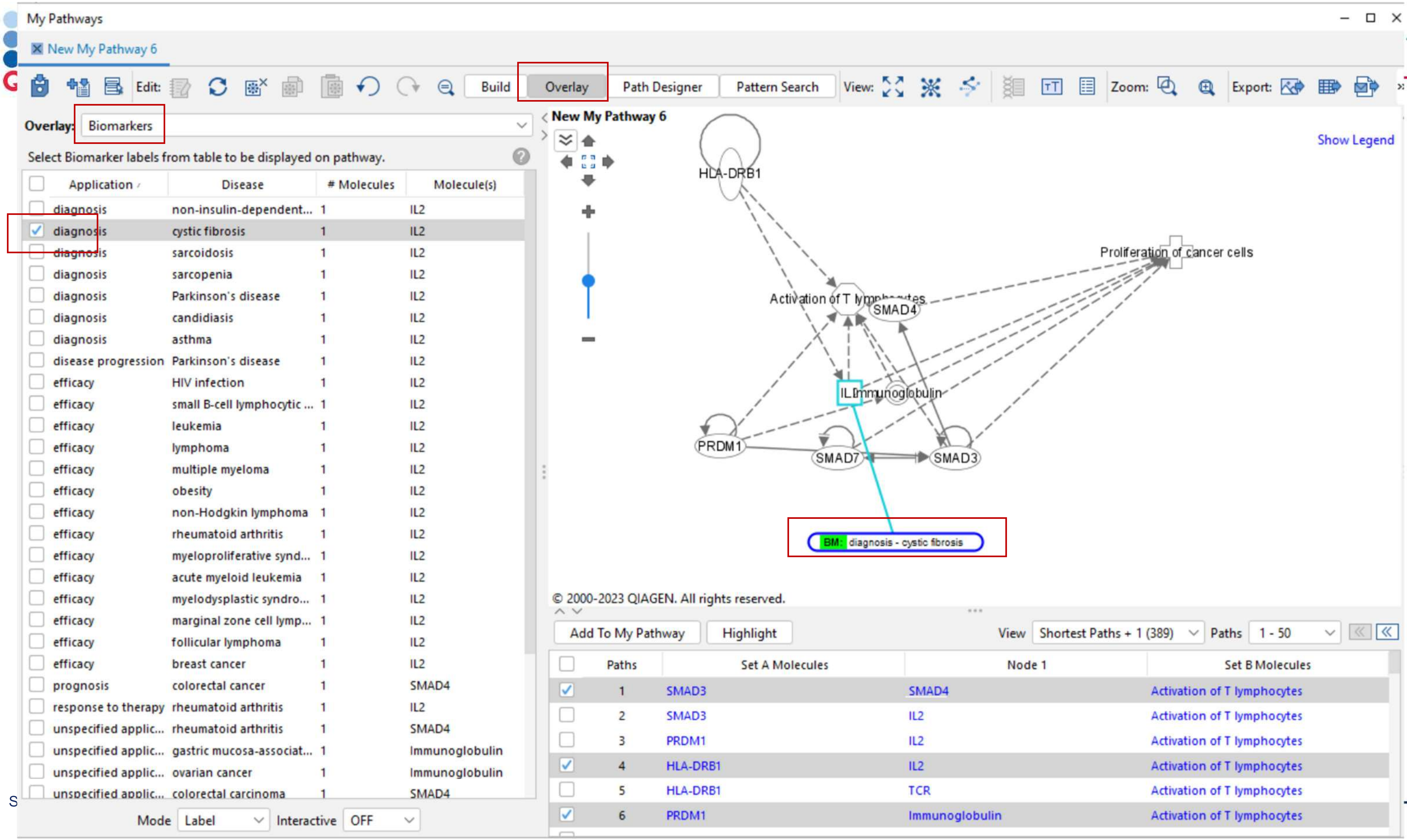
View Shortest Paths + 1 (389) Paths 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes



Overlay: Biomarkers

Select Biomarker labels from table to be displayed on pathway.

☐	Application	Disease	# Molecules	Molecule(s)
☐	diagnosis	non-insulin-dependent...	1	IL2
☑	diagnosis	cystic fibrosis	1	IL2
☐	diagnosis	sarcoidosis	1	IL2
☐	diagnosis	sarcopenia	1	IL2
☐	diagnosis	Parkinson's disease	1	IL2
☐	diagnosis	candidiasis	1	IL2
☐	diagnosis	asthma	1	IL2
☐	disease progression	Parkinson's disease	1	IL2
☐	efficacy	HIV infection	1	IL2
☐	efficacy	small B-cell lymphocytic ...	1	IL2
☐	efficacy	leukemia	1	IL2
☐	efficacy	lymphoma	1	IL2
☐	efficacy	multiple myeloma	1	IL2
☐	efficacy	obesity	1	IL2
☐	efficacy	non-Hodgkin lymphoma	1	IL2
☐	efficacy	rheumatoid arthritis	1	IL2
☐	efficacy	myeloproliferative synd...	1	IL2
☐	efficacy	acute myeloid leukemia	1	IL2
☐	efficacy	myelodysplastic syndro...	1	IL2
☐	efficacy	marginal zone cell lymp...	1	IL2
☐	efficacy	follicular lymphoma	1	IL2
☐	efficacy	breast cancer	1	IL2
☐	prognosis	colorectal cancer	1	SMAD4
☐	response to therapy	rheumatoid arthritis	1	IL2
☐	unspecified applic...	rheumatoid arthritis	1	SMAD4
☐	unspecified applic...	gastric mucosa-associat...	1	Immunoglobulin
☐	unspecified applic...	ovarian cancer	1	Immunoglobulin
☐	unspecified applic...	colorectal carcinoma	1	SMAD4

Mode: Label
Interactive: OFF

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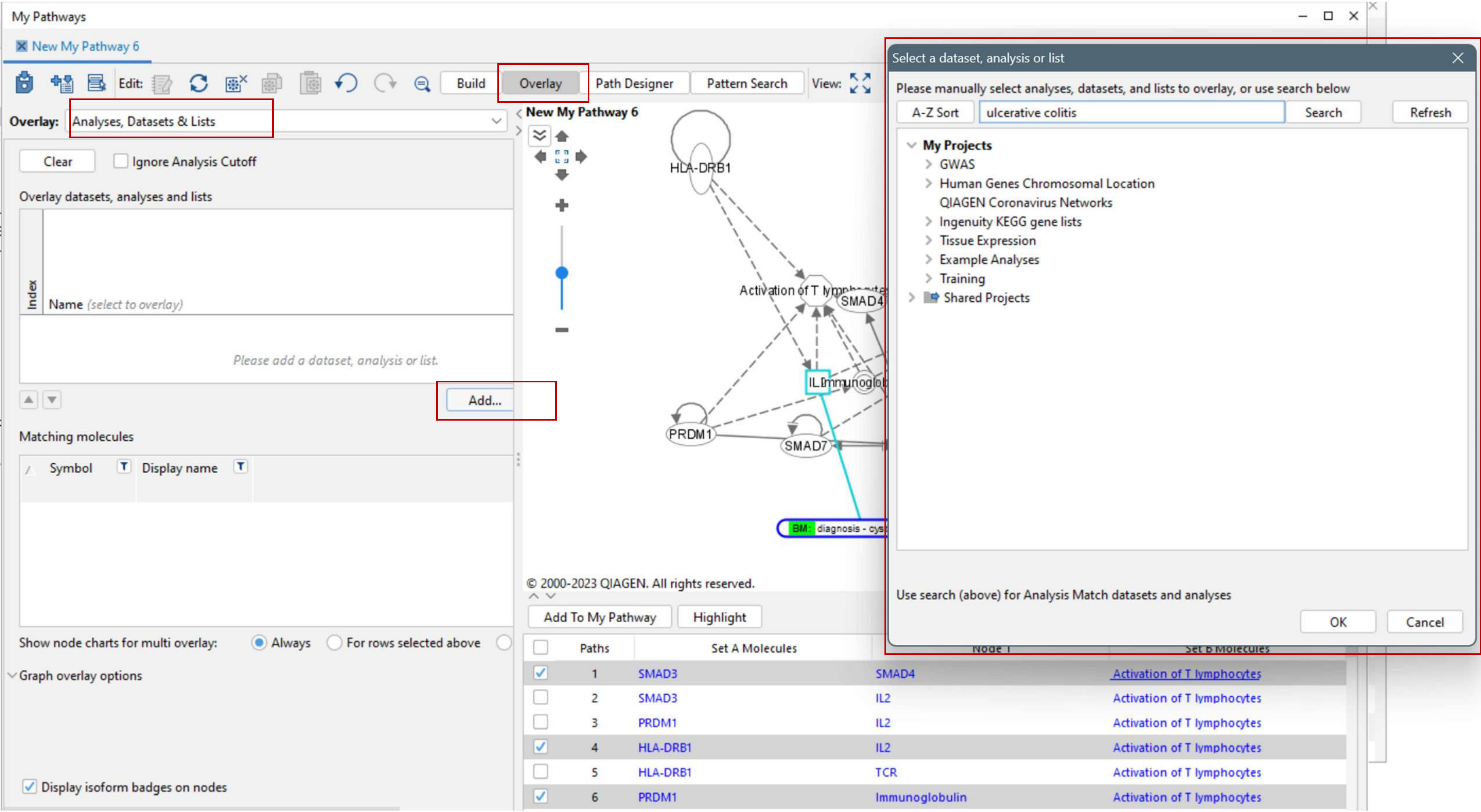
View: Shortest Paths + 1 (389)
Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes



Overlay: Analyses, Datasets & Lists

☐ Ignore Analysis Cutoff

Please add a dataset, analysis or list.

Show node charts for multi overlay: ● Always ○ For rows selected above

☑ Display isoform badges on nodes

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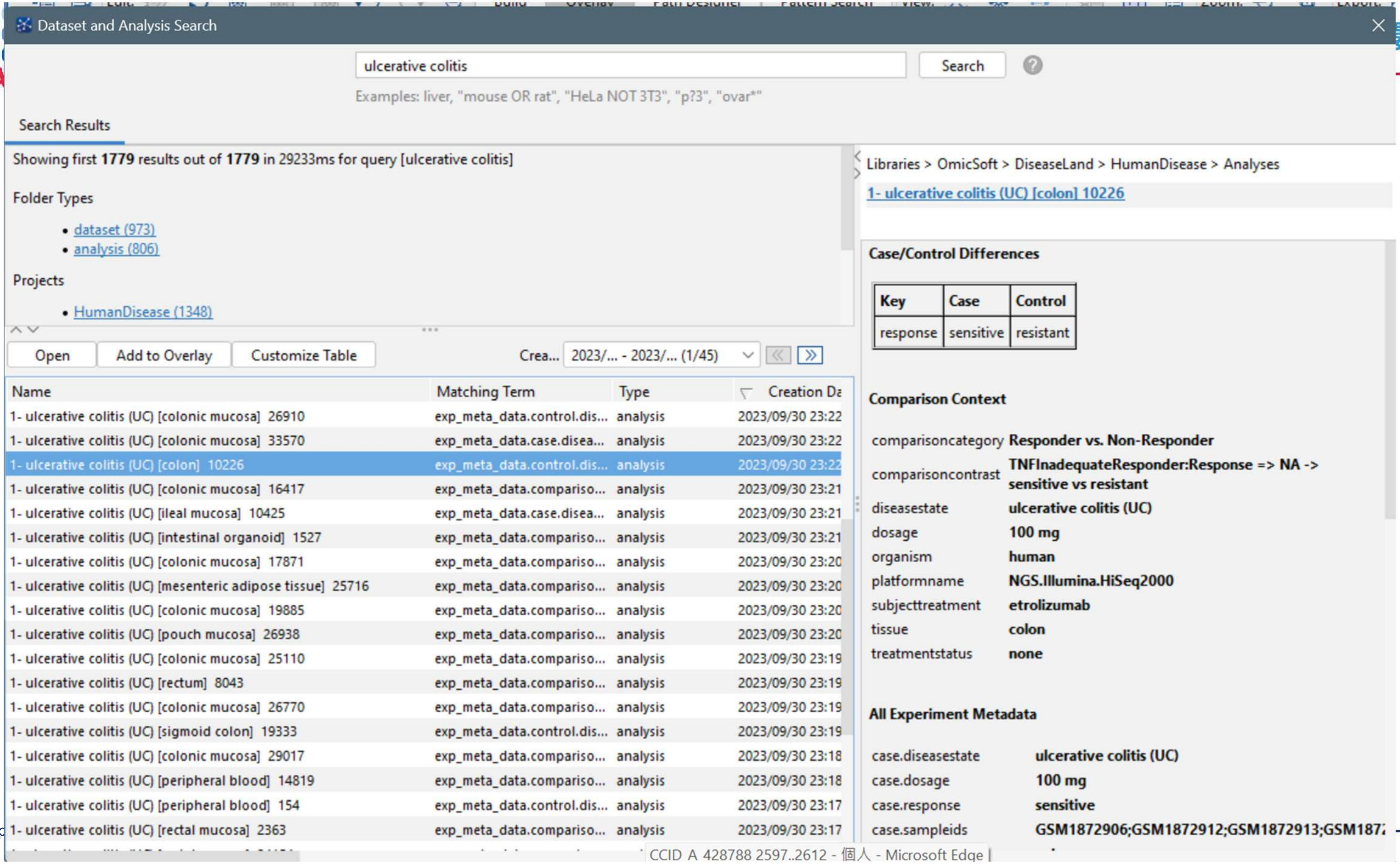
Please manually select analyses, datasets, and lists to overlay, or use search below

ulcerative colitis

Use search (above) for Analysis Match datasets and analyses

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

數位



ulcerative colitis

Examples: liver, "mouse OR rat", "HeLa NOT 3T3", "p?3", "ovar*"

Search Results

Showing first **1779** results out of **1779** in 29233ms for query [ulcerative colitis]

Folder Types

- dataset (973)
- analysis (806)

Projects

- HumanDisease (1348)

Crea... 2023/... - 2023/... (1/45)

Name	Matching Term	Type	Creation Da
1- ulcerative colitis (UC) [colonic mucosa] 26910	exp_meta_data.control.dis...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colonic mucosa] 33570	exp_meta_data.case.disea...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colon] 10226	exp_meta_data.control.dis...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colonic mucosa] 16417	exp_meta_data.compariso...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [ileal mucosa] 10425	exp_meta_data.case.disea...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [intestinal organoid] 1527	exp_meta_data.compariso...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [colonic mucosa] 17871	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [mesenteric adipose tissue] 25716	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [colonic mucosa] 19885	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [pouch mucosa] 26938	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [colonic mucosa] 25110	exp_meta_data.compariso...	analysis	2023/09/30 23:19
1- ulcerative colitis (UC) [rectum] 8043	exp_meta_data.compariso...	analysis	2023/09/30 23:19
1- ulcerative colitis (UC) [colonic mucosa] 26770	exp_meta_data.compariso...	analysis	2023/09/30 23:19
1- ulcerative colitis (UC) [sigmoid colon] 19333	exp_meta_data.control.dis...	analysis	2023/09/30 23:19
1- ulcerative colitis (UC) [colonic mucosa] 29017	exp_meta_data.compariso...	analysis	2023/09/30 23:18
1- ulcerative colitis (UC) [peripheral blood] 14819	exp_meta_data.compariso...	analysis	2023/09/30 23:18
1- ulcerative colitis (UC) [peripheral blood] 154	exp_meta_data.control.dis...	analysis	2023/09/30 23:17
1- ulcerative colitis (UC) [rectal mucosa] 2363	exp_meta_data.compariso...	analysis	2023/09/30 23:17

Libraries > OmicSoft > DiseaseLand > HumanDisease > Analyses

1- ulcerative colitis (UC) [colon] 10226

Case/Control Differences

Key	Case	Control
response	sensitive	resistant

Comparison Context

comparisoncategory	**Responder vs. Non-Responder**
comparisoncontrast	**TNFInadequateResponder:Response => NA -> sensitive vs resistant**
diseasestate	**ulcerative colitis (UC)**
dosage	**100 mg**
organism	**human**
platformname	**NGS.Illumina.HiSeq2000**
subjecttreatment	**etrolizumab**
tissue	**colon**
treatmentstatus	**none**

All Experiment Metadata

case.diseasestate	**ulcerative colitis (UC)**
case.dosage	**100 mg**
case.response	**sensitive**
case.sampleids	**GSM1872906;GSM1872912;GSM1872913;GSM187**

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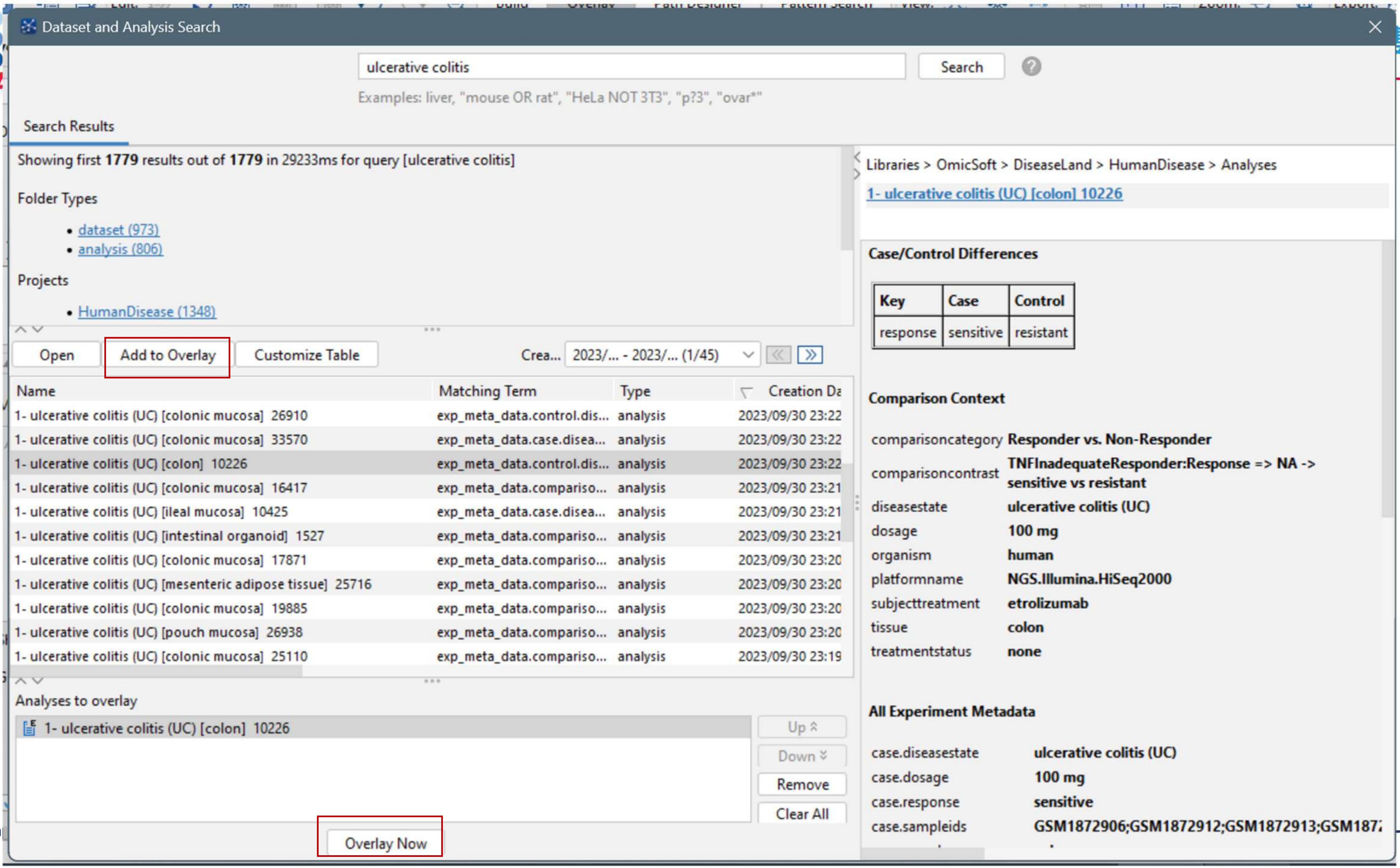
Samp

數位



ulcerative colitis

Showing first **1779** results out of **1779** in 29233ms for query [ulcerative colitis]

Folder Types

- dataset (973)
- analysis (806)

Projects

- HumanDisease (1348)

Name	Matching Term	Type	Creation Da
1- ulcerative colitis (UC) [colonic mucosa] 26910	exp_meta_data.control.dis...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colonic mucosa] 33570	exp_meta_data.case.disea...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colon] 10226	exp_meta_data.control.dis...	analysis	2023/09/30 23:22
1- ulcerative colitis (UC) [colonic mucosa] 16417	exp_meta_data.compariso...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [ileal mucosa] 10425	exp_meta_data.case.disea...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [intestinal organoid] 1527	exp_meta_data.compariso...	analysis	2023/09/30 23:21
1- ulcerative colitis (UC) [colonic mucosa] 17871	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [mesenteric adipose tissue] 25716	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [colonic mucosa] 19885	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [pouch mucosa] 26938	exp_meta_data.compariso...	analysis	2023/09/30 23:20
1- ulcerative colitis (UC) [colonic mucosa] 25110	exp_meta_data.compariso...	analysis	2023/09/30 23:19

Analyses to overlay

1- ulcerative colitis (UC) [colon] 10226

Libraries > OmicSoft > DiseaseLand > HumanDisease > Analyses

1- ulcerative colitis (UC) [colon] 10226

Case/Control Differences

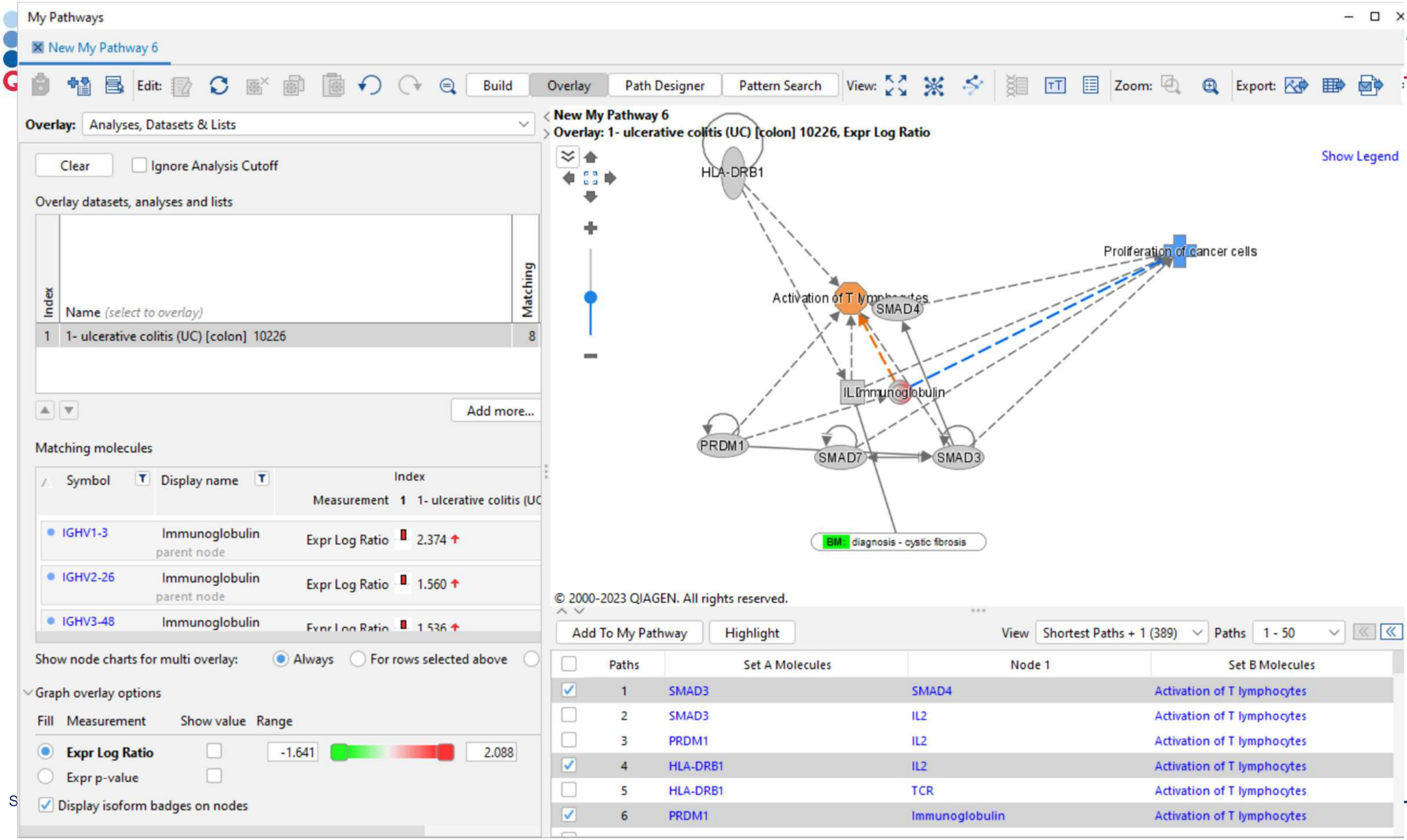
Key	Case	Control
response	sensitive	resistant

Comparison Context

comparisoncategory	**Responder vs. Non-Responder**
comparisoncontrast	**TNFInadequateResponder:Response => NA -> sensitive vs resistant**
diseasestate	**ulcerative colitis (UC)**
dosage	**100 mg**
organism	**human**
platformname	**NGS.Illumina.HiSeq2000**
subjecttreatment	**etrolizumab**
tissue	**colon**
treatmentstatus	**none**

All Experiment Metadata

case.diseasestate	**ulcerative colitis (UC)**
case.dosage	**100 mg**
case.response	**sensitive**
case.sampleids	**GSM1872906;GSM1872912;GSM1872913;GSM187**



Overlay: Analyses, Datasets & Lists

☐ Ignore Analysis Cutoff

Overlay datasets, analyses and lists

Index	Name *(select to overlay)*	Matching
1	1- ulcerative colitis (UC) [colon] 10226	8

Matching molecules

Symbol	Display name	Measurement	1 1- ulcerative colitis (UC
IGHV1-3	Immunoglobulin parent node	Expr Log Ratio	2.374 ↑
IGHV2-26	Immunoglobulin parent node	Expr Log Ratio	1.560 ↑
IGHV3-48	Immunoglobulin	Expr Log Ratio	1.536 ↑

Show node charts for multi overlay: ● Always ○ For rows selected above ○

Graph overlay options

Fill	Measurement	Show value	Range
●	Expr Log Ratio	☐	-1.641 – 2.088
○	Expr p-value	☐	

☑ Display isoform badges on nodes

New My Pathway 6

Overlay: 1- ulcerative colitis (UC) [colon] 10226, Expr Log Ratio

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View: Shortest Paths + 1 (389) Paths: 1 - 50

☐	Paths	Set A Molecules	Node 1	Set B Molecules
☑	1	SMAD3	SMAD4	Activation of T lymphocytes
☐	2	SMAD3	IL2	Activation of T lymphocytes
☐	3	PRDM1	IL2	Activation of T lymphocytes
☑	4	HLA-DRB1	IL2	Activation of T lymphocytes
☐	5	HLA-DRB1	TCR	Activation of T lymphocytes
☑	6	PRDM1	Immunoglobulin	Activation of T lymphocytes

Clinical, Cosmetic and Investigational Dermatology Dovepress

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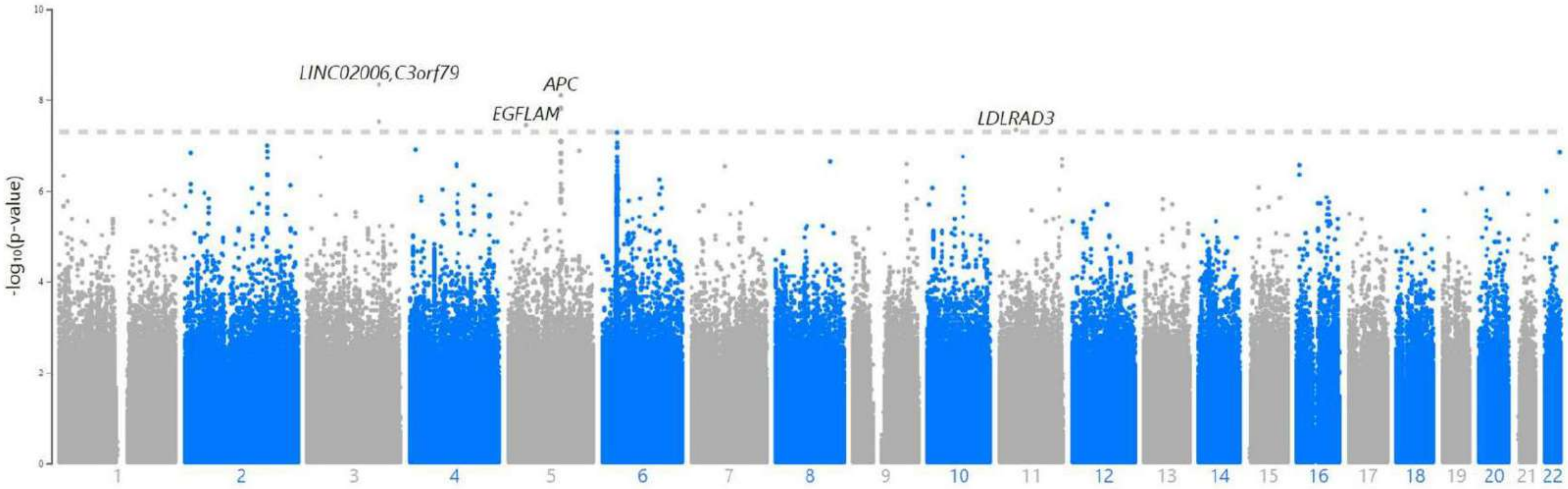
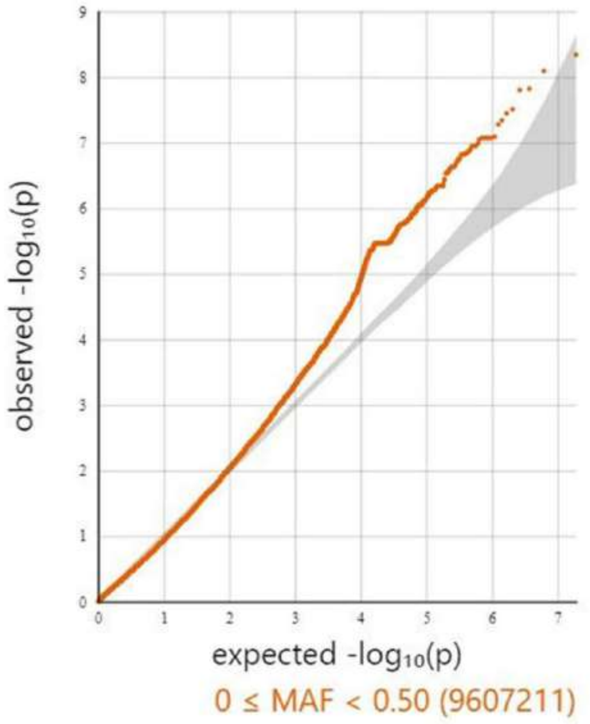


[1]Department of Medical Research, China Medical University Hospital, China Medical University, Taichung, 404327, Taiwan; [2]Million-Person Precision Medicine Initiative, Department of Medical Research, China Medical University Hospital, Taichung, 404327, Taiwan; [3]Department of Biological Science and Technology, China Medical University, Taichung, 406040, Taiwan; [4]Division of Plastic and Reconstructive Surgery, Department of Surgery, Taipei



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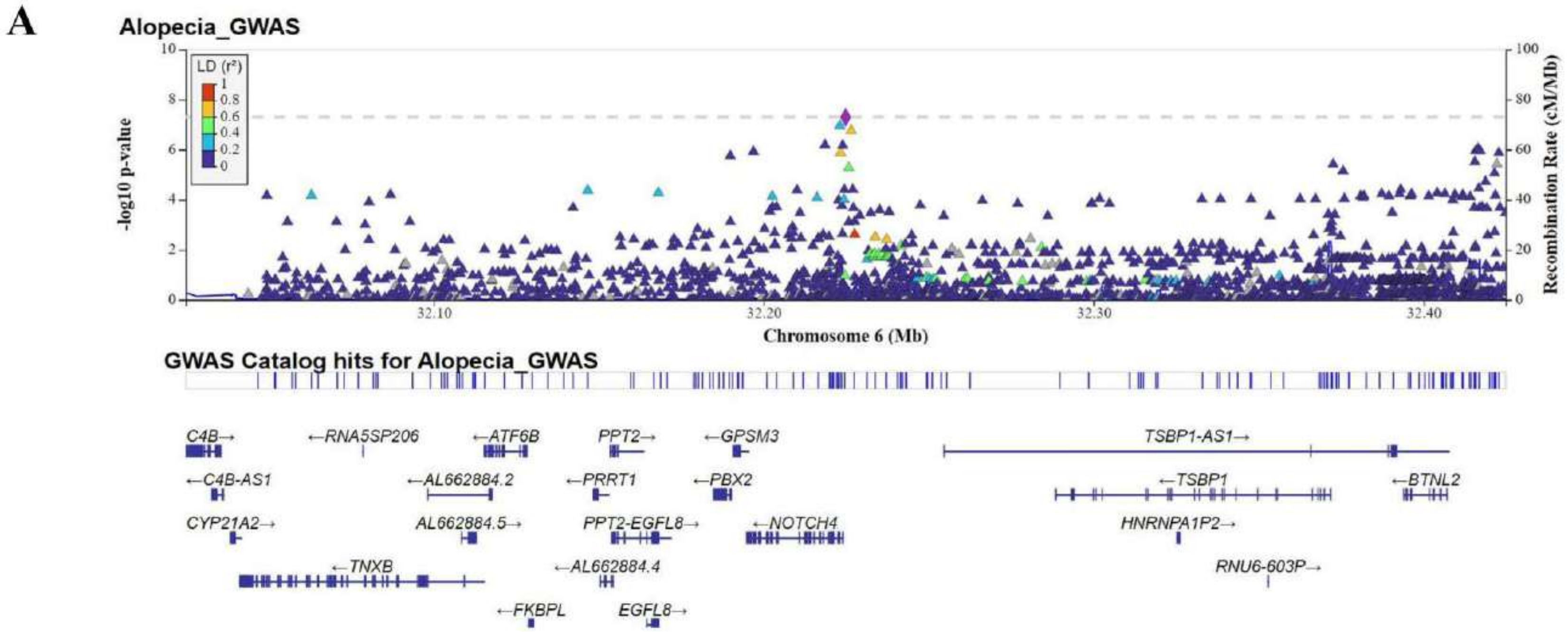

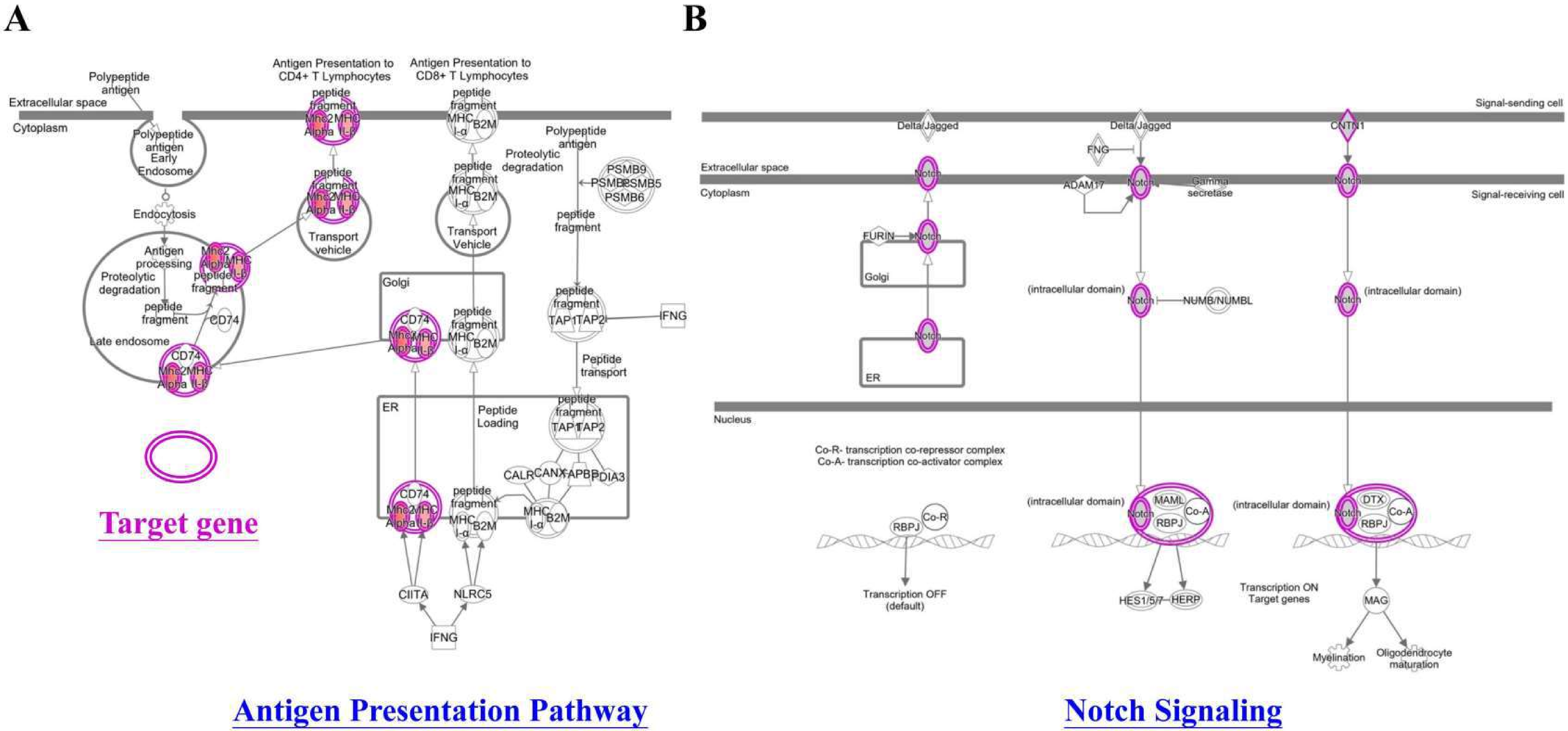

Figure 5 Network analyses of the antigen presentation pathway target gene (**A**) and the gene that Notch signaling targets (**B**). IPA software analyzed network analysis (SNPs gene loci, P<1E-05).

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:

周儀柔 資深業務專員	GraceChou@gga.asia	02-2795 1777 #3019
林文賢 經理	BryceLin@gga.asia	02-2795 1777 #3665
	Bioinfo@GGA.ASIA	