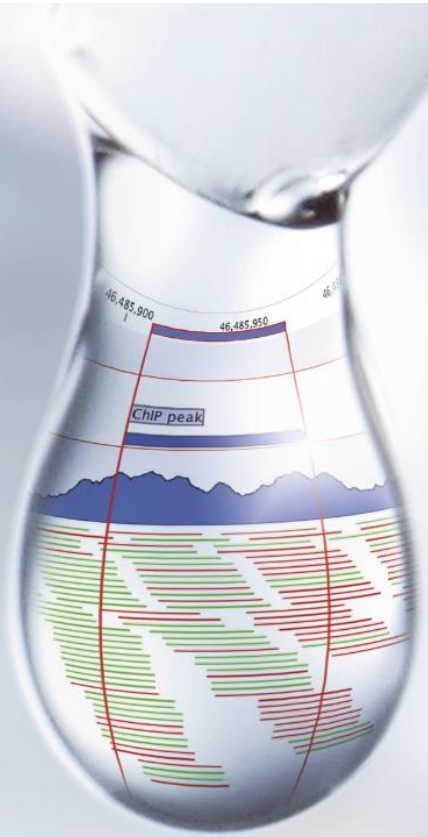
Analyzing genetic risk locations from GWAS in relation to vital genes and pathways using QIAGEN Ingenuity Pathway Analysis



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

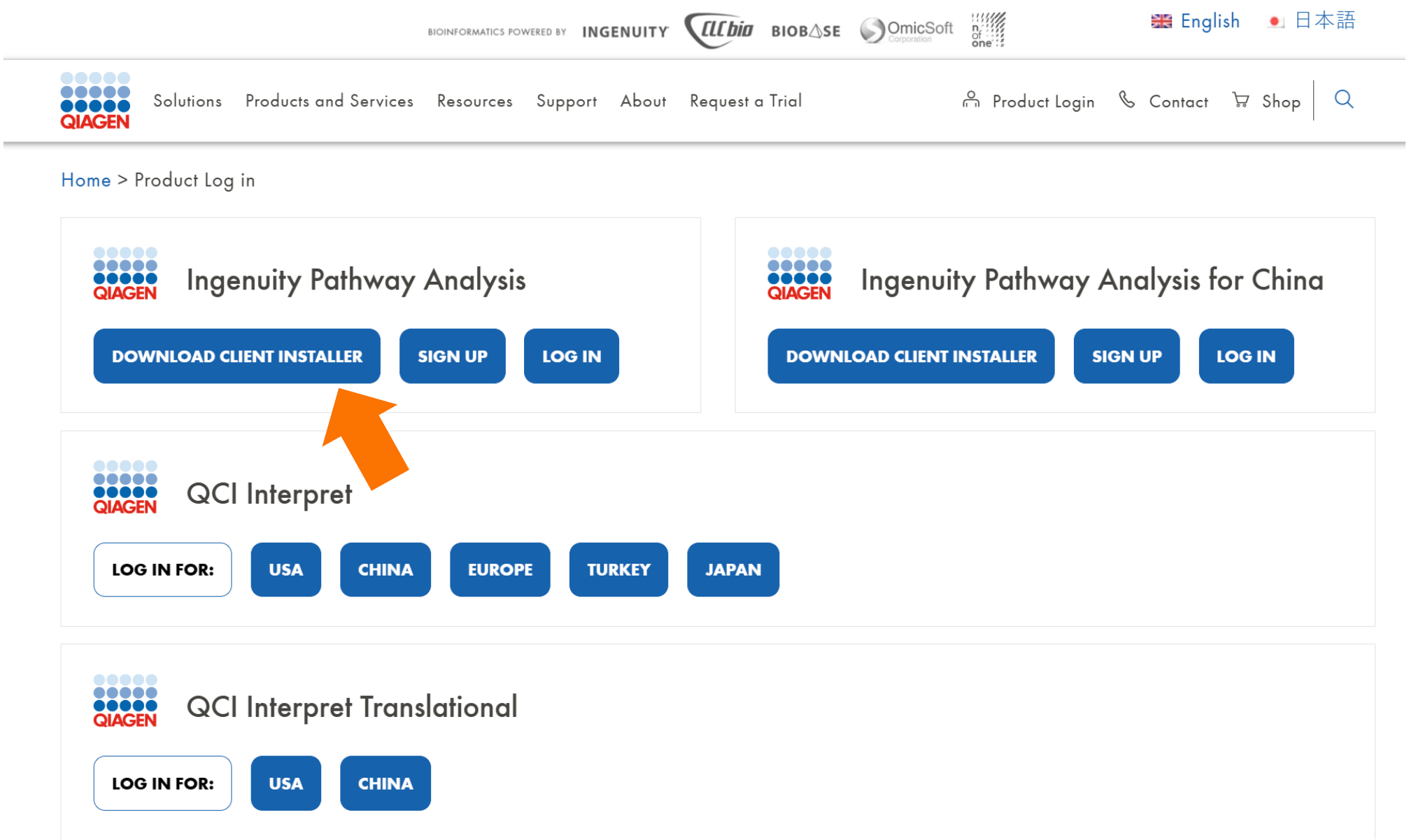
IPA Training Account & Demo Data

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

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

Client: (IPA Login)

IPA Download webpage



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

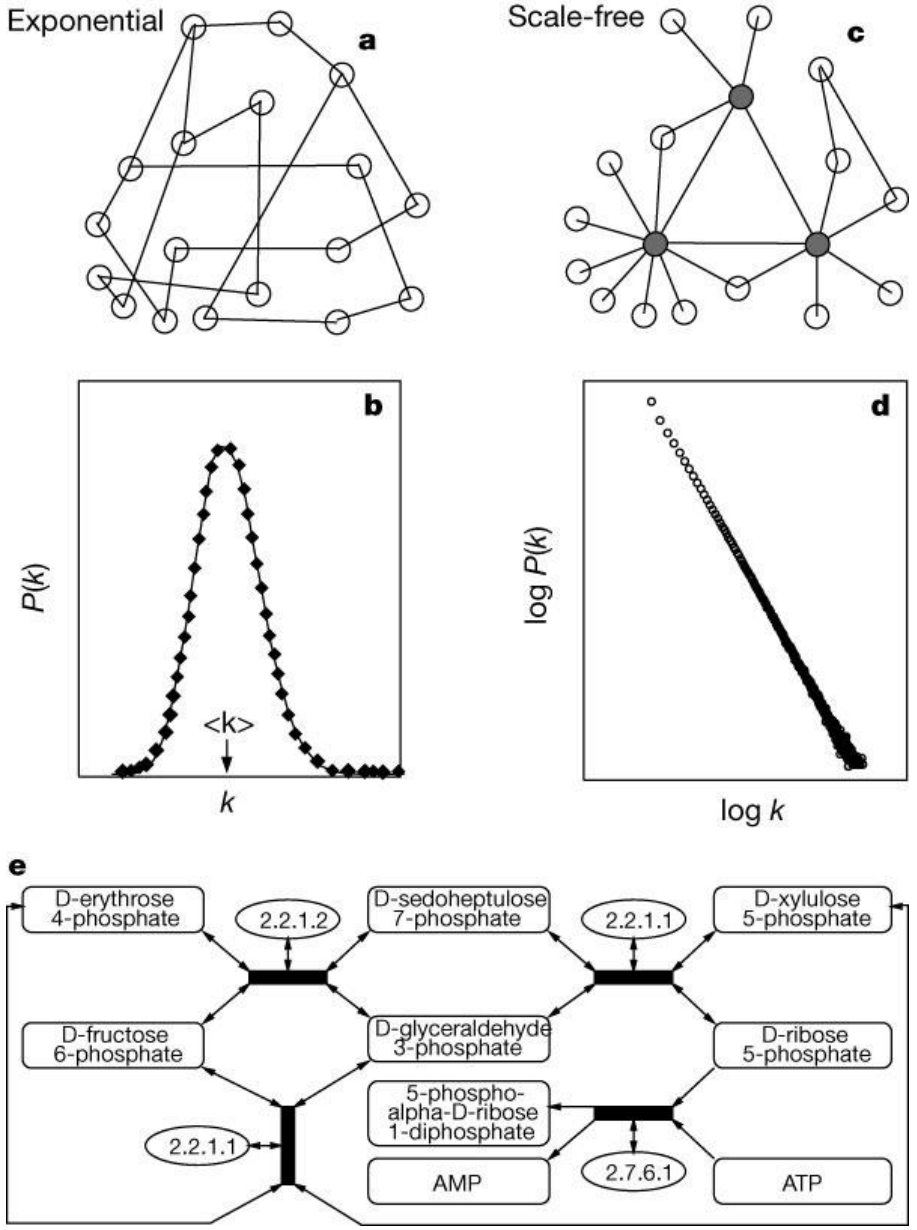
For more information see this help page.

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.

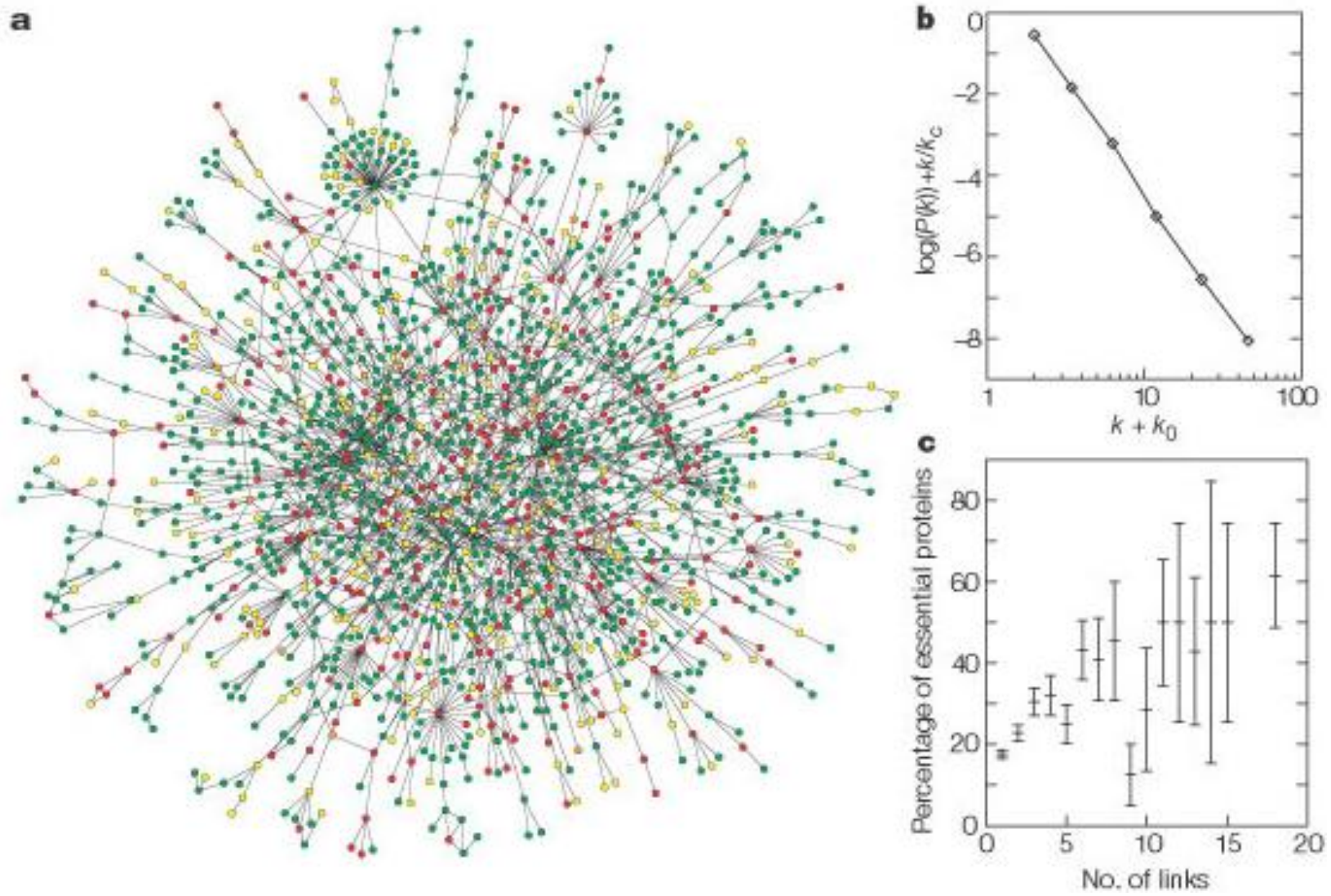


Nature 407, 651-654 (2000)

Lethality and centrality in protein networks

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

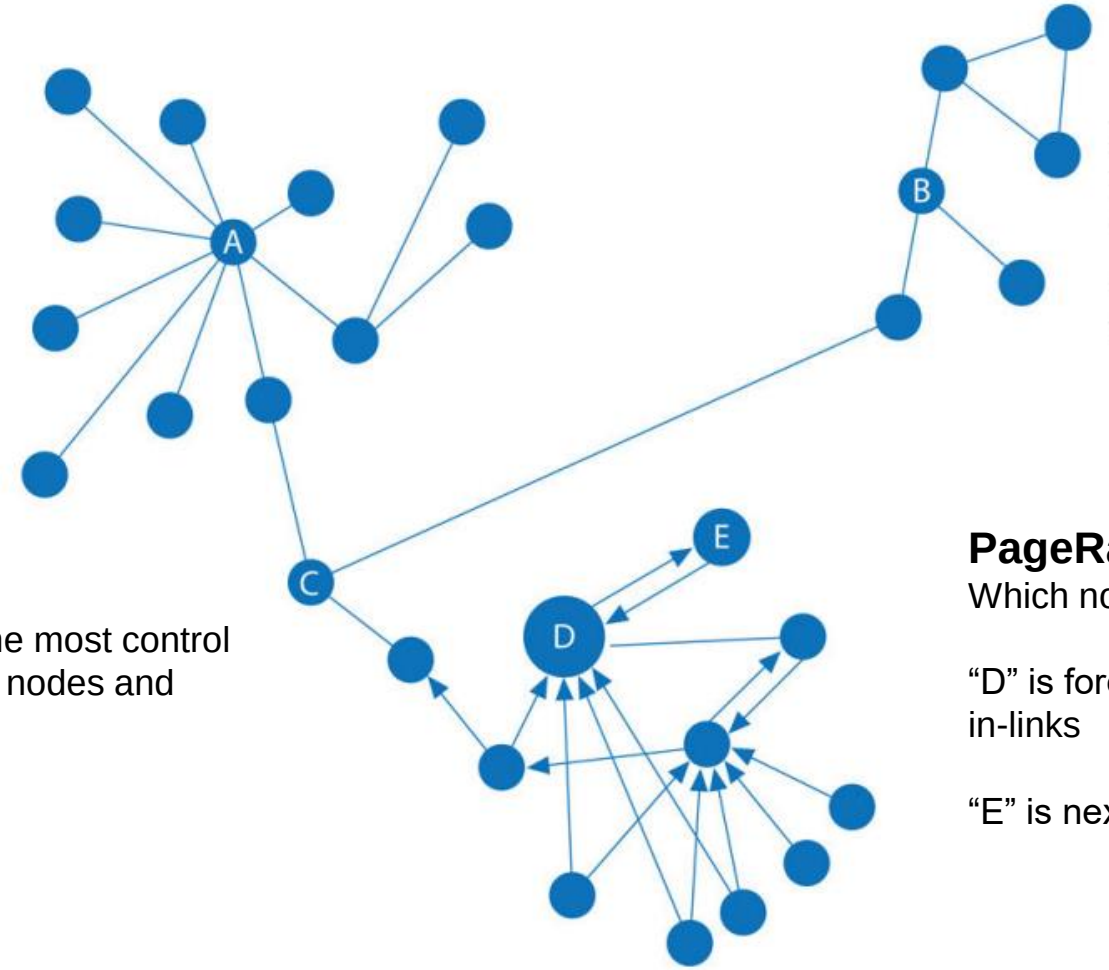
Nature 411, 41-42 (2001)



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?

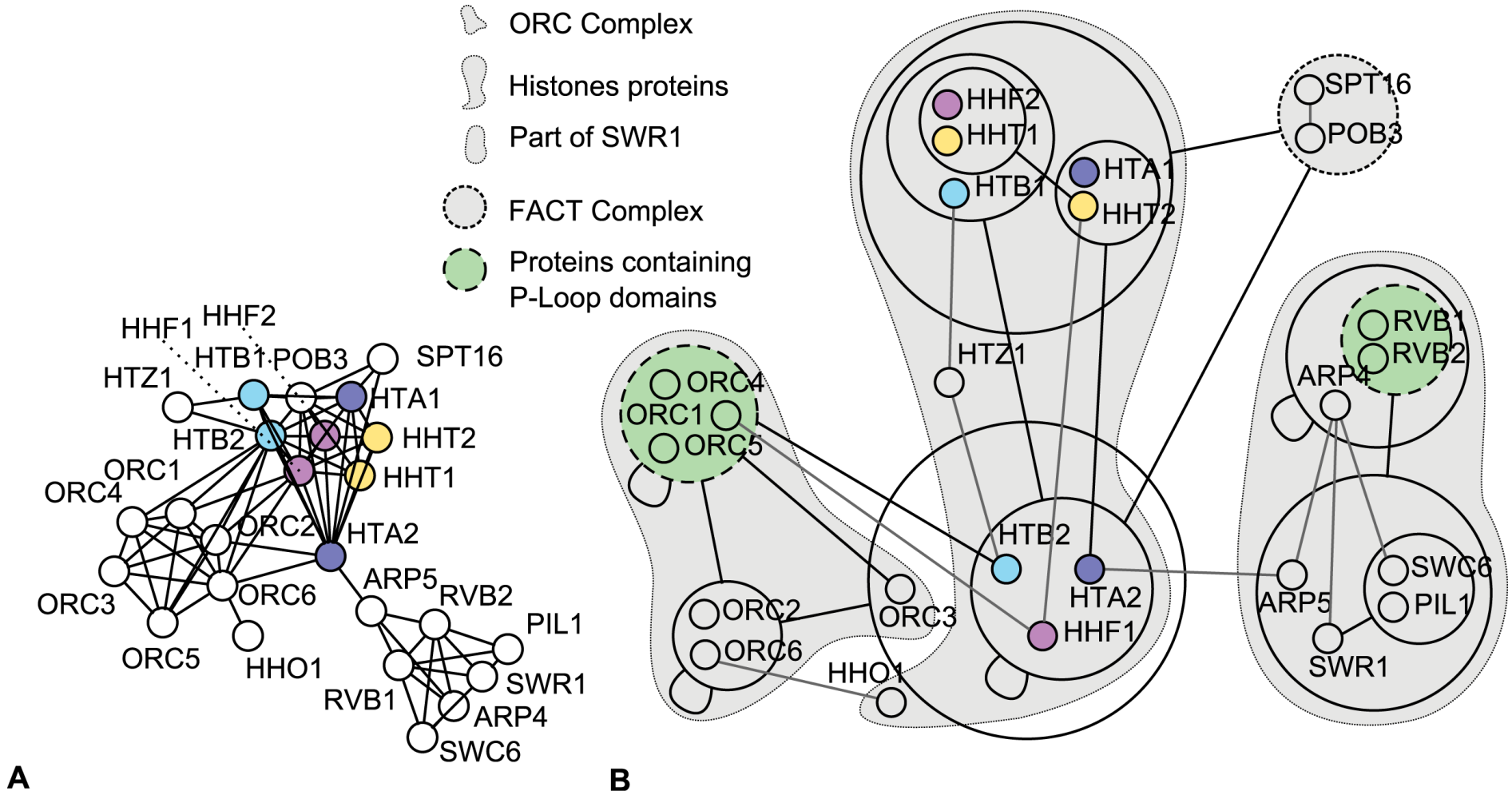
“C” is a bridge

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

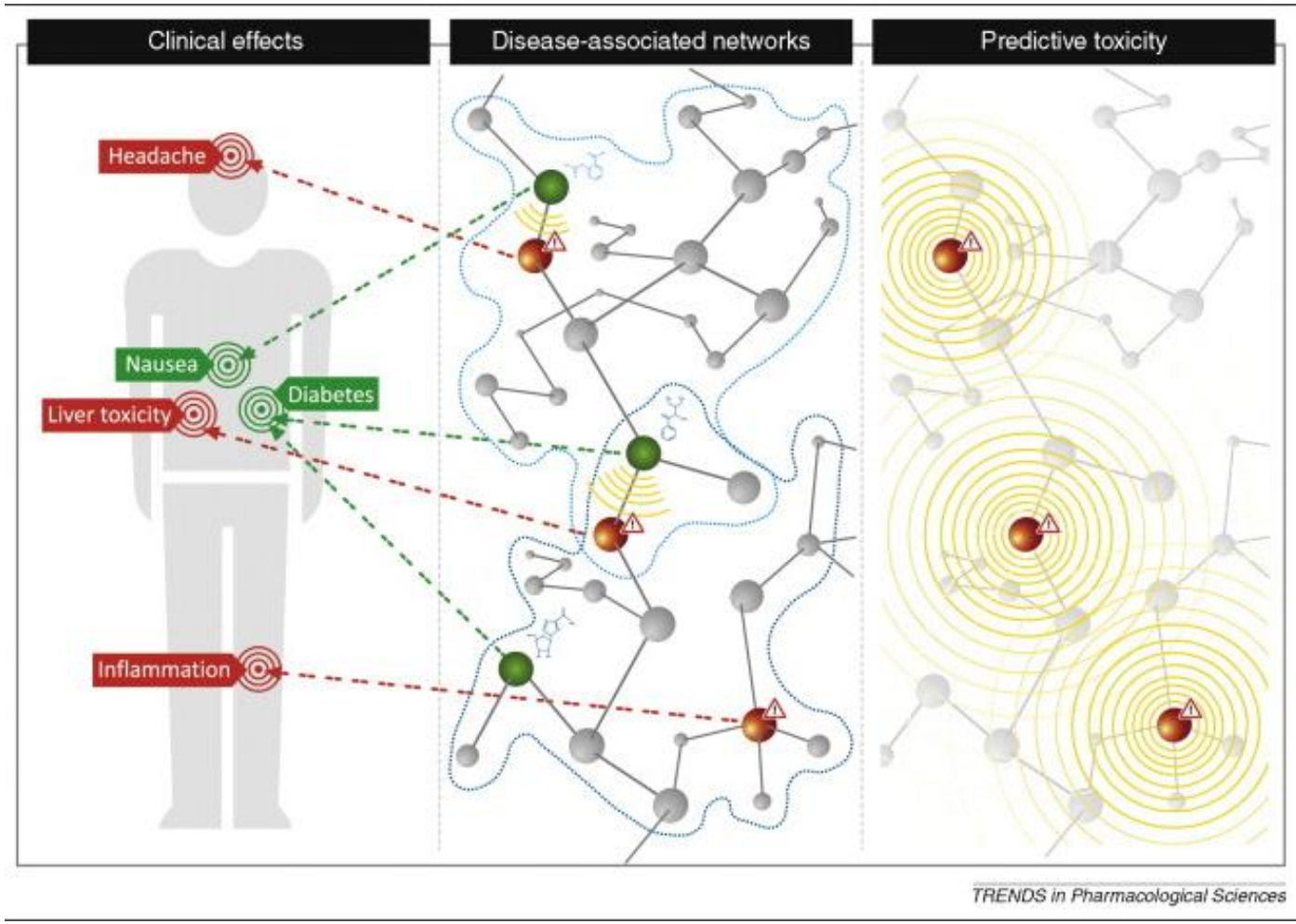
(Source: Needham & Hodler, 2019)

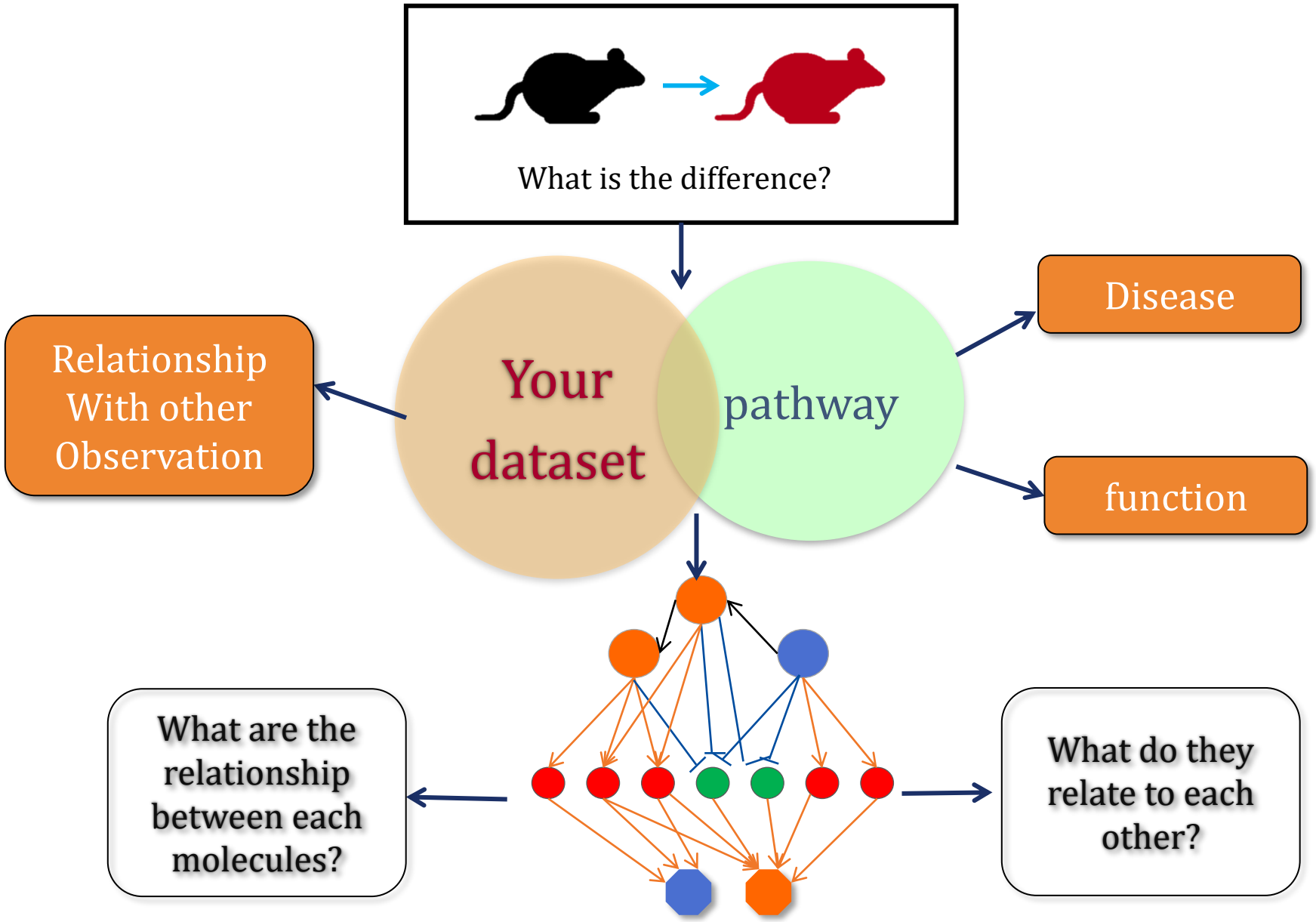


•https://doi.org/10.1371/journal.pcbi.1000108

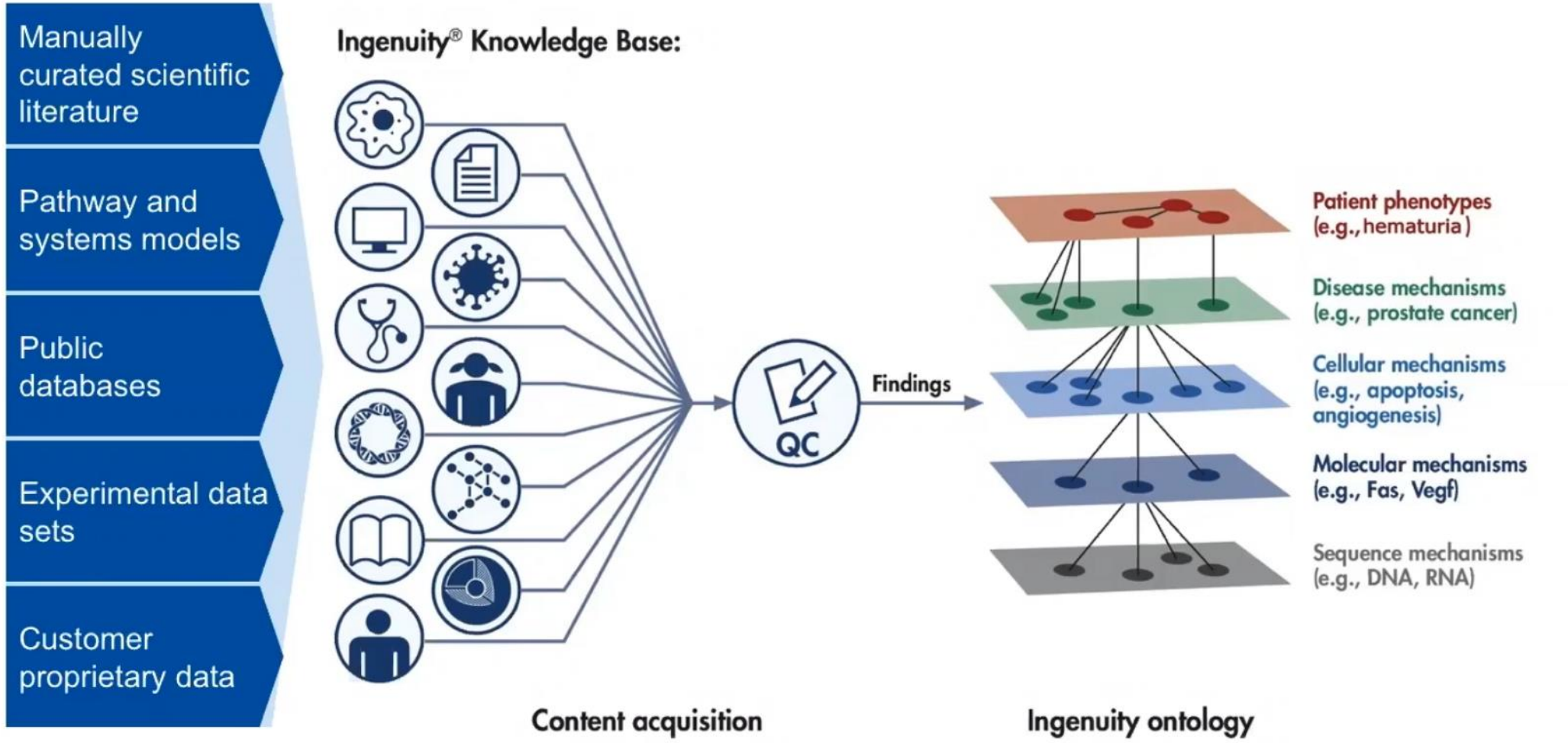
Models can identify the areas of influence of proteins leading to undesired effects, and to explore how they are related to network connectivity.

- 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).




What is the difference?
Your dataset
pathway
Disease
function
Relationship With other Observation
What are the relationship between each molecules?
What do they relate to each other?

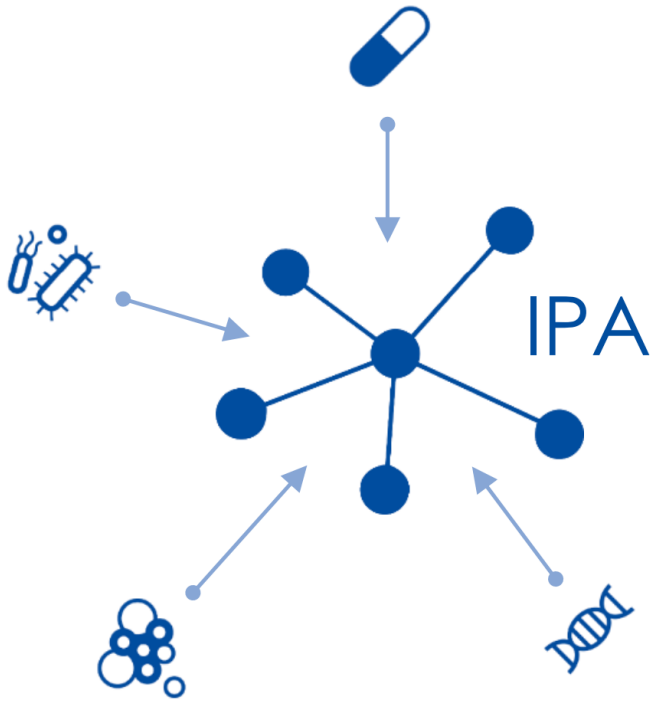
The Ingenuity Platform: a 20-year massive investment



Updated weekly with the latest clinical trials and manuscripts

12+ million findings curated using controlled vocabulary

Decades of accumulated knowledge mapped in directional networks

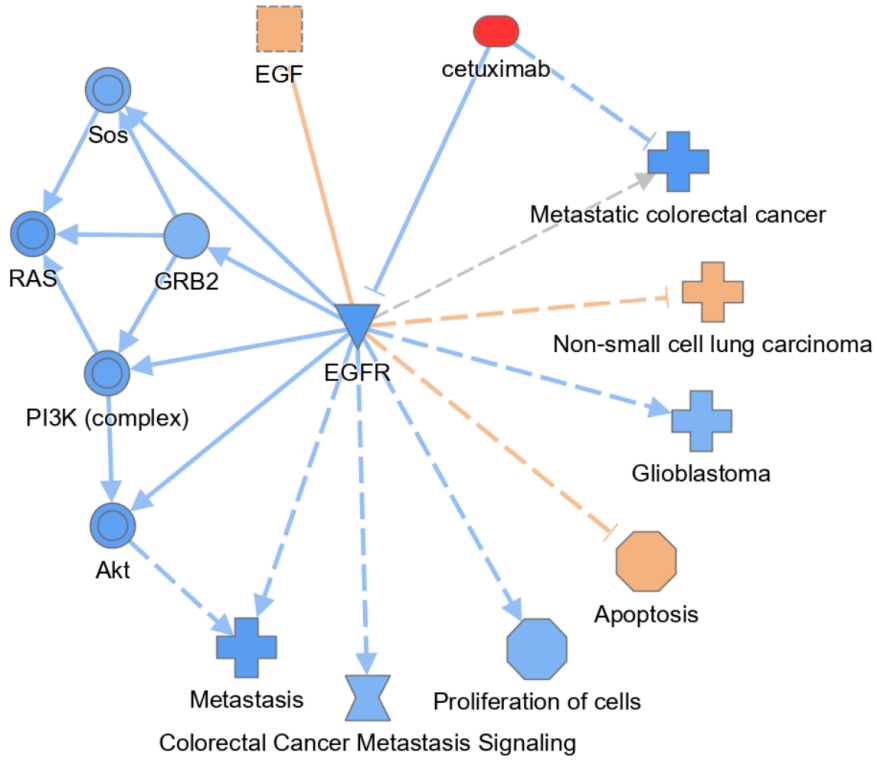


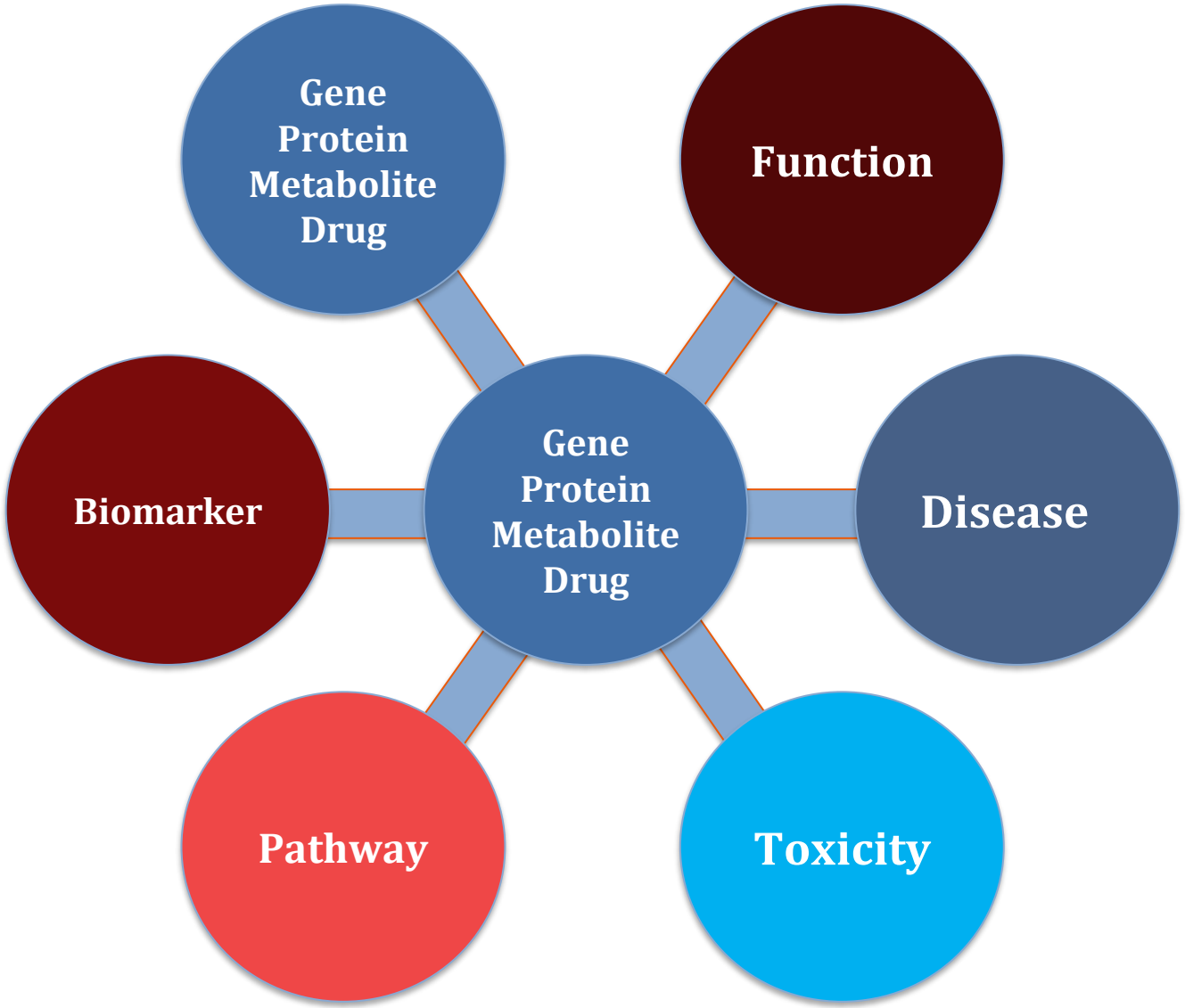
EGF – EGFR
[one of many]

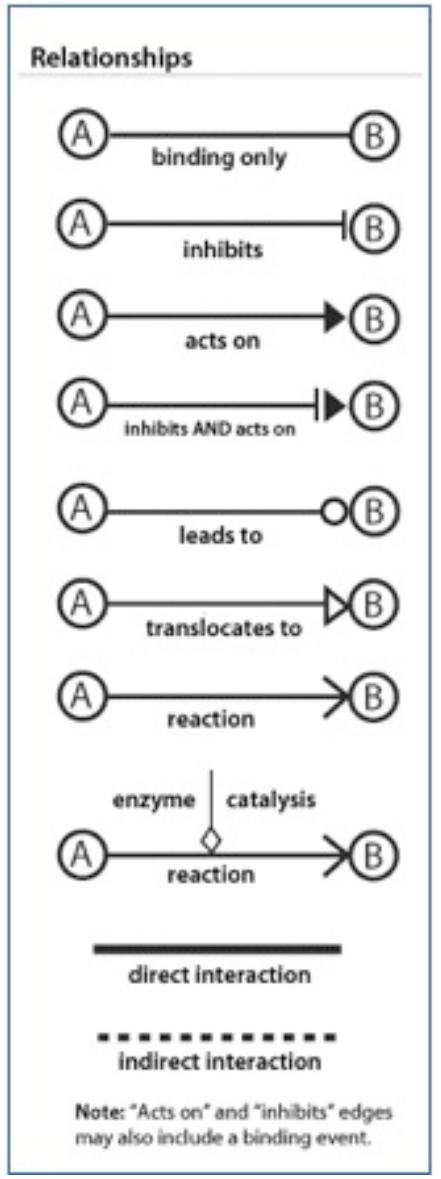
Type:	**activation**
Direction:	**directional**
Effect:	**increases**
Directness:	**direct**
Tissue:	**epithelial cells**
Location:	**plasma membrane**
Source:	**PMID: 17909010**

cetuximab – EGFR
[one of many]

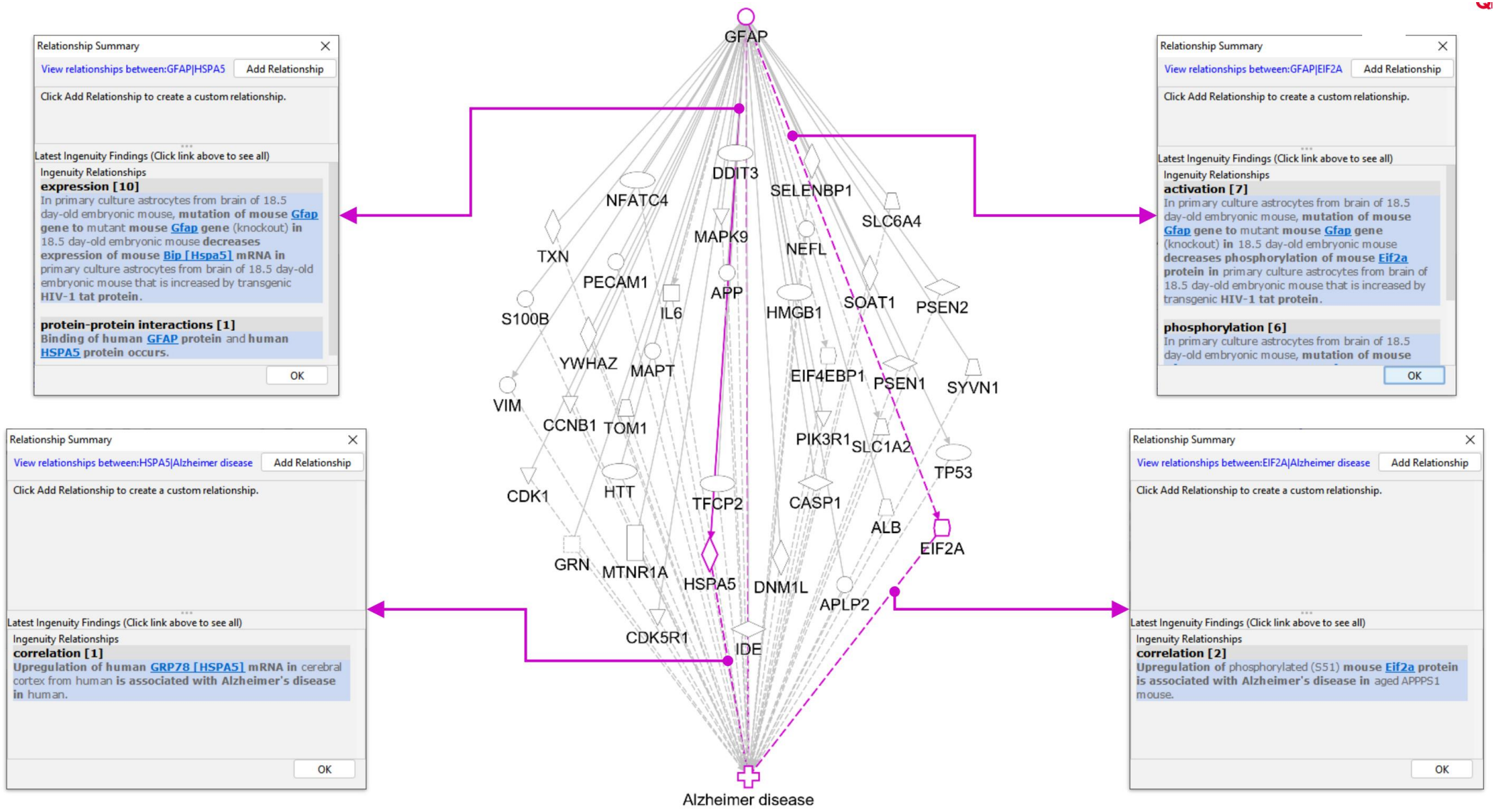
Type:	**phosphorylation**
Direction:	**directional**
Effect:	**decreases**
Cell line:	**CaR1 cells**
Organism:	**human**
Experiment:	**immunoblot**
Source:	**PMID: 23213241**




Gene
Protein
Metabolite
Drug
Function
Biomarker
Gene
Protein
Metabolite
Drug
Disease
Pathway
Toxicity

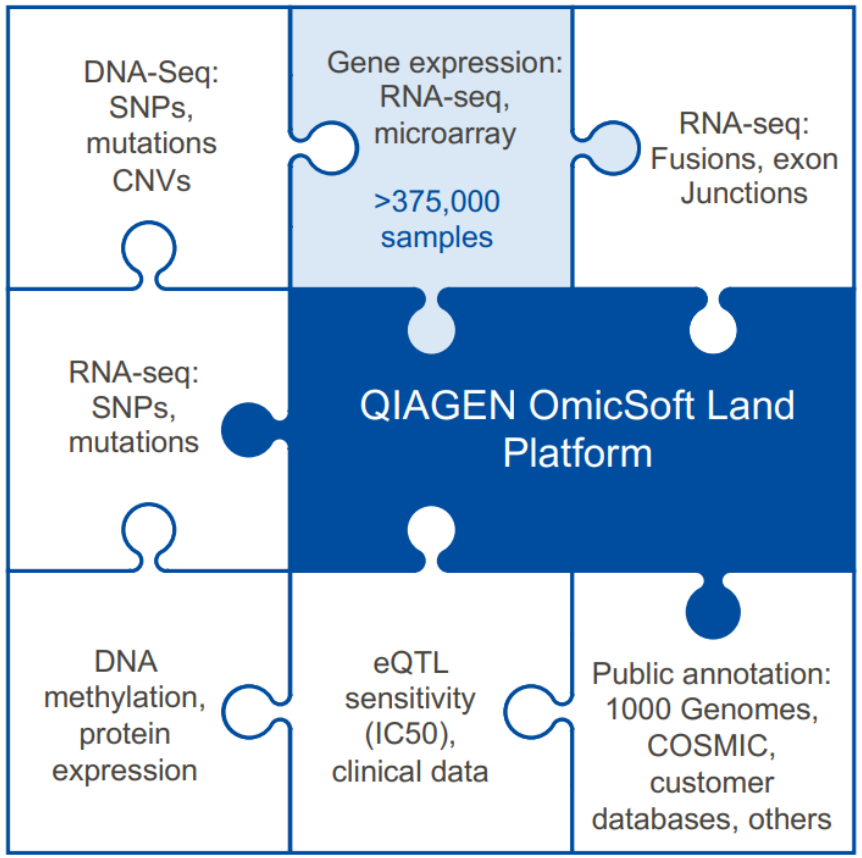

Relationships
binding only
inhibits
acts on
inhibits AND acts on
leads to
translocates to
reaction
enzyme
catalysis
reaction
direct interaction
indirect interaction
Note: "Acts on" and "inhibits" edges may also include a binding event.

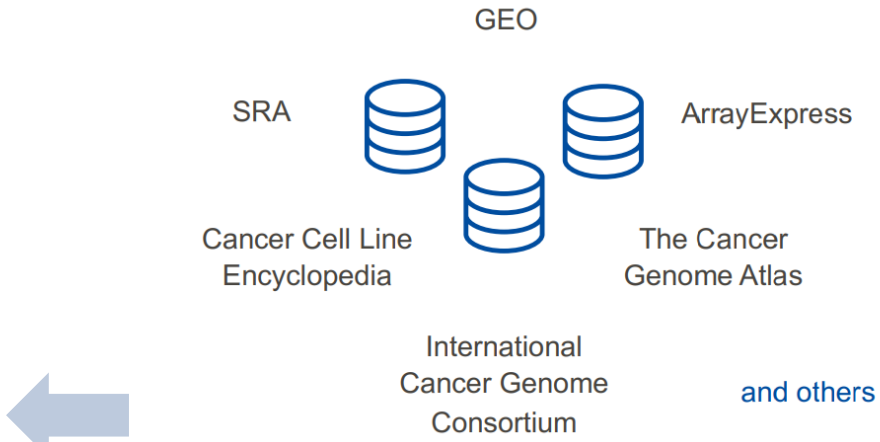
Every connection in IPA is backed by literature findings



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

Lands provide expression data to QIAGEN IPA





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

Species support within IPA

Fully supported:


Human


Mouse

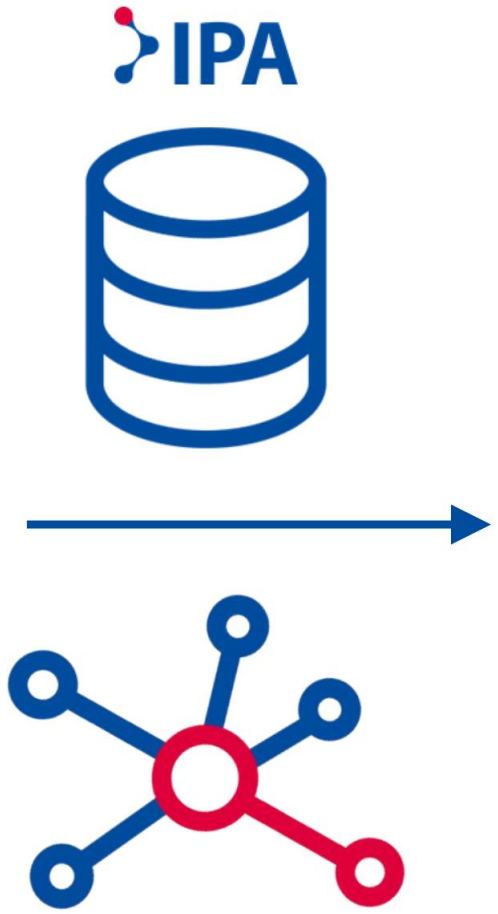

Rat

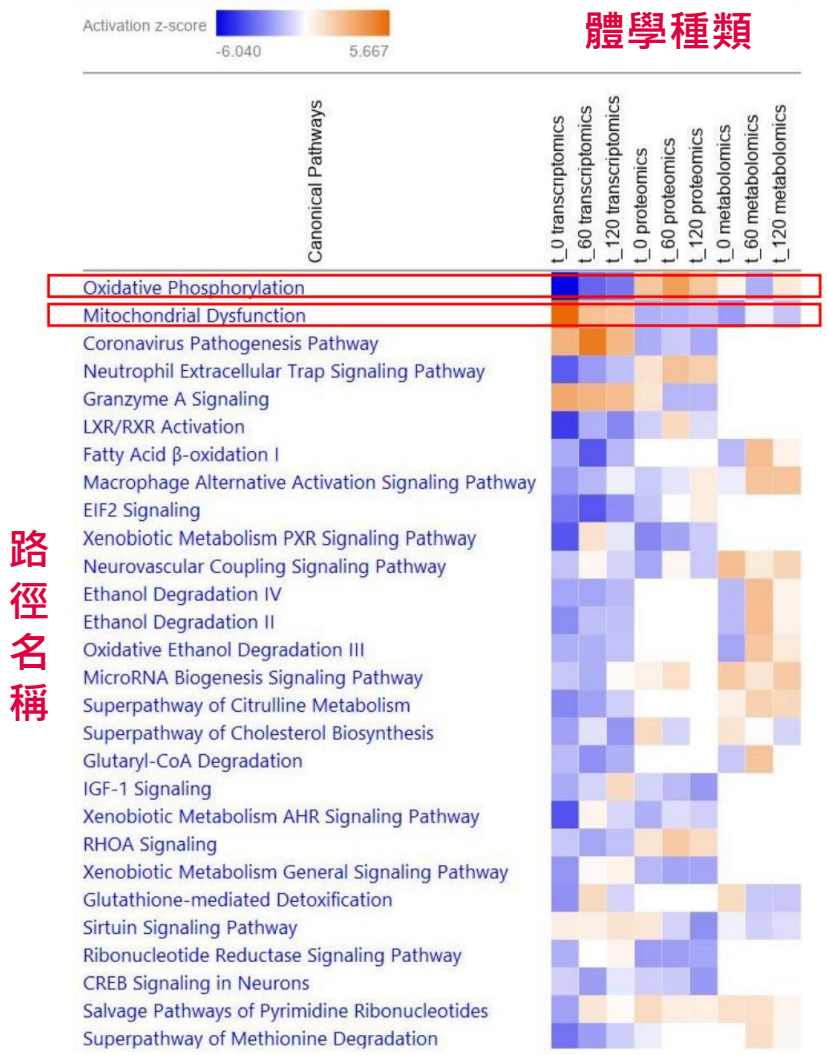
IPA can remap orthologous identifiers from the following species:

- 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*)

Omics data type

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





Supported Identifiers for Data Upload

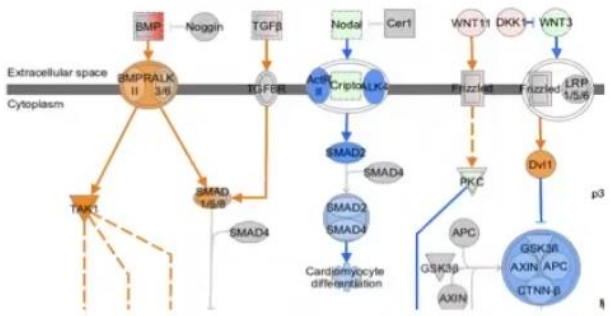
Get more complete mapping during dataset upload!

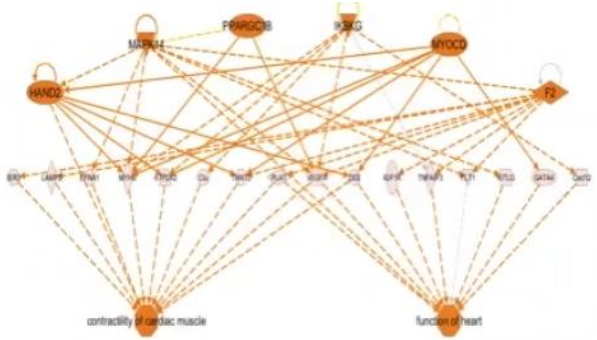
Vendor IDs	Gene	Protein	Transcript	microRNA	SNP	Chemical
Affymetrix (na36)	Entrez Gene (2020/10)	GenPept	Ensembl (101)	miRBase (mature)	Affy SNP IDs	CAS Registry Number
Agilent	GenBank (239)	International Protein Index (IPI)	RefSeq (human、mouse)	miRBase (stemloop)	dbSNP	HMDB
Life Tech (ABI)	Symbol-human (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					

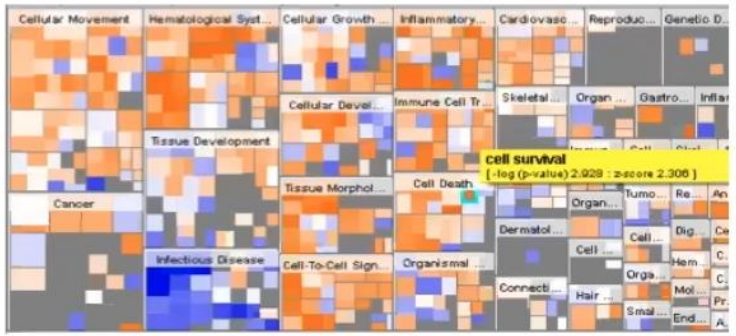
Questions you can address

We can ask which …

- …signaling and metabolic **canonical pathways** are enriched in the data?
- …predicted **upstream regulators** are significant?
- …**diseases and functions** are over-represented?
- …**molecular networks** (potential molecular interactions) pinpoint important molecules in the system?
- …molecules and biological processes are predicted to be **activated or inhibited**?
- …analyses are **similar** or **dissimilar** from my own?





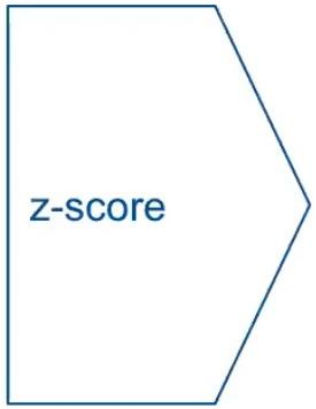


Statistical analyses used in IPA



- The null hypothesis: molecules in your dataset do not overlap with a particular disease, function, pathway, etc.
- Calculated using the right-tailed Fisher's Exact test
- Significant p-value ≤ 0.05

Note: Benjamini-Hochberg correction for multiple testing can be implemented.



- Used in two ways:
  - **1. Predicts activation or inhibition**
    - Requires directional expression or phosphorylation data
    - Correlation between what is known (Ingenuity Knowledge Base) and your data
    - z-score ≥ 2 (activation) and ≤ –2 (inhibition)
  - **2. Measures the match between two analyses (Analysis Match)**
    - z-score ≥ 2 (match) and ≤ –2 (anti-match)

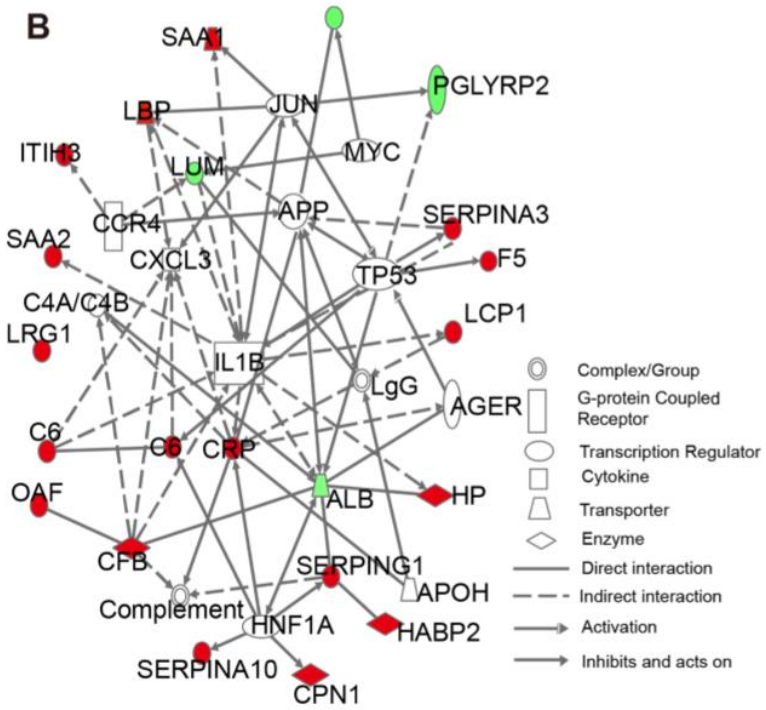
FAQ - Statistical Calculations

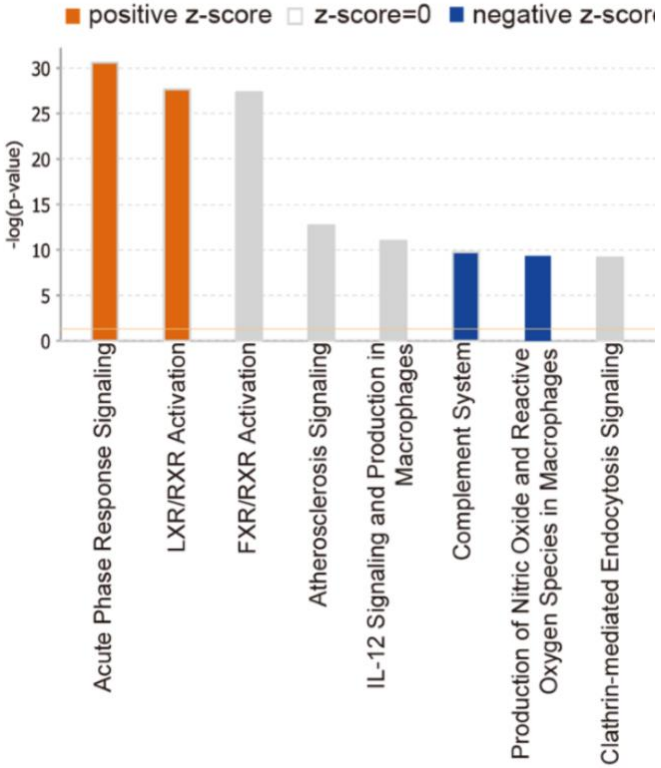
The statistics used depends on the analysis

Analysis type	p-value of overlap	z-score
Canonical pathways	●	●
Upstream Analysis	●	●
Diseases & Functions	●	●
Regulator Effects	●	○
Networks	●	○
Analysis Match	●	●

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.





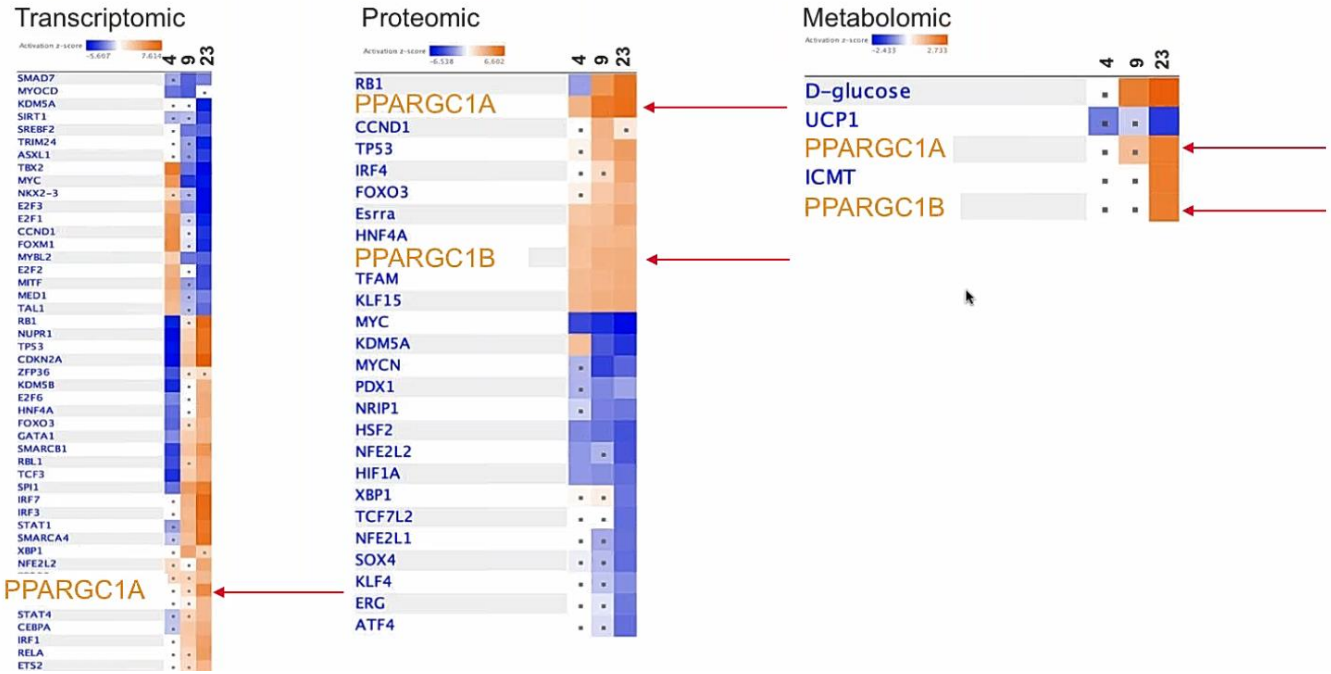
https://www.medrxiv.org/content/10.1101/2020.04.07.20054585v1

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

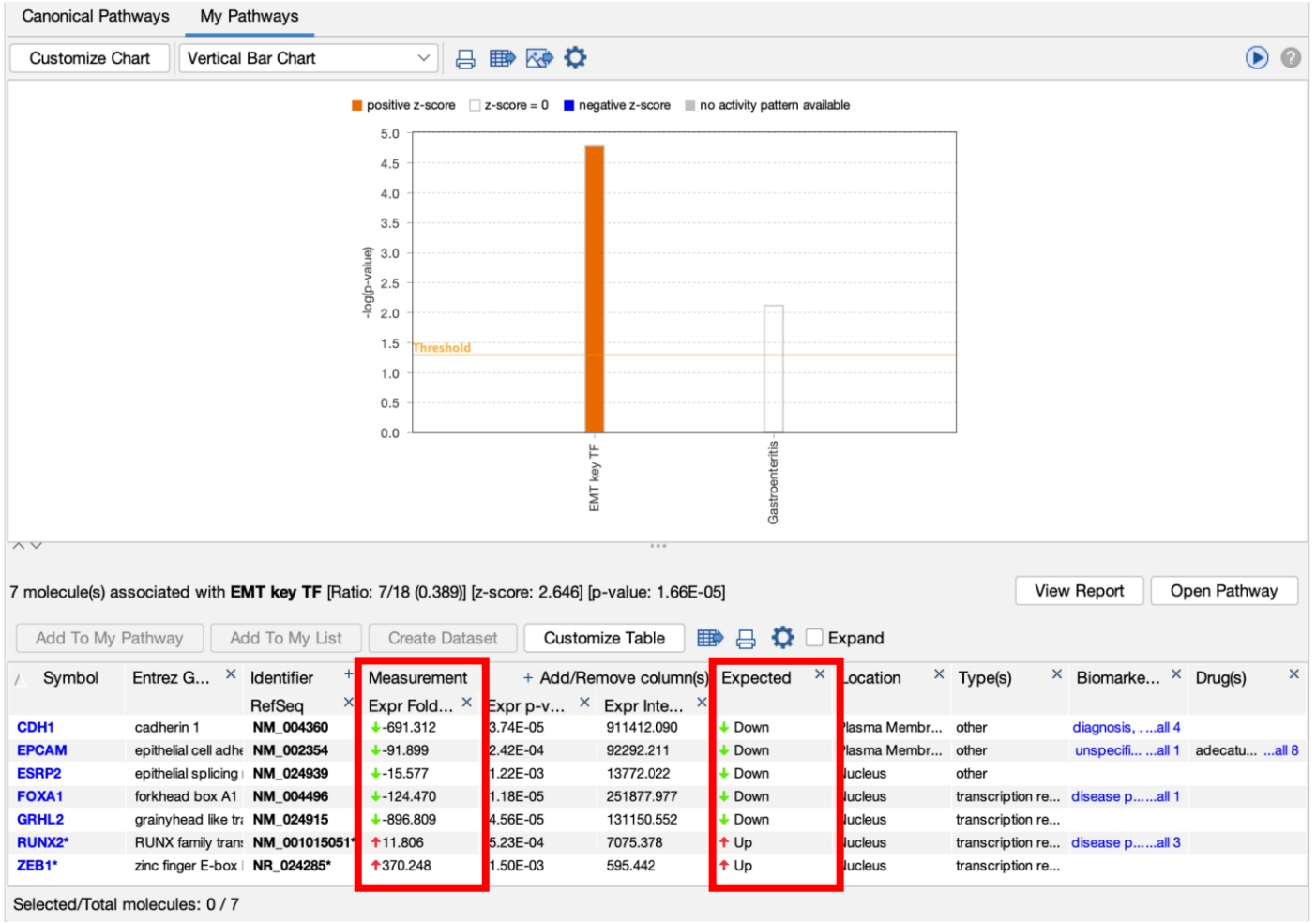
Multi-omics analysis indicate similar transcriptional drivers

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

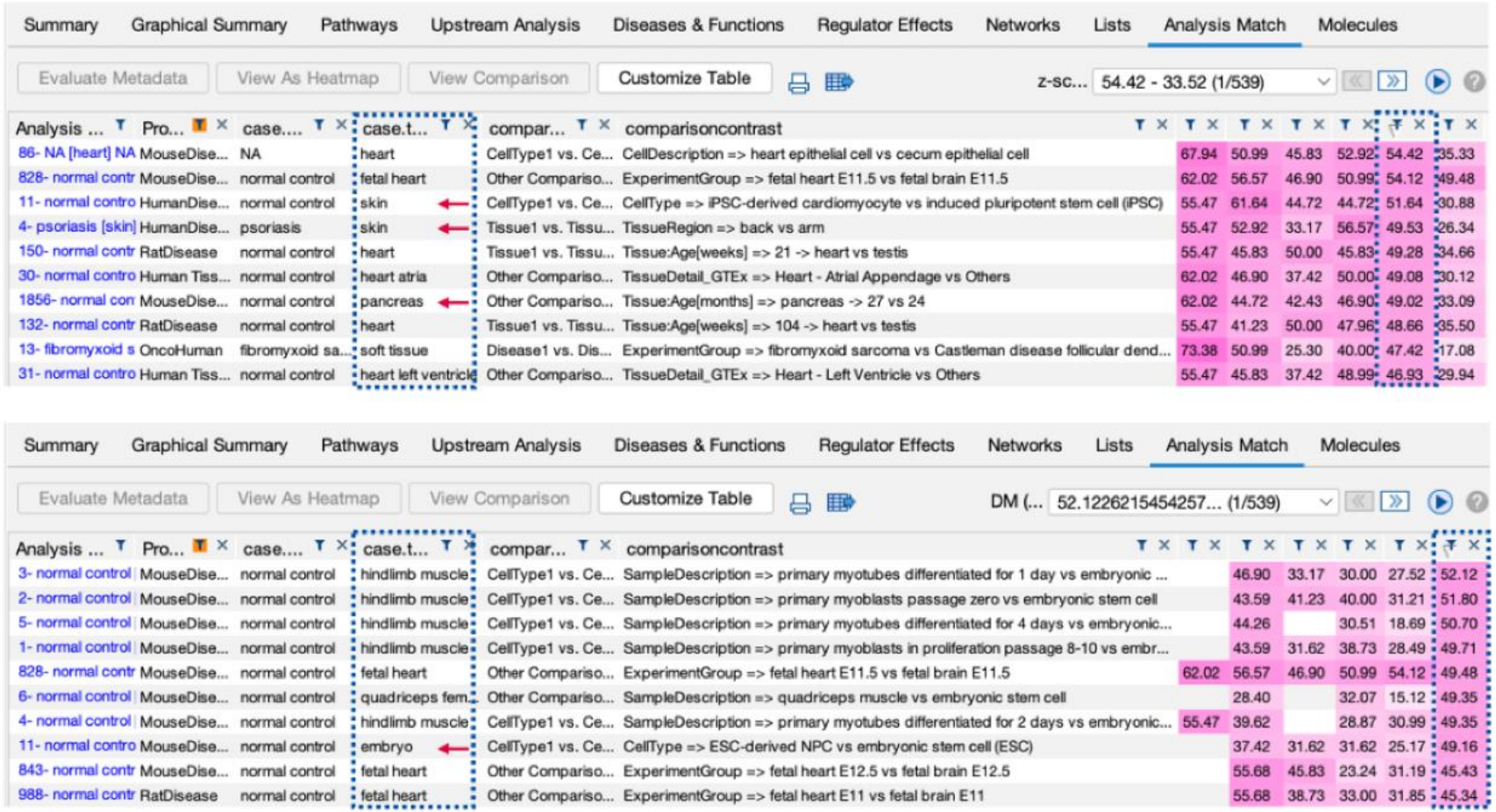
Causally score My Pathways in Core Analysis



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

Causally scoring a My Pathway.

Discover more precise matches in Analysis Match



Sorted by original overall z-score match

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

Sorted by new DM "dataset match" column

Results are more strictly heart or muscle cells vs embryonic cells

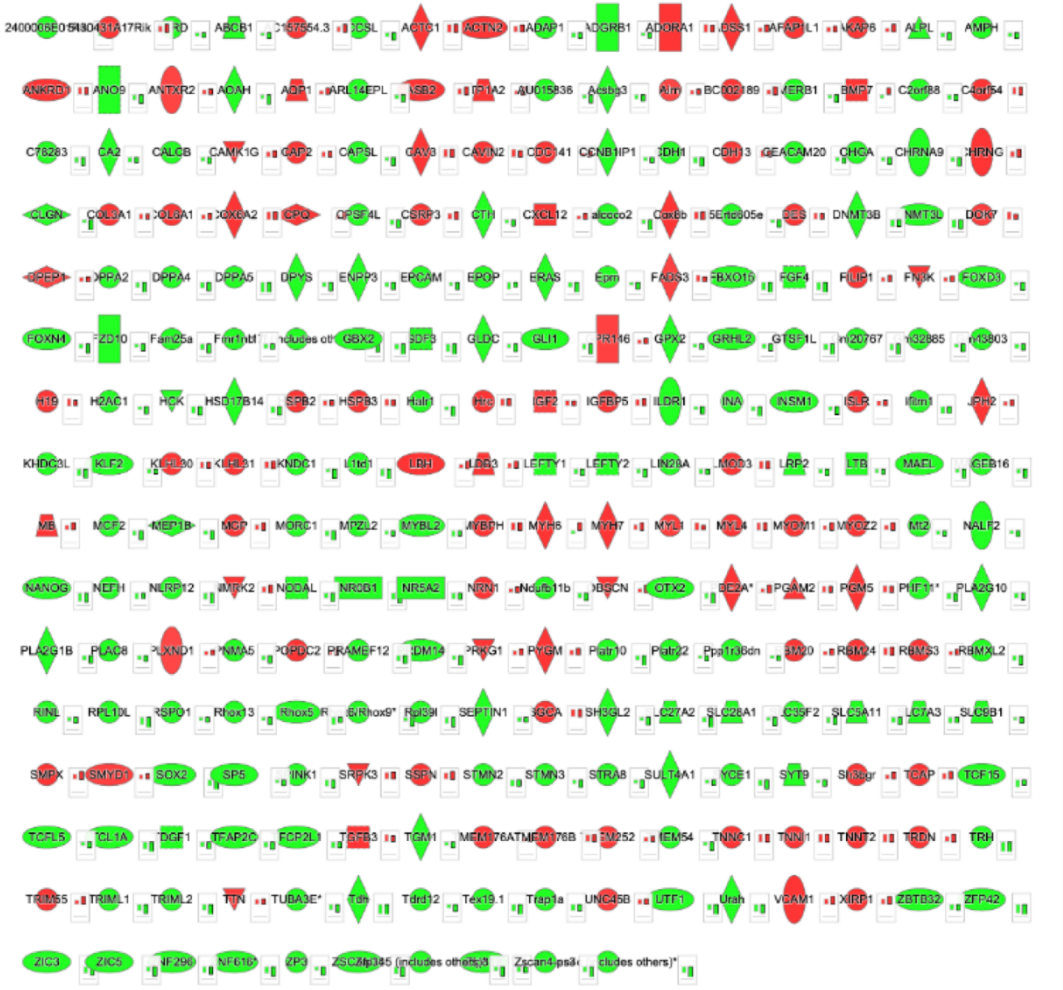
Analysis Match results sorted by the original score (top) and new score (bottom).

Heatmap of the top forty matching analyses



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

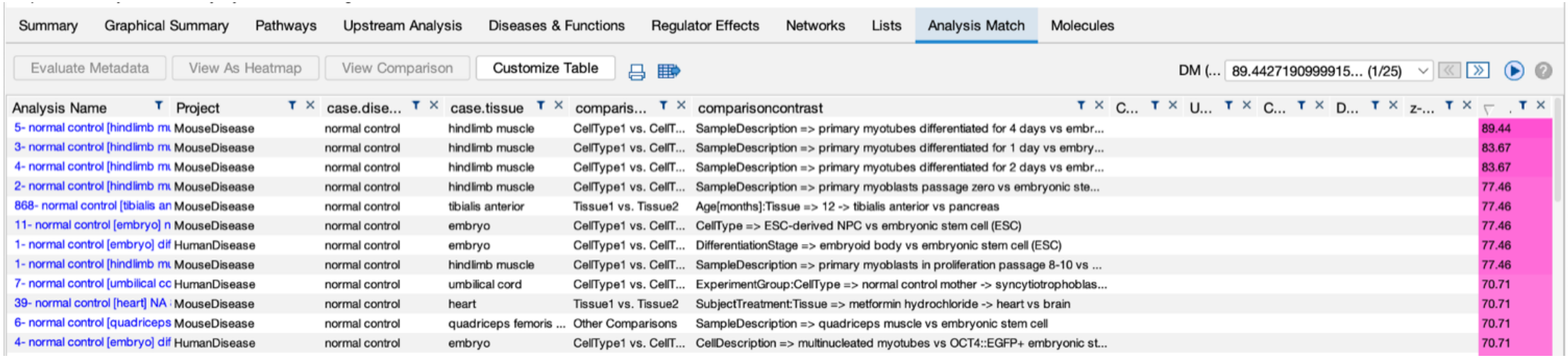
Heatmap of the top forty matching analyses



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

The new scoring method using a small dataset.

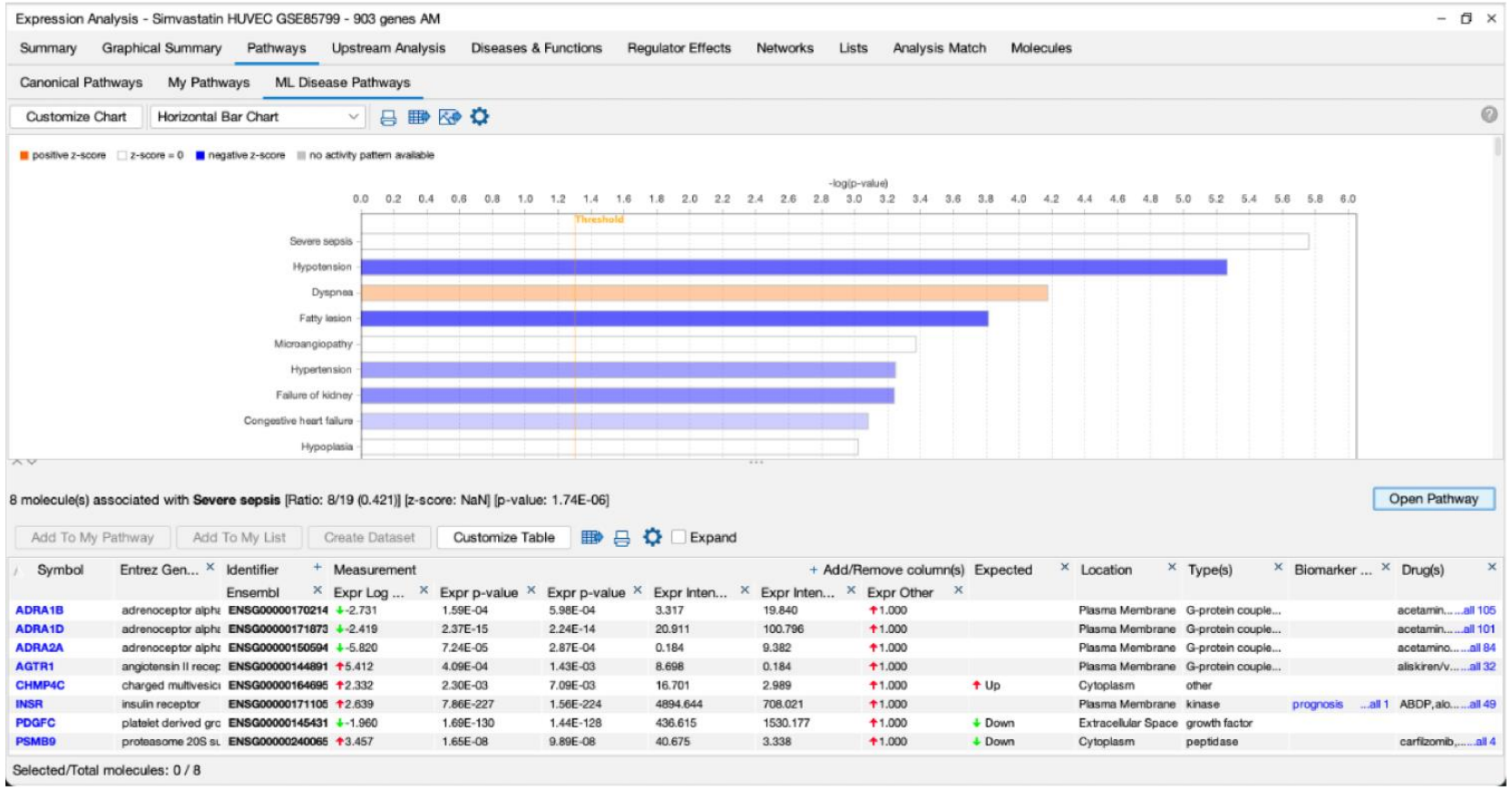
The new scoring method often works on small datasets, where there are typically too few genes to generate robust Upstream Regulator, Causal Network, Canonical Pathway, and Disease and Function signatures to match to other analyses.



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

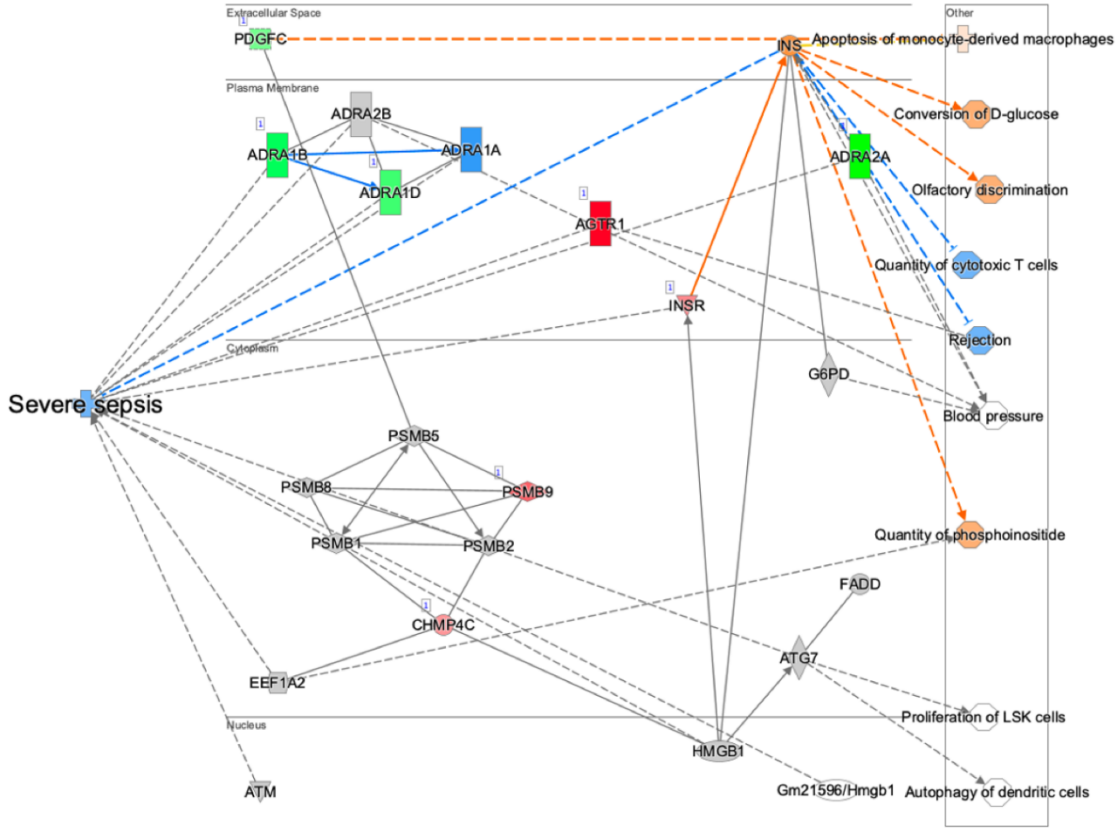
The analysis of a 10-gene dataset from the cardiomyocytes versus embryonic stem cells matches the expected types of analyses.

Find the unexpected with ML Disease Pathways in Core Analyses



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

Find the unexpected with ML Disease Pathways in Core Analyses

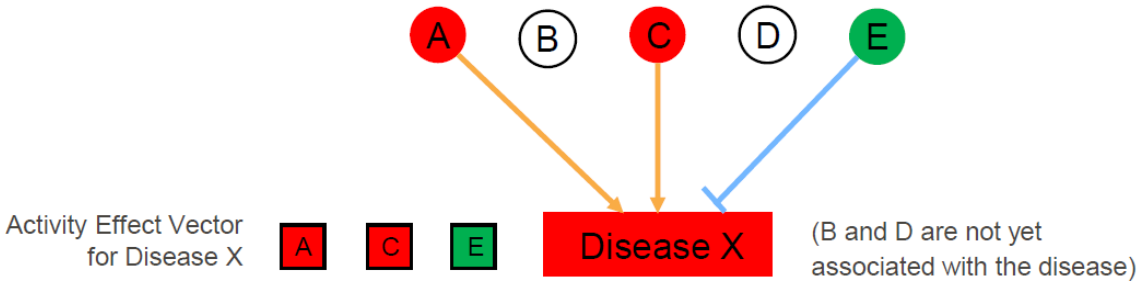


The severe sepsis ML pathway overlaid with simvastatin differential expression data. IPA predicts that simvastatin may decrease severe sepsis.

Enhancing the KB through Machine Learning

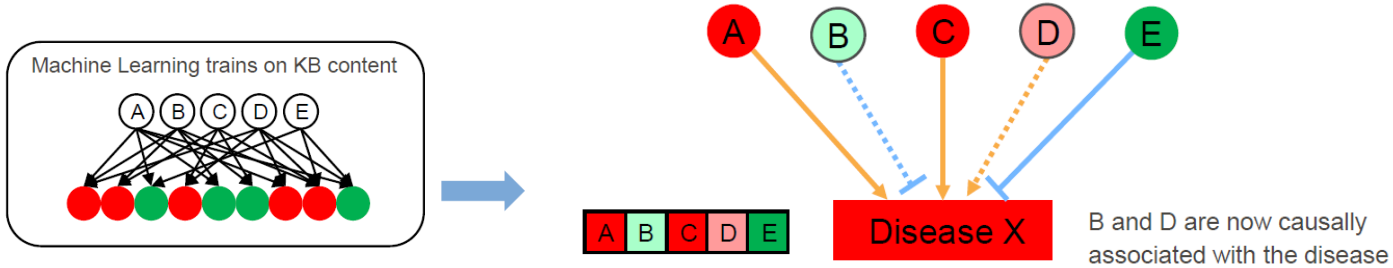
Standard KB

- 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.

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。

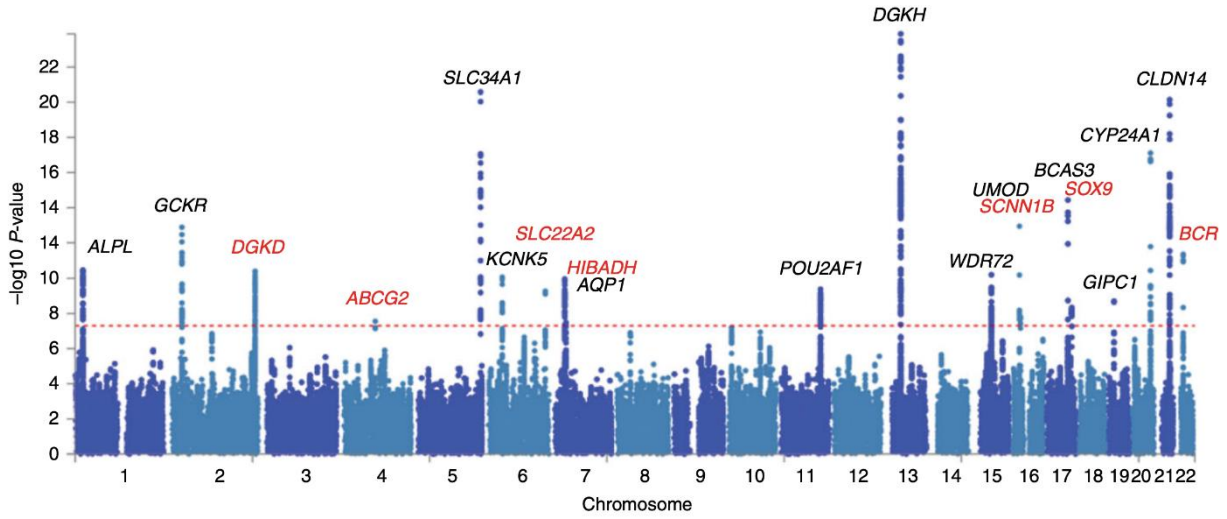
IPA與市售系統生物學分析工具比較

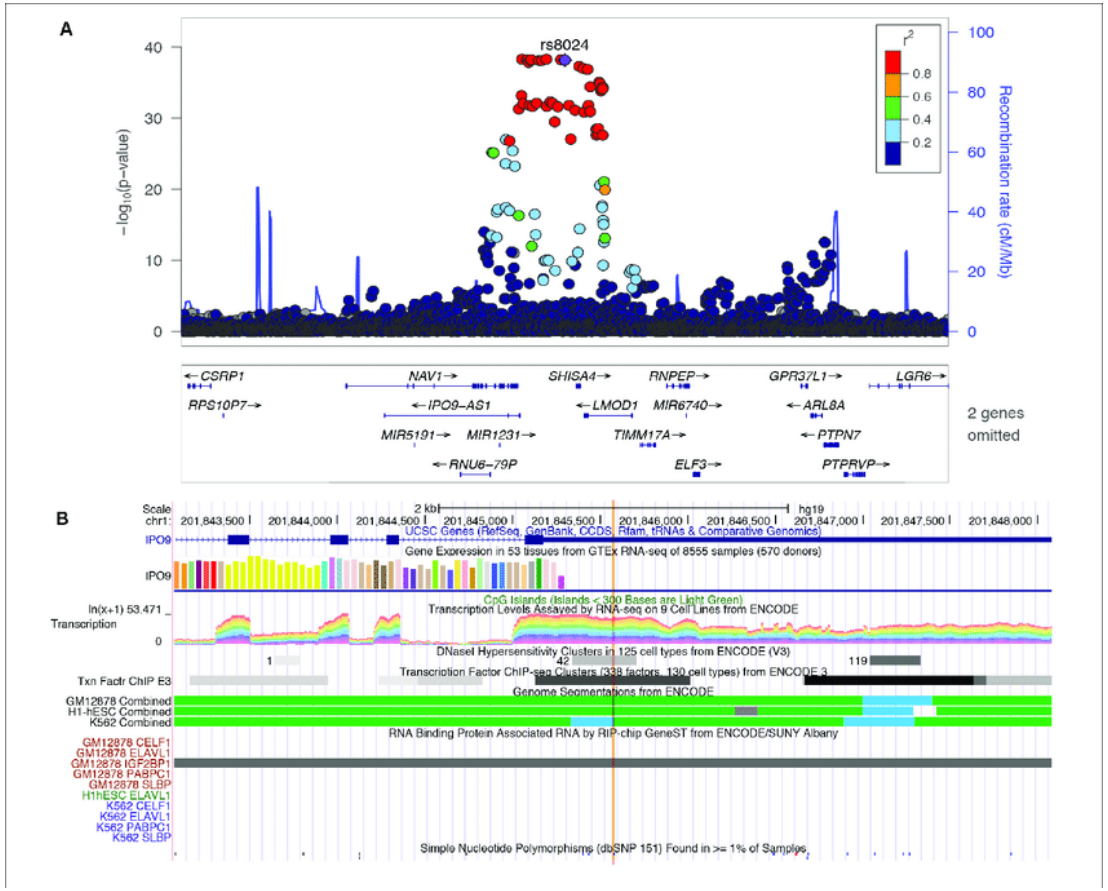
	IPA	Metacore	KEGG	Note
Enrichment Analysis				
基因體、蛋白質體表現分析	O	O	O	
代謝體	O	O	O	
毒物分析	O	O	O	
Enrichment Analysis結果視覺化表現	O	X	X	將各項Enrichment結果以不同的視覺化分析圖表呈現。
Enrichment Analysis Expression Pattern比較	O	X	X	將本次Enrichment結果與其他疾病、實驗的Dataset進行相似性比較。
因果網路分析	O	X	X	將Enrichment結果與感興趣的生物分子或者疾病、生物功能產生關連。
疾病熱圖	O	X	X	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

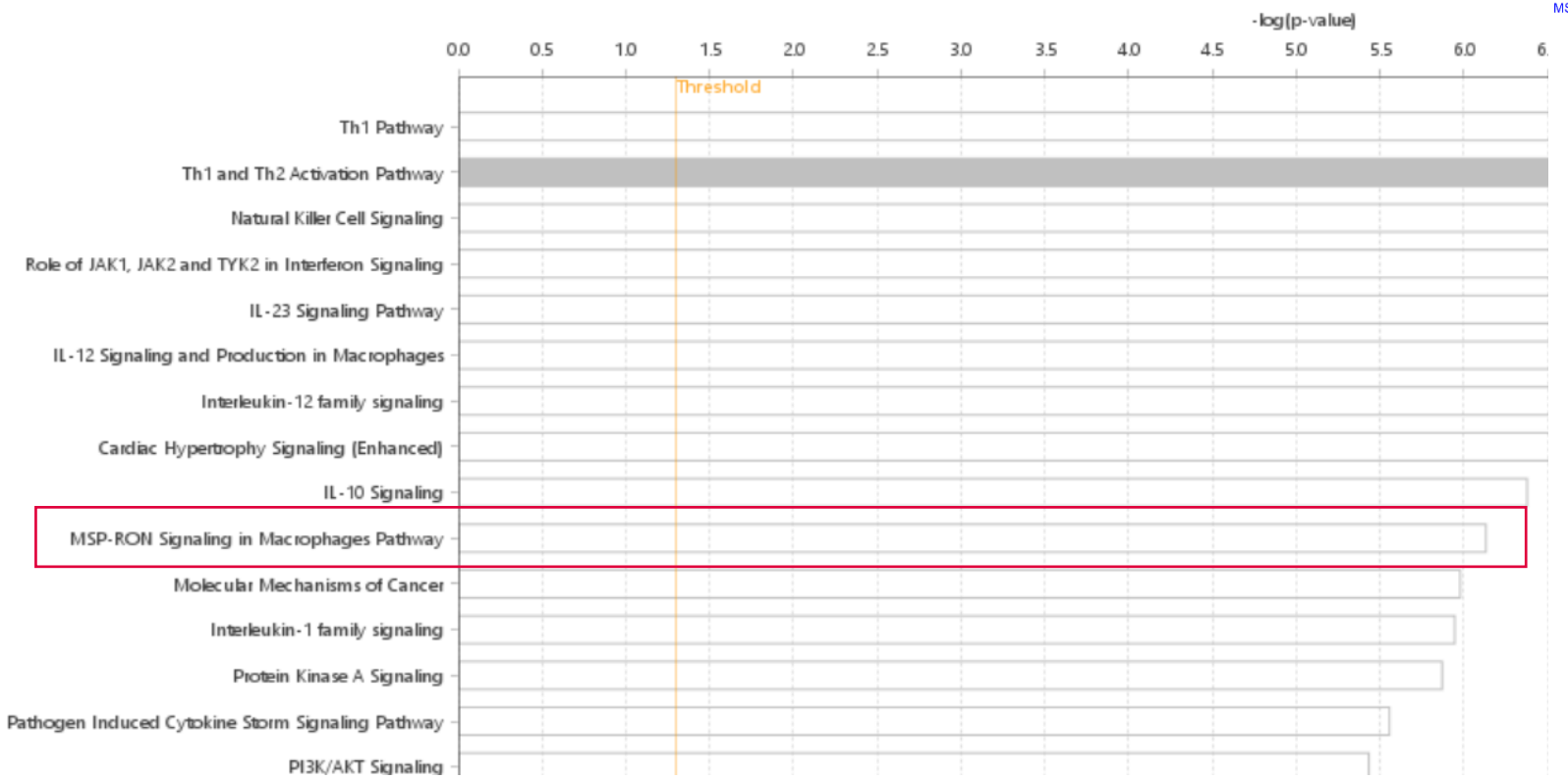
	IPA	Metacore	KEGG	Note
其他功能				
生物特性篩選	O	X	X	Bioprofiler，可篩選出具有相同生物特性的訊息傳遞因子。
Isoform篩選	O	X	X	Isoprofiler，可鑑別出同基因不同Isoform的生物表現結果。
基因於組織差異表現分析	O	X	X	GTEx Expression Pattern，用作於比較相同基因在不同組織的差異分析。
miRNA調控目標預測分析	O	X	X	miRNA Target filter，可進行miRNA與mRNA配對，進而比較出miRNA的作用方式。
磷酸化蛋白質體分析	O	X	X	用於確認不同位點的磷酸化蛋白質功能。
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。

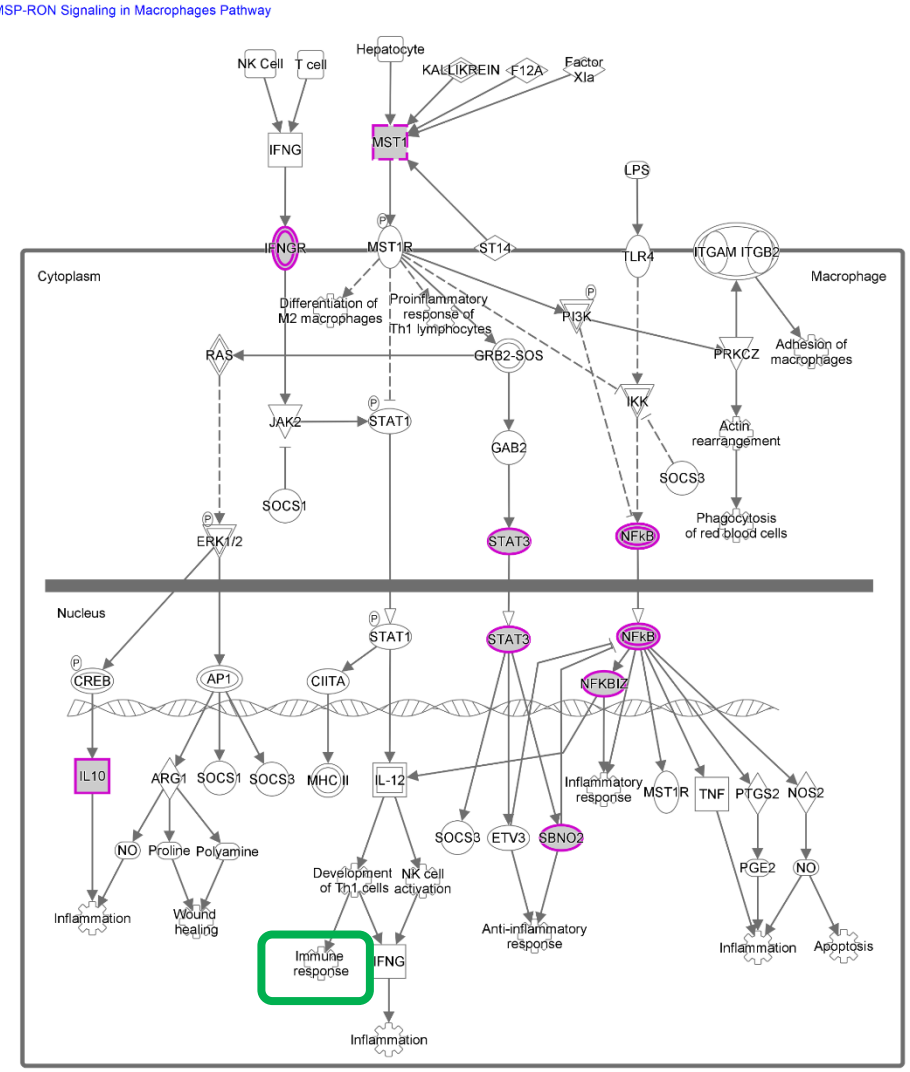
A genome-wide association study (GWA study, or GWAS), is an observational study of a genome-wide set of genetic variants in different individuals to see if any variant is associated with a trait. GWAS typically focus on associations between single-nucleotide polymorphisms (SNPs) and traits like major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





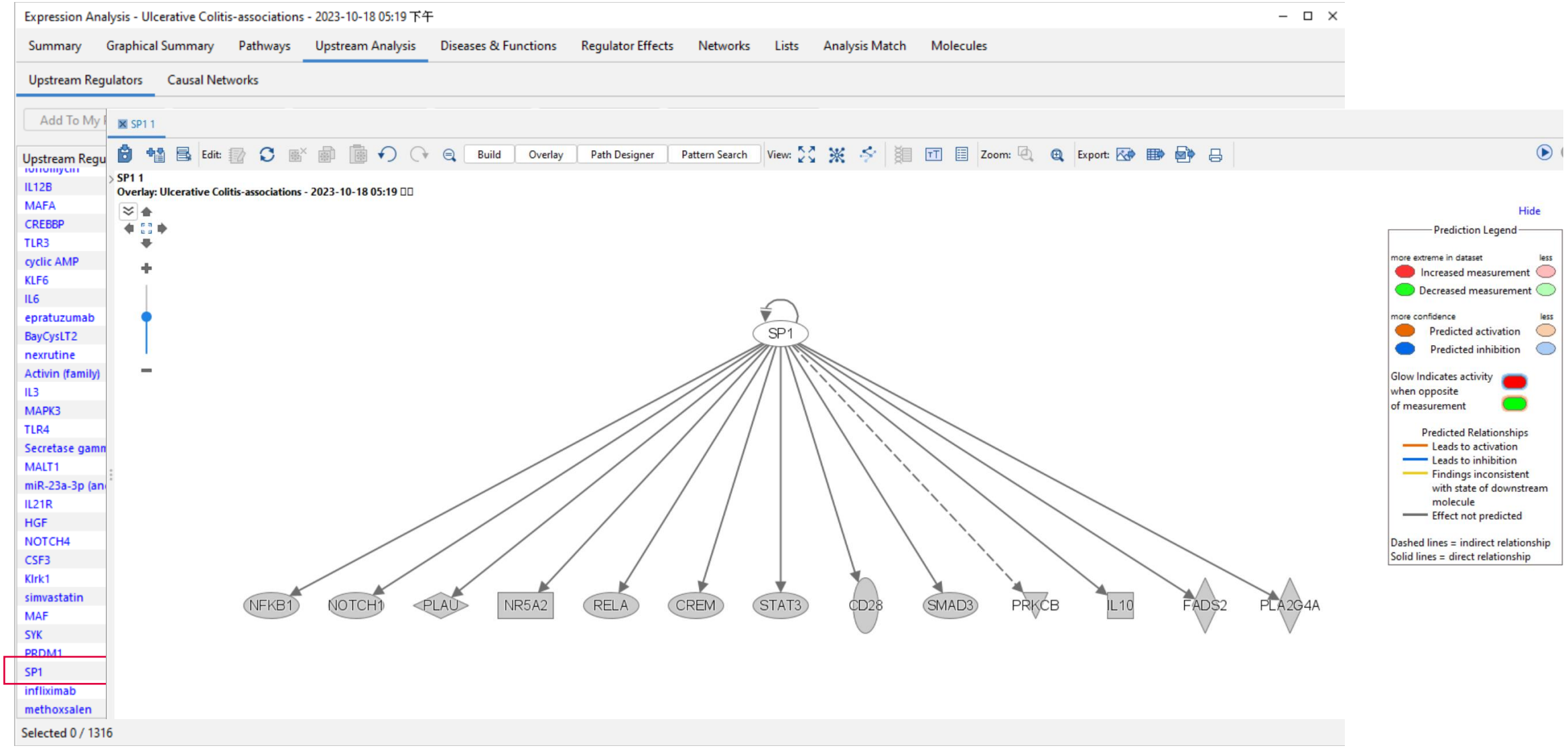
Analyze risk loci to identify enriched pathways





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Discover regulatory molecules influencing genes associated with risk loci

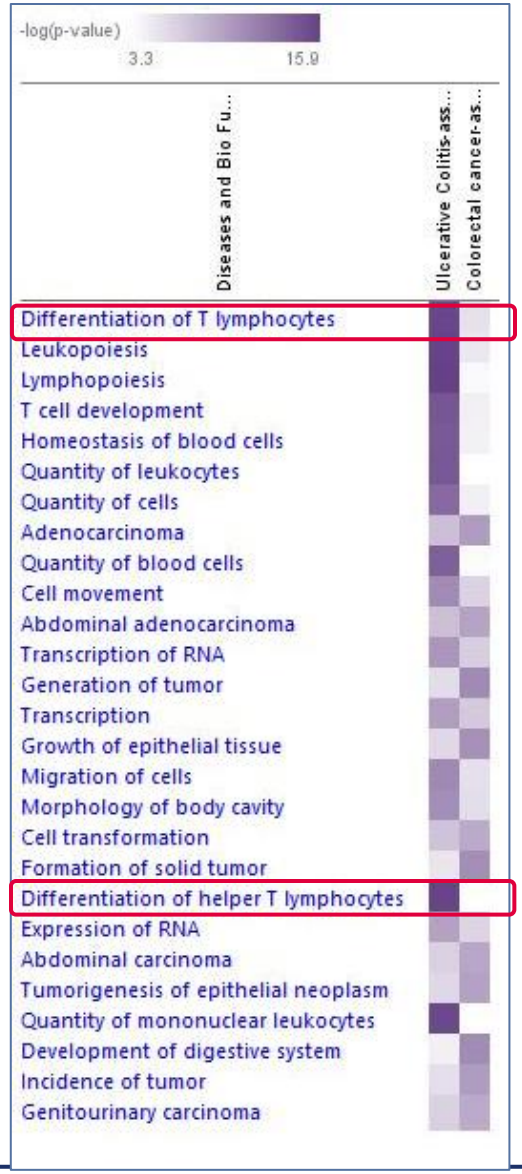


Compare multiple GWAS risk loci analysis using heatmaps

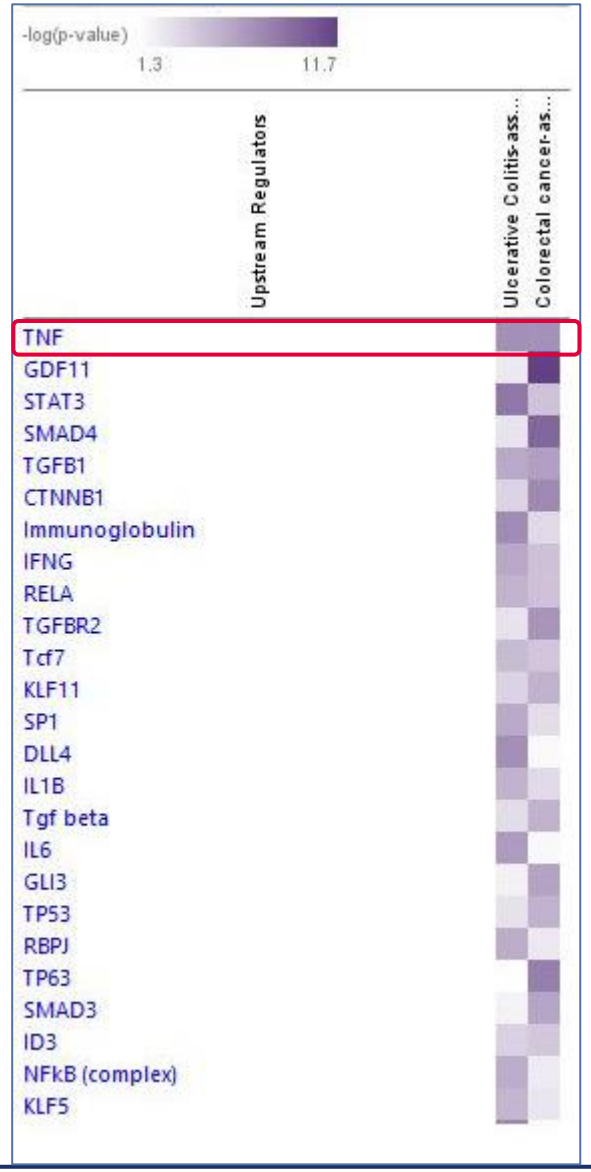
Canonical pathways



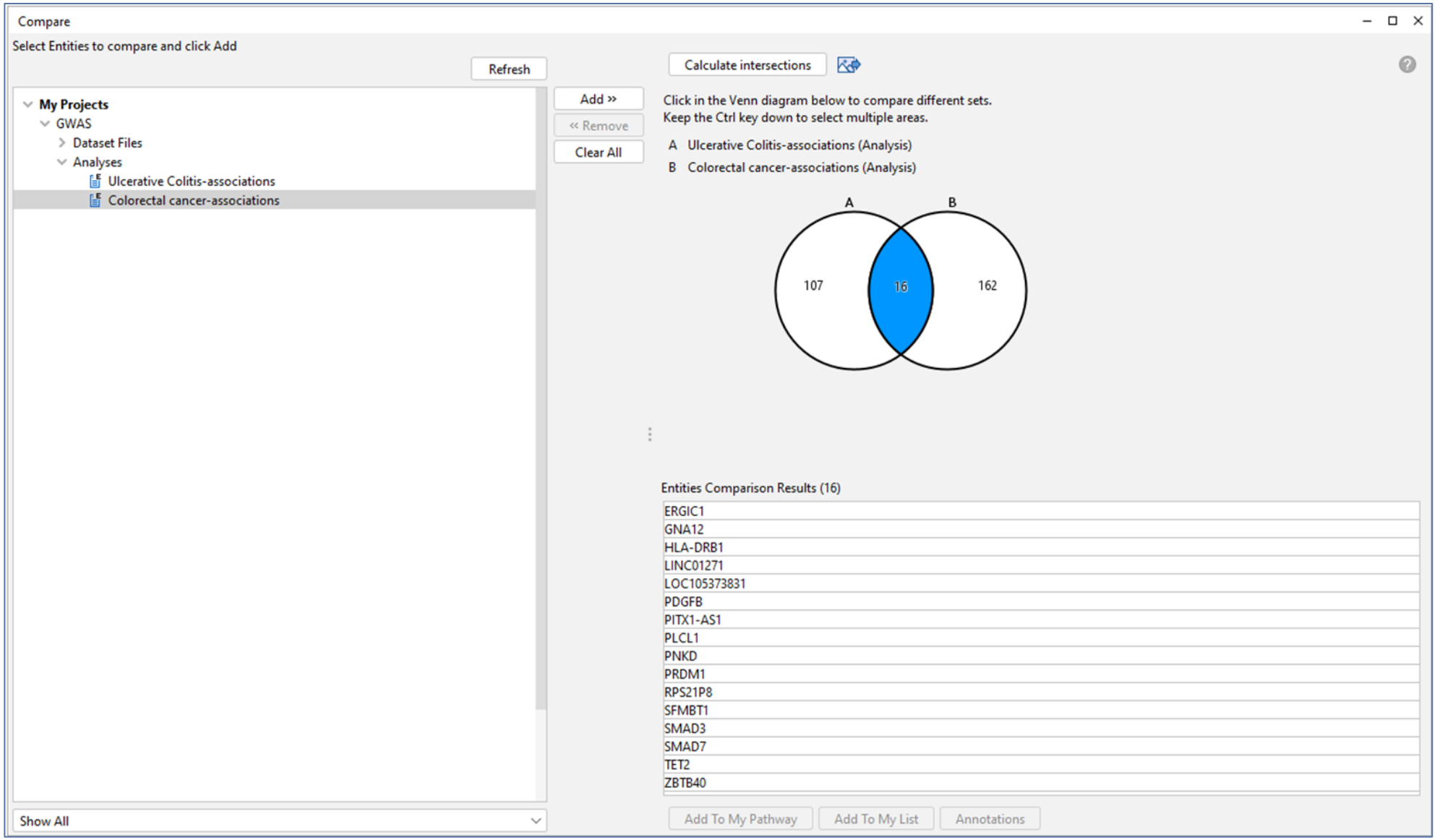
Disease and bio-functions



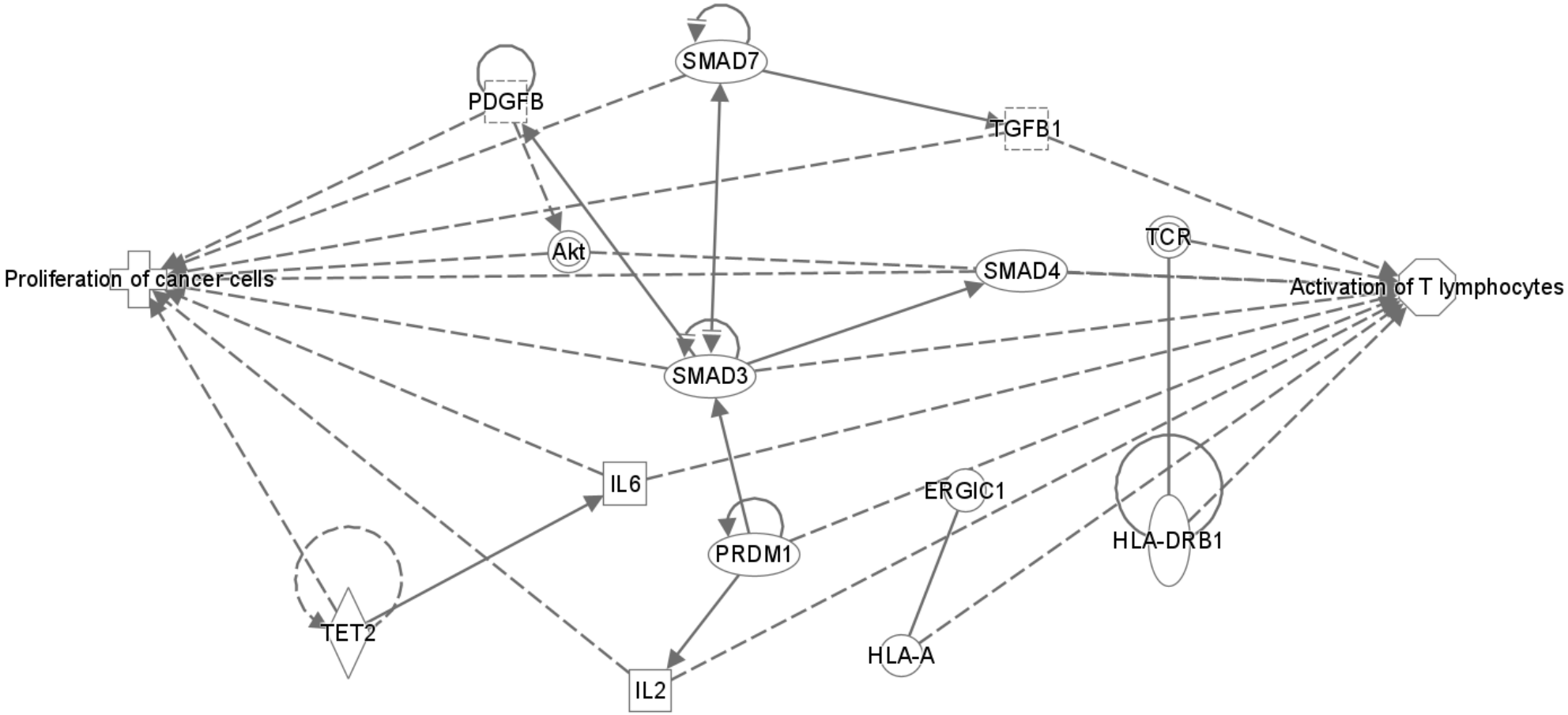
Upstream Regulators



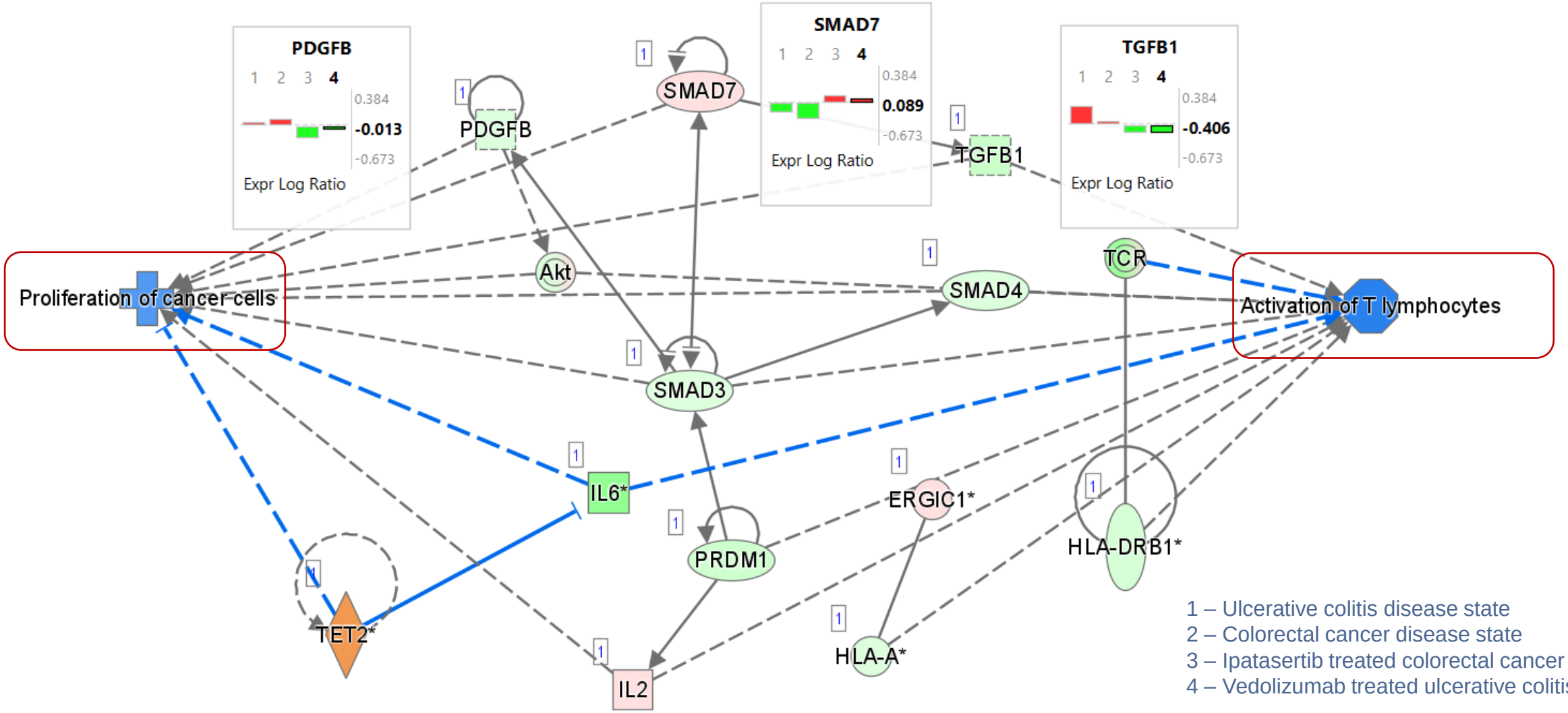
Compare and identify common molecules between risk loci list



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



Contextualize a network using public omic data

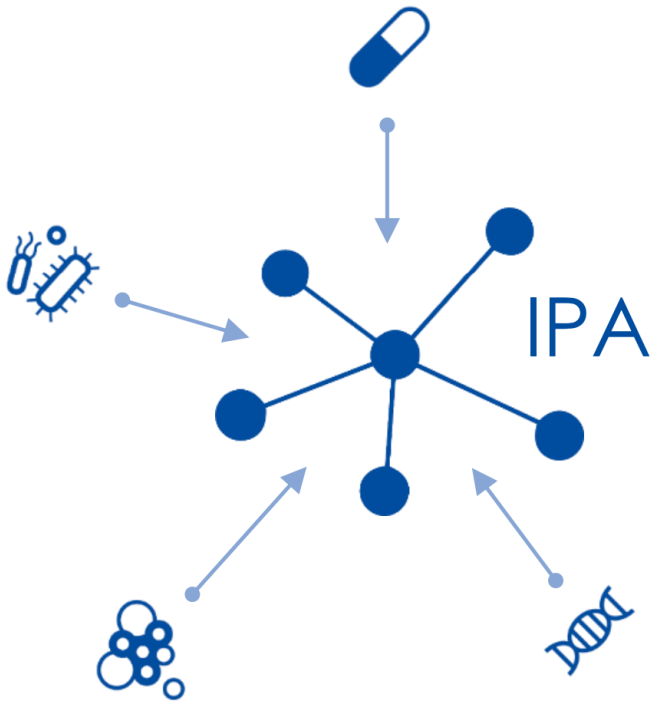


IPA is powered by the QIAGEN Knowledge Base

Updated weekly with the latest clinical trials and manuscripts

12+ million findings curated using controlled vocabulary

Decades of accumulated knowledge mapped in directional networks

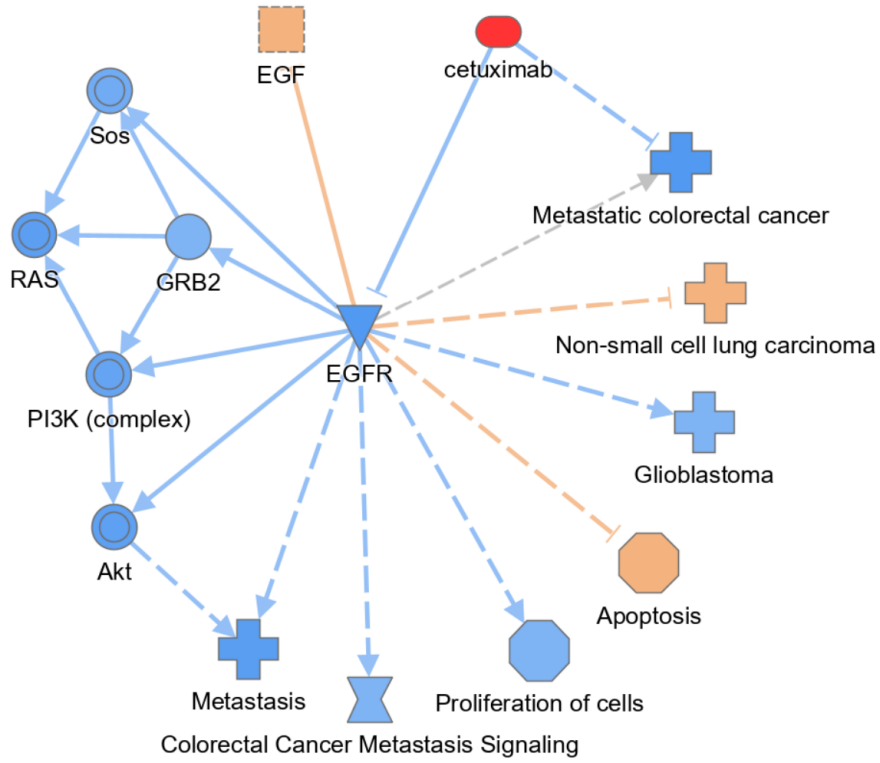


EGF – EGFR
[one of many]

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**



	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

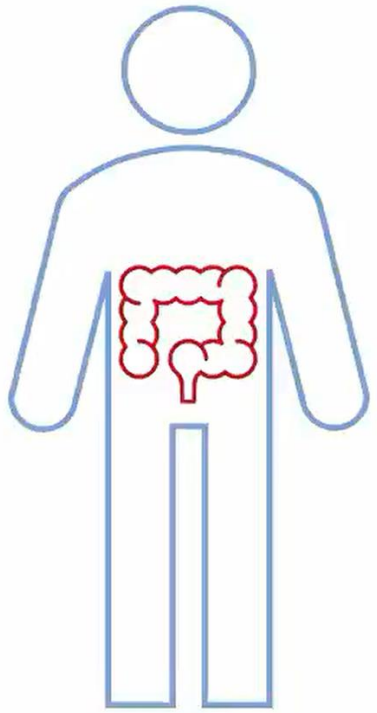
Accepted Files Formats

.txt (tab delimited text files)

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

.diff (cuffdiff files)

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



Ulcerative Colitis

(PMID: 26192919)

	A	B	C	D	E	F
1	Variant	Mapped gene				
2	rs9847710	SFMBT1				
3	rs6087990	DNMT3B				
4	rs3740415	MFSD13A				
5	rs616597	NFKBIZ				
6	rs11150589	Y_RNA				
7	rs254560	C5orf66				
8	rs11641184	LITAF				
9	rs7657746	KIAA1109				
10	rs1405108	'-				
11	rs113010081	LINC02009				
12	rs12103	INTS11				
13	rs1517352	STAT4				
14	rs4976646	RGS14				
15	rs8005161	GPR65				
16	rs4656958	ITLN2				
17	rs4743820	LINC00484				
18	rs1077773	LINC02888				
19	rs907611	LSP1				
20	rs6062504	ZGPAT				
21	rs11229555	GLYAT				
22	rs913678	LINC01271				

Ulcerative Colitis-asso

Ready Display Settings 100%

IPA Training Account & Demo Data

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

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

Client: (IPA Login)

File Edit View Window Help

Provide Feedback | Su

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

Create New...

Enter gene names/symbols/IDs or chemical/drug names here

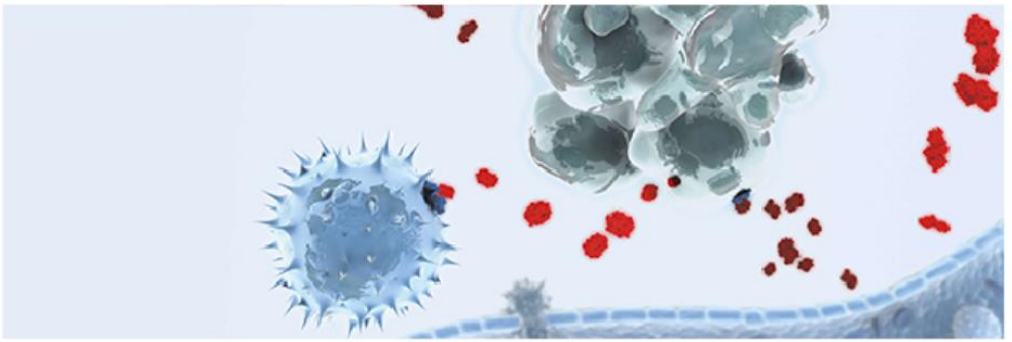
Search

Advanced Search

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

Quick Start

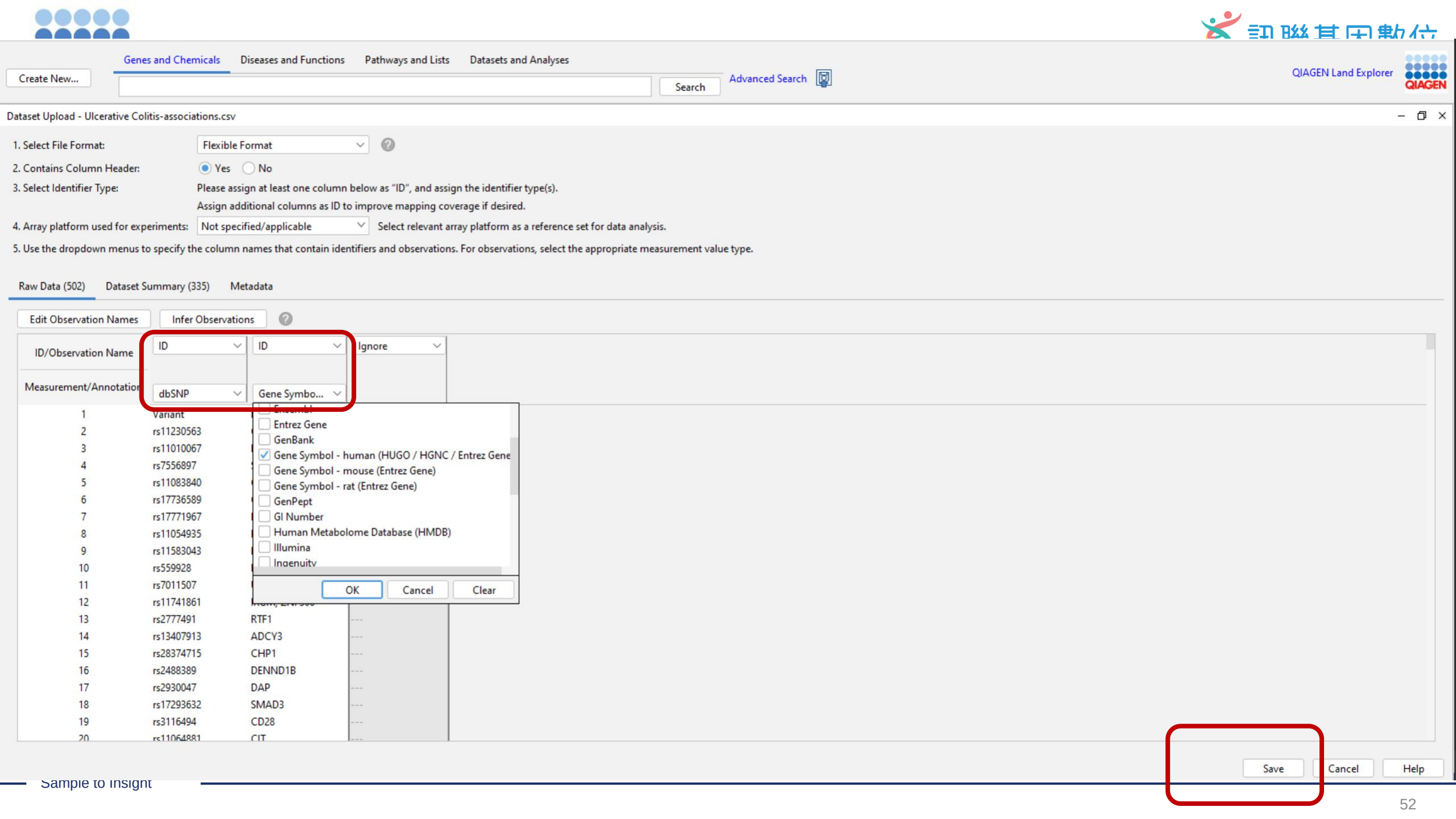
- News
- Getting started
- Exploring large public data resources through IPA
- Exploring IPA knowledge
- Analyzing mRNA or proteomics data
- Analyzing microRNA data
- Analyzing phosphoproteomics data
- Analyzing genetic gain/loss data
- Analyzing metabolomics data
- Case studies and Support webinars
- Top help articles and FAQs
- Contacting Support
- Shortcuts



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.

Don't Show at Startup


Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses
Create New...
Search
Advanced Search
QIAGEN Land Explorer
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.
Raw Data (502)
Dataset Summary (335)
Metadata
Edit Observation Names
Infer Observations
ID/Observation Name
ID
ID
Ignore
Measurement/Annotation
dbSNP
Gene Symbo...
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
OK
Cancel
Clear
Save
Cancel
Help

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.

Raw Data (502) | Dataset Summary (335) | Metadata

Edit Observation Names | Infer Observations

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

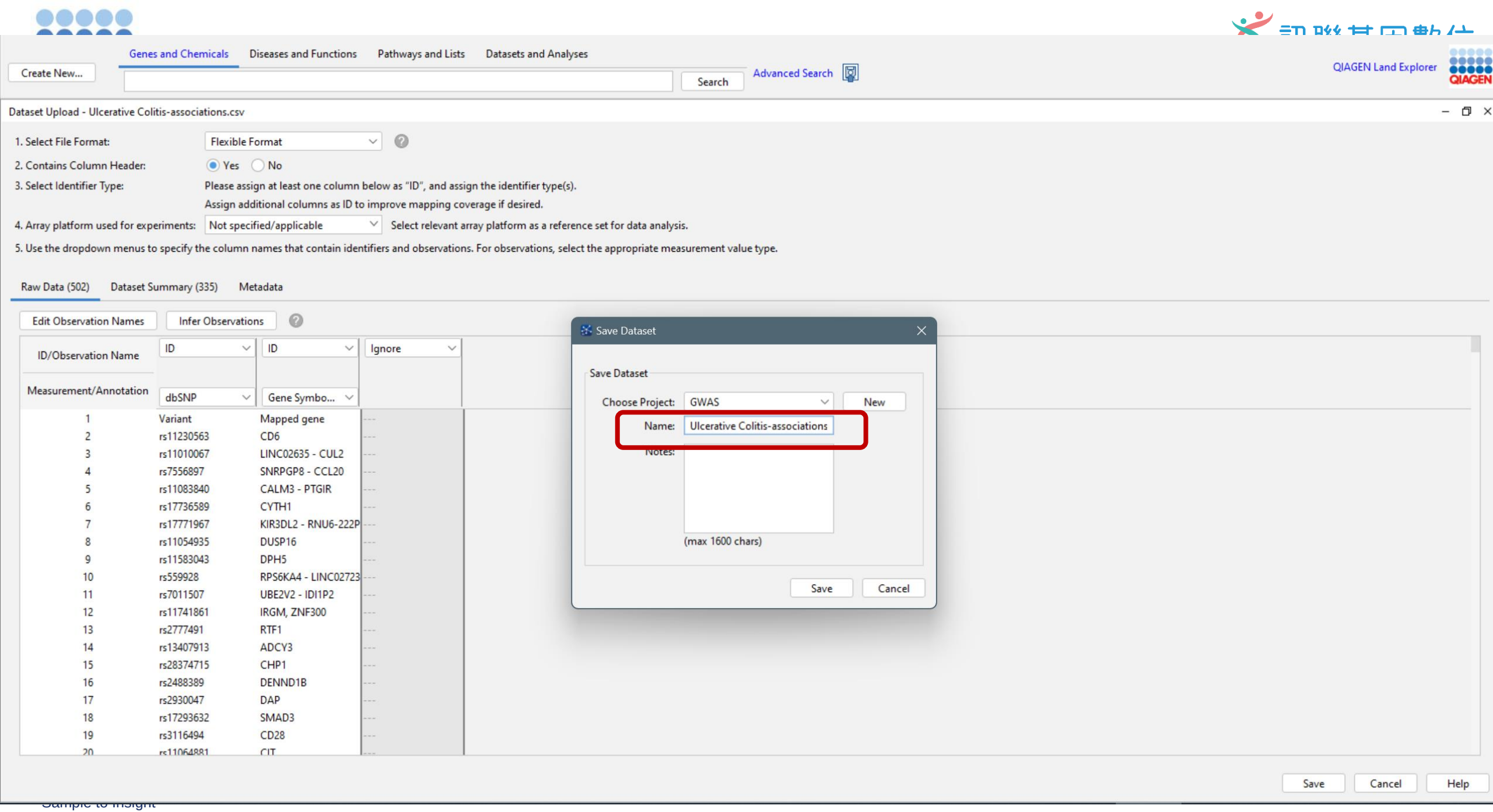
Your dataset does not contain any metadata.
Metadata is useful when you search for datasets or subsequent analyses.

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

Click OK to continue to save the dataset without metadata.

OK Cancel

Save Cancel Help


Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses
Create New...
Search
Advanced Search
QIAGEN Land Explorer
Dataset Upload - Ulcerative Colitis-associations.csv
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No
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Dataset Summary (335)
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Edit Observation Names
Infer Observations
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
New
Name:
Ulcerative Colitis-associations
Notes:
(max 1600 chars)
Save
Cancel
Save
Cancel
Help

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

Annotated Dataset: Ulcerative Colitis-associations2

Preview Dataset Ulcerative Colitis-associations2

Mapped IDs (335) | Unmapped IDs (166) | All IDs (501) | Metadata

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

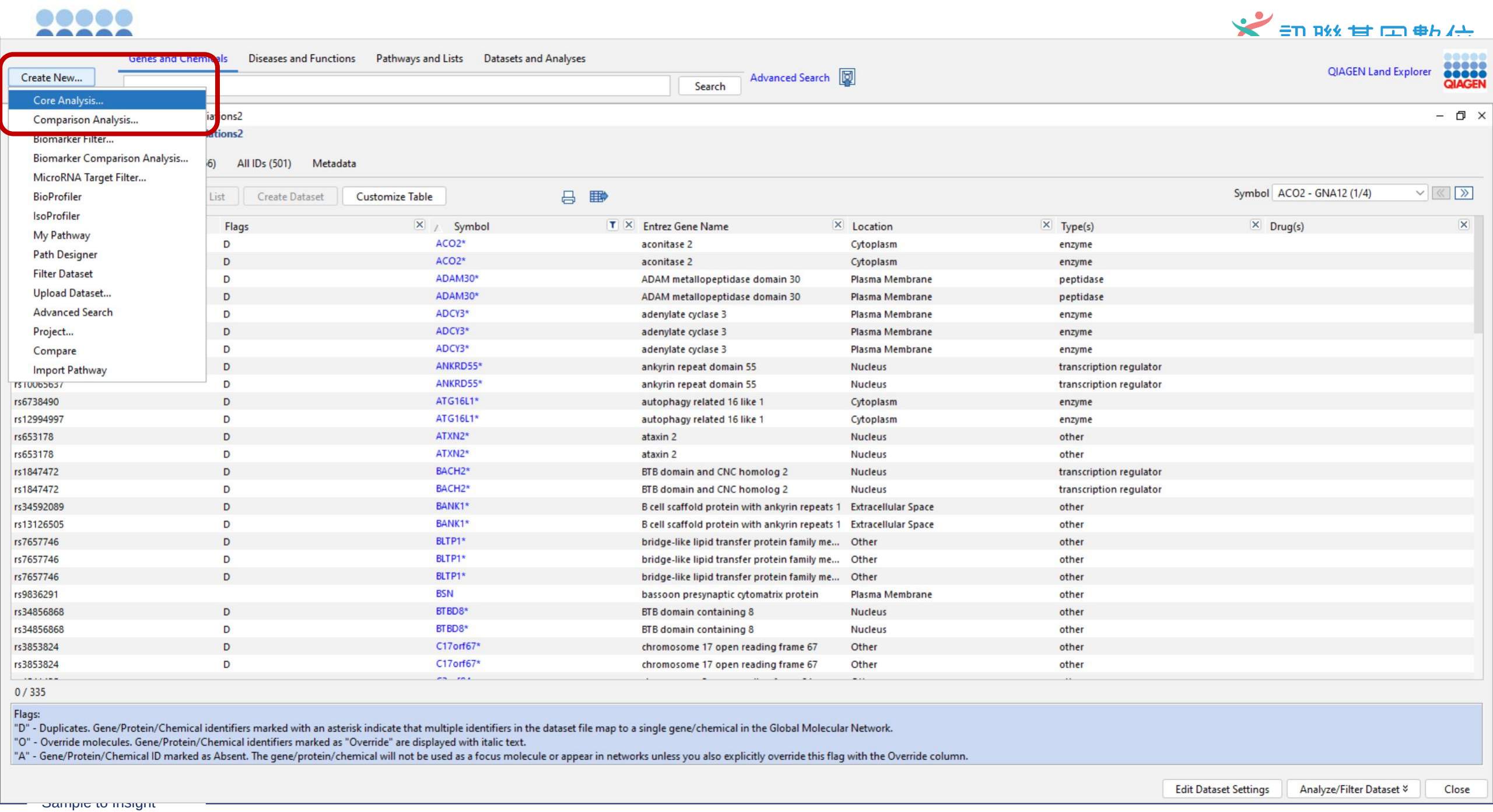
Symbol ACO2 - GNA12 (1/4)

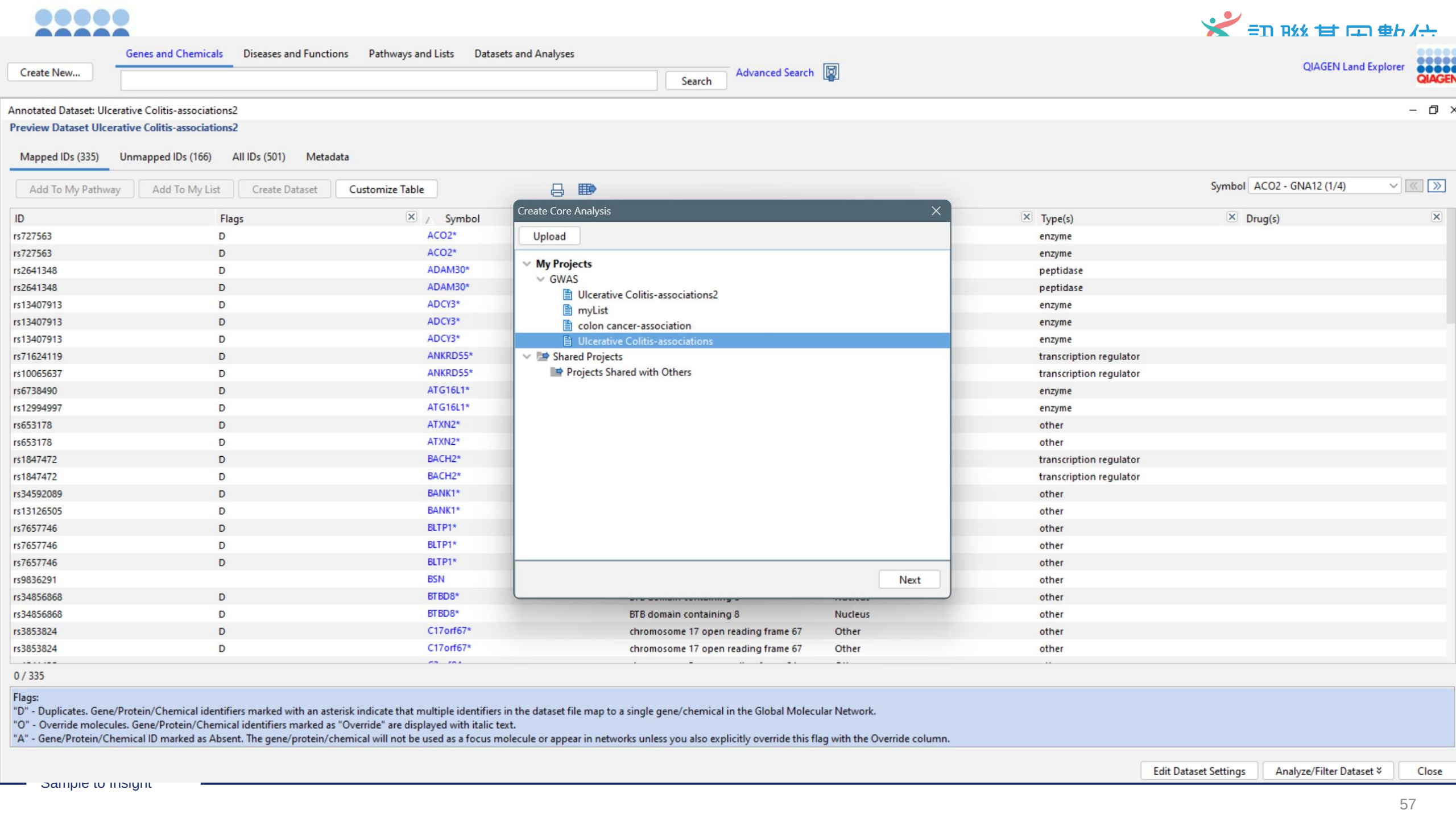
ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
rs727563	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
rs727563	D	ACO2*	aconitase 2	Cytoplasm	enzyme	
rs2641348	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
rs2641348	D	ADAM30*	ADAM metallopeptidase domain 30	Plasma Membrane	peptidase	
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	

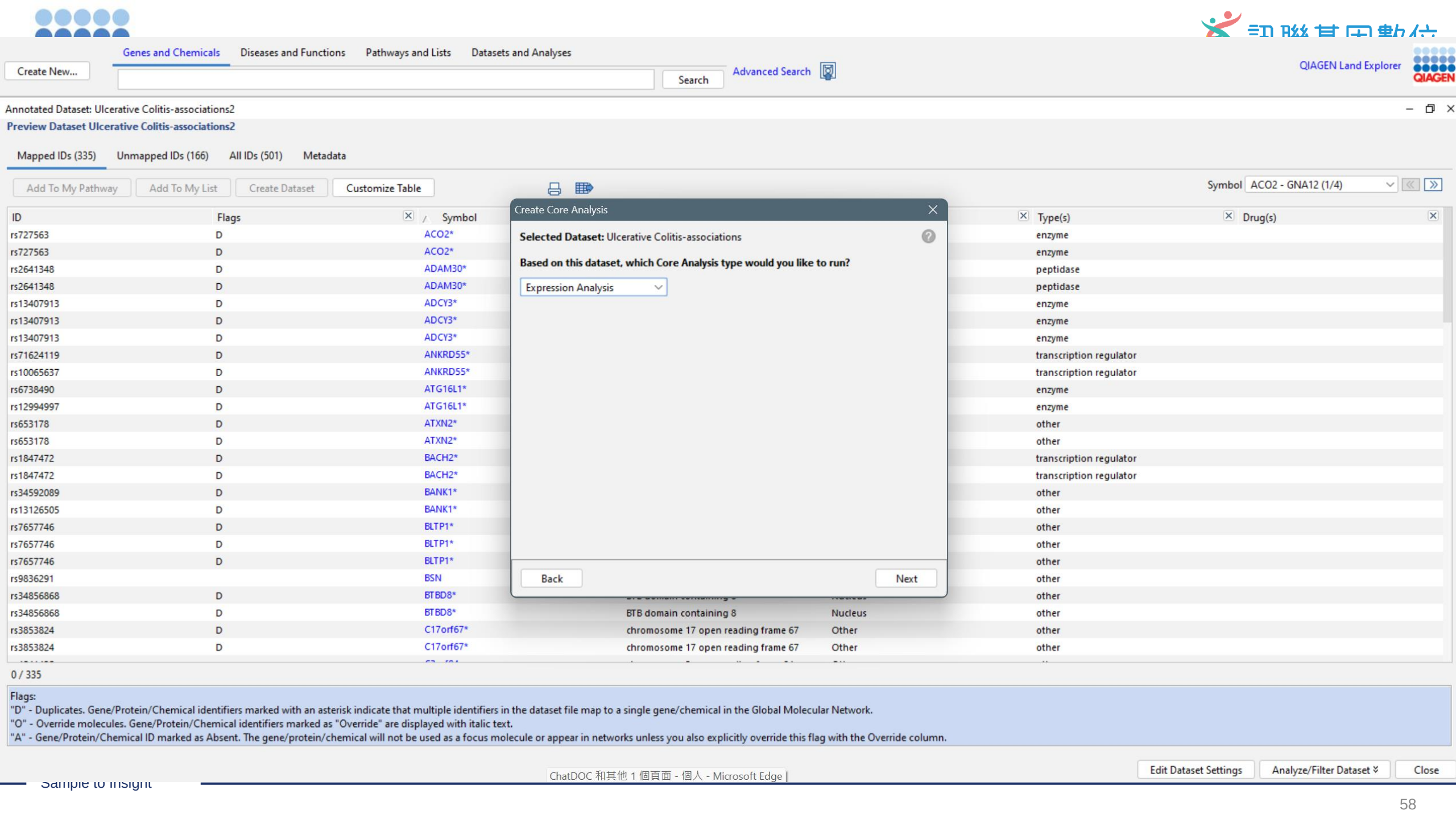
0 / 335

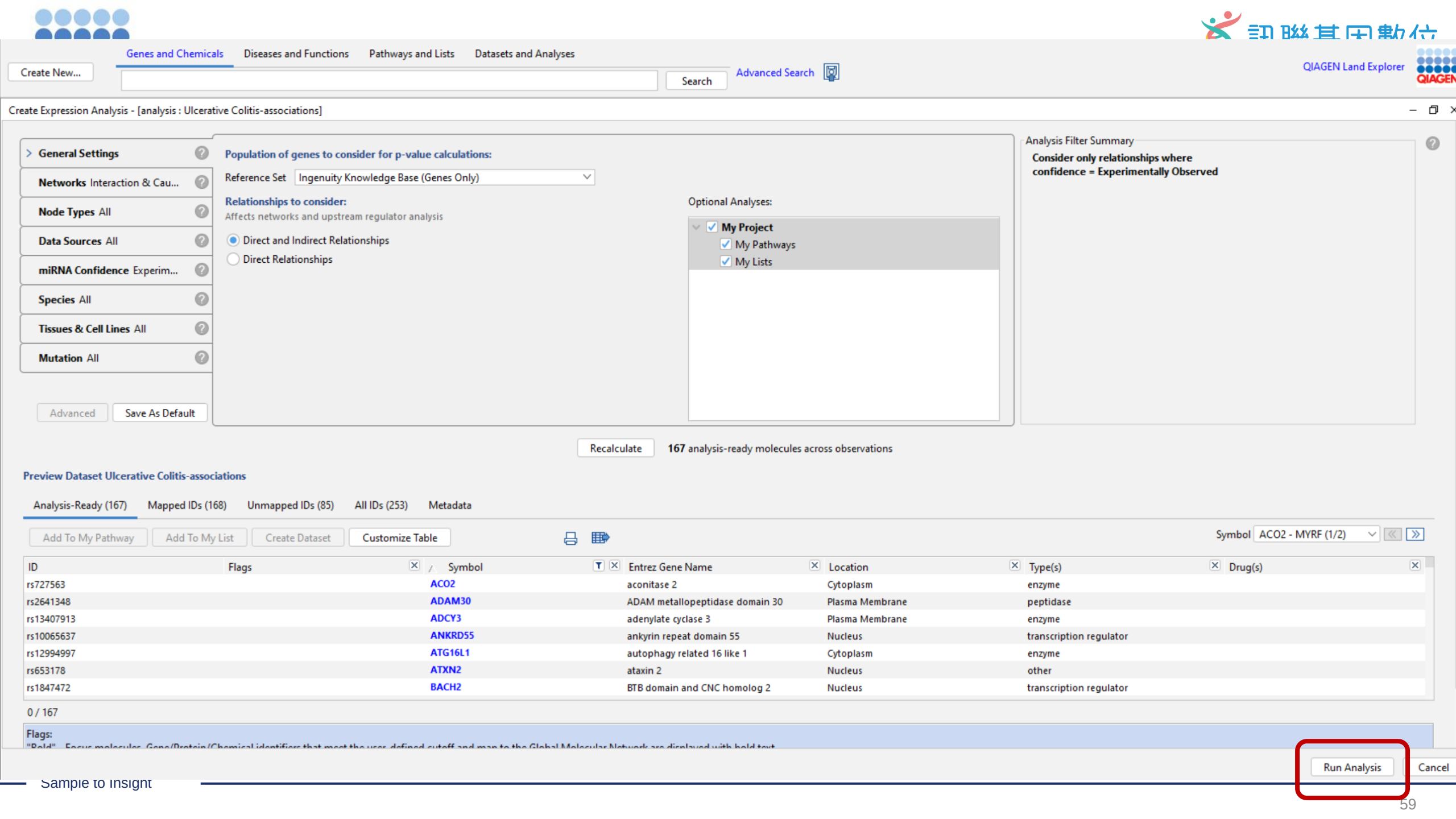
Flags:
"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.
"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with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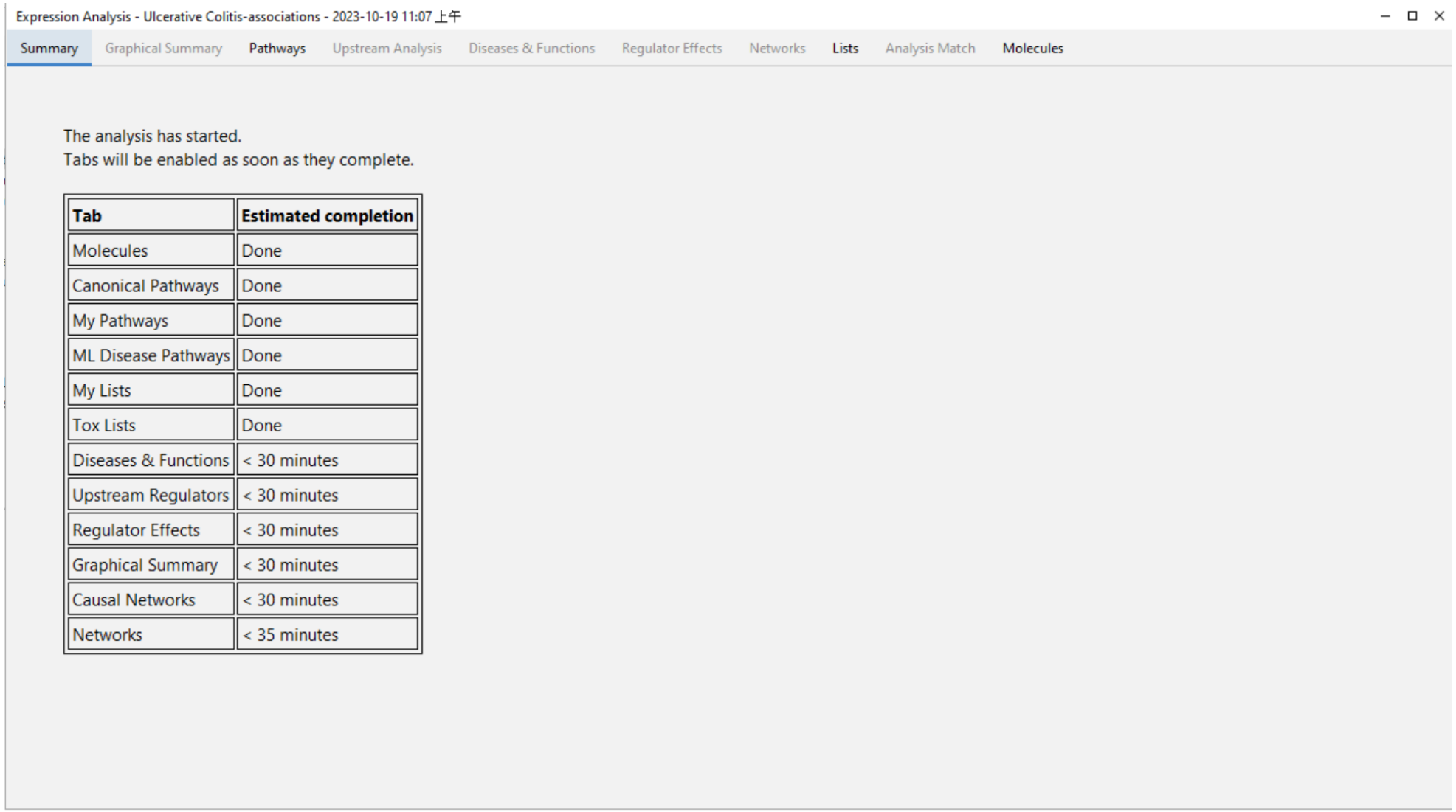
Edit Dataset Settings | Analyze/Filter Dataset | Close


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Core Analysis...
Comparison Analysis...
Biomarker Filter...
Biomarker Comparison Analysis...
MicroRNA Target Filter...
BioProfiler
IsoProfiler
My Pathway
Path Designer
Filter Dataset
Upload Dataset...
Advanced Search
Project...
Compare
Import Pathway
Search
Advanced Search
QIAGEN Land Explorer
All IDs (501)
Metadata
List
Create Dataset
Customize Table
Symbol ACO2 - GNA12 (1/4)
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
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
Flags:
"D" - Duplicates. Gene/Protein/Chemical identifiers marked with an asterisk indicate that multiple identifiers in the dataset file map to a single gene/chemical in the Global Molecular Network.
"O" - Override molecules. Gene/Protein/Chemical identifiers marked as "Override" are displayed with italic text.
"A" - Gene/Protein/Chemical ID marked as Absent. The gene/protein/chemical will not be used as a focus molecule or appear in networks unless you also explicitly override this flag with the Override column.
Edit Dataset Settings
Analyze/Filter Dataset
Close


Genes and Chemicals
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Datasets and Analyses
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QIAGEN Land Explorer
Annotated Dataset: Ulcerative Colitis-associations2
Preview Dataset Ulcerative Colitis-associations2
Mapped IDs (335)
Unmapped IDs (166)
All IDs (501)
Metadata
Add To My Pathway
Add To My List
Create Dataset
Customize Table
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
Create Core Analysis
Upload
My Projects
GWAS
Ulcerative Colitis-associations2
myList
colon cancer-association
Ulcerative Colitis-associations
Shared Projects
Projects Shared with Others
Next
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.
Edit Dataset Settings
Analyze/Filter Dataset
Close


Genes and Chemicals
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Annotated Dataset: Ulcerative Colitis-associations2
Preview Dataset Ulcerative Colitis-associations2
Mapped IDs (335)
Unmapped IDs (166)
All IDs (501)
Metadata
Add To My Pathway
Add To My List
Create Dataset
Customize Table
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
Back
Next
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.
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Edit Dataset Settings
Analyze/Filter Dataset
Close
ChatDOC 和其他 1 個頁面 - 個人 - Microsoft Edge


Genes and Chemicals
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Pathways and Lists
Datasets and Analyses
Create New...
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QIAGEN Land Explorer
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
Advanced
Save As Default
Population of genes to consider for p-value calculations:
Reference Set
Ingenuity Knowledge Base (Genes Only)
Relationships to consider:
Affects networks and upstream regulator analysis
Direct and Indirect Relationships
Direct Relationships
Optional Analyses:
My Project
My Pathways
My Lists
Analysis Filter Summary
Consider only relationships where
confidence = Experimentally Observed
Recalculate
167 analysis-ready molecules across observations
Preview Dataset Ulcerative Colitis-associations
Analysis-Ready (167)
Mapped IDs (168)
Unmapped IDs (85)
All IDs (253)
Metadata
Add To My Pathway
Add To My List
Create Dataset
Customize Table
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:
Run Analysis
Cancel



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

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

Export :

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

1 2 3 4 5 6 7 8 9 >

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	

1 2 3 4 5 6 7 8 9 >

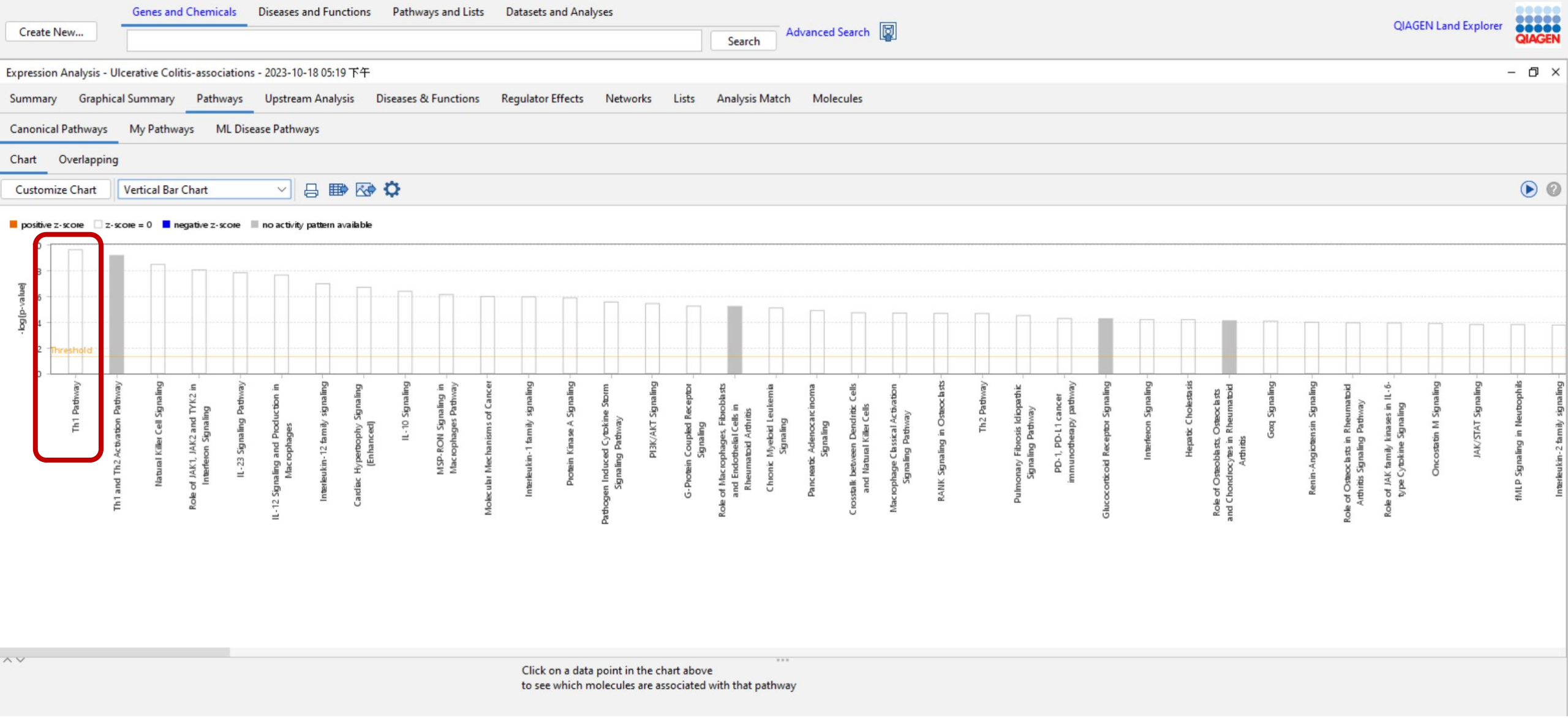
Causal Network

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	

1 2 3 4 5 6 7 8 9 >

Top Diseases and Bio Functions

Diseases and Disorders


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Molecules
Canonical Pathways
My Pathways
ML Disease Pathways
Chart
Overlapping
Customize Chart
Vertical Bar Chart
positive z-score
z-score = 0
negative z-score
no activity pattern available
-log[p-value]
Threshold
Th1 Pathway
Th1 and Th2 Activation Pathway
Natural Killer Cell Signaling
Role of JAK1, JAK2 and TYK2 in Interferon Signaling
IL-23 Signaling Pathway
IL-12 Signaling and Production in Macrophages
Interleukin-12 family signaling
Cardiac Hypertrophy Signaling (Enhanced)
IL-10 Signaling
MSP-RON Signaling in Macrophages Pathway
Molecular Mechanisms of Cancer
Interleukin-1 family signaling
Protein Kinase A Signaling
Pathogen Induced Cytokine Storm Signaling Pathway
PI3K/AKT Signaling
G-Protein Coupled Receptor Signaling
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis
Chronic Myeloid Leukemia Signaling
Pancreatic Adenocarcinoma Signaling
Crosstalk between Dendritic Cells and Natural Killer Cells
Macrophage Classical Activation Signaling Pathway
RANK Signaling in Osteoclasts
Th2 Pathway
Pulmonary Fibrosis Idiopathic Signaling Pathway
PD-1, PD-L1 cancer immunotherapy pathway
Glucocorticoid Receptor Signaling
Interferon Signaling
Hepatic Cholestasis
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis
Gαq Signaling
Renin-Angiotensin Signaling
Role of Osteoclasts in Rheumatoid Arthritis Signaling Pathway
Role of JAK family kinases in IL-6-type Cytokine Signaling
Oncostatin M Signaling
JAK/STAT Signaling
fMLP Signaling in Neutrophils
Interleukin-2 family signaling
Click on a data point in the chart above
to see which molecules are associated with that pathway

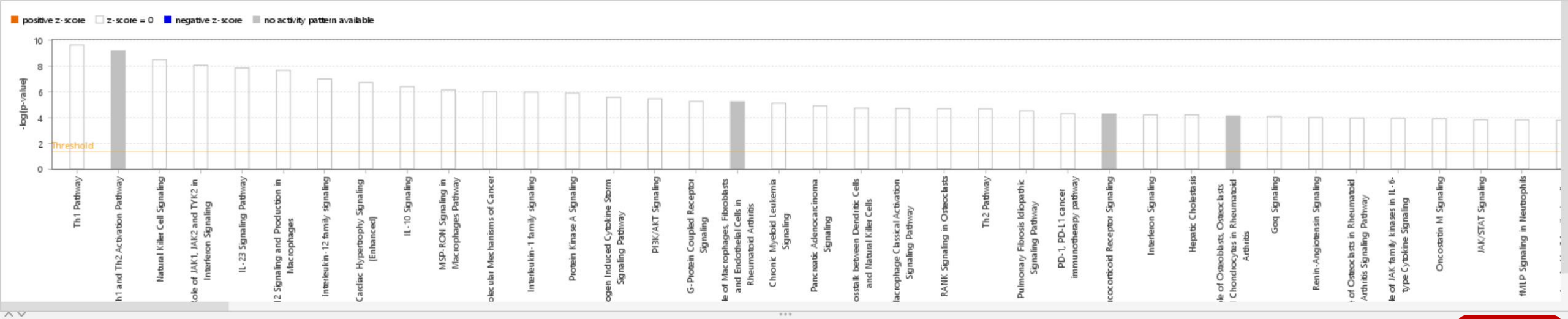
Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

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

Canonical Pathways | My Pathways | ML Disease Pathways

Chart | Overlapping

Customize Chart | Vertical Bar Chart



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

Activity Plot | View Report | Open Pathway

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

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

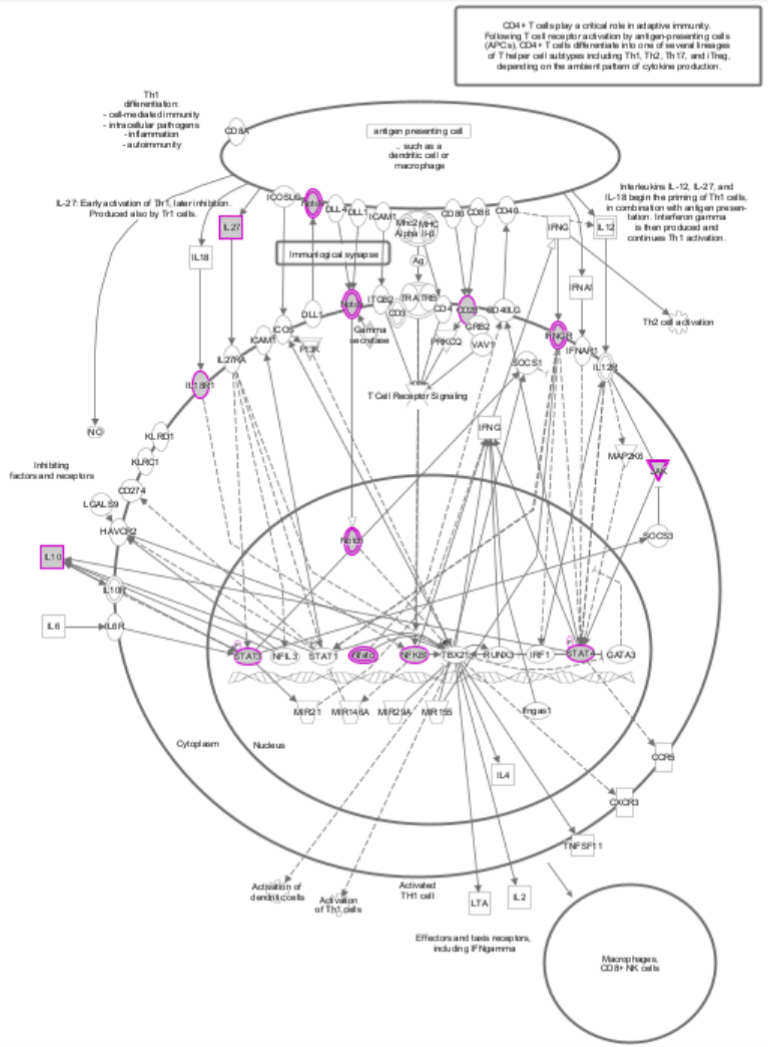
Canonical Pathways

Th1 Pathway

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

Th1 Pathway

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



Hide

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

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

Upstream Regulators | Causal Networks

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

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

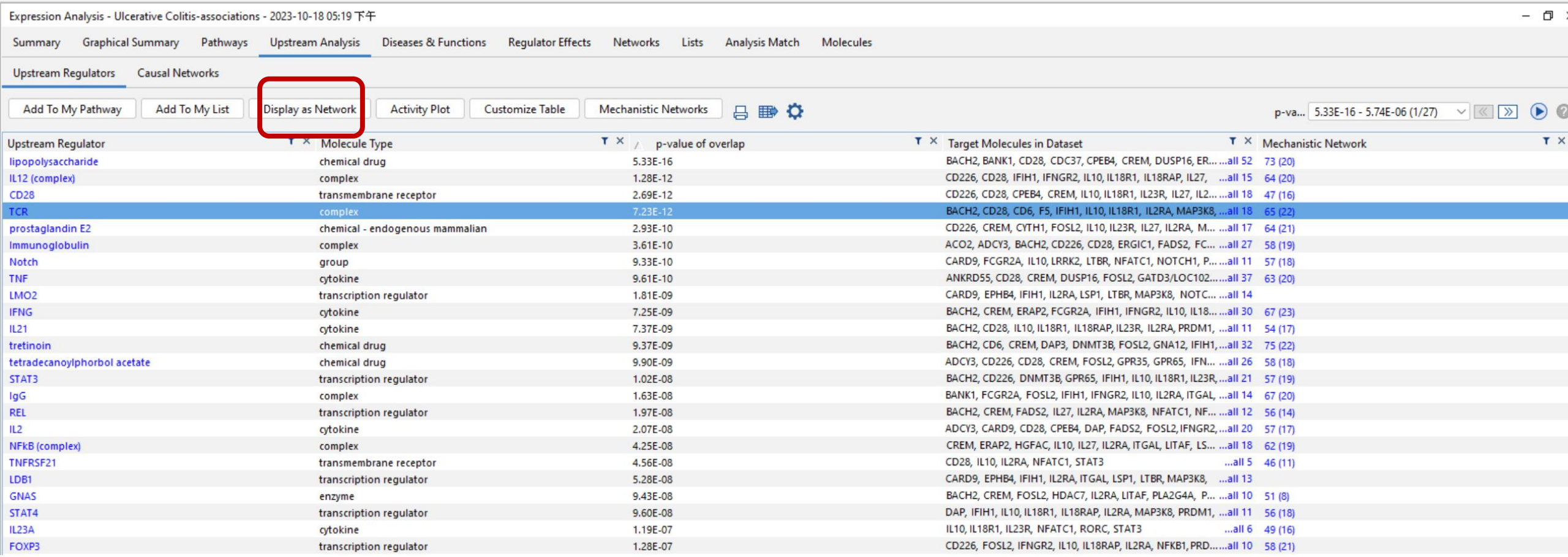
Upstream Regulator	Molecule Type	p-value of overlap	Target Molecules in Dataset	Mechanistic Network
lipopolysaccharide	chemical drug		BACH2, BANK1, CD28, CDC37, CPEB4, CREM, DUSP16, ER... ...all 52	73 (20)
IL12 (complex)	complex		CD226, CD28, IFIH1, IFNGR2, IL10, IL18R1, IL18RAP, IL27, ...all 15	64 (20)
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		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)

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

Apply | Cancel

Selected 0 / 1316



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

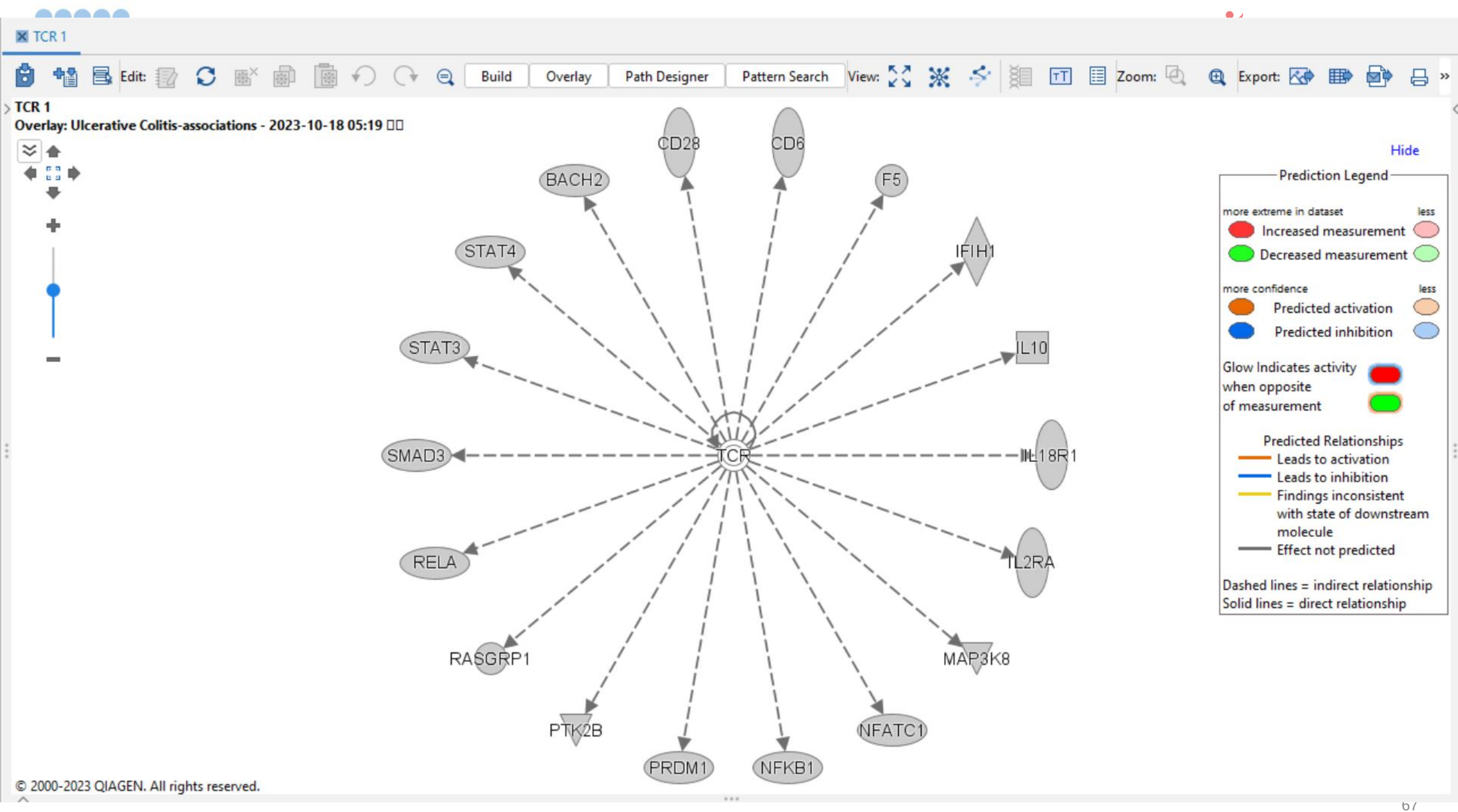
Summary | Graphical Summary | Pathways | Upstream Analysis | Diseases & Functions | Regulator Effects | Networks | Lists | Analysis Match | Molecules

Upstream Regulators | Causal Networks

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

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

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)
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FOXP3	transcription regulator	1.28E-07	CD226, FOSL2, IFNGR2, IL10, IL18RAP, IL2RA, NFKB1, PRD... ...all 10	58 (21)


TCR 1
Build
Overlay
Path Designer
Pattern Search
Edit:
View:
Zoom:
Export:
TCR 1
Overlay: Ulcerative Colitis-associations - 2023-10-18 05:19
Hide
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
CD28
CD6
BACH2
F5
STAT4
IFIH1
STAT3
IL10
SMAD3
TCR
IL18R1
RELA
IL2RA
RASGRP1
MAP3K8
PTK2B
NFATC1
PRDM1
NFKB1
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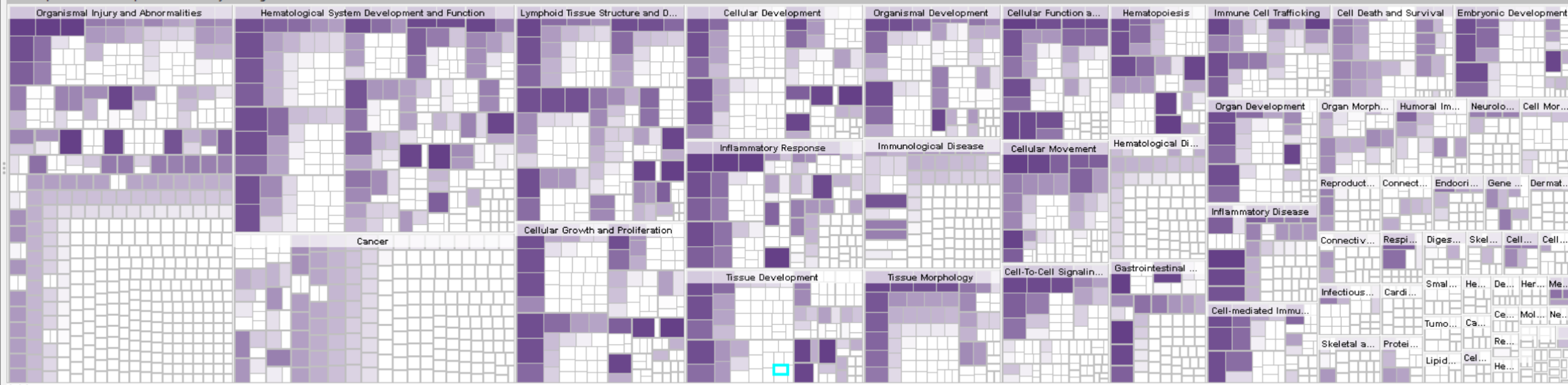
Expression Analysis - Ulcerative Colitis-associations - 2023-10-18 05:19 下午

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

Diseases and Bio Functions | Tox Functions

Size by: -log(p-value) Color by: -log(p-value) -log(p-value) <5.872 18.416-log(p-value) Highlight: None Show Label Show Barchart

Click squares below to explore Currently Viewing: All



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

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

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

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

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

Symbol ACO2 - MYRF (1/2)

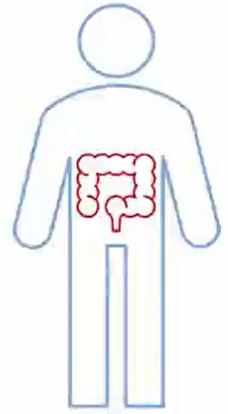
Symbol	Entrez Gene Name	Identifier (dbSNP/Gene Symbol - human (HU...)	Location	Type(s)	Biomarker Application(s)	Drug(s)
ACO2	aconitase 2	rs727563	Cytoplasm	enzyme		
ADAM30	ADAM metallopeptidase domain 30	rs2641348	Plasma Membrane	peptidase		
ADCY3	adenylate cyclase 3	rs13407913	Plasma Membrane	enzyme		
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

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.



Ulcerative Colitis GWAS

(PMID: 26192919)

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

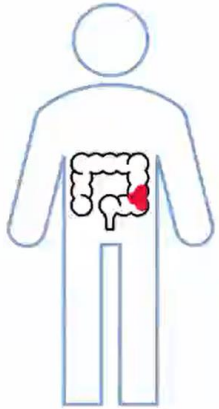
Matsuda K, Hashiguchi Y, Asako K, Okada Y, Ohno K, Tsukamoto M, Fukushima Y, Shimada R, Ozawa T, Hayama T, Nozawa K, Fukagawa T, Kikuchi Y, Sasajima Y.

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



Colorectal Cancer GWAS

(PMID: 36539618)

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

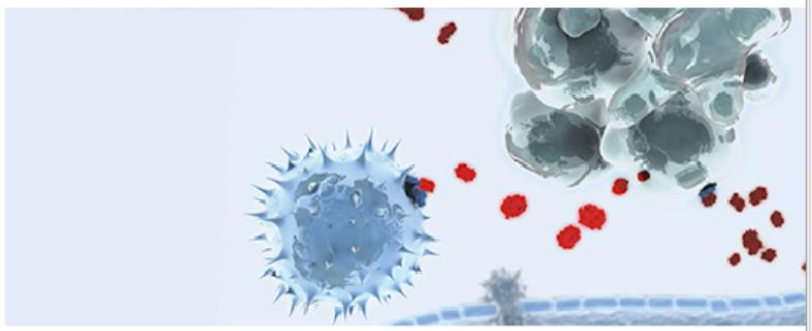
- Core Analysis...
- Comparison Analysis...
- Biomarker Filter...
- Biomarker Comparison Analysis...
- MicroRNA Target Filter...
- BioProfiler
- IsoProfiler
- My Pathway
- Path Designer
- Filter Dataset
- Upload Dataset...
- Advanced Search
- Project...
- Compare
- Import Pathway

A-Z Sort | Refresh

associations - 2023-10-19 11:07 □□
ciation - 2023-10-18 05:52 □□
associations - 2023-10-18 05:19 □□
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My Lists
Human Genes Chromosomal Location
QIAGEN Coronavirus Networks
Ingenuity KEGG gene lists
Tissue Expression
Example Analyses
Training
Shared Projects

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or proteomics data
NA data
hoproteomics data
Analyzing genetic gain/loss data
Analyzing metabolomics data
Case studies and Support webinars
Top help articles and FAQs
Contacting Support
Shortcuts



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 (No
  - **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.

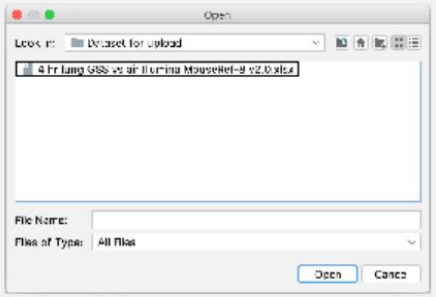
Don't Show at Startup

Dataset Upload Workflow Instructions

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

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

Project Manager

A-Z Sort

- My Projects
  - GWAS
    - Dataset Files
    - 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
    - Comparison Analyses
    - Biomarker Filter Results
    - Biomarker Comparison Analyses
    - MicroRNA Target Filter Results
    - BioProfiler Results
    - IsoProfiler Results
    - My Pathways
    - My Lists
  - Human Genes Chromosomal Location
  - QIAGEN Coronavirus Networks
  - Ingenuity KEGG gene lists
  - Tissue Expression
  - Example Analyses
  - Training
- Shared Projects

Create Comparison Analysis

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

Create Comparison Analysis

Select Analyses | A-Z Sort

- My Projects
  - GWAS
    - Ulcerative Colitis-associations - 2023-
    - colon cancer-association - 2023-10-18
    - Ulcerative Colitis-associations - 2023-
- Shared Projects

Add »

Analyses to Compare

- Ulcerative Colitis-associations - 2023-10-18 05:1
- colon cancer-association - 2023-10-18 05:52

Move Up | Move Down

« Remove

View Comparison | Cancel

Comparison Analysis Workflow Instructions

arison Analyses Workflow

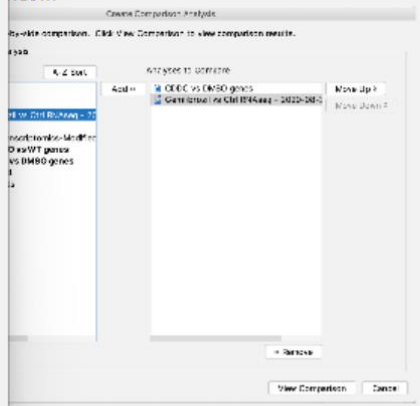
Analyses are available for Core, Tox and Metabolomics analyses.

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".

rmation, 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**.

Read our news and sign up for our newsletter.

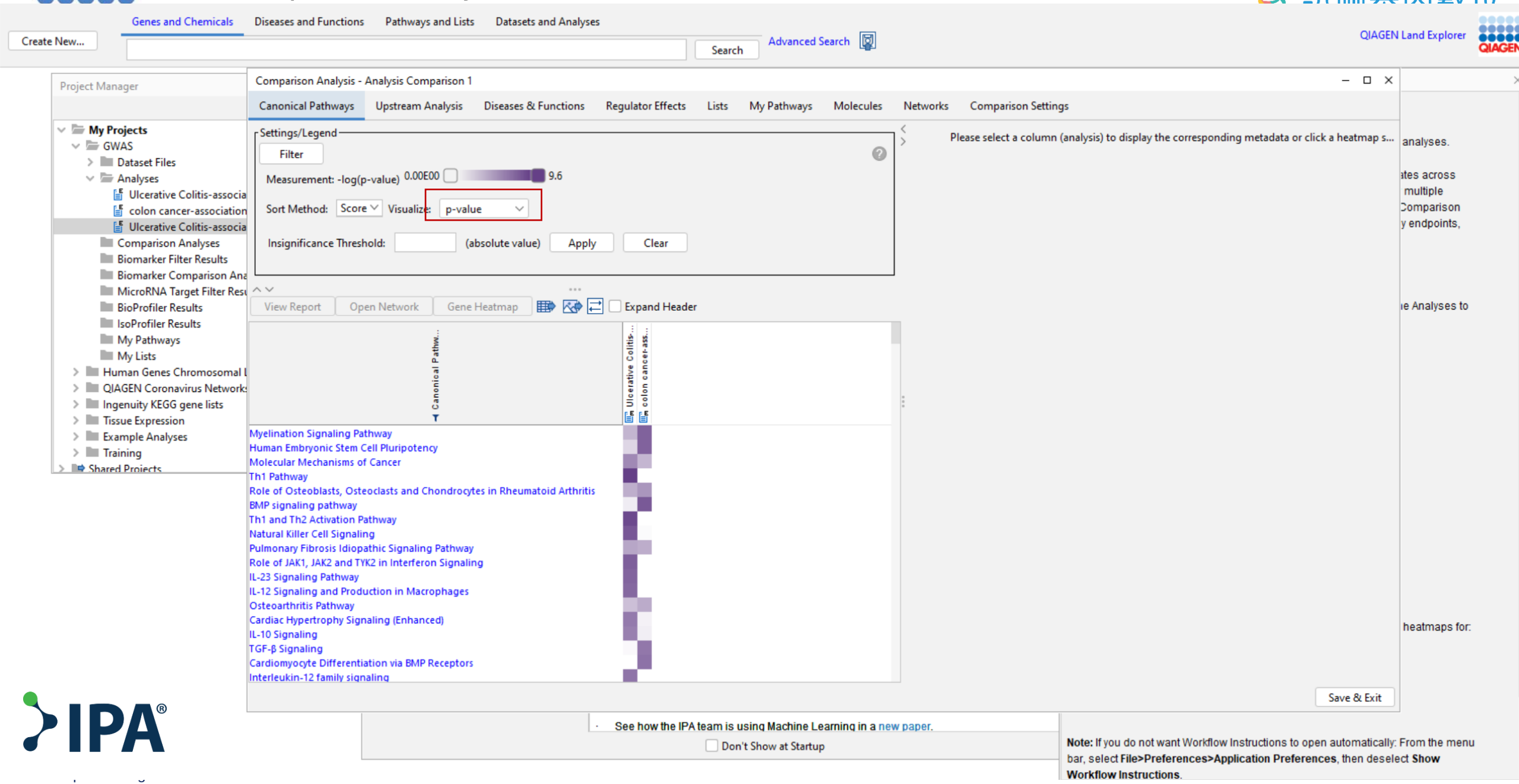
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See how the IPA team is using Machine Learning in a new paper.

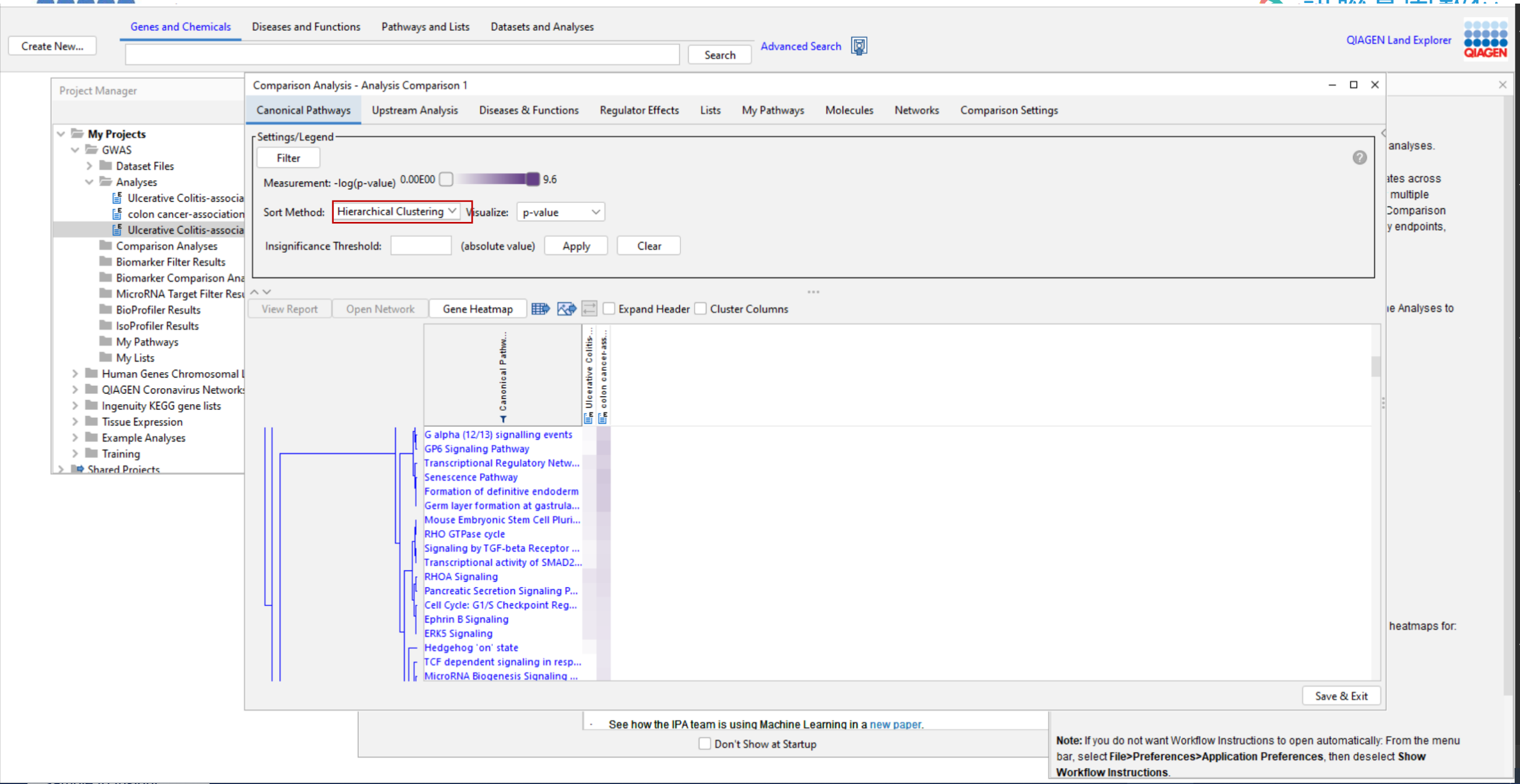
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Comparison Analysis – P-value



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


Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses
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Advanced Search
QIAGEN Land Explorer
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BioProfiler Results
IsoProfiler Results
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Ingenuity KEGG gene lists
Tissue Expression
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Training
Shared Projects
Comparison Analysis - Analysis Comparison 1
Canonical Pathways
Upstream Analysis
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Hierarchical Clustering
Visualize:
p-value
Insignificance Threshold:
(absolute value)
Apply
Clear
View Report
Open Network
Gene Heatmap
Expand Header
Cluster Columns
Canonical Pathw...
Ulcerative Colitis-...
colon cancer-ass...
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 ...
Save & Exit
analyses.
tes 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
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.

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

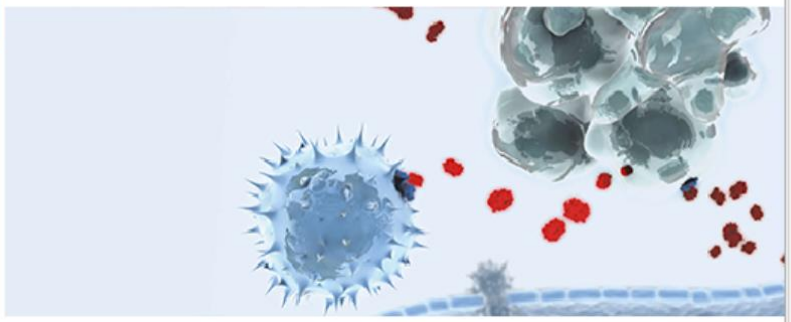
- Core Analysis...
- Comparison Analysis...
- Biomarker Filter...
- Biomarker Comparison Analysis...
- MicroRNA Target Filter...
- BioProfiler
- IsoProfiler
- My Pathway
- Path Designer
- Filter Dataset
- Upload Dataset...
- Advanced Search
- Project...
- Compare
- Import Pathway

A-Z Sort | Refresh

associations - 2023-10-19 11:07 □□
ciation - 2023-10-18 05:52 □□
associations - 2023-10-18 05:19 □□
es
ults
son Analyses
ter Results

My Lists
Human Genes Chromosomal Location
QIAGEN Coronavirus Networks
Ingenuity KEGG gene lists
Tissue Expression
Example Analyses
Training
Shared Projects

ublic data resources
wledge
or proteomics data
NA data
oproteomics data
Analyzing genetic gain/loss data
Analyzing metabolomics data
Case studies and Support webinars
Top help articles and FAQs
Contacting Support
Shortcuts



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 (No
  - **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.

Don't Show at Startup

Comparison Analysis Workflow Instructions

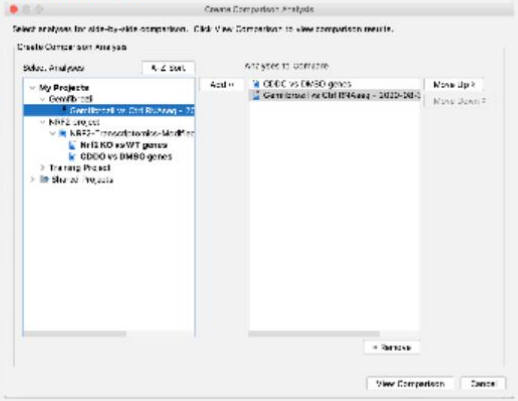
Comparison Analyses Workflow

Comparison Analyses are available for Core, Tox and Metabolomics analyses.

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

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**.

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

Compare

Select Entities to compare and click Add

Refresh

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

Show All

Add »

« Remove

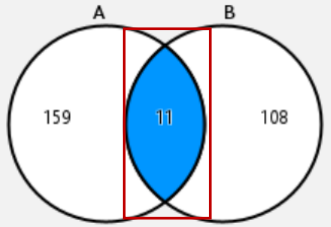
Clear All

Calculate intersections

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

Add To My Pathway | Add To My List | Annotations

s Workflow

e, Tox and Metabolomics analyses.

changes in biological states across
olomics Analysis on your multiple
e treatments. Then use Comparison
cesses, clinical pathology endpoints,
n timepoint or dose.

e.

lick Add to add them to the Analyses to

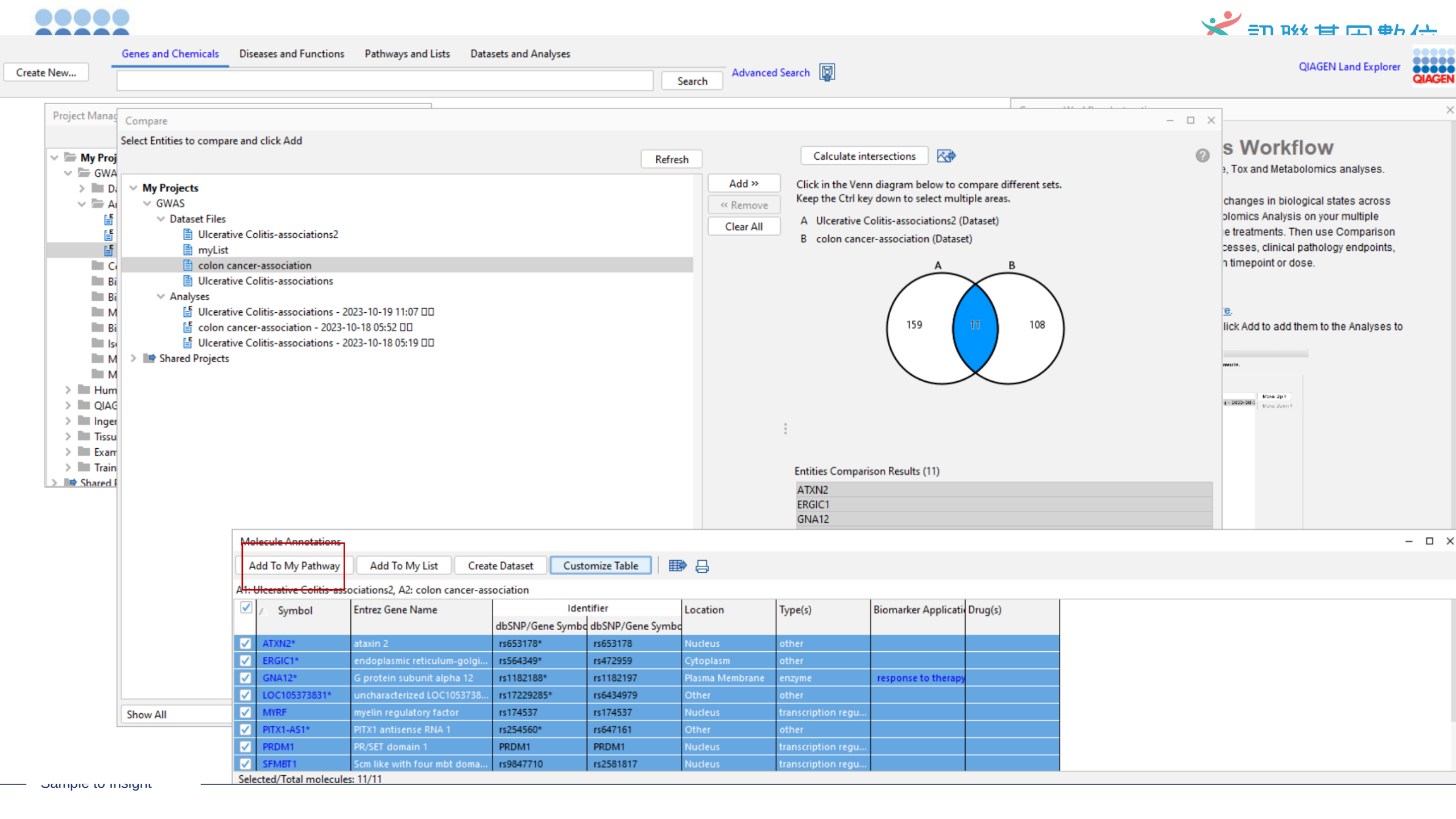
or Comparison Analysis heatmaps for:

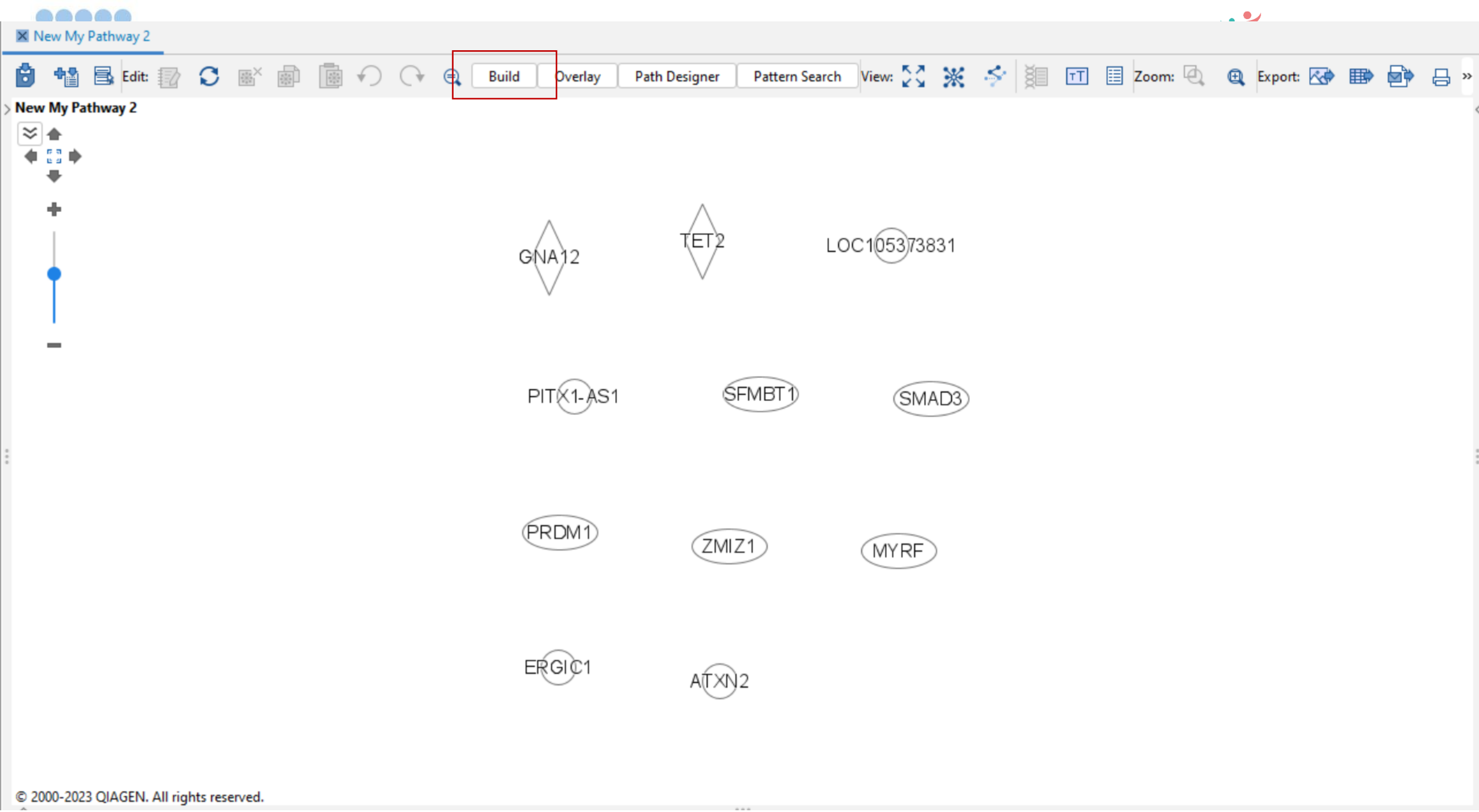
See how the IPA team is using Machine Learning in a new paper.

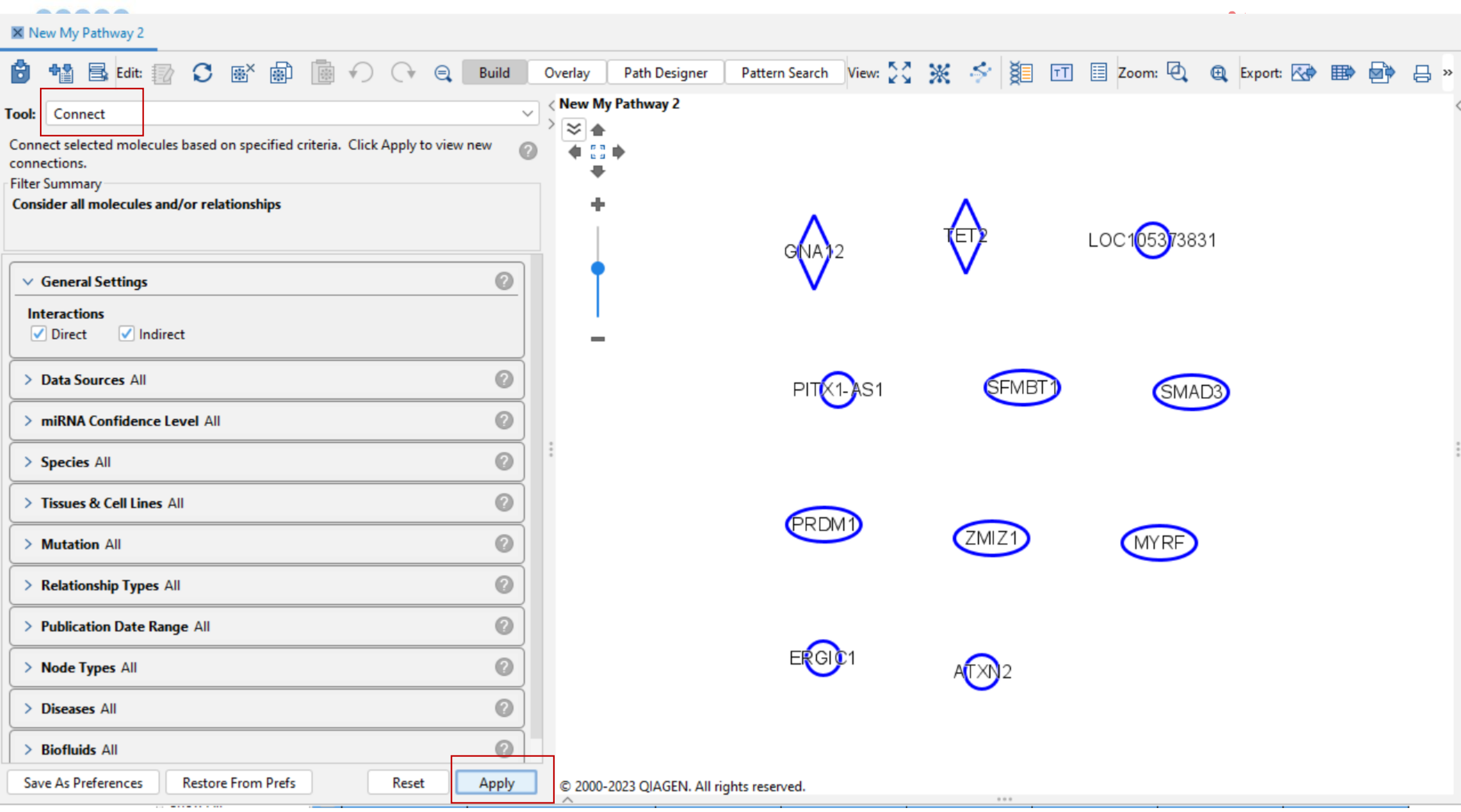
Don't Show at Startup

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**.

Sample to Insight


Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses
Create New...
Search
Advanced Search
QIAGEN Land Explorer
Compare
Select Entities to compare and click Add
Refresh
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
Add »
« Remove
Clear All
Calculate intersections
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)
A
B
159
11
108
Entities Comparison Results (11)
ATXN2
ERGIC1
GNA12
Show All
Molecule Annotations
Add To My Pathway
Add To My List
Create Dataset
Customize Table
A1: Ulcerative Colitis-associations2, A2: colon cancer-association
Symbol
Entrez Gene Name
Identifier
dbSNP/Gene Symbo
dbSNP/Gene Symbo
Location
Type(s)
Biomarker Applicati
Drug(s)
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
s Workflow
, Tox and Metabolomics analyses.
changes in biological states across
olomics Analysis on your multiple
e treatments. Then use Comparison
cesses, clinical pathology endpoints,
timepoint or dose.
e.
lick Add to add them to the Analyses to


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
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New My Pathway 2
Edit:
Build
Overlay
Path Designer
Pattern Search
View:
Zoom:
Export:
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
Save As Preferences
Restore From Prefs
Reset
Apply
New My Pathway 2
GNA12
TET2
LOC105373831
PITX1-AS1
SFMBT1
SMAD3
PRDM1
ZMIZ1
MYRF
ERGIC1
ATXN2
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New My Pathway 2

Edit: | Build | Overlay | Path Designer | Pattern Search | View: | Zoom: | Export:

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

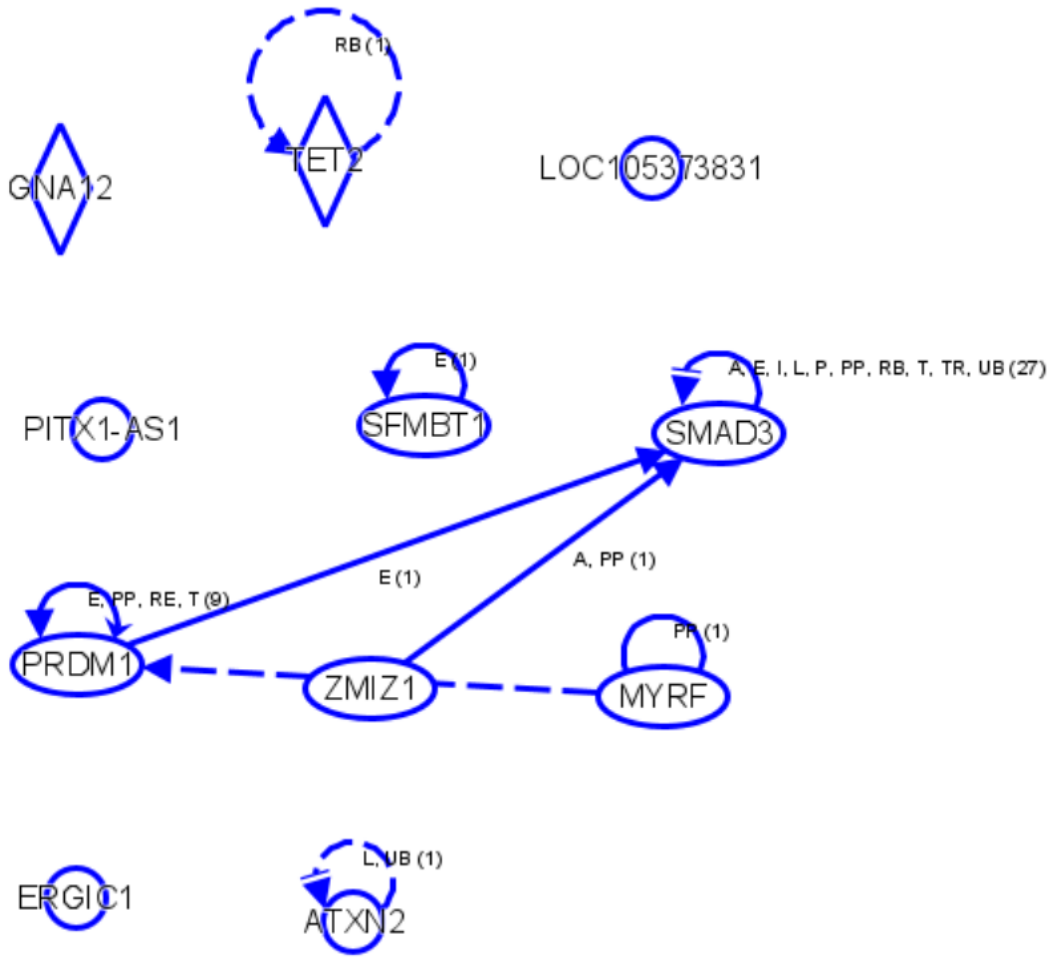
Node Types All

Diseases All

Biofluids All

Save As Preferences | Restore From Prefs | Reset | Apply

New My Pathway 2



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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.

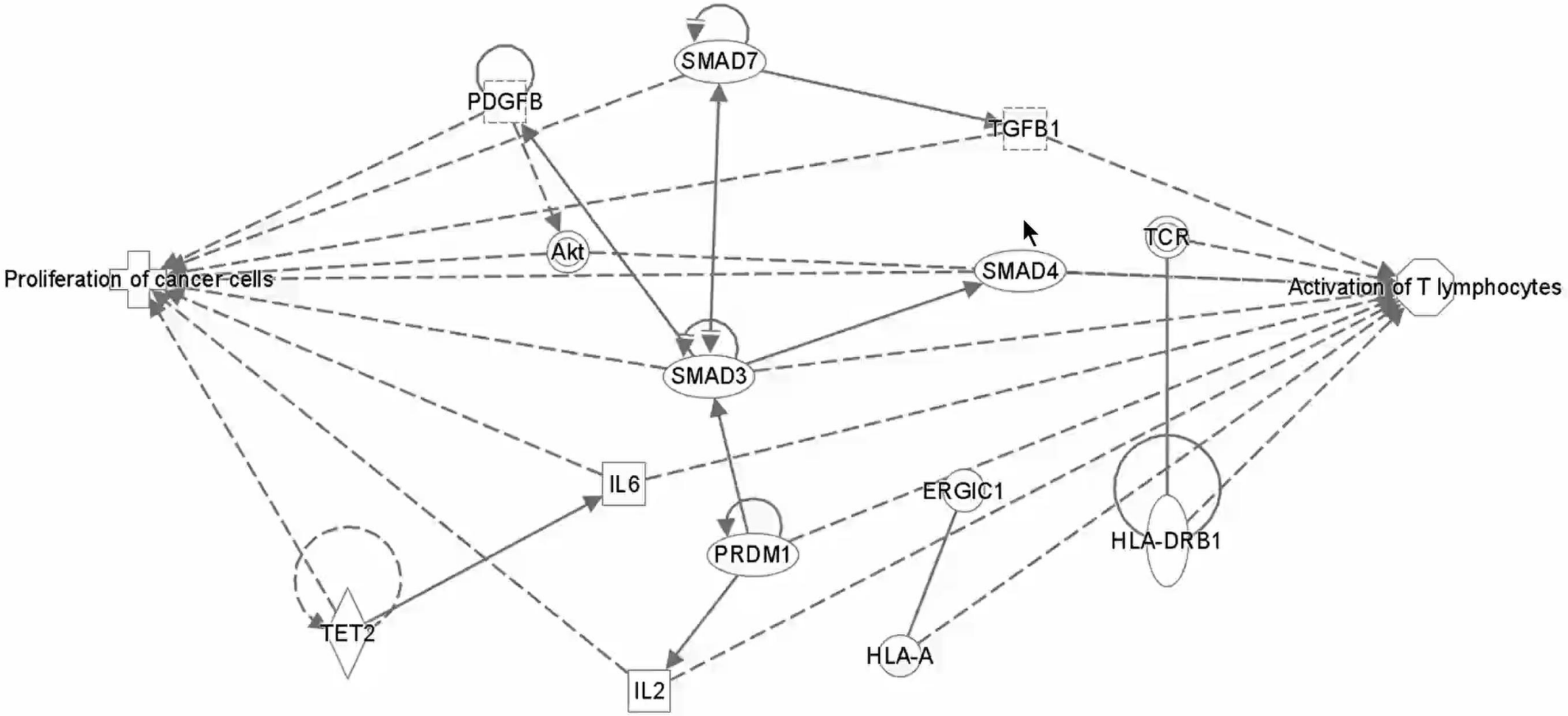
Cytotoxic T lymphocytes efficiently recognize human colon cancer stem-like cells

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





訊磁基因動位

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

Create New... | Search | Advanced Search | QIAGEN Land Explorer

Annotated Dataset: myList

Preview Dataset myList

Mapped IDs (16) | Unmapped IDs (0) | All IDs (16) | Metadata

Add To My Pathway | New My Pathway | Saved My Pathway | New My Pathway 6 | eate Dataset | Customize Table

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.

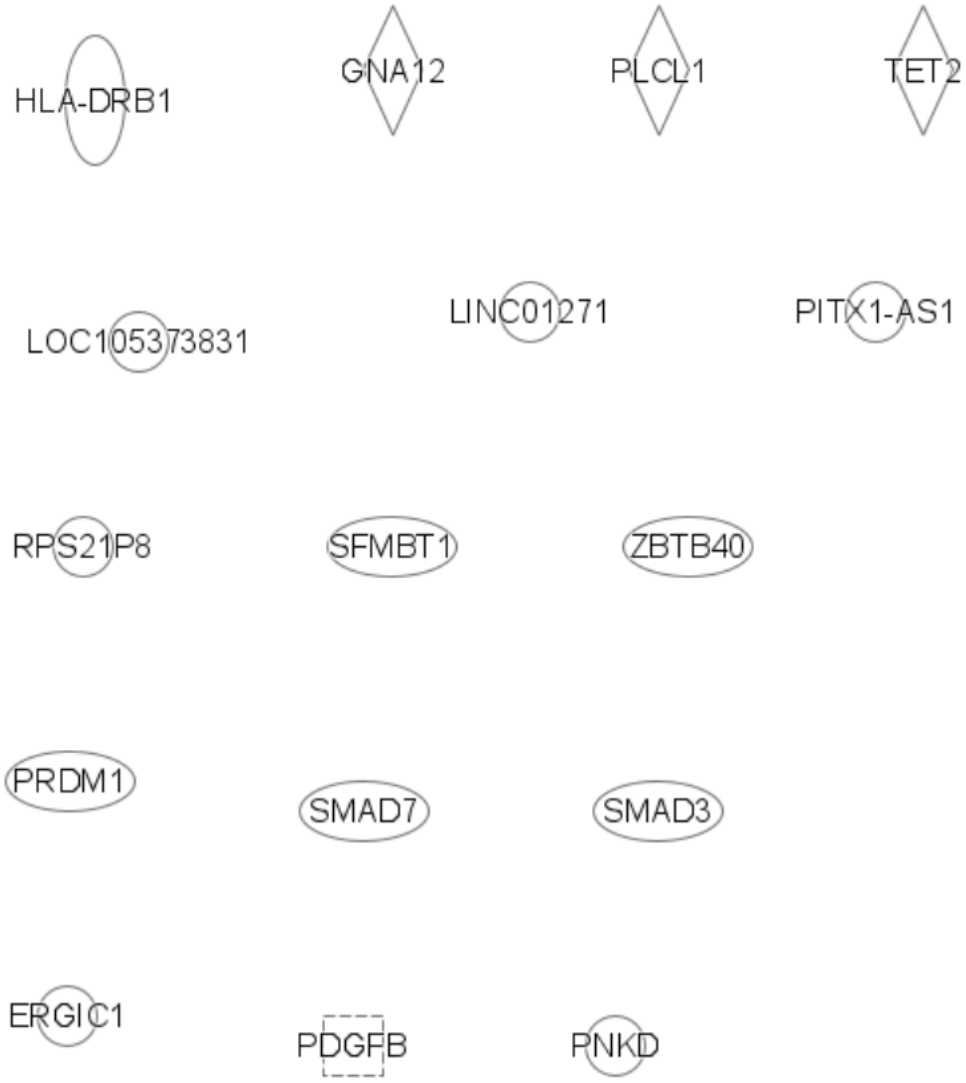
Edit Dataset Settings | Analyze/Filter Dataset | Close

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

New My Pathway 6



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My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

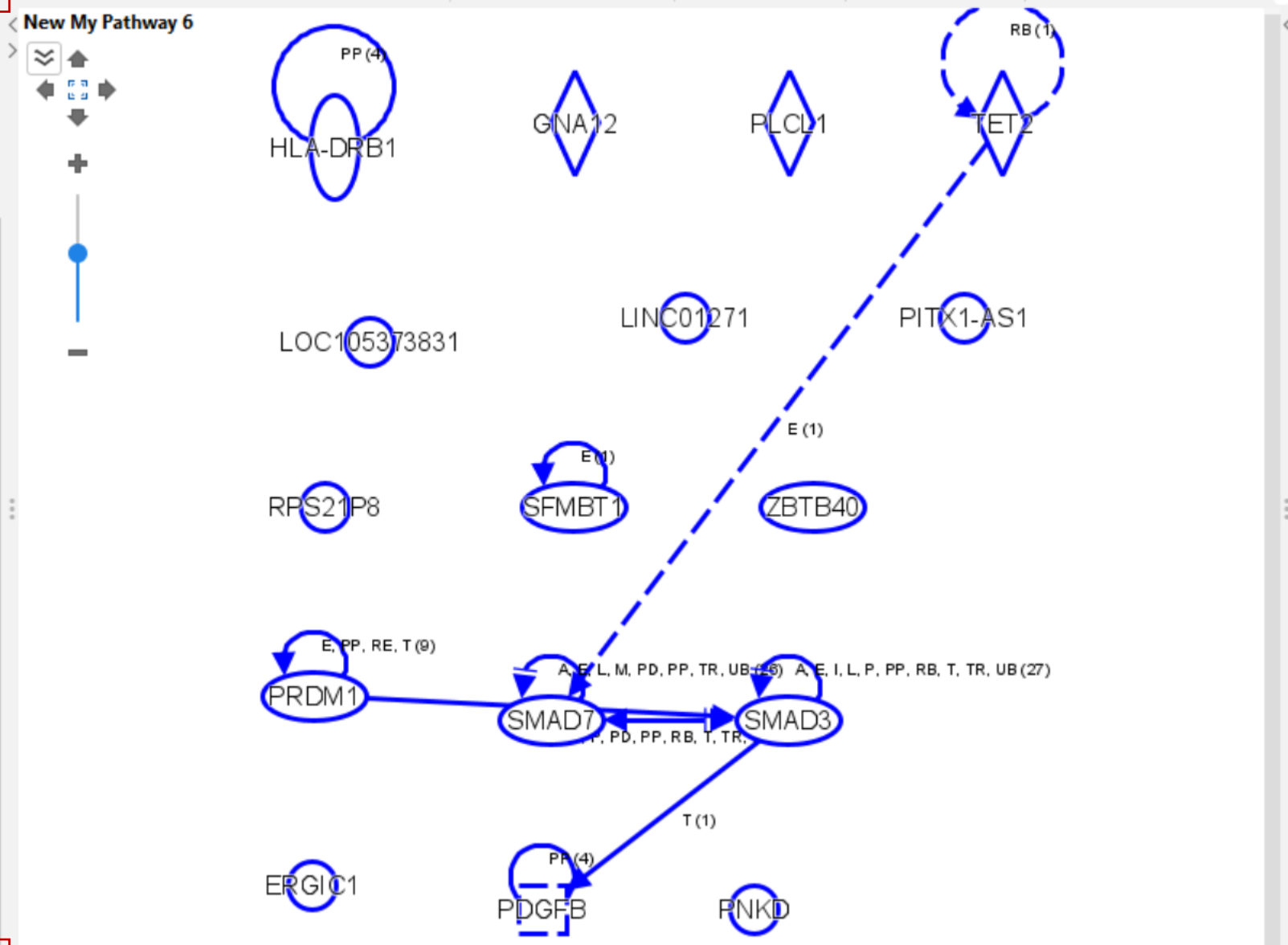
Publication Date Range All

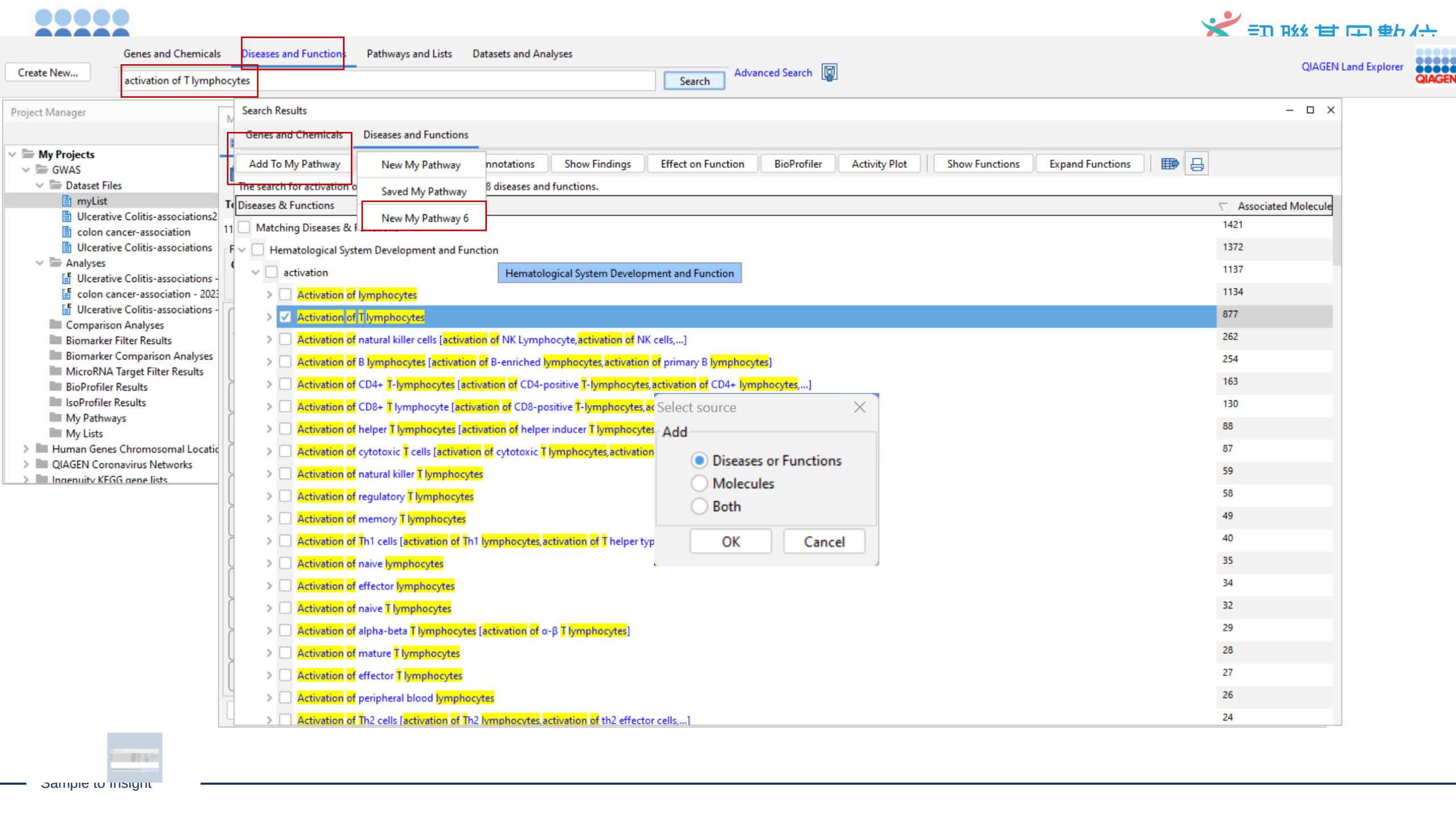
Node Types All

Diseases All

Biofluids All

Save As Preferences | Restore From Prefs | Reset | Apply




Genes and Chemicals
Diseases and Functions
Pathways and Lists
Datasets and Analyses
Create New...
activation of T lymphocytes
Search
Advanced Search
QIAGEN Land Explorer
Project Manager
My Projects
GWAS
Dataset Files
myList
Ulcerative Colitis-associations2
colon cancer-association
Ulcerative Colitis-associations
Analyses
Ulcerative Colitis-associations -
colon cancer-association - 2023
Ulcerative Colitis-associations -
Comparison Analyses
Biomarker Filter Results
Biomarker Comparison Analyses
MicroRNA Target Filter Results
BioProfiler Results
IsoProfiler Results
My Pathways
My Lists
Human Genes Chromosomal Locatic
QIAGEN Coronavirus Networks
Ingenuity KEGG gene lists
Search Results
Genes and Chemicals
Diseases and Functions
Add To My Pathway
New My Pathway
Saved My Pathway
New My Pathway 6
Show Findings
Effect on Function
BioProfiler
Activity Plot
Show Functions
Expand Functions
8 diseases and functions.
Diseases & Functions
Associated Molecule
Matching Diseases &
Hematological System Development and Function
activation
Hematological System Development and Function
Activation of lymphocytes
Activation of T lymphocytes
Activation of natural killer cells [activation of NK Lymphocyte,activation of NK cells,...]
Activation of B lymphocytes [activation of B-enriched lymphocytes,activation of primary B lymphocytes]
Activation of CD4+ T-lymphocytes [activation of CD4-positive T-lymphocytes,activation of CD4+ lymphocytes,...]
Activation of CD8+ T lymphocyte [activation of CD8-positive T-lymphocytes,ac
Activation of helper T lymphocytes [activation of helper inducer T lymphocytes
Activation of cytotoxic T cells [activation of cytotoxic T lymphocytes,activation
Activation of natural killer T lymphocytes
Activation of regulatory T lymphocytes
Activation of memory T lymphocytes
Activation of Th1 cells [activation of Th1 lymphocytes,activation of T helper typ
Activation of naive lymphocytes
Activation of effector lymphocytes
Activation of naive T lymphocytes
Activation of alpha-beta T lymphocytes [activation of α-β T lymphocytes]
Activation of mature T lymphocytes
Activation of effector T lymphocytes
Activation of peripheral blood lymphocytes
Activation of Th2 cells [activation of Th2 lymphocytes,activation of th2 effector cells,...]
1421
1372
1137
1134
877
262
254
163
130
88
87
59
58
49
40
35
34
32
29
28
27
26
24
Select source
Add
Diseases or Functions
Molecules
Both
OK
Cancel

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

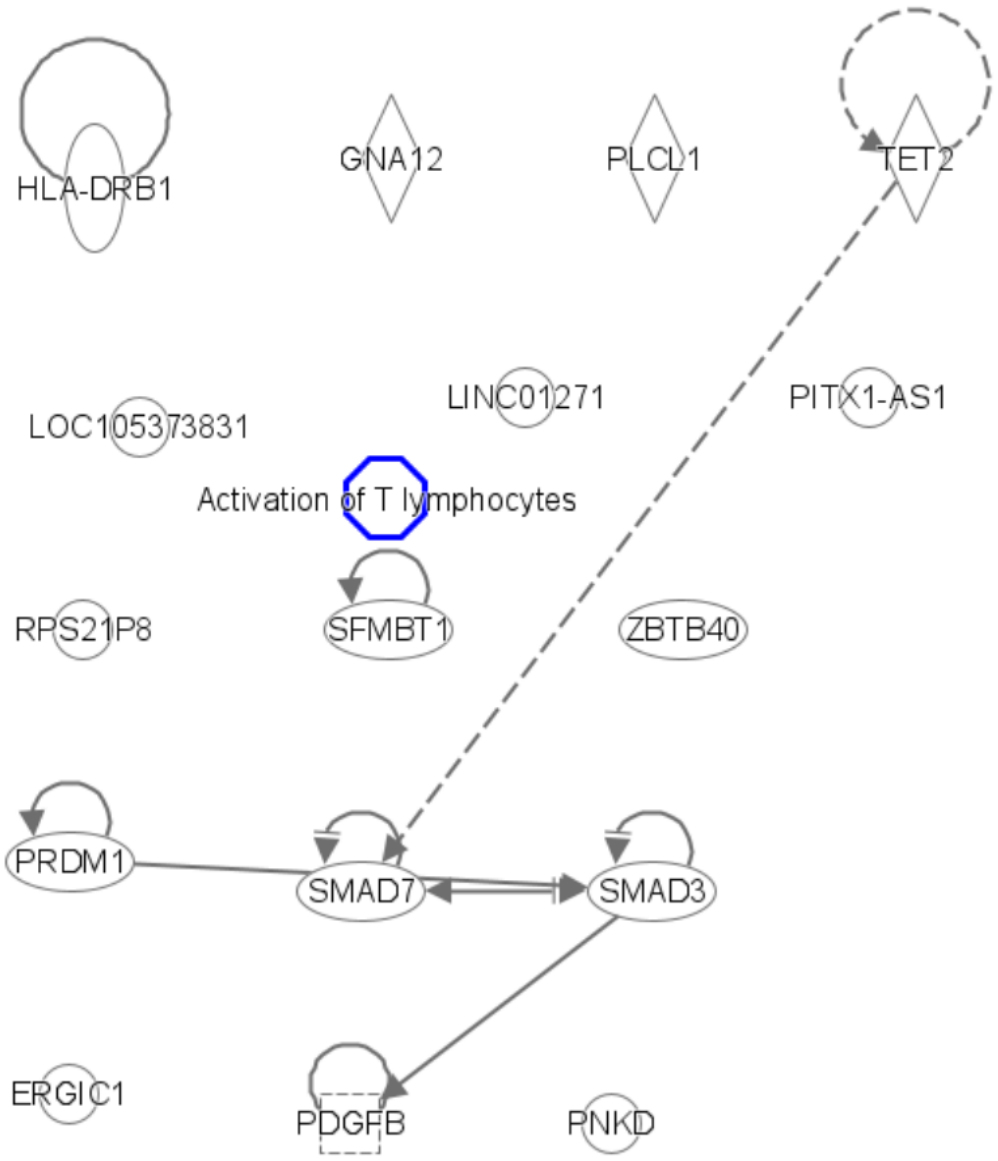
Node Types All

Diseases All

Biofluids All

Save As Preferences Restore From Prefs Reset Apply

New My Pathway 6



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Chinese (Traditiona

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

Tool: Path Explorer

Add molecules to set A and B and explore shortest path(s) based on specified criteria. Click Apply to view list of shortest path(s).

Filter Summary

Consider all molecules and/or relationships

General Settings

Interactions

Direct Indirect

Set A Add Remove

ERGIC1
GNA12
HLA-DRB1

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...

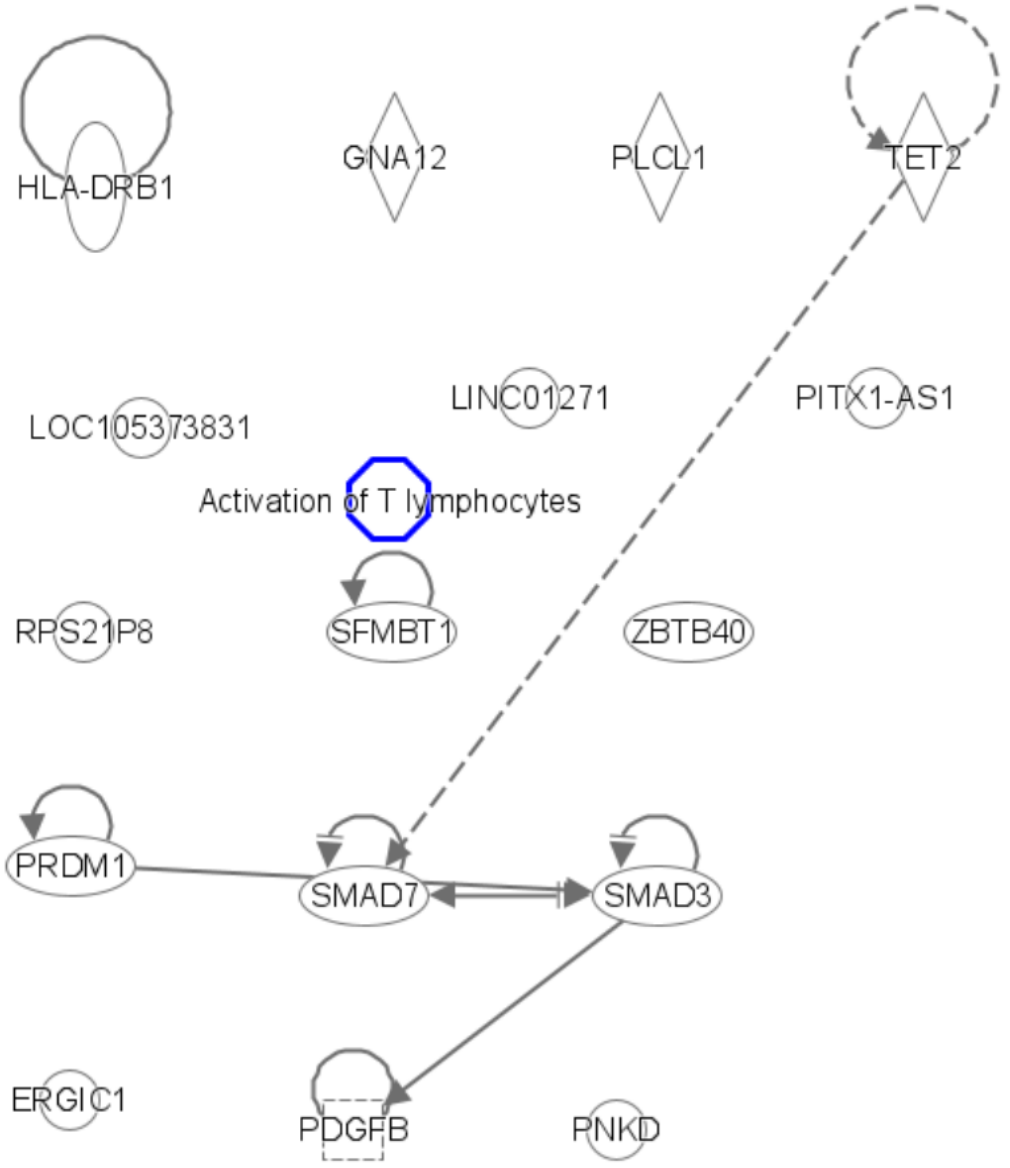
Current Analysis/Dataset/List: None selected

Change Analysis/Dataset/List

Data Sources All

Save As Preferences Restore From Prefs Reset Apply

New My Pathway 6



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My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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...

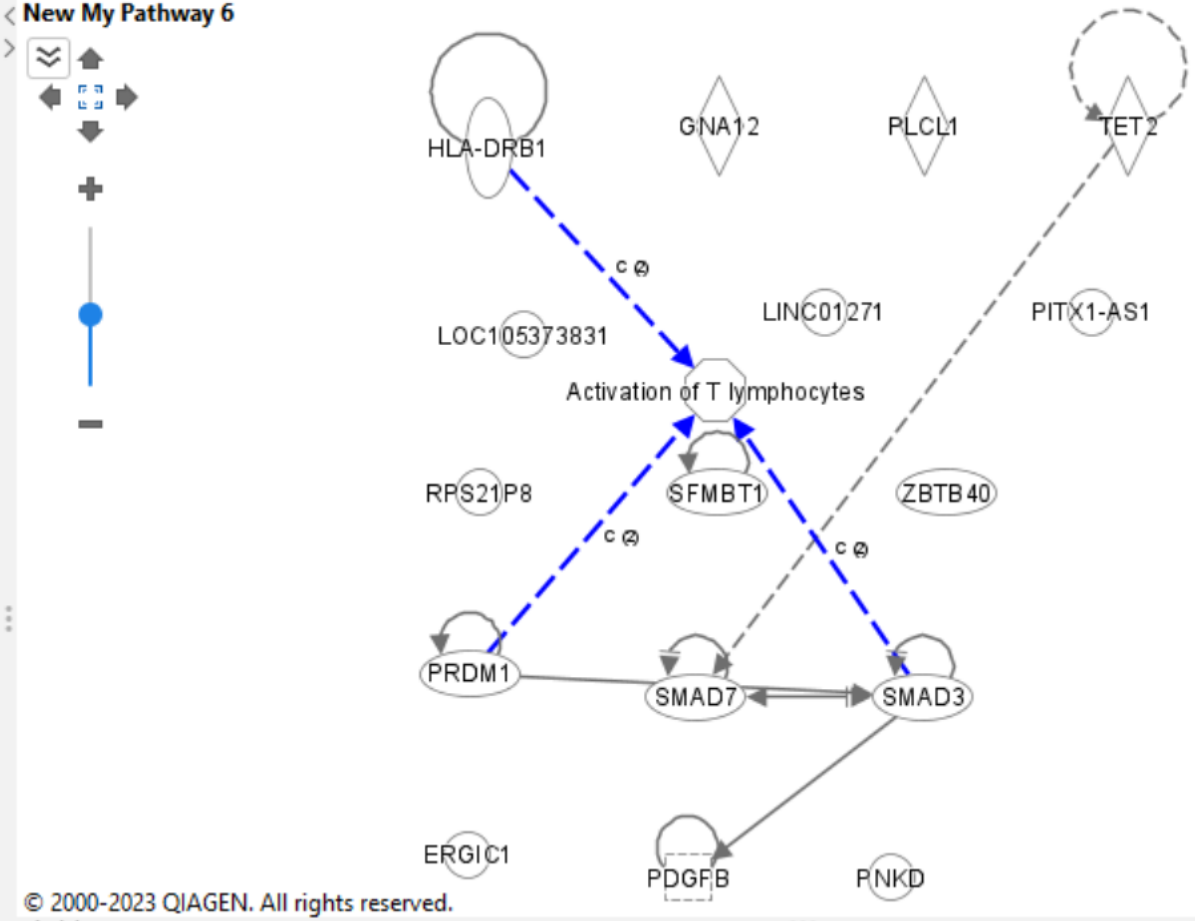
Current Analysis/Dataset/List: None selected

Change Analysis/Dataset/List

Data Sources All

Save As Preferences Restore From Prefs Reset Apply

New My Pathway 6



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Add To My Pathway Highlight 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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...

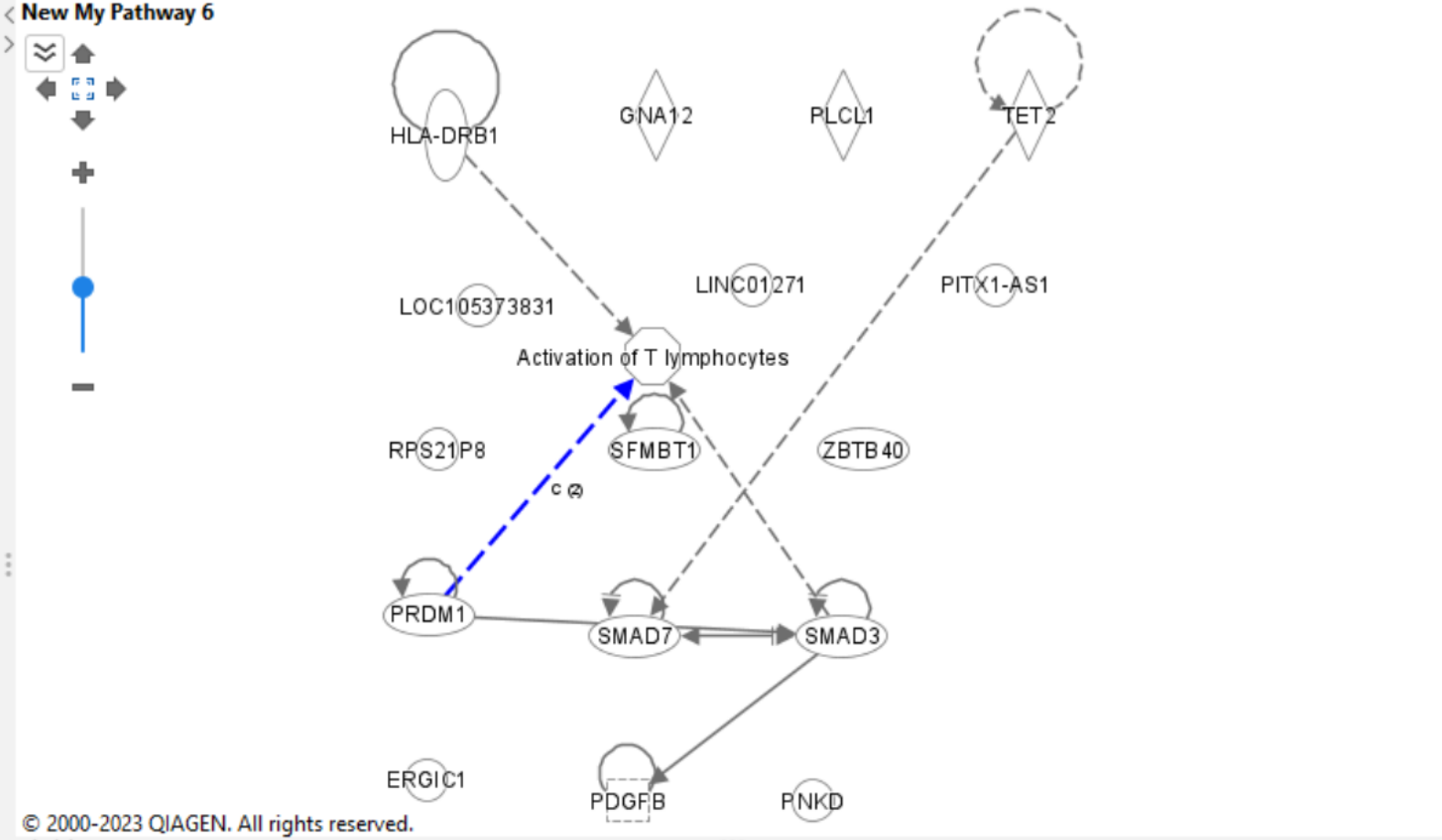
Current Analysis/Dataset/List: None selected

Change Analysis/Dataset/List

Data Sources All

Save As Preferences | Restore From Prefs | Reset | Apply

New My Pathway 6



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Add To My Pathway | Highlight | View: Shortest Paths (3) | Paths: 1 - 3

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

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

My Pathways

New My Pathway 6

Build | Overlay | Path Designer | Pattern Search

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

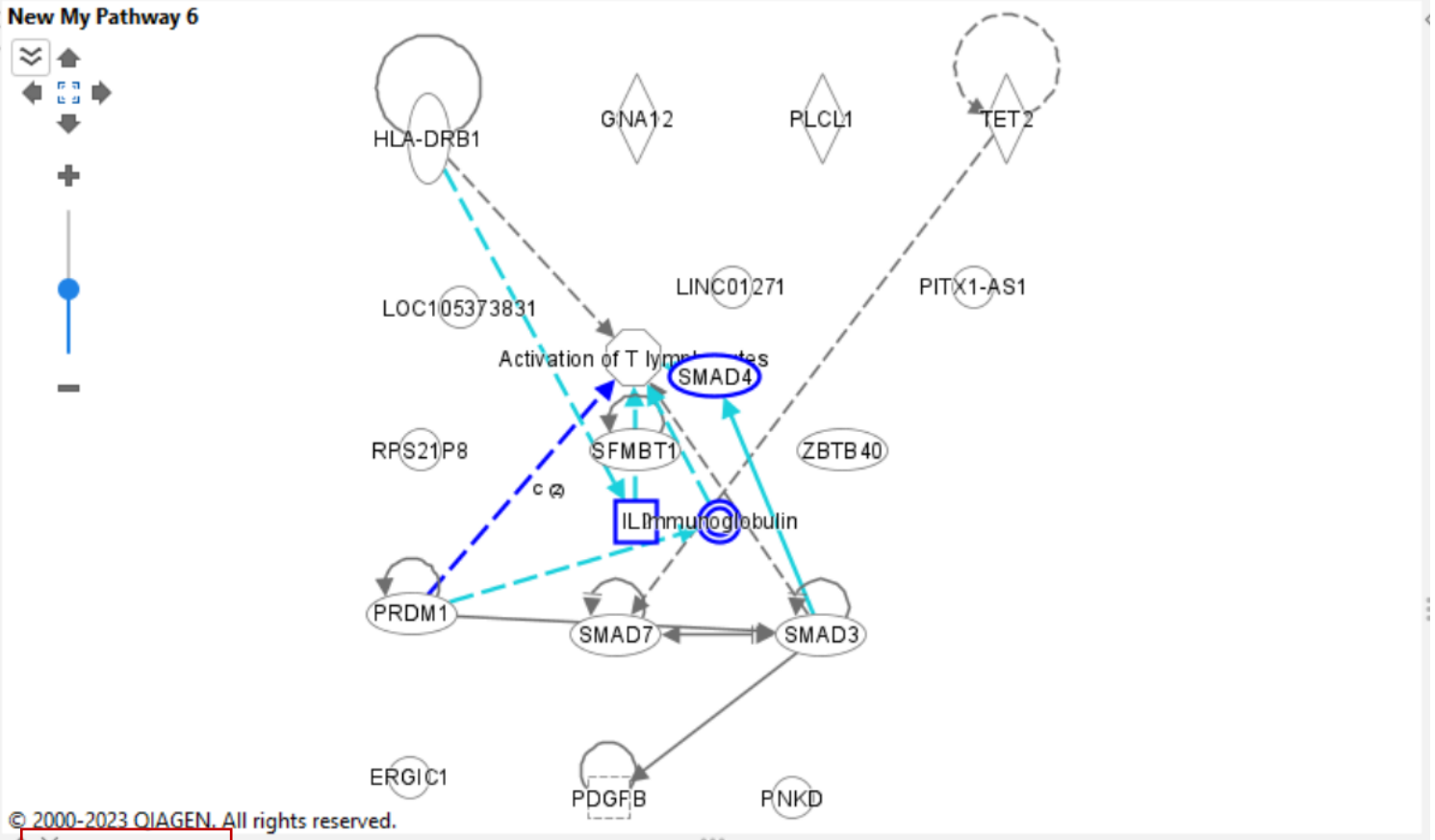
Change Analysis/Dataset/List

Data Sources All

miRNA Confidence Level All

Species All

Save As Preferences | Restore From Prefs | Reset | Apply



Add To My Pathway | Highlight

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

My Pathways

New My Pathway 6

Edit: | Build | Overlay | Path Designer | Pattern Search | View: | Zoom: | Export:

Tool: Keep

8 nodes and 15 relationships were kept

Filter Summary

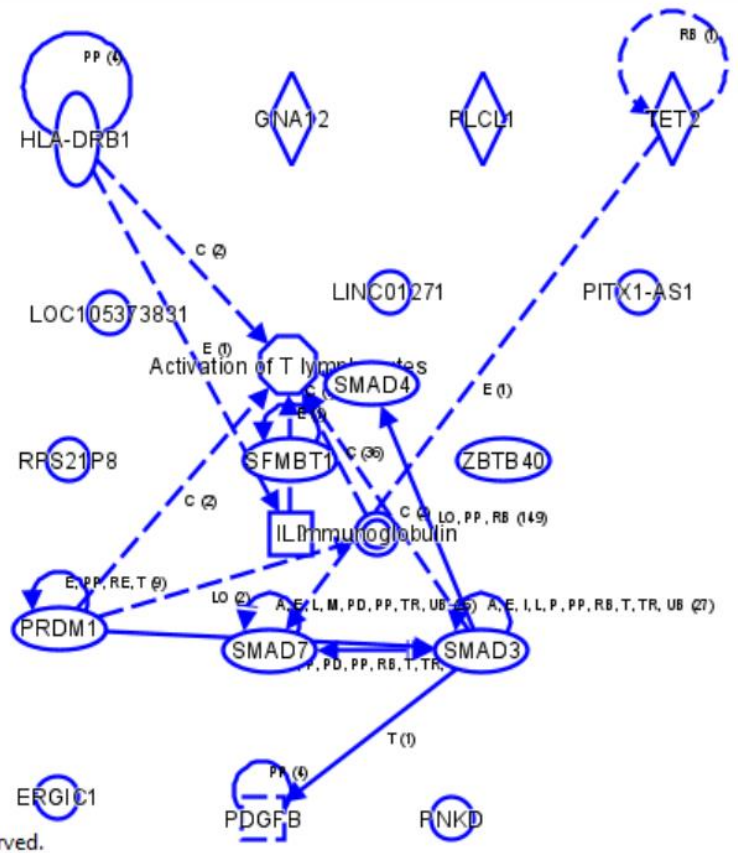
Keep all molecules where connectedness > 1

- 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

Reset | Apply

New My Pathway 6



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Add To My Pathway | Highlight | 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

Tool: Keep

8 nodes and 15 relationships were kept

Filter Summary

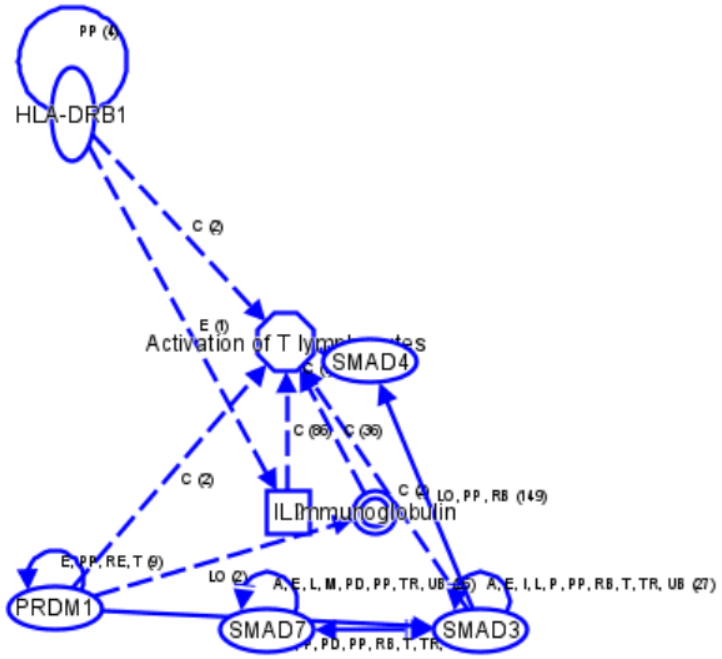
Keep all molecules where connectedness > 1

- 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

Reset Apply

New My Pathway 6



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Add To My Pathway Highlight 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

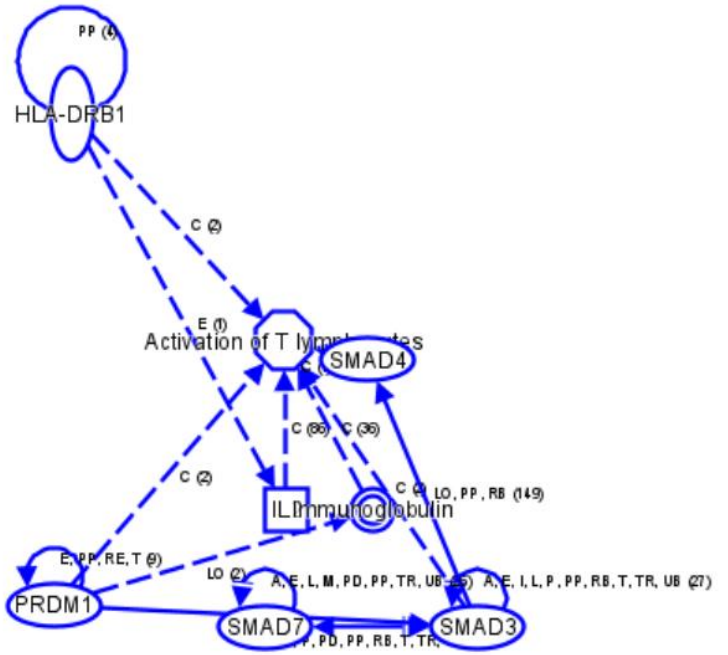
Consider all functions

Recalculate

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 Reset Apply

New My Pathway 6



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Add To My Pathway | Highlight | 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

Recalculate

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...
Differentiation of regulat		HLA-DRB1...all 4
Cytostasis of epithelial ce		AD3, 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
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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

Diseases and Functions

Functions to include: (use * for wildcard)

proliferation*

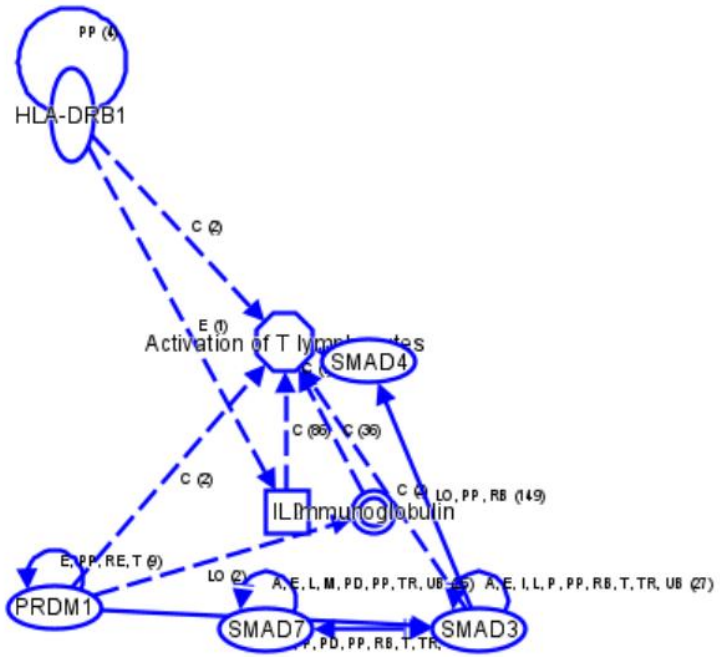
Functions to exclude:

Apply Cancel

SMAD4

0/355 Reset Apply

New My Pathway 6



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Add To My Pathway | Highlight | 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

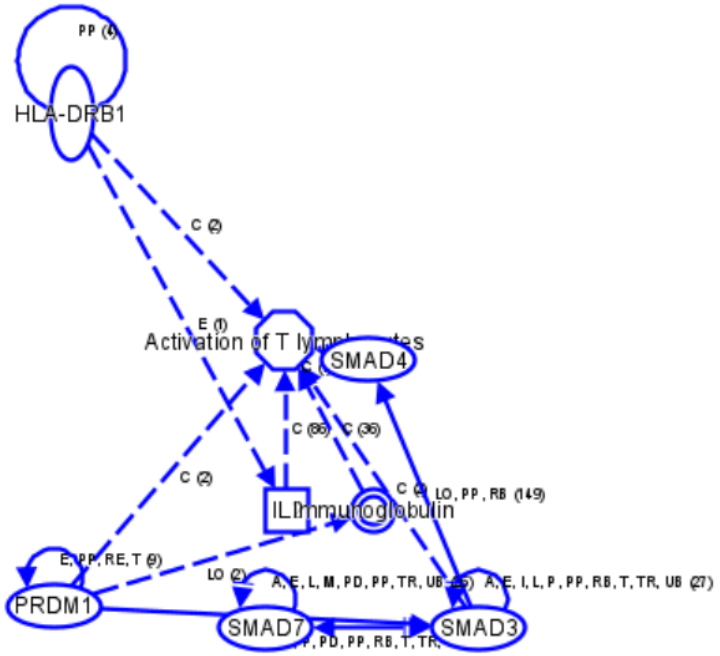
Consider only functions with names like proliferation*

Recalculate

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

1/14 Reset Apply

New My Pathway 6



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Add To My Pathway | Highlight | 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

My Pathways

New My Pathway 6

Edit: Build Overlay Path Designer Pattern Search View: Zoom: Export:

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

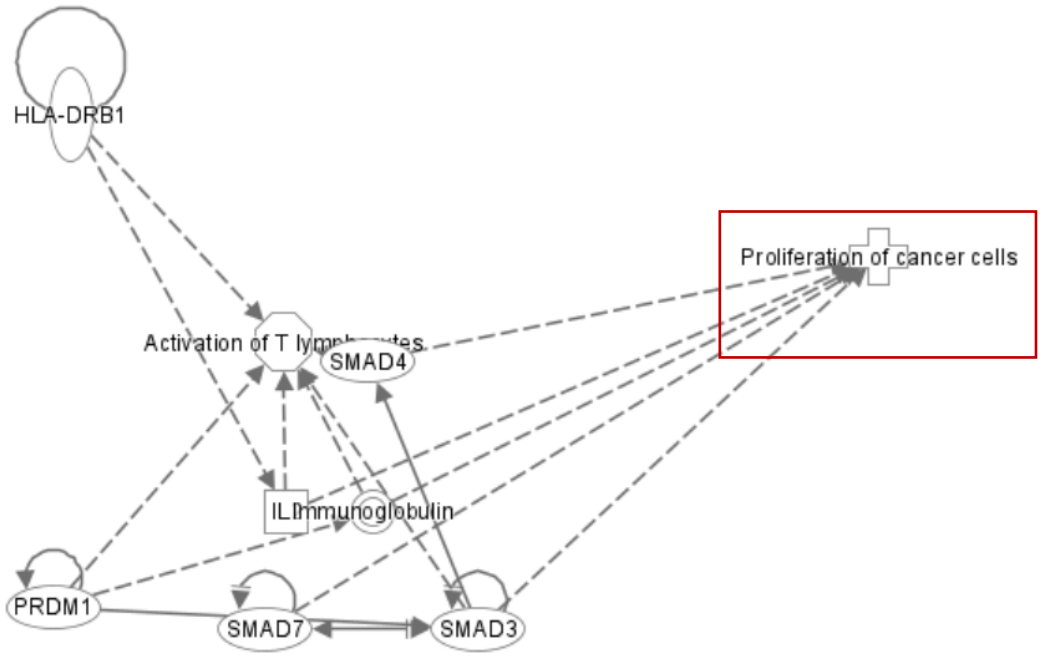
Consider only functions with names like proliferation*

Recalculate

Diseases and Functions	p-value	Molecules
Proliferation of activated T ly	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 Reset Apply

New My Pathway 6



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Add To My Pathway | Highlight | 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

My Pathways

New My Pathway 6

Edit: | Build | Overlay | Path Designer | Pattern Search | View: | Zoom: | Export:

Overlay: Biomarkers

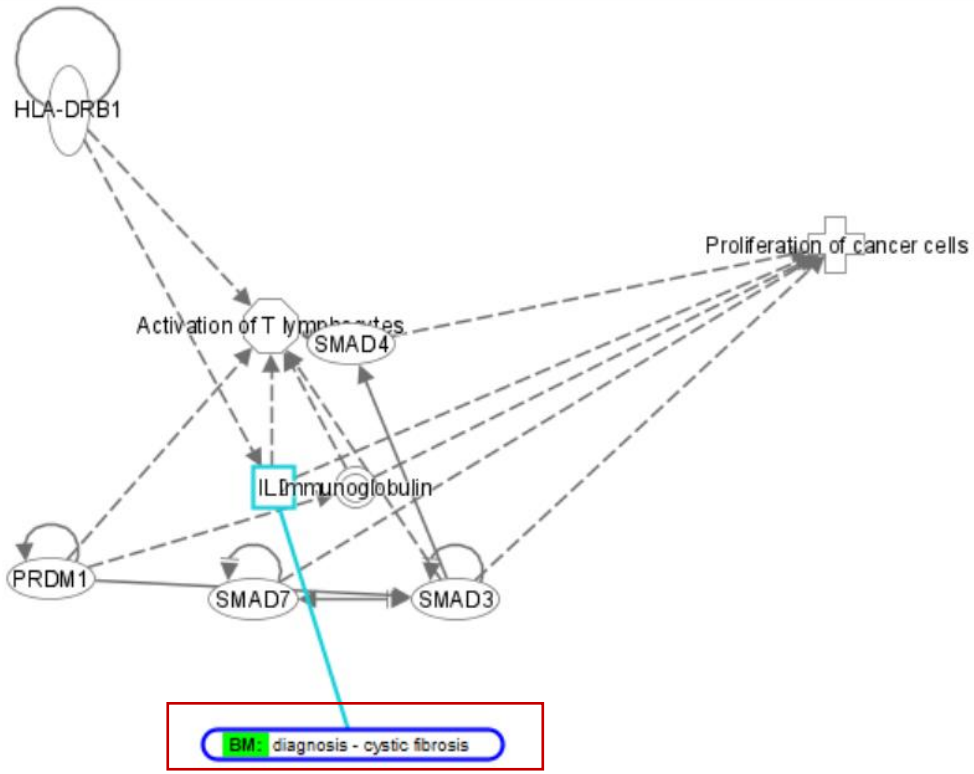
Select Biomarker labels from table to be displayed on pathway.

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

New My Pathway 6

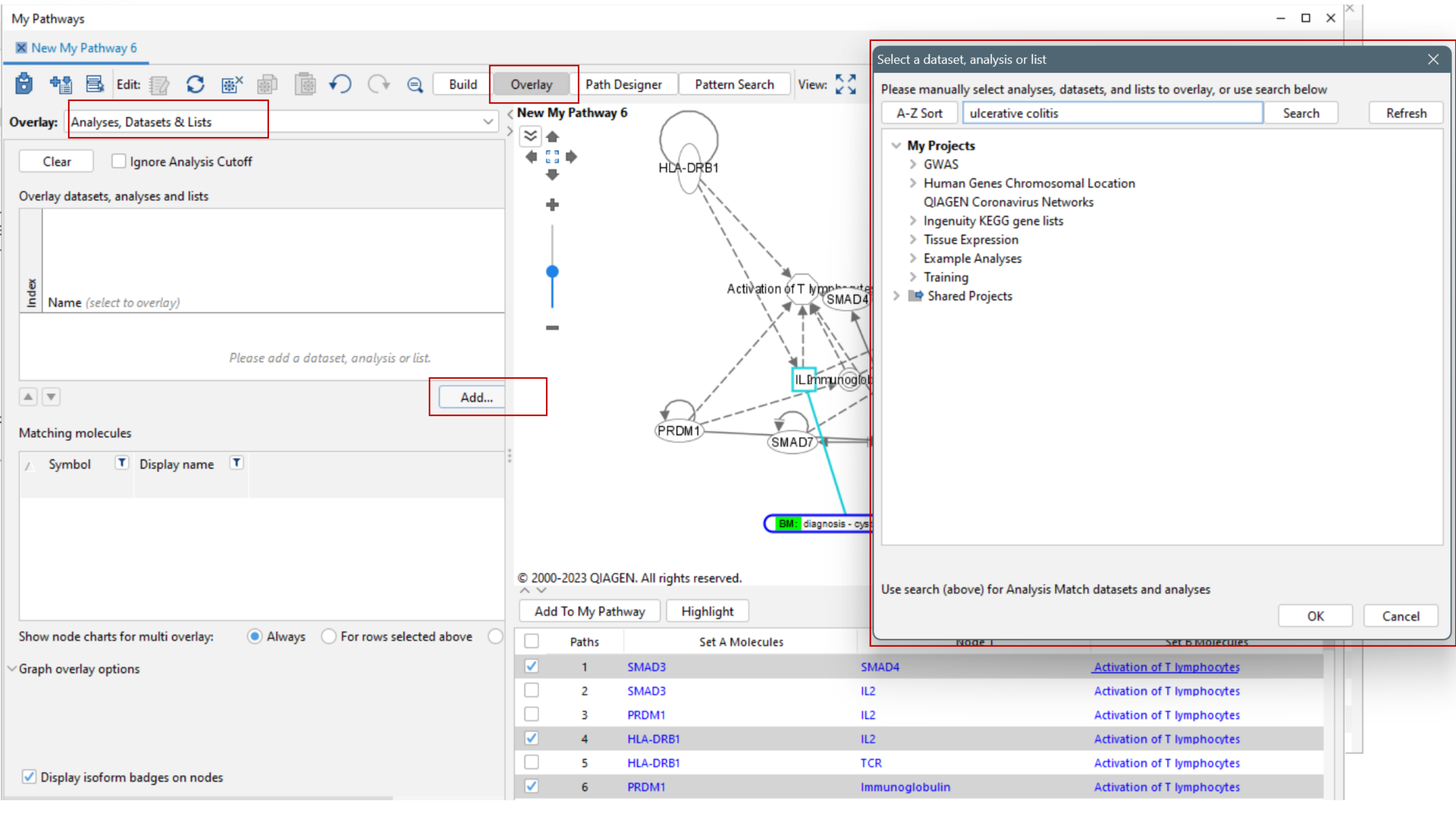
Show Legend

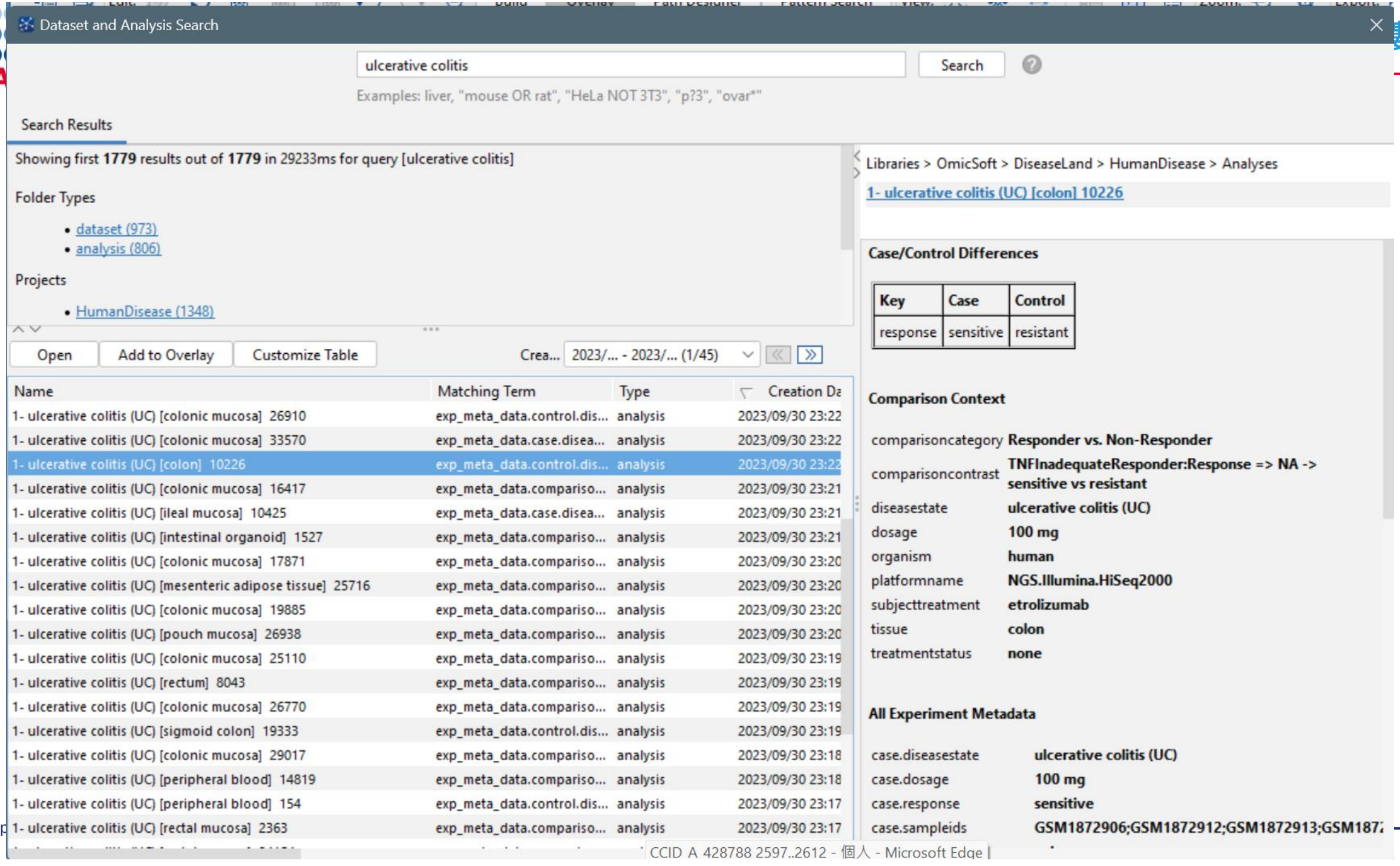


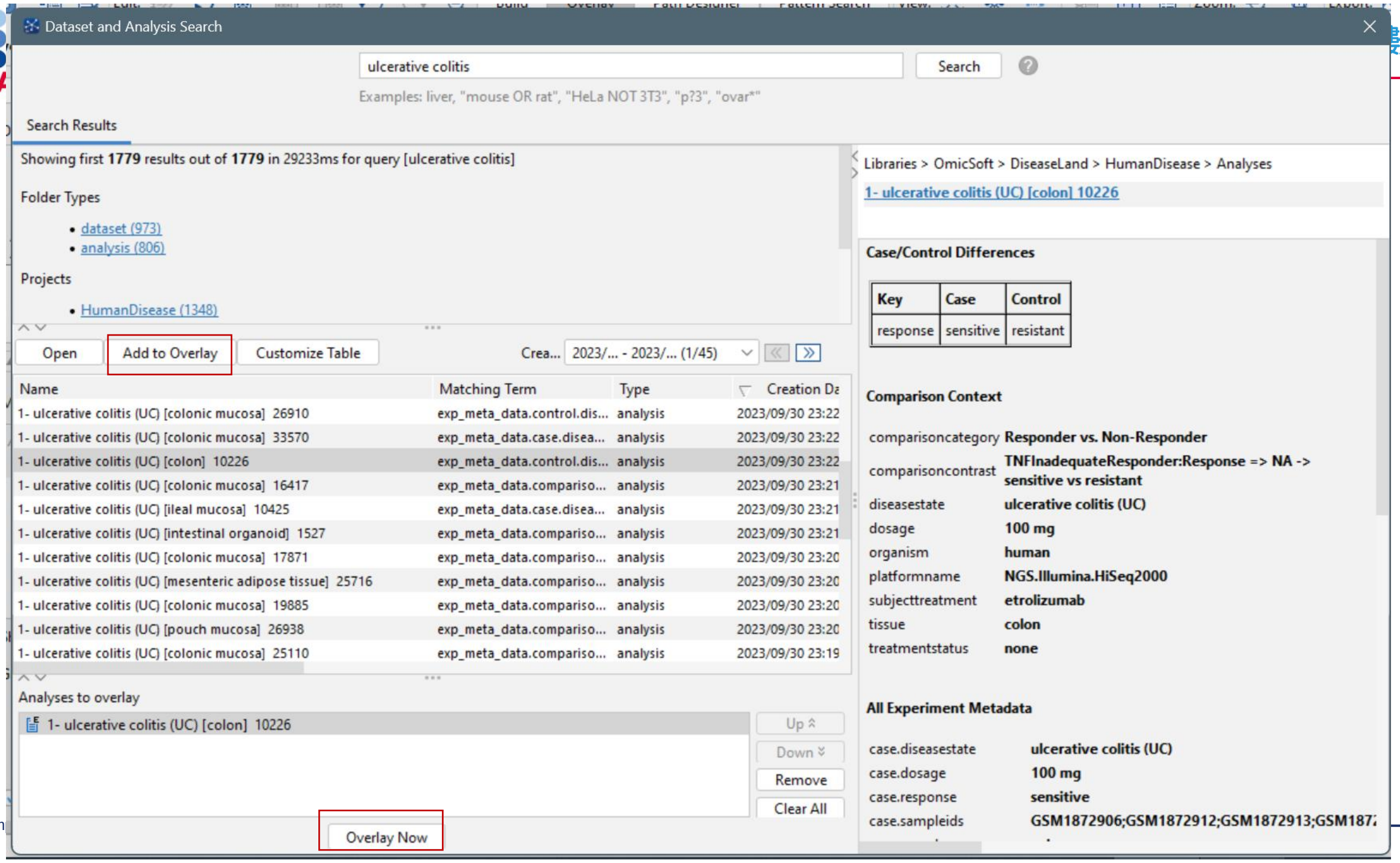
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Add To My Pathway | Highlight | View: Shortest Paths + 1 (389) | Paths: 1 - 50

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


My Pathways
New My Pathway 6
Edit:
Build
Overlay
Path Designer
Pattern Search
View:
Overlay:
Analyses, Datasets & Lists
Clear
Ignore Analysis Cutoff
Overlay datasets, analyses and lists
Index
Name (select to overlay)
Please add a dataset, analysis or list.
Add...
Matching molecules
Symbol
Display name
Show node charts for multi overlay:
Always
For rows selected above
Graph overlay options
Display isoform badges on nodes
New My Pathway 6
HLA-DRB1
Activation of T lymphocytes
SMAD4
IL2
Immunoglob
PRDM1
SMAD7
BM: diagnosis - cyst
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Add To My Pathway
Highlight
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
Select a dataset, analysis or list
Please manually select analyses, datasets, and lists to overlay, or use search below
A-Z Sort
ulcerative colitis
Search
Refresh
My Projects
GWAS
Human Genes Chromosomal Location
QIAGEN Coronavirus Networks
Ingenuity KEGG gene lists
Tissue Expression
Example Analyses
Training
Shared Projects
Use search (above) for Analysis Match datasets and analyses
OK
Cancel


Dataset and Analysis Search
ulcerative colitis
Search
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)
Open
Add to Overlay
Customize Table
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
CCID A 428788 2597..2612 - 個人 - Microsoft Edge


Dataset and Analysis Search
ulcerative colitis
Search
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)
Open
Add to Overlay
Customize Table
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
Analyses to overlay
1- ulcerative colitis (UC) [colon] 10226
Up
Down
Remove
Clear All
Overlay Now
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

My Pathways

New My Pathway 6

Edit: | Build | Overlay | Path Designer | Pattern Search | View: | Zoom: | Export:

Overlay: Analyses, Datasets & Lists

Clear | Ignore Analysis Cutoff

Overlay datasets, analyses and lists

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

Add more...

Matching molecules

Symbol	Display name	Index: 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

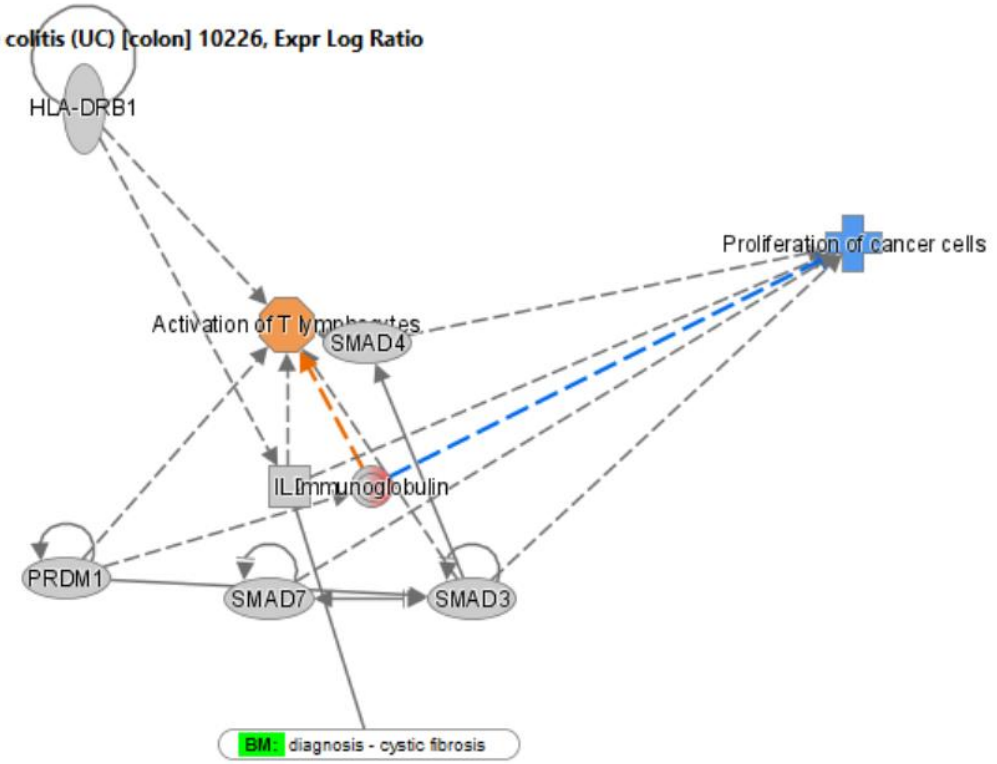
Fill	Measurement	Show value	Range
●	**Expr Log Ratio**	☐	-1.641 … 2.088
○	Expr p-value	☐	

☑ Display isoform badges on nodes

New My Pathway 6

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

Show Legend



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Add To My Pathway | Highlight | 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

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ORIGINAL RESEARCH

Genome-Wide Association Study of Alopecia Areata in Taiwan: The Conflict Between Individuals and Hair Follicles

Jai-Sing Yang[1,*], Ting-Yuan Liu[2,*], Yu-Chia Chen[2], Shih-Chang Tsai[3], Yu-Jen Chiu[4,5], Chi-Chou Liao[2], Fuu-Jen Tsai[6–8]

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Purpose: Alopecia areata (AA) is one of the most prevalent autoimmune diseases affecting humans. Given that hair follicles are immune-privileged, autoimmunity can result in disfiguring hair loss. However, the genetic basis for AA in the Taiwanese population remains unknown.

Materials and Methods: A genome-wide association study was conducted using a cohort of 408 AA cases and 8167 controls. To link variants to gene relationships, we used 882 SNPs (P<1E-05) within 74 genes that were associated with AA group to build the biological networks by IPA software. HLA diplotypes and haplotypes were analyzed using Attribute Bagging (HIBAG)-R package and chi-square analysis.

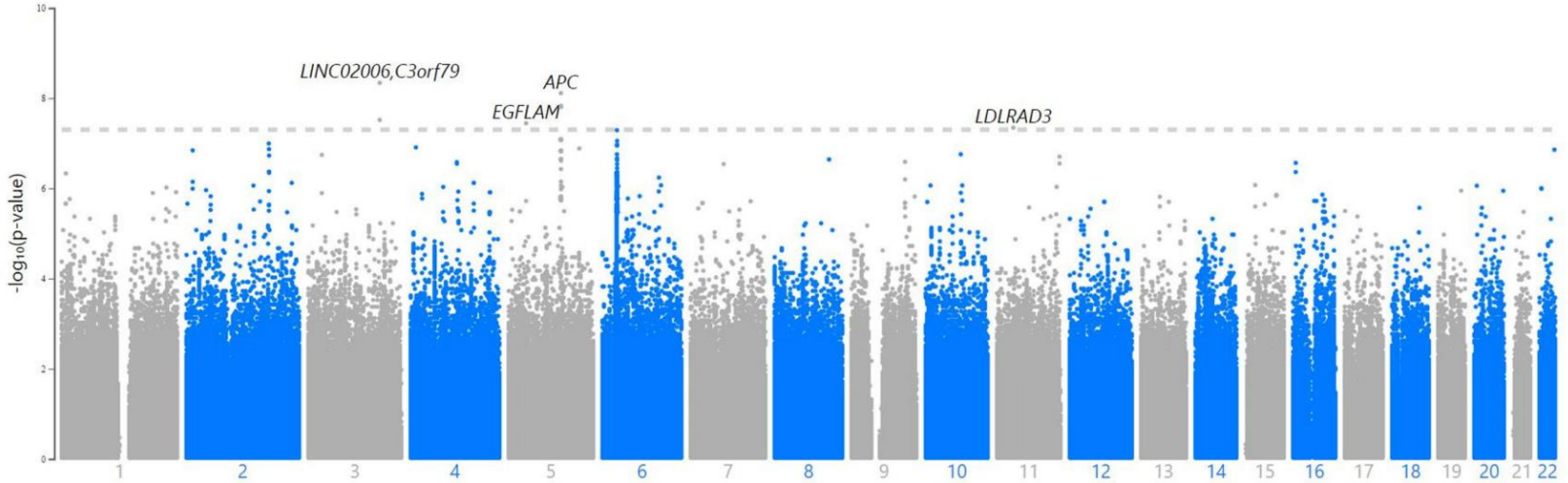
Results: Seven single nucleotide polymorphisms (SNPs) including LINC02006 (rs531166736, rs187306735), APC (rs112800832_C_CAT), SRP19 (rs139948960, rs144784670), EGFLAM (rs16903975) and LDLRAD3 (rs79874564) were closely associated with the AA phenotype (P<5E-08). Examination of biological networks revealed that these genomic areas are associated with antigen presentation signaling, B cell and T cell development, Th1 and Th2 activation pathways, Notch signaling, crosstalk signaling between dendritic cells and natural killer cells, and phagosome maturation. Based on human leukocyte antigen (HLA) genotype analysis, four HLA genotypes (HLA-B*15:01-*40:01, HLA-DQA1*01:02-*03:03, HLA-DQA1*01:02, and HLA-DQB1*02:01) were found to be associated with AA (adjusted p-value<0.05). HLA-DQA1*01:02 is the most significantly related gene in the Taiwanese population (adjusted p-value = 2.09E-05).

Conclusion: This study successfully identified susceptibility loci associated with AA in the Taiwanese population. These findings not only shed light on the origins of AA within the Taiwanese context but also contribute to a comprehensive understanding of the genetic factors influencing AA susceptibility.

PMID: 37752970

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ORIGINAL RESEARCH

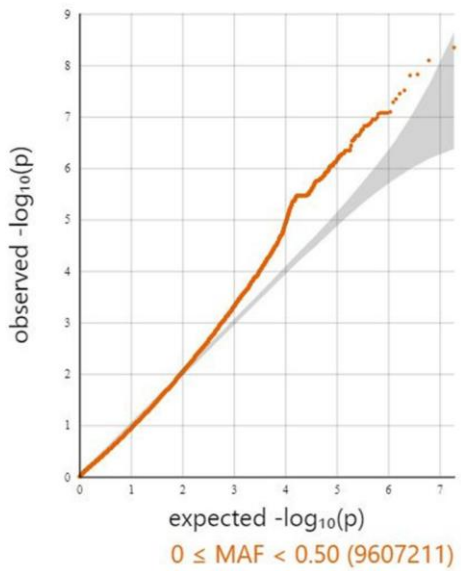
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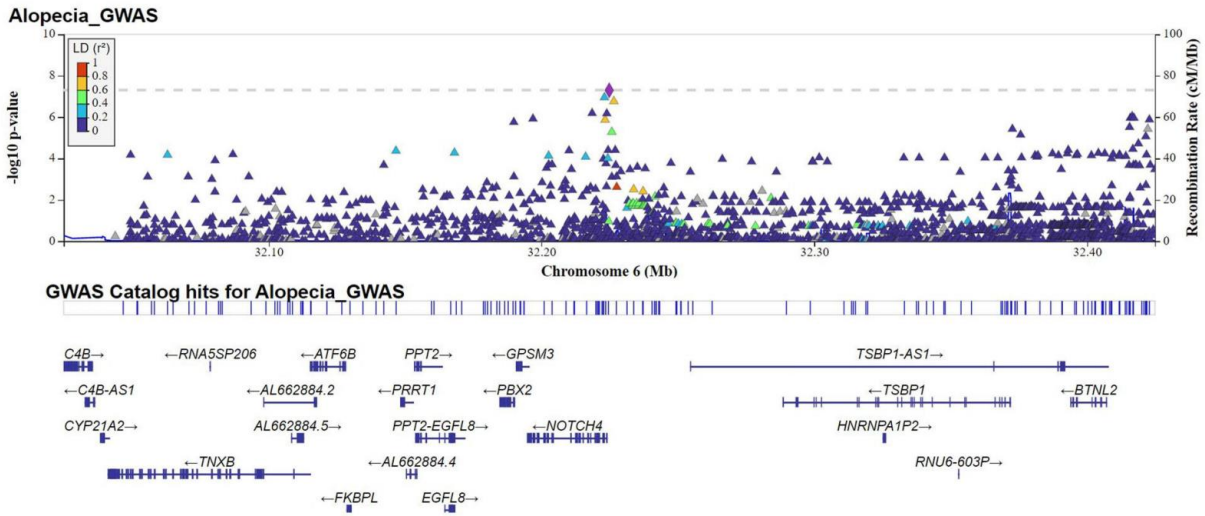
Jai-Sing Yang
Fuu-Jen Tsa

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Accepted:
Published:



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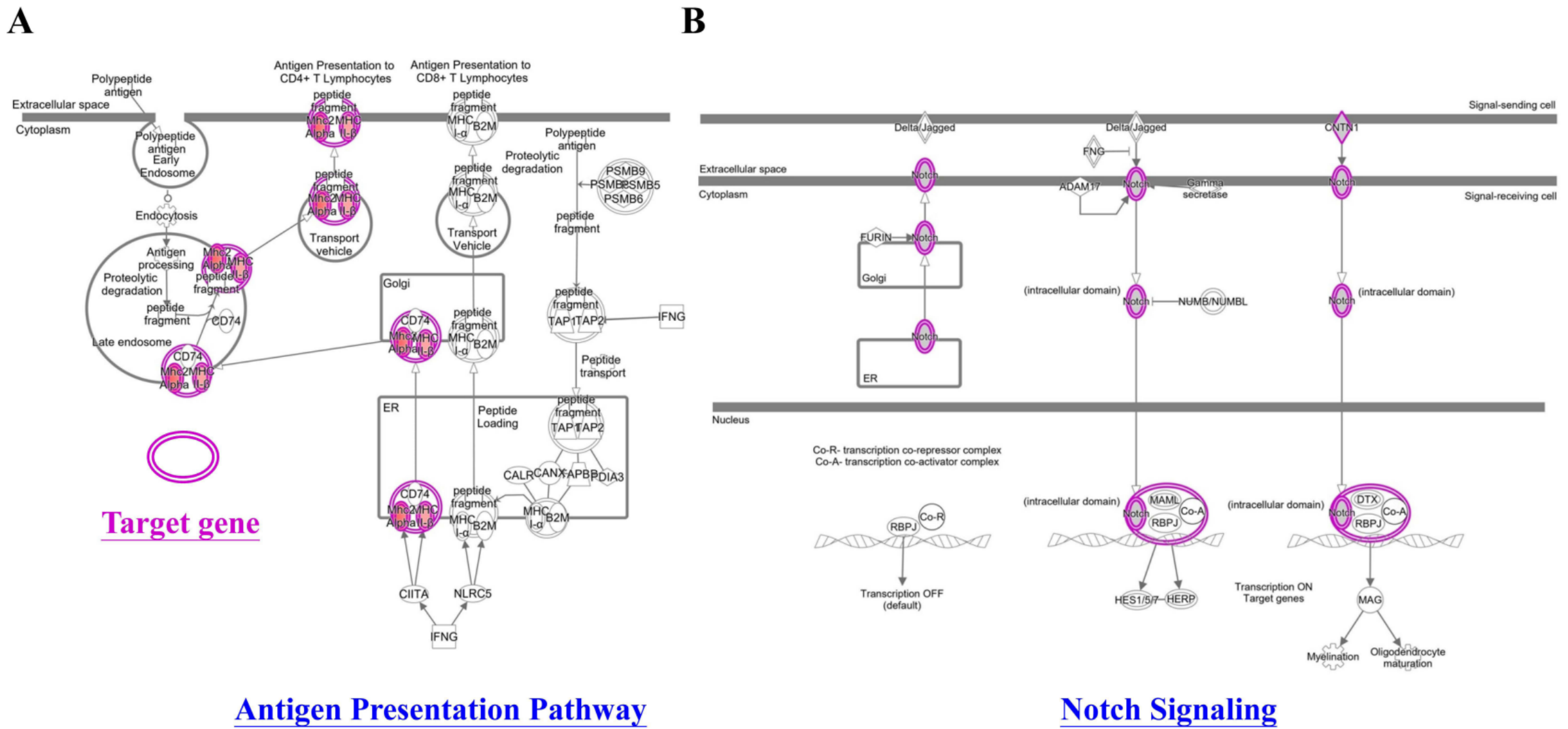


Figure 5 Network analyses of the antigen presentation pathway target gene (**A**) and the gene that Notch signaling targets (**B**). IPA software analyzed network analysis (SNPs gene loci, P<1E-05).



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:

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