Previous recordings, slides, etc.

Popular recordings from recent trainings (2022)

RNA-seq analysis and interpretation:
https://qiagen.showpad.com/share/FFpWhr5b1aVbQbcQD0bs5

miRNA analysis using Ingenuity Pathway Analysis:
https://qiagen.showpad.com/share/aDzTaHl4GBasbDcuyJWQp

Single-cell RNA-seq analysis and interpretation:
https://qiagen.showpad.com/share/u5Sv8rbZzED2aLe2bc4s4

Public single cell data analysis and interpretation:
https://qiagen.showpad.com/share/wMpUrxwnrJk4Zc6iP9jzm

Single-cell ATAC-seq analysis:
https://qiagen.showpad.com/share/weaxKgKrGxtnW4Udz5Toa

SARS-CoV-2 detection in wastewater w/ CLC Genomics Workbench:
https://qiagen.showpad.com/share/PZmv2KNXNT1yDTlTUNmca

Long reads sequencing analysis:
https://qiagen.showpad.com/share/EXDUJ3RKHsjXNxQpCiVnA

Software trials

CLC Genomics Workbench trial:
https://qiagen.showpad.com/share/I6MqdhIybpllyvuYW3AKy

Human Somatic Mutation Database trial:
https://qiagen.showpad.com/share/ELhnINyfamHr1Q1mmQnuv

Ingenuity Pathway Analysis resources

IPA beginner training recording:
https://qiagen.showpad.com/share/t2cGMdF3NjVucBA0b9tIT

IPA deeper dive training recording:
https://qiagen.showpad.com/share/wCQrTeE2ftSQkgFTooHSu

IPA step-by-step guide w/ data format (slide 9) and upload (slide 28) instructions:
https://qiagen.showpad.com/share/VjizSLJVBw1qfVnyoVJ8B

Resources in this presentation

- Formatting transcriptomics data before uploading to IPA
- Data upload step by step
- How to access Land Explorer data
- Land Explorer navigation
- Colors and z-scores in IPA
- Enrichment in IPA
- IPA Analysis Tabs
- IPA Help

QIAGEN IPA Boston University Workshop

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Technical Support: ts-bioinformatics@qiagen.com

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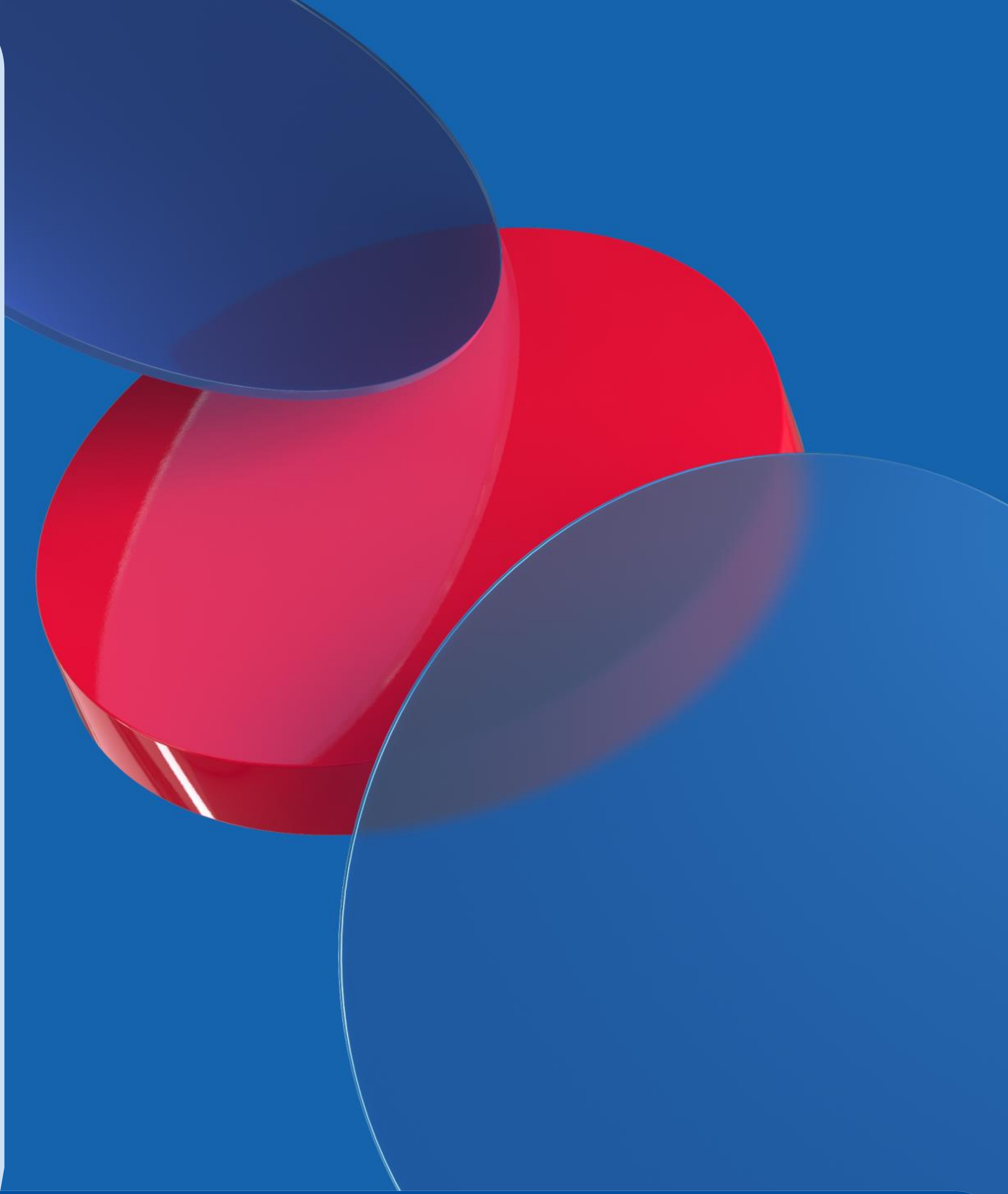


Agenda

Topics for today’s workshop

Interpreting your ′omics data using IPA Core Analysis

- Setting up a core analysis
- Canonical pathways
- Comparison analysis

Creating networks from scratch

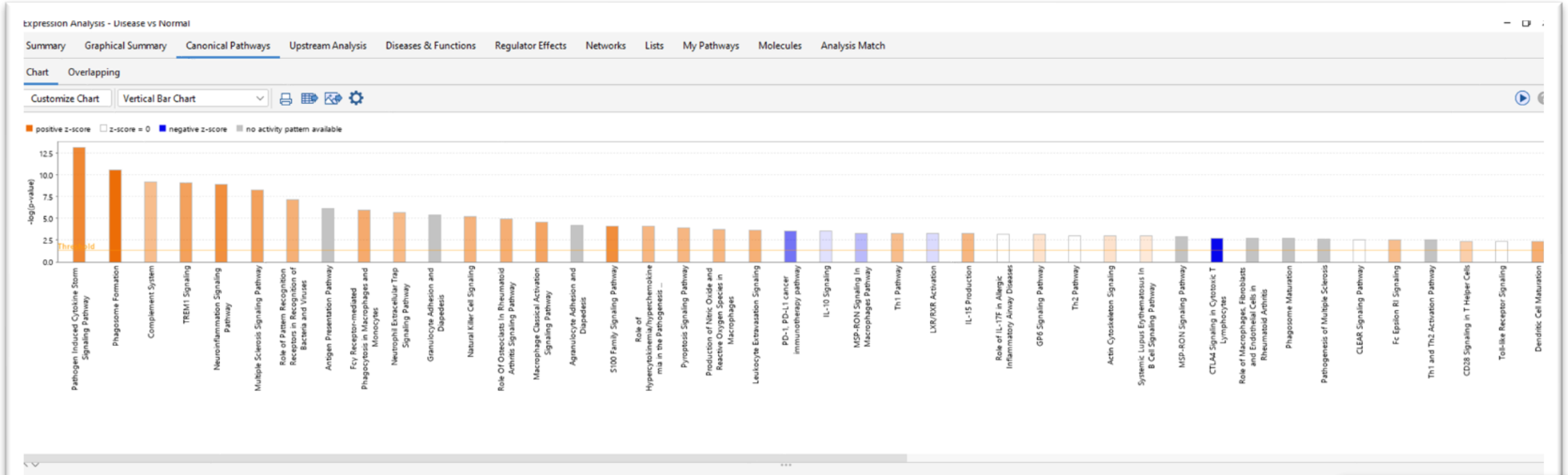
- Connecting genes in a network
- In silico testing
- Overlay drugs and biomarkers

Exploring publicly available data

- Activity plot, pattern search, Analysis Match
- Land Explorer

Summary

Interpret your data with causal analytics and find key pathways

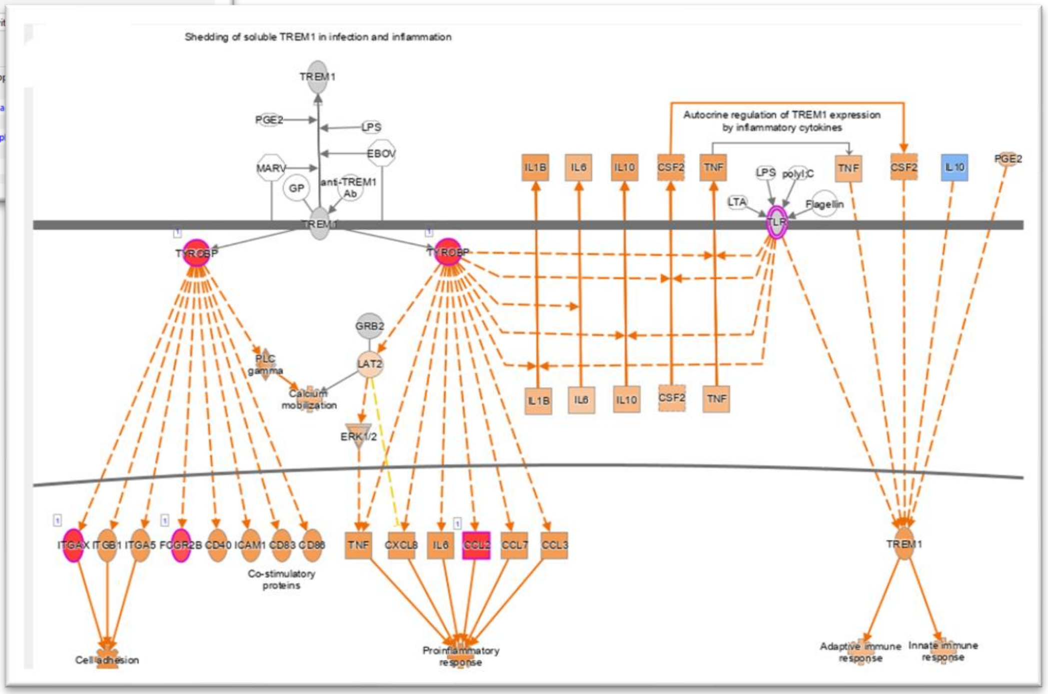


Expression Analysis - Disease vs Normal

0 molecule(s) associated with **TREM1 Signaling** [Ratio: 10/77 (0.13)] [z-score: 3.162] [p-value: 8.24E-10]

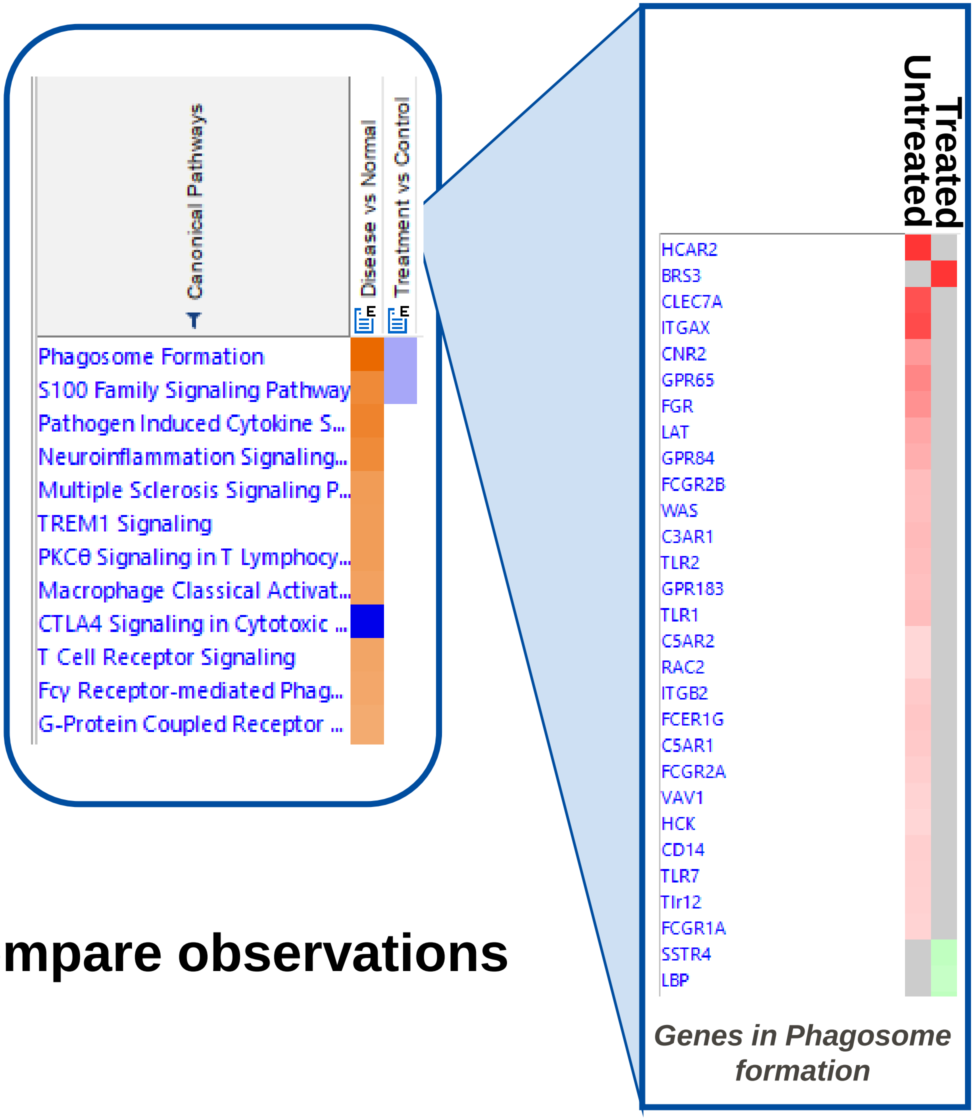
Symbol	Entrez Gene Name	Identifier Ensembl	Measurement Expr Log Ratio	Expr p-value	Expr p-value	Expected	Location	Type(s)	Biomarker App
CCL2	C-C motif chemokine ligand 2	ENSMUSG00000035352.3	↑2.296	3.85E-03	1.44E-01	↑ Up	Extracellular Space	cytokine	diagnosis, effica
FCGR2B	Fc gamma receptor IIb	ENSMUSG00000026656.15	↑1.652	8.16E-18	4.68E-15	↑ Up	Plasma Membrane	transmembrane receptor	
ITGAX	integrin subunit alpha X	ENSMUSG00000030789.9	↑4.554	1.51E-32	3.35E-29	↑ Up	Plasma Membrane	transmembrane receptor	unspecified appl
Naip1 (includes others)*	NLR family, apoptosis inhibitory pr	ENSMUSG00000071203.6*	↑1.343	1.17E-03	6.48E-02	↑ Up	Cytoplasm	other	
NLRC5	NLR family CARD domain containi	ENSMUSG00000074151.13	↑1.125	8.54E-03	2.36E-01	↑ Up	Cytoplasm	transcription regulator	
TLR1	toll like receptor 1	ENSMUSG00000044827.10	↑1.666	2.92E-03	1.21E-01	↑ Up	Plasma Membrane	transmembrane receptor	

Explore canonical pathway enrichment and activity prediction



Get more granular with your data with pathway maps

Compare multiple experiments and build hypotheses without data



Canonical Pathways | Disease vs Normal | Treatment vs Control

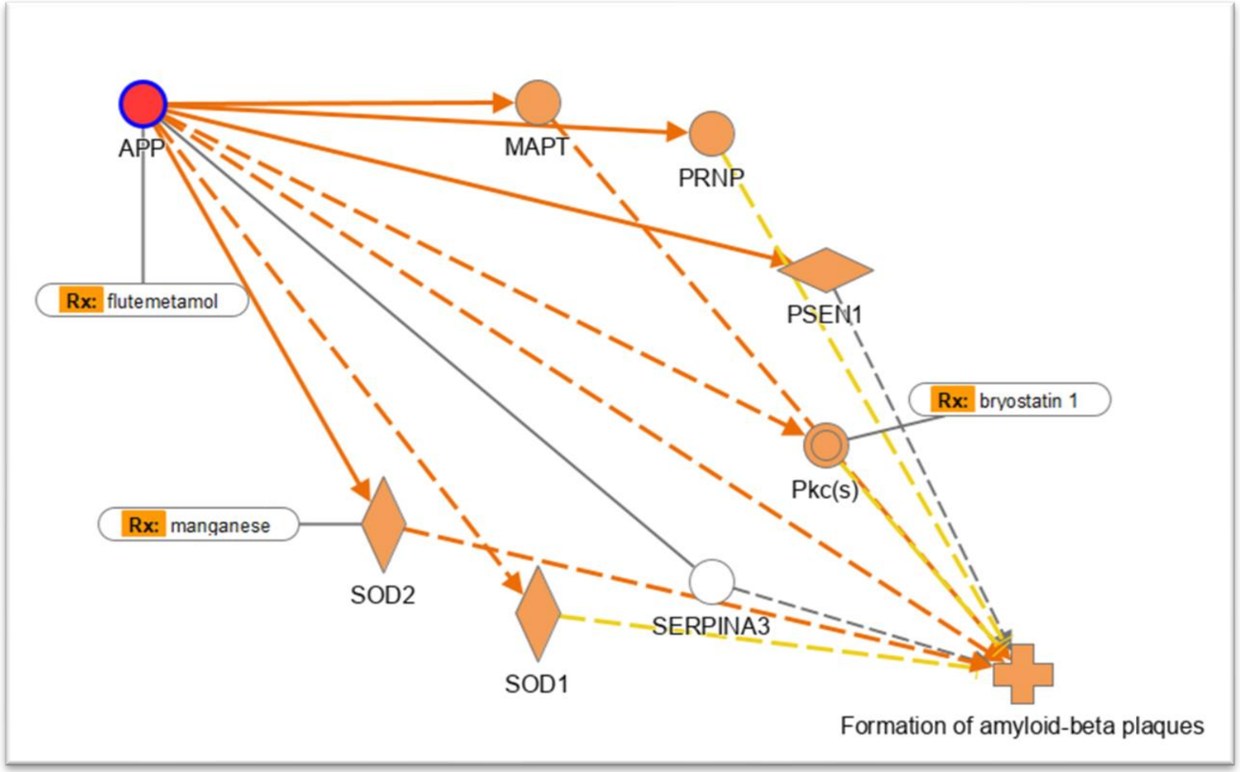
- Phagosome Formation
- S100 Family Signaling Pathway
- Pathogen Induced Cytokine S...
- Neuroinflammation Signaling...
- Multiple Sclerosis Signaling P...
- TREM1 Signaling
- PKCθ Signaling in T Lymphocy...
- Macrophage Classical Activat...
- CTLA4 Signaling in Cytotoxic ...
- T Cell Receptor Signaling
- Fcγ Receptor-mediated Phag...
- G-Protein Coupled Receptor ...

Treated
Untreated

HCAR2
BRS3
CLEC7A
ITGAX
CNR2
GPR65
FGR
LAT
GPR84
FCGR2B
WAS
C3AR1
TLR2
GPR183
TLR1
C5AR2
RAC2
ITGB2
FCER1G
C5AR1
FCGR2A
VAV1
HCK
CD14
TLR7
Tlr12
FCGR1A
SSTR4
LBP

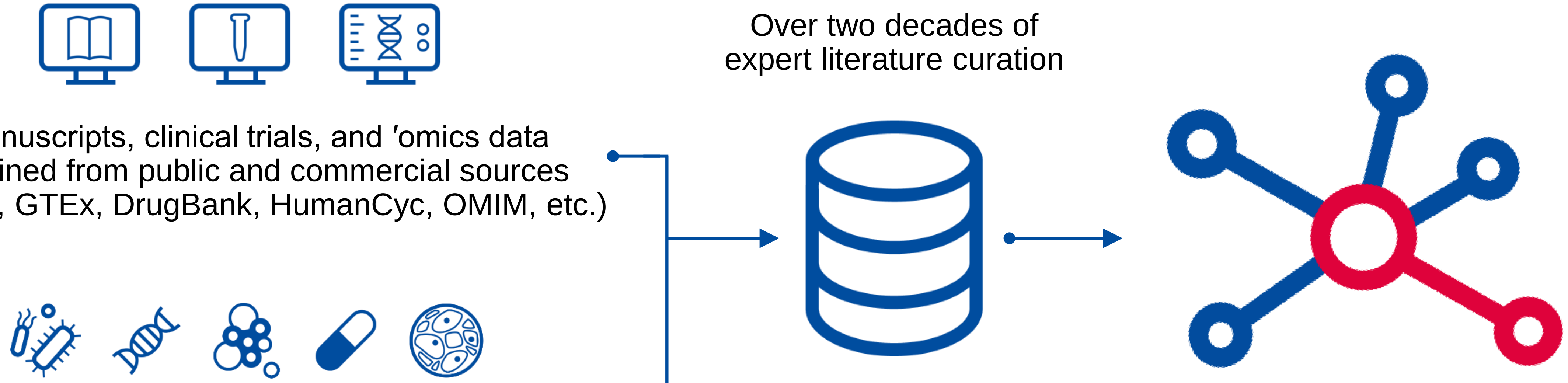
Genes in Phagosome formation

Compare observations



Build networks from scratch

IPA is powered by the QIAGEN Knowledge Base



Manuscripts, clinical trials, and ′omics data obtained from public and commercial sources (TCGA, GTEx, DrugBank, HumanCyc, OMIM, etc.)

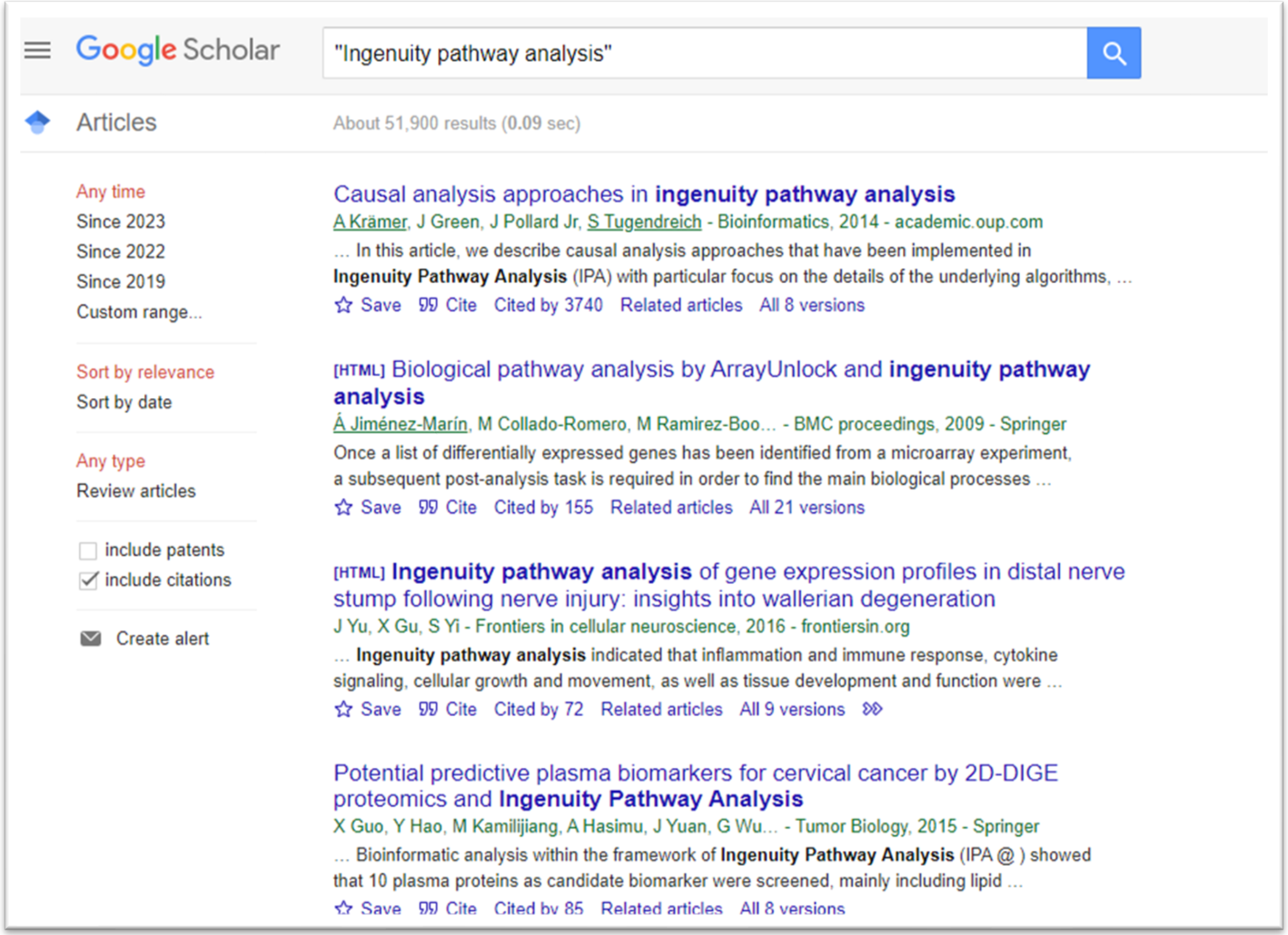
Weekly and quarterly updates with the latest disease, genetics, cancer and drug findings

Over two decades of expert literature curation

Over 12.2 million research findings accessible by you in **seconds**

The high-quality, manually curated data allows for **causality prediction**

IPA is used and cited widely across many scientific disciplines



Google Scholar

"Ingenuity pathway analysis"

Articles

About 51,900 results (**0.09** sec)

Any time
Since 2023
Since 2022
Since 2019
Custom range...

Sort by relevance
Sort by date

Any type
Review articles

☐ include patents
☑ include citations

Create alert

Causal analysis approaches in **ingenuity pathway analysis**
A Krämer, J Green, J Pollard Jr, S Tugendreich - Bioinformatics, 2014 - academic.oup.com
... In this article, we describe causal analysis approaches that have been implemented in **Ingenuity Pathway Analysis** (IPA) with particular focus on the details of the underlying algorithms, ...
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[HTML] Biological pathway analysis by ArrayUnlock and **ingenuity pathway analysis**
Á Jiménez-Marín, M Collado-Romero, M Ramirez-Boo... - BMC proceedings, 2009 - Springer
Once a list of differentially expressed genes has been identified from a microarray experiment, a subsequent post-analysis task is required in order to find the main biological processes ...
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[HTML] **Ingenuity pathway analysis** of gene expression profiles in distal nerve stump following nerve injury: insights into wallerian degeneration
J Yu, X Gu, S Yi - Frontiers in cellular neuroscience, 2016 - frontiersin.org
... **Ingenuity pathway analysis** indicated that inflammation and immune response, cytokine signaling, cellular growth and movement, as well as tissue development and function were ...
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Potential predictive plasma biomarkers for cervical cancer by 2D-DIGE proteomics and **Ingenuity Pathway Analysis**
X Guo, Y Hao, M Kamilijiang, A Hasimu, J Yuan, G Wu... - Tumor Biology, 2015 - Springer
... Bioinformatic analysis within the framework of **Ingenuity Pathway Analysis** (IPA @) showed that 10 plasma proteins as candidate biomarker were screened, mainly including lipid ...
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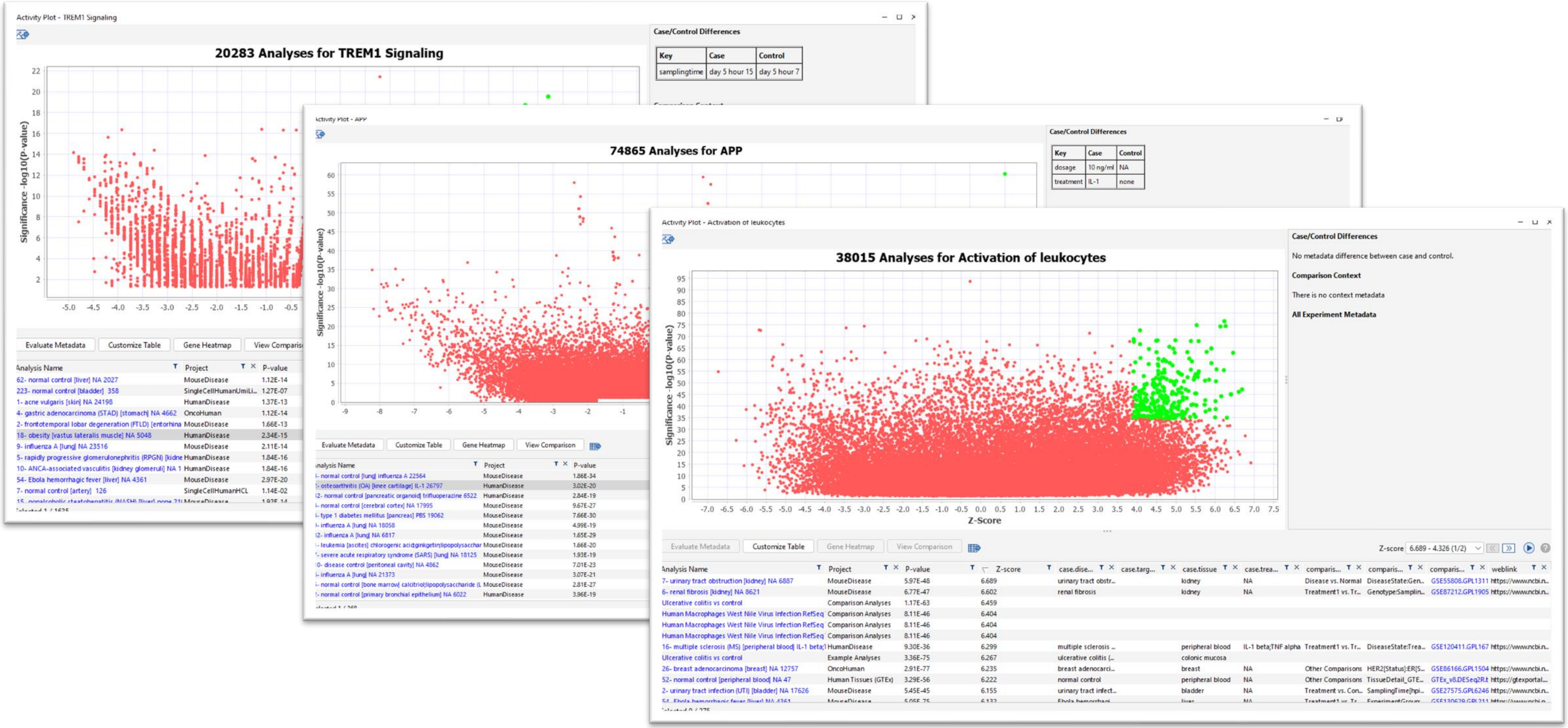
Find public data with similar or dissimilar activation patterns for key pathways, regulators, diseases and functions with Activity Plot



Case/Control Differences

Key	Case	Control
samplingtime	day 5 hour 15	day 5 hour 7

Analysis Name	Project	P-value
62- normal control [liver] NA 2027	MouseDisease	1.12E-14
223- normal control [bladder] 358	SingleCellHumanUmiLi...	1.27E-07
1- acne vulgaris [skin] NA 24198	HumanDisease	1.37E-13
4- gastric adenocarcinoma (STAD) [stomach] NA 4662	OncoHuman	1.12E-14
2- frontotemporal lobar degeneration (FTLD) [entorhina	MouseDisease	1.66E-13
18- obesity [vastus lateralis muscle] NA 5048	HumanDisease	2.34E-15
9- influenza A [lung] NA 23516	MouseDisease	2.11E-14
5- rapidly progressive glomerulonephritis (RPGN) [kidne	HumanDisease	1.84E-16
10- ANCA-associated vasculitis [kidney glomeruli] NA 1	HumanDisease	1.84E-16
54- Ebola hemorrhagic fever [liver] NA 4361	MouseDisease	2.97E-20
7- normal control [artery] 126	SingleCellHumanHCL	1.14E-02

Case/Control Differences

Key	Case	Control
dosage	10 ng/ml	NA
treatment	IL-1	none

Analysis Name	Project	P-value
-normal control [lung] influenza A 22564	MouseDisease	1.86E-34
- osteoarthritis (OA) [knee cartilage] IL-1 26797	HumanDisease	3.02E-20
2- normal control [pancreatic organoid] trifluoperazine 6522	HumanDisease	2.84E-19
- normal control [cerebral cortex] NA 17995	MouseDisease	9.67E-27
- type 1 diabetes mellitus [pancreas] PBS 19062	MouseDisease	7.66E-30
- influenza A [lung] NA 18058	MouseDisease	4.99E-19
2- influenza A [lung] NA 6817	MouseDisease	1.65E-29
- leukemia [ascites] chlorogenic acid;ginkgetin;lipopolysacchar	MouseDisease	1.66E-20
- severe acute respiratory syndrome (SARS) [lung] NA 18125	MouseDisease	1.93E-19
0- disease control [peritoneal cavity] NA 4862	MouseDisease	7.01E-23
- influenza A [lung] NA 21373	MouseDisease	3.07E-21
- normal control [bone marrow] calcitriol;lipopolysaccharide (L	MouseDisease	2.81E-27
- normal control [primary bronchial epithelium] NA 6022	HumanDisease	3.96E-19

Case/Control Differences

No metadata difference between case and control.

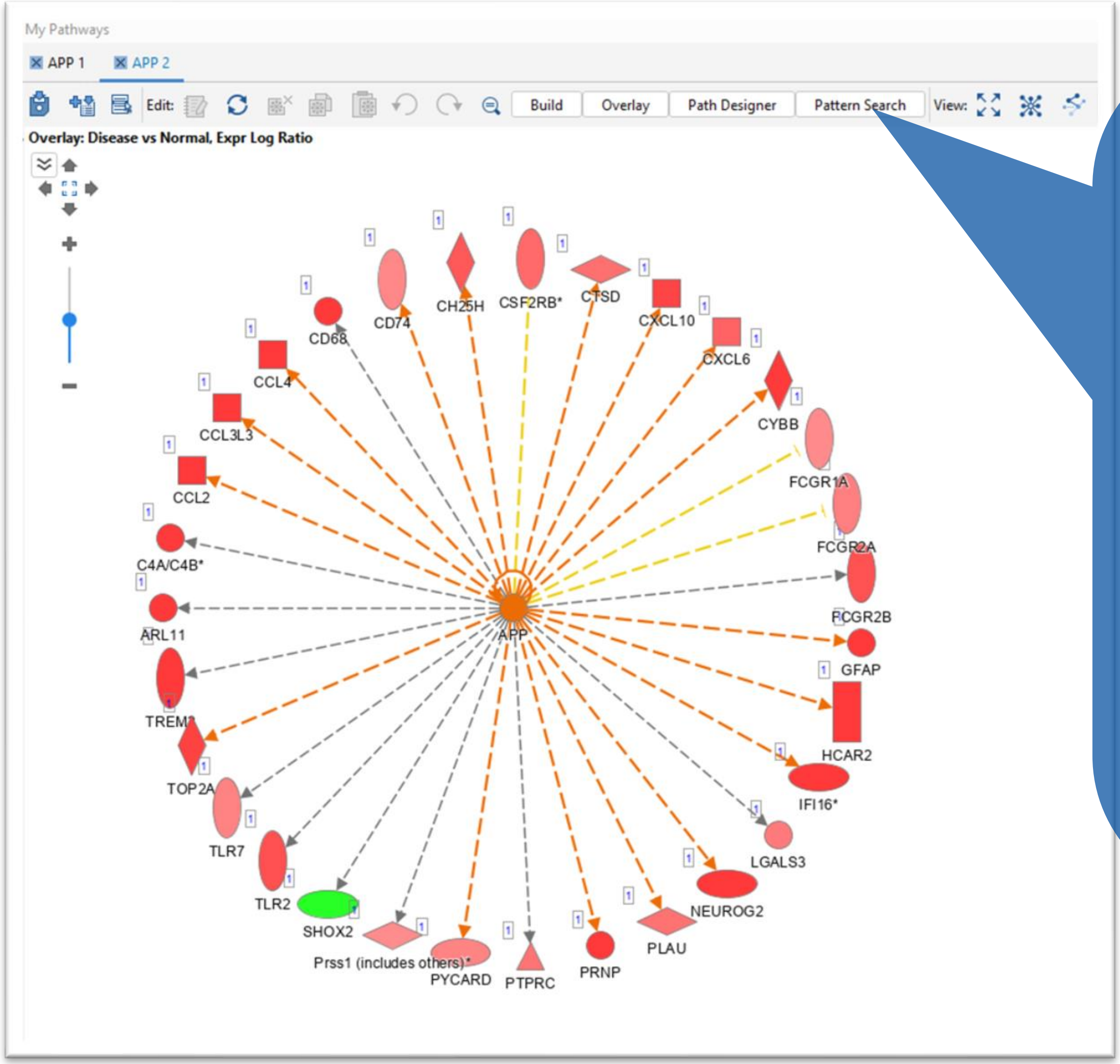
Comparison Context

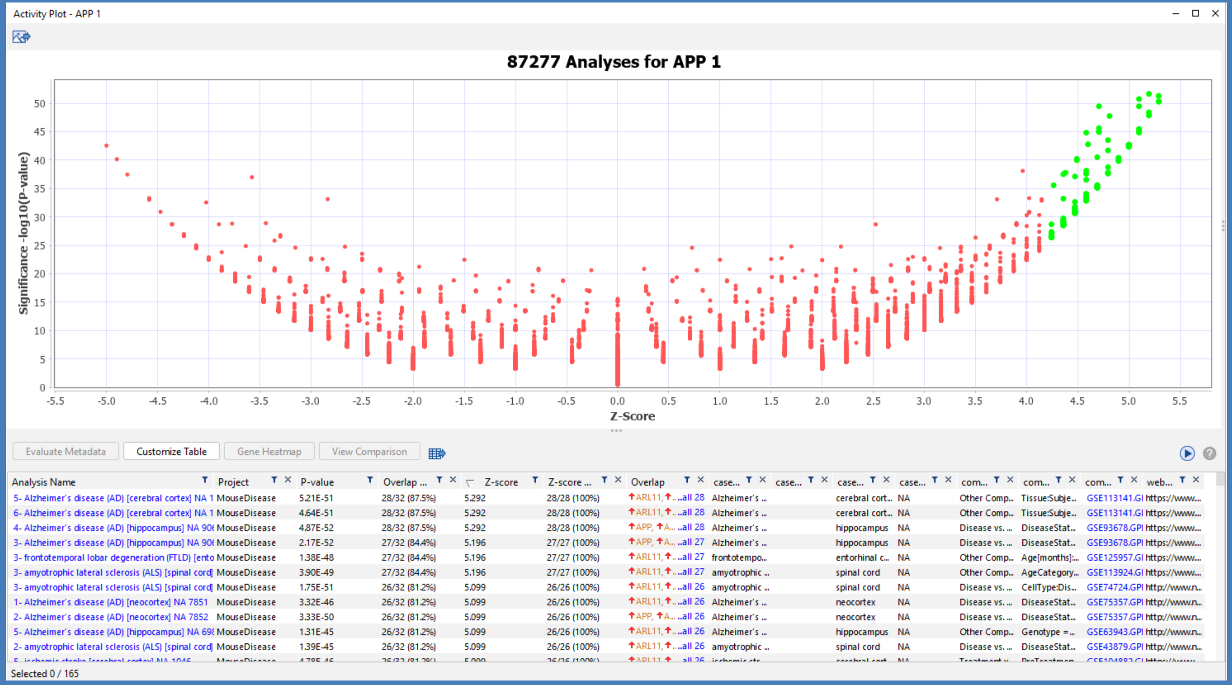
There is no context metadata

All Experiment Metadata

Analysis Name	Project	P-value	Z-score	case.dise...	case.targ...	case.tissue	case.trea...	comparis...	comparis...	comparis...	weblink
7- urinary tract obstruction [kidney] NA 6887	MouseDisease	5.97E-48	6.689	urinary tract obstr...		kidney	NA	Disease vs. Normal	DiseaseState:Gen...	GSE55808.GPL1311	https://www.ncbi.n...
6- renal fibrosis [kidney] NA 8621	MouseDisease	6.77E-47	6.602	renal fibrosis		kidney	NA	Treatment1 vs. Tr...	Genotype:Samplin...	GSE87212.GPL1905	https://www.ncbi.n...
Ulcerative colitis vs control	Comparison Analyses	1.17E-63	6.459								
Human Macrophages West Nile Virus Infection RefSeq	Comparison Analyses	8.11E-46	6.404								
Human Macrophages West Nile Virus Infection RefSeq	Comparison Analyses	8.11E-46	6.404								
Human Macrophages West Nile Virus Infection RefSeq	Comparison Analyses	8.11E-46	6.404								
16- multiple sclerosis (MS) [peripheral blood] IL-1 beta;1	HumanDisease	9.30E-36	6.299	multiple sclerosis ...		peripheral blood	IL-1 beta;TNF alpha	Treatment1 vs. Tr...	DiseaseState:Trea...	GSE120411.GPL167	https://www.ncbi.n...
Ulcerative colitis vs control	Example Analyses	3.36E-75	6.267	ulcerative colitis (...		colonic mucosa					
26- breast adenocarcinoma [breast] NA 12757	OncoHuman	2.91E-77	6.235	breast adenocarci...		breast	NA	Other Comparisons	HER2[Status]:ER[S...	GSE86166.GPL1504	https://www.ncbi.n...
52- normal control [peripheral blood] NA 47	Human Tissues (GTEx)	3.29E-56	6.222	normal control		peripheral blood	NA	Other Comparisons	TissueDetail_GTE...	GTEx_v8.DESeq2R.t	https://gtexportal...
2- urinary tract infection (UTI) [bladder] NA 17626	MouseDisease	5.45E-45	6.155	urinary tract infect...		bladder	NA	Treatment vs. Con...	SamplingTime[hpi...	GSE27575.GPL6246	https://www.ncbi.n...

Identify patterns seen in your data and match with public data sets





Analysis Name	Project	P-value	Overlap ...	Z-score	Z-score ...	Overlap	case...	case...	case...	case...	com...	com...	com...	web...
5- Alzheimer's disease (AD) [cerebral cortex] NA 1	MouseDisease	5.21E-51	28/32 (87.5%)	5.292	28/28 (100%)	↑ARL11, ↑… …all 28	Alzheimer's …		cerebral cort…	NA	Other Comp…	Tissue:Subje…	GSE113141.GI	https://www.…
6- Alzheimer's disease (AD) [cerebral cortex] NA 1	MouseDisease	4.64E-51	28/32 (87.5%)	5.292	28/28 (100%)	↑ARL11, ↑… …all 28	Alzheimer's …		cerebral cort…	NA	Other Comp…	Tissue:Subje…	GSE113141.GI	https://www.…
4- Alzheimer's disease (AD) [hippocampus] NA 90	MouseDisease	4.87E-52	28/32 (87.5%)	5.292	28/28 (100%)	↑APP, ↑A… …all 28	Alzheimer's …		hippocampus	NA	Disease vs. …	DiseaseStat…	GSE93678.GPI	https://www.…
3- Alzheimer's disease (AD) [hippocampus] NA 90	MouseDisease	2.17E-52	27/32 (84.4%)	5.196	27/27 (100%)	↑APP, ↑A… …all 27	Alzheimer's …		hippocampus	NA	Disease vs. …	DiseaseStat…	GSE93678.GPI	https://www.…
3- frontotemporal lobar degeneration (FTLD) [ento	MouseDisease	1.38E-48	27/32 (84.4%)	5.196	27/27 (100%)	↑ARL11, ↑… …all 27	frontotempo…		entorhinal c…	NA	Other Comp…	Age[months]:…	GSE125957.GI	https://www.…
3- amyotrophic lateral sclerosis (ALS) [spinal cord]	MouseDisease	3.90E-49	27/32 (84.4%)	5.196	27/27 (100%)	↑ARL11, ↑… …all 27	amyotrophic …		spinal cord	NA	Other Comp…	AgeCategory…	GSE113924.GI	https://www.…
3- amyotrophic lateral sclerosis (ALS) [spinal cord]	MouseDisease	1.75E-51	26/32 (81.2%)	5.099	26/26 (100%)	↑ARL11, ↑… …all 26	amyotrophic …		spinal cord	NA	Disease vs. …	CellType:Dis…	GSE74724.GPI	http://www.n…
1- Alzheimer's disease (AD) [neocortex] NA 7851	MouseDisease	3.32E-46	26/32 (81.2%)	5.099	26/26 (100%)	↑ARL11, ↑… …all 26	Alzheimer's …		neocortex	NA	Disease vs. …	DiseaseStat…	GSE75357.GPI	http://www.n…
2- Alzheimer's disease (AD) [neocortex] NA 7852	MouseDisease	3.33E-50	26/32 (81.2%)	5.099	26/26 (100%)	↑APP, ↑A… …all 26	Alzheimer's …		neocortex	NA	Disease vs. …	DiseaseStat…	GSE75357.GPI	http://www.n…
5- Alzheimer's disease (AD) [hippocampus] NA 69	MouseDisease	1.31E-45	26/32 (81.2%)	5.099	26/26 (100%)	↑ARL11, ↑… …all 26	Alzheimer's …		hippocampus	NA	Other Comp…	Genotype = …	GSE63943.GPI	http://www.n…
2- amyotrophic lateral sclerosis (ALS) [spinal cord]	MouseDisease	1.39E-45	26/32 (81.2%)	5.099	26/26 (100%)	↑ARL11, ↑… …all 26	amyotrophic …		spinal cord	NA	Disease vs. …	DiseaseStat…	GSE43879.GPI	http://www.n…

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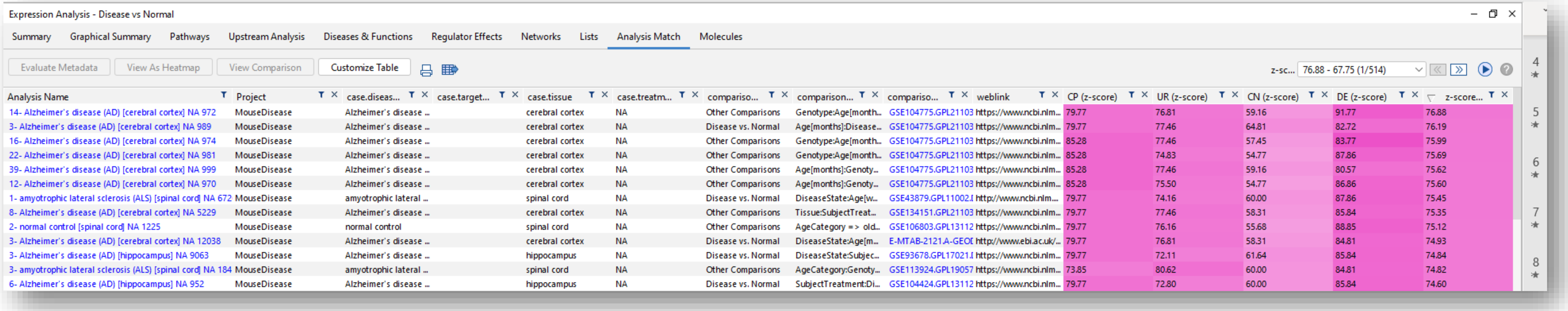
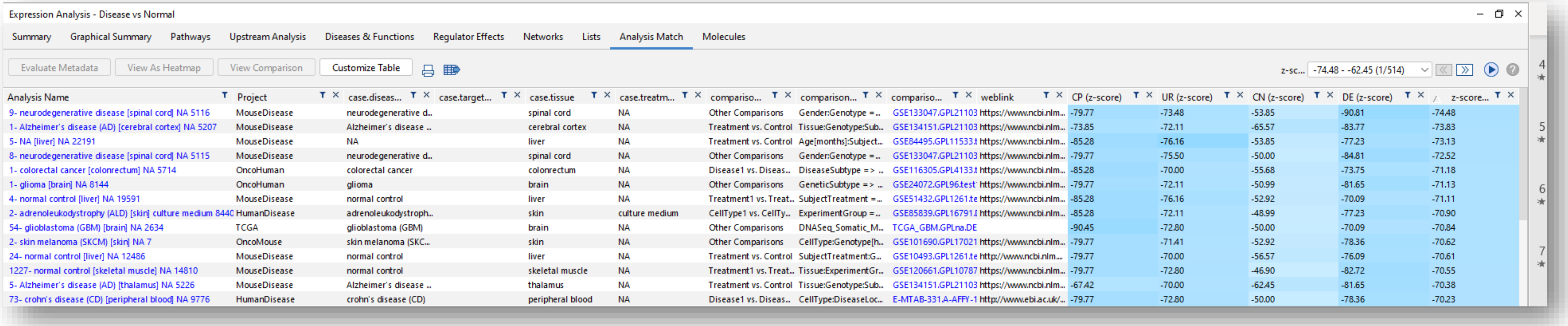
Compare your entire core analysis with public data sets



z-sc... 76.88 - 67.75 (1/514)

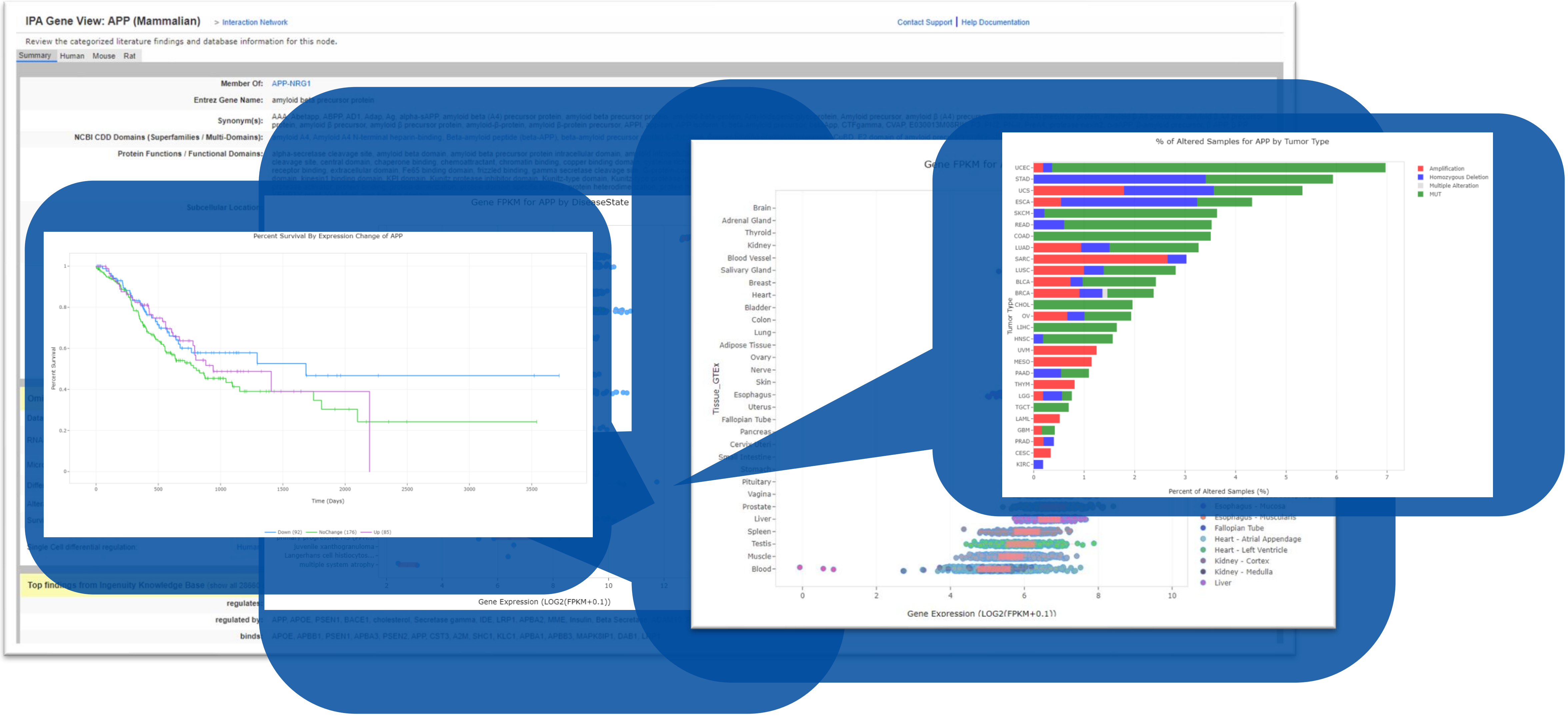
Analysis Name	Project	case.diseas...	case.target...	case.tissue	case.treatm...	compariso...	comparison...	compariso...	weblink	CP (z-score)	UR (z-score)	CN (z-score)	DE (z-score)	z-score...
14- Alzheimer's disease (AD) [cerebral cortex] NA 972	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Genotype:Age[month...	GSE104775.GPL21103	https://www.ncbi.nlm...	79.77	76.81	59.16	91.77	76.88
3- Alzheimer's disease (AD) [cerebral cortex] NA 989	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Disease vs. Normal	Age[months]:Disease...	GSE104775.GPL21103	https://www.ncbi.nlm...	79.77	77.46	64.81	82.72	76.19
16- Alzheimer's disease (AD) [cerebral cortex] NA 974	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Genotype:Age[month...	GSE104775.GPL21103	https://www.ncbi.nlm...	85.28	77.46	57.45	83.77	75.99
22- Alzheimer's disease (AD) [cerebral cortex] NA 981	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Genotype:Age[month...	GSE104775.GPL21103	https://www.ncbi.nlm...	85.28	74.83	54.77	87.86	75.69
39- Alzheimer's disease (AD) [cerebral cortex] NA 999	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Age[months]:Genoty...	GSE104775.GPL21103	https://www.ncbi.nlm...	85.28	77.46	59.16	80.57	75.62
12- Alzheimer's disease (AD) [cerebral cortex] NA 970	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Age[months]:Genoty...	GSE104775.GPL21103	https://www.ncbi.nlm...	85.28	75.50	54.77	86.86	75.60
1- amyotrophic lateral sclerosis (ALS) [spinal cord] NA 672	MouseDisease	amyotrophic lateral ...		spinal cord	NA	Disease vs. Normal	DiseaseState:Age[w...	GSE43879.GPL11002.I	http://www.ncbi.nlm....	79.77	74.16	60.00	87.86	75.45
8- Alzheimer's disease (AD) [cerebral cortex] NA 5229	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Other Comparisons	Tissue:SubjectTreat...	GSE134151.GPL21103	https://www.ncbi.nlm...	79.77	77.46	58.31	85.84	75.35
2- normal control [spinal cord] NA 1225	MouseDisease	normal control		spinal cord	NA	Other Comparisons	AgeCategory => old...	GSE106803.GPL13112	https://www.ncbi.nlm...	79.77	76.16	55.68	88.85	75.12
3- Alzheimer's disease (AD) [cerebral cortex] NA 12038	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Disease vs. Normal	DiseaseState:Age[m...	E-MTAB-2121.A-GEOI	http://www.ebi.ac.uk/...	79.77	76.81	58.31	84.81	74.93
3- Alzheimer's disease (AD) [hippocampus] NA 9063	MouseDisease	Alzheimer's disease ...		hippocampus	NA	Disease vs. Normal	DiseaseState:Subjec...	GSE93678.GPL17021.I	https://www.ncbi.nlm...	79.77	72.11	61.64	85.84	74.84
3- amyotrophic lateral sclerosis (ALS) [spinal cord] NA 184	MouseDisease	amyotrophic lateral ...		spinal cord	NA	Other Comparisons	AgeCategory:Genoty...	GSE113924.GPL19057	https://www.ncbi.nlm...	73.85	80.62	60.00	84.81	74.82
6- Alzheimer's disease (AD) [hippocampus] NA 952	MouseDisease	Alzheimer's disease ...		hippocampus	NA	Disease vs. Normal	SubjectTreatment:Di...	GSE104424.GPL13112	https://www.ncbi.nlm...	79.77	72.80	60.00	85.84	74.60



z-sc... -74.48 - -62.45 (1/514)

Analysis Name	Project	case.diseas...	case.target...	case.tissue	case.treatm...	compariso...	comparison...	compariso...	weblink	CP (z-score)	UR (z-score)	CN (z-score)	DE (z-score)	z-score...
9- neurodegenerative disease [spinal cord] NA 5116	MouseDisease	neurodegenerative d...		spinal cord	NA	Other Comparisons	Gender:Genotype =...	GSE133047.GPL21103	https://www.ncbi.nlm...	-79.77	-73.48	-53.85	-90.81	-74.48
1- Alzheimer's disease (AD) [cerebral cortex] NA 5207	MouseDisease	Alzheimer's disease ...		cerebral cortex	NA	Treatment vs. Control	Tissue:Genotype:Sub...	GSE134151.GPL21103	https://www.ncbi.nlm...	-73.85	-72.11	-65.57	-83.77	-73.83
5- NA [liver] NA 22191	MouseDisease	NA		liver	NA	Treatment vs. Control	Age[months]:Subject...	GSE84495.GPL11533.t	https://www.ncbi.nlm...	-85.28	-76.16	-53.85	-77.23	-73.13
8- neurodegenerative disease [spinal cord] NA 5115	MouseDisease	neurodegenerative d...		spinal cord	NA	Other Comparisons	Gender:Genotype =...	GSE133047.GPL21103	https://www.ncbi.nlm...	-79.77	-75.50	-50.00	-84.81	-72.52
1- colorectal cancer [colonrectum] NA 5714	OncoHuman	colorectal cancer		colonrectum	NA	Disease1 vs. Diseas...	DiseaseSubtype => ...	GSE116305.GPL4133.t	https://www.ncbi.nlm...	-85.28	-70.00	-55.68	-73.75	-71.18
1- glioma [brain] NA 8144	OncoHuman	glioma		brain	NA	Other Comparisons	GeneticSubtype => ...	GSE24072.GPL96.test	https://www.ncbi.nlm...	-79.77	-72.11	-50.99	-81.65	-71.13
4- normal control [liver] NA 19591	MouseDisease	normal control		liver	NA	Treatment1 vs. Treat...	SubjectTreatment =...	GSE51432.GPL1261.te	https://www.ncbi.nlm...	-85.28	-76.16	-52.92	-70.09	-71.11
2- adrenoleukodystrophy (ALD) [skin] culture medium 8440	HumanDisease	adrenoleukodystroph...		skin	culture medium	CellType1 vs. CellTy...	ExperimentGroup =...	GSE85839.GPL16791.I	https://www.ncbi.nlm...	-85.28	-72.11	-48.99	-77.23	-70.90
54- glioblastoma (GBM) [brain] NA 2634	TCGA	glioblastoma (GBM)		brain	NA	Other Comparisons	DNASeq_Somatic_M...	TCGA_GBM.GPLna.DE		-90.45	-72.80	-50.00	-70.09	-70.84
2- skin melanoma (SKCM) [skin] NA 7	OncoMouse	skin melanoma (SKC...		skin	NA	Other Comparisons	CellType:Genotype[h...	GSE101690.GPL17021	https://www.ncbi.nlm...	-79.77	-71.41	-52.92	-78.36	-70.62
24- normal control [liver] NA 12486	MouseDisease	normal control		liver	NA	Treatment vs. Control	SubjectTreatment:G...	GSE10493.GPL1261.te	http://www.ncbi.nlm....	-79.77	-70.00	-56.57	-76.09	-70.61
1227- normal control [skeletal muscle] NA 14810	MouseDisease	normal control		skeletal muscle	NA	Treatment1 vs. Treat...	Tissue:ExperimentGr...	GSE120661.GPL10787	https://www.ncbi.nlm...	-79.77	-72.80	-46.90	-82.72	-70.55
5- Alzheimer's disease (AD) [thalamus] NA 5226	MouseDisease	Alzheimer's disease ...		thalamus	NA	Treatment vs. Control	Tissue:Genotype:Sub...	GSE134151.GPL21103	https://www.ncbi.nlm...	-67.42	-70.00	-62.45	-81.65	-70.38
73- crohn's disease (CD) [peripheral blood] NA 9776	HumanDisease	crohn's disease (CD)		peripheral blood	NA	Disease1 vs. Diseas...	CellType:DiseaseLoc...	E-MTAB-331.A-AFFY-1	http://www.ebi.ac.uk/...	-79.77	-72.80	-50.00	-78.36	-70.23

Explore genes in Land Explorer



IPA Gene View: APP (Mammalian) > Interaction Network

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

Member Of: APP-NRG1

Entrez Gene Name: amyloid beta precursor protein

Synonym(s): AAA, Abetapp, ABPP, AD1, Adap, Ag, alpha-sAPP, amyloid beta (A4) precursor protein, amyloid beta precursor protein, amyloid β precursor, amyloid β precursor protein, amyloid-β-protein, amyloid β-protein precursor, APPI

NCBI CDD Domains (Superfamilies / Multi-Domains): amyloid A4, Amyloid A4 N-terminal heparin-binding, Beta-amyloid peptide (beta-APP), beta-amyloid precursor

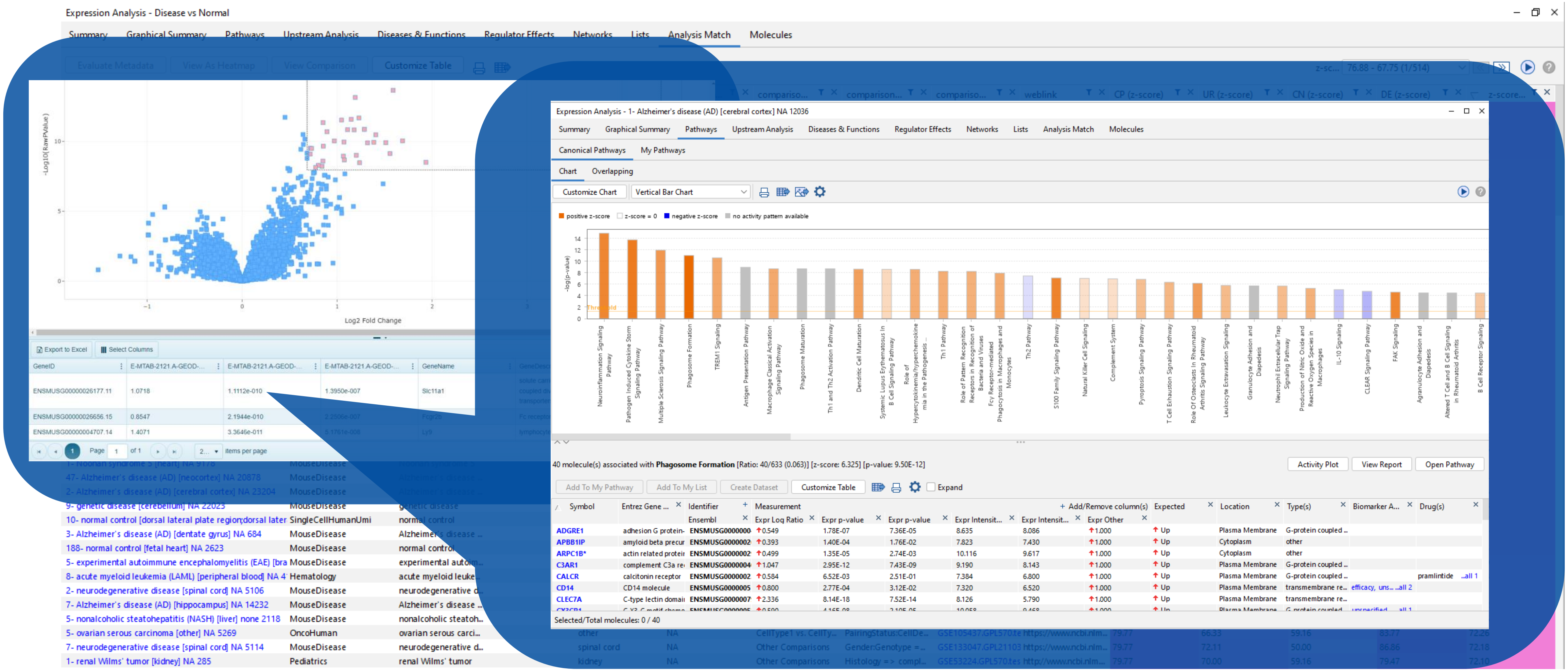
Protein Functions / Functional Domains: alpha-secretase cleavage site, amyloid beta domain, amyloid beta precursor protein intracellular domain, cleavage site, central domain, chaperone binding, chemoattractant, chromatin binding, copper binding domain, receptor binding, extracellular domain, Fe65 binding domain, frizzled binding, gamma secretase cleavage site, domain, kinesin1 binding domain, KPI domain, Kunitz protease inhibitor domain, Kunitz-type domain, protein heterodimerization

Top findings from Ingenuity Knowledge Base

regulated by: APP, APOE, PSEN1, BACE1, cholesterol, Secretase gamma, IDE, LRP1, APBA2, MME, Insulin, Beta Secretase

binds: APOE, APBB1, PSEN1, APBA3, PSEN2, APP, CST3, A2M, SHC1, KLC1, APBA1, APBB3, MAPK8IP1, DAB1

Explore public data comparisons in Land Explorer and IPA



GeneID	E-MTAB-2121.A-GEOD-...	E-MTAB-2121.A-GEOD-...	E-MTAB-2121.A-GEOD-...	GeneName
ENSMUSG00000026177.11	1.0718	1.1112e-010	1.3950e-007	Slc11a1
ENSMUSG00000026656.15	0.8547	2.1944e-010	2.2506e-007	Fcgr2b
ENSMUSG00000004707.14	1.4071	3.3646e-011	5.1761e-008	Ly9

Page 1 of 1 2... items per page

1- Noonan syndrome 5 [heart] NA 9178	MouseDisease	Noonan syndrome 5
47- Alzheimer's disease (AD) [neocortex] NA 20878	MouseDisease	Alzheimer's disease ...
2- Alzheimer's disease (AD) [cerebral cortex] NA 23204	MouseDisease	Alzheimer's disease ...
9- genetic disease [cerebellum] NA 22023	MouseDisease	genetic disease
10- normal control [dorsal lateral plate region;dorsal later	SingleCellHumanUmi	normal control
3- Alzheimer's disease (AD) [dentate gyrus] NA 684	MouseDisease	Alzheimer's disease ...
188- normal control [fetal heart] NA 2623	MouseDisease	normal control
5- experimental autoimmune encephalomyelitis (EAE) [bra	MouseDisease	experimental autoim...
8- acute myeloid leukemia (LAML) [peripheral blood] NA 4	Hematology	acute myeloid leuke...
2- neurodegenerative disease [spinal cord] NA 5106	MouseDisease	neurodegenerative d...
7- Alzheimer's disease (AD) [hippocampus] NA 14232	MouseDisease	Alzheimer's disease ...
5- nonalcoholic steatohepatitis (NASH) [liver] none 2118	MouseDisease	nonalcoholic steatoh...
5- ovarian serous carcinoma [other] NA 5269	OncoHuman	ovarian serous carci...
7- neurodegenerative disease [spinal cord] NA 5114	MouseDisease	neurodegenerative d...
1- renal Wilms' tumor [kidney] NA 285	Pediatrics	renal Wilms' tumor

other	NA	CellType1 vs. CellTy...	PairingStatus:CellDe...	GSE105437.GPL570.te	https://www.ncbi.nlm...	79.77	66.33	59.16	83.77	72.26
spinal cord	NA	Other Comparisons	Gender:Genotype =...	GSE133047.GPL21103	https://www.ncbi.nlm...	79.77	72.11	50.00	86.86	72.18
kidney	NA	Other Comparisons	Histology => compl...	GSE53224.GPL570.tes	http://www.ncbi.nlm...	79.77	70.00	59.16	79.47	72.10

40 molecule(s) associated with **Phagosome Formation** [Ratio: 40/633 (0.063)] [z-score: 6.325] [p-value: 9.50E-12]

Symbol	Entrez Gene ...	Identifier Ensembl	Measurement Expr Log Ratio	Expr p-value	Expr p-value	Expr Intensit...	Expr Intensit...	Expr Other	Expected	Location	Type(s)	Biomarker A...	Drug(s)
ADGRE1	adhesion G protein-	ENSMUSG0000000	↑0.549	1.78E-07	7.36E-05	8.635	8.086	↑1.000	↑ Up	Plasma Membrane	G-protein coupled ...		
APBB1IP	amyloid beta precur	ENSMUSG0000002	↑0.393	1.40E-04	1.76E-02	7.823	7.430	↑1.000	↑ Up	Cytoplasm	other		
ARPC1B*	actin related protei	ENSMUSG0000002	↑0.499	1.35E-05	2.74E-03	10.116	9.617	↑1.000	↑ Up	Cytoplasm	other		
C3AR1	complement C3a re	ENSMUSG0000004	↑1.047	2.95E-12	7.43E-09	9.190	8.143	↑1.000	↑ Up	Plasma Membrane	G-protein coupled ...		
CALCR	calcitonin receptor	ENSMUSG0000002	↑0.584	6.52E-03	2.51E-01	7.384	6.800	↑1.000	↑ Up	Plasma Membrane	G-protein coupled ...		pramlintide ...all 1
CD14	CD14 molecule	ENSMUSG0000005	↑0.800	2.77E-04	3.12E-02	7.320	6.520	↑1.000	↑ Up	Plasma Membrane	transmembrane re...	efficacy, uns... ...all 2	
CLEC7A	C-type lectin domai	ENSMUSG0000007	↑2.336	8.14E-18	7.52E-14	8.126	5.790	↑1.000	↑ Up	Plasma Membrane	transmembrane re...		

Selected/Total molecules: 0 / 40

Agenda

Topics for today’s workshop

Interpreting your ′omics data using IPA Core Analysis

- Setting up a core analysis
- Canonical pathways
- Comparison analysis

Creating networks from scratch

- Connecting genes in a network
- In silico testing
- Overlay drugs and biomarkers

Exploring publicly available data

- Activity plot, pattern search, Analysis Match
- Land Explorer

Summary

Previous recordings, slides, etc.

Popular recordings from recent trainings (2022)

RNA-seq analysis and interpretation:
https://qiagen.showpad.com/share/FFpWhr5b1aVbQbcQD0bs5

miRNA analysis using Ingenuity Pathway Analysis:
https://qiagen.showpad.com/share/aDzTaHl4GBasbDcuyJWQp

Single-cell RNA-seq analysis and interpretation:
https://qiagen.showpad.com/share/u5Sv8rbZzED2aLe2bc4s4

Public single cell data analysis and interpretation:
https://qiagen.showpad.com/share/wMpUrxwnrJk4Zc6iP9jzm

Single-cell ATAC-seq analysis:
https://qiagen.showpad.com/share/weaxKgKrGxtnW4Udz5Toa

SARS-CoV-2 detection in wastewater w/ CLC Genomics Workbench:
https://qiagen.showpad.com/share/PZmv2KNXNT1yDTlTUNmca

Long reads sequencing analysis:
https://qiagen.showpad.com/share/EXDUJ3RKHsjXNxQpCiVnA

Software trials

CLC Genomics Workbench trial:
https://qiagen.showpad.com/share/I6MqdhIybpllyvuYW3AKy

Human Somatic Mutation Database trial:
https://qiagen.showpad.com/share/ELhnINyfamHr1Q1mmQnuv

Ingenuity Pathway Analysis resources

IPA beginner training recording:
https://qiagen.showpad.com/share/t2cGMdF3NjVucBA0b9tIT

IPA deeper dive training recording:
https://qiagen.showpad.com/share/wCQrTeE2ftSQkgFTooHSu

IPA step-by-step guide w/ data format (slide 9) and upload (slide 28) instructions:
https://qiagen.showpad.com/share/VjizSLJVBw1qfVnyoVJ8B

Resources in this presentation

Formatting transcriptomics data before uploading to IPA

Data upload step by step

How to access Land Explorer data

Land Explorer navigation

Colors and z-scores in IPA

IPA investigates biology of anti-PD1 immunotherapy resistance in Metastatic Melanoma

Volume 26, Issue 14

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CLINICAL CANCER RESEARCH

The Journal of Clinical and Translational Research

AACR

CLINICAL CANCER RESEARCH | TRANSLATIONAL CANCER MECHANISMS AND THERAPY

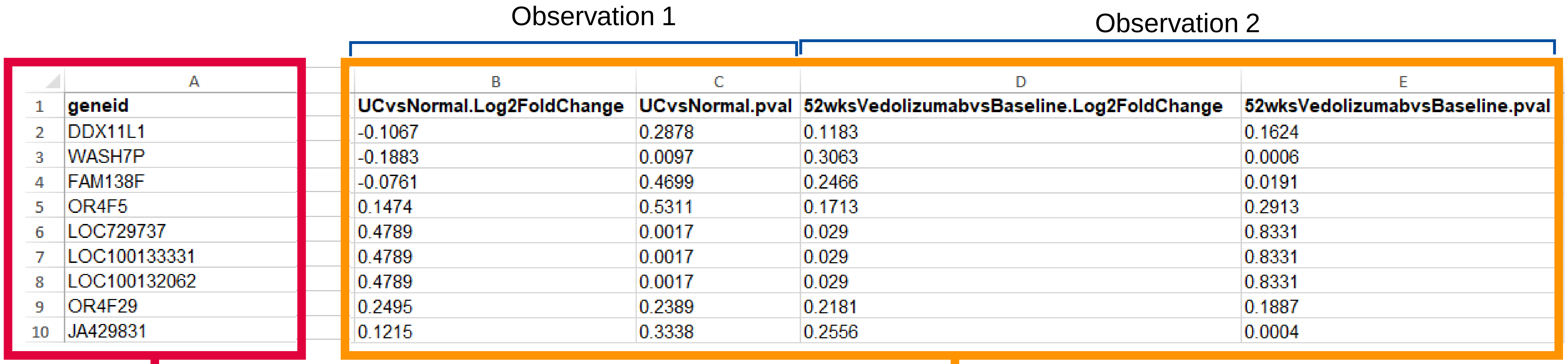
Tumor CD155 Expression Is Associated with Resistance to Anti-PD1 Immunotherapy in Metastatic Melanoma

Check for updates

Ailin Lepletier[1], Jason Madore[1], Jake S. O'Donnell[1,2,3], Rebecca L. Johnston[4], Xian-Yang Li[1], Elizabeth McDonald[2], Elizabeth Ahern[1,3,5], Anna Kuchel[1,3,5], Melissa Eastgate[3,5], Sally-Ann Pearson[1], Domenico Mallardo[6], Paolo A. Ascierto[6], Daniela Massi[7], Barbara Merelli[8], Mario Mandala[8], James S. Wilmott[9], Alexander M. Menzies[9], Charles Leduc[10], John Stagg[1,11], Bertrand Routy[11], Georgina V. Long[9], Richard A. Scolyer[9,12,13], Tobias Bald[14], Nicola Waddell[4], William C. Dougall[1], Michele W.L. Teng[2,3], and Mark J. Smyth[1,3]

- **Metastatic melanoma treated with immune checkpoint blockade therapy (n=155) and BRAF/MEK-directed targeted therapy (n=50)**
- **RNA sequencing performed on samples and clinical RECIST response and progression-free survival data were collected**
- **High pretreatment levels of CD155 correlated with high parenchymal PD1+CD8+/CD8+ T-cell ratios and poor response to anti-PD1 therapy**

Formatting ‘omics data before uploading to IPA



Observation 1

Observation 2

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

Analyte identifier REQUIRED to explore enrichment

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

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

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

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

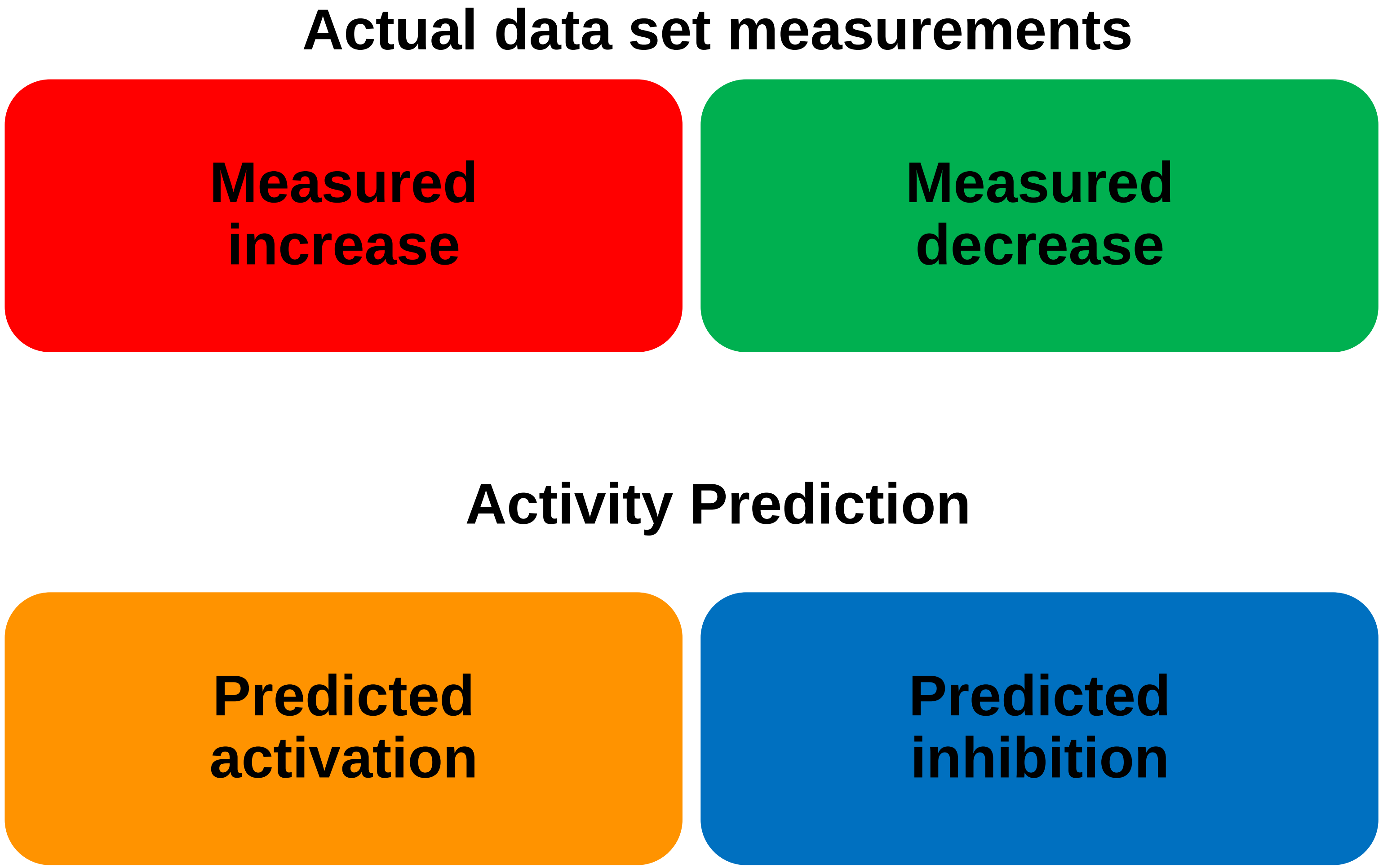
Significance values: P-values **optional but recommended to enable filtering for significance*

Accepted file formats:

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

Multiple comparisons or observations may be uploaded in one file

IPA important colors



Actual data set measurements

Measured increase

Measured decrease

Activity Prediction

Predicted activation

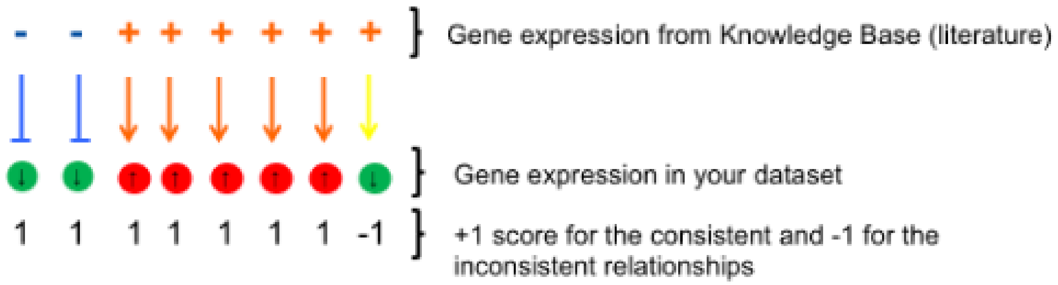
Predicted inhibition

Z-scores predict activity

Compares the EXPECTED gene expression pattern for activation in the knowledgebase to the ACTUAL gene expression measurements

Z-scores are used throughout IPA to predict activation or inhibition of:

- **Canonical pathways**
- **Upstream regulators**
- **Master regulators**
- **Diseases and functions**



Gene expression from Knowledge Base (literature)

Gene expression in your dataset

+1 score for the consistent and -1 for the inconsistent relationships

Simplified z-score formula:

$$z = \frac{x}{\sigma_x} = \frac{\sum_i x_i}{\sqrt{N}} = \frac{N_+ - N_-}{\sqrt{N}}$$

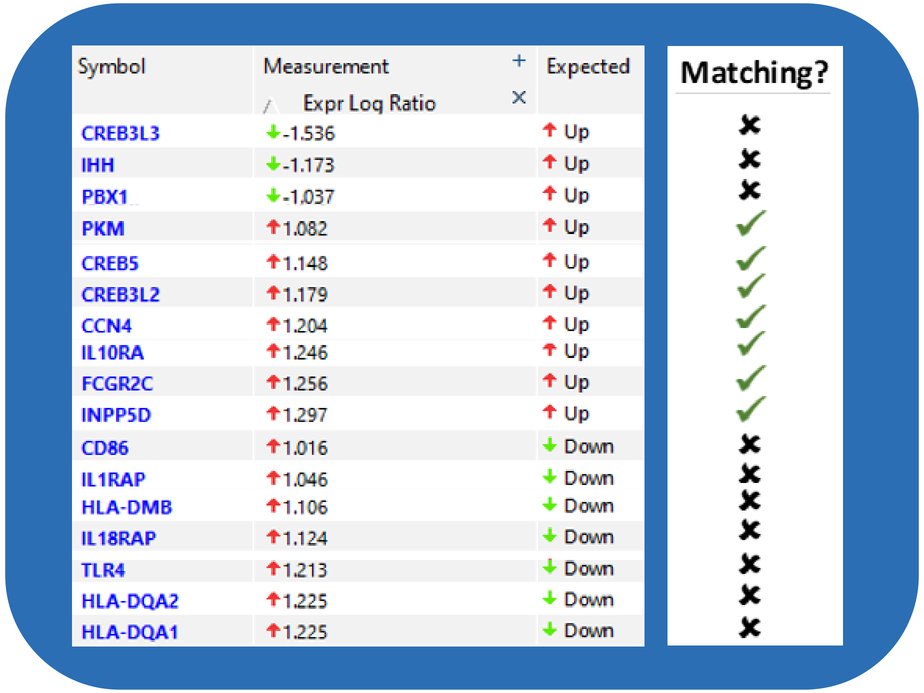
Z-score calculation summary

Compares the EXPECTED gene expression pattern for activation in the knowledgebase to the ACTUAL data set gene expression measurements

Does the expected pattern of activation *mostly* match the actual gene expression measurements?

NO! a NEGATIVE Z-score is calculated indicating predicted inhibition

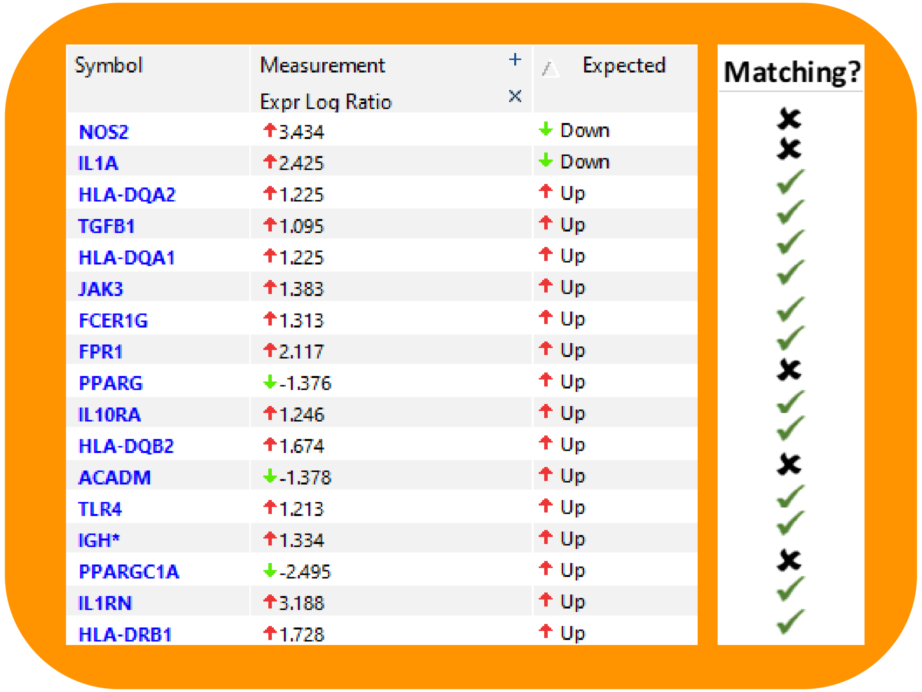
Z-score= -2.236



Symbol	Measurement Expr Log Ratio	Expected	Matching?
CREB3L3	↓-1.536	↑ Up	✗
IHH	↓-1.173	↑ Up	✗
PBX1	↓-1.037	↑ Up	✗
PKM	↑1.082	↑ Up	✓
CREB5	↑1.148	↑ Up	✓
CREB3L2	↑1.179	↑ Up	✓
CCN4	↑1.204	↑ Up	✓
IL10RA	↑1.246	↑ Up	✓
FCGR2C	↑1.256	↑ Up	✓
INPP5D	↑1.297	↑ Up	✓
CD86	↑1.016	↓ Down	✗
IL1RAP	↑1.046	↓ Down	✗
HLA-DMB	↑1.106	↓ Down	✗
IL18RAP	↑1.124	↓ Down	✗
TLR4	↑1.213	↓ Down	✗
HLA-DQA2	↑1.225	↓ Down	✗
HLA-DQA1	↑1.225	↓ Down	✗

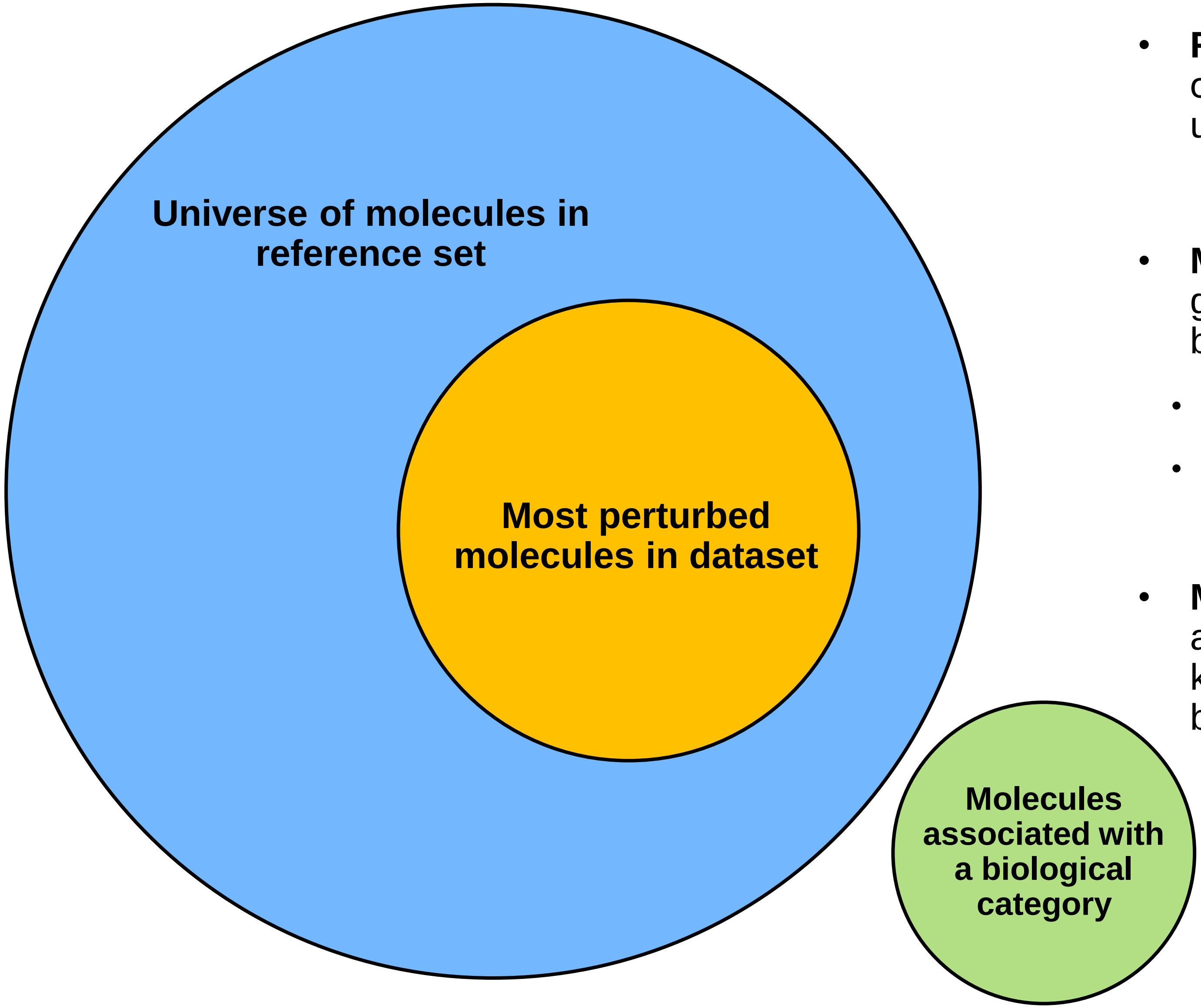
YES! a POSITIVE Z-score is calculated indicating predicted activation

Z-score= 2.427



Symbol	Measurement Expr Log Ratio	Expected	Matching?
NOS2	↑3.434	↓ Down	✗
IL1A	↑2.425	↓ Down	✗
HLA-DQA2	↑1.225	↑ Up	✓
TGFB1	↑1.095	↑ Up	✓
HLA-DQA1	↑1.225	↑ Up	✓
JAK3	↑1.383	↑ Up	✓
FCER1G	↑1.313	↑ Up	✓
FPR1	↑2.117	↑ Up	✓
PPARG	↓-1.376	↑ Up	✗
IL10RA	↑1.246	↑ Up	✓
HLA-DQB2	↑1.674	↑ Up	✓
ACADM	↓-1.378	↑ Up	✗
TLR4	↑1.213	↑ Up	✓
IGH*	↑1.334	↑ Up	✓
PPARGC1A	↓-2.495	↑ Up	✗
IL1RN	↑3.188	↑ Up	✓
HLA-DRB1	↑1.728	↑ Up	✓

Pathway enrichment: P-value of overlap

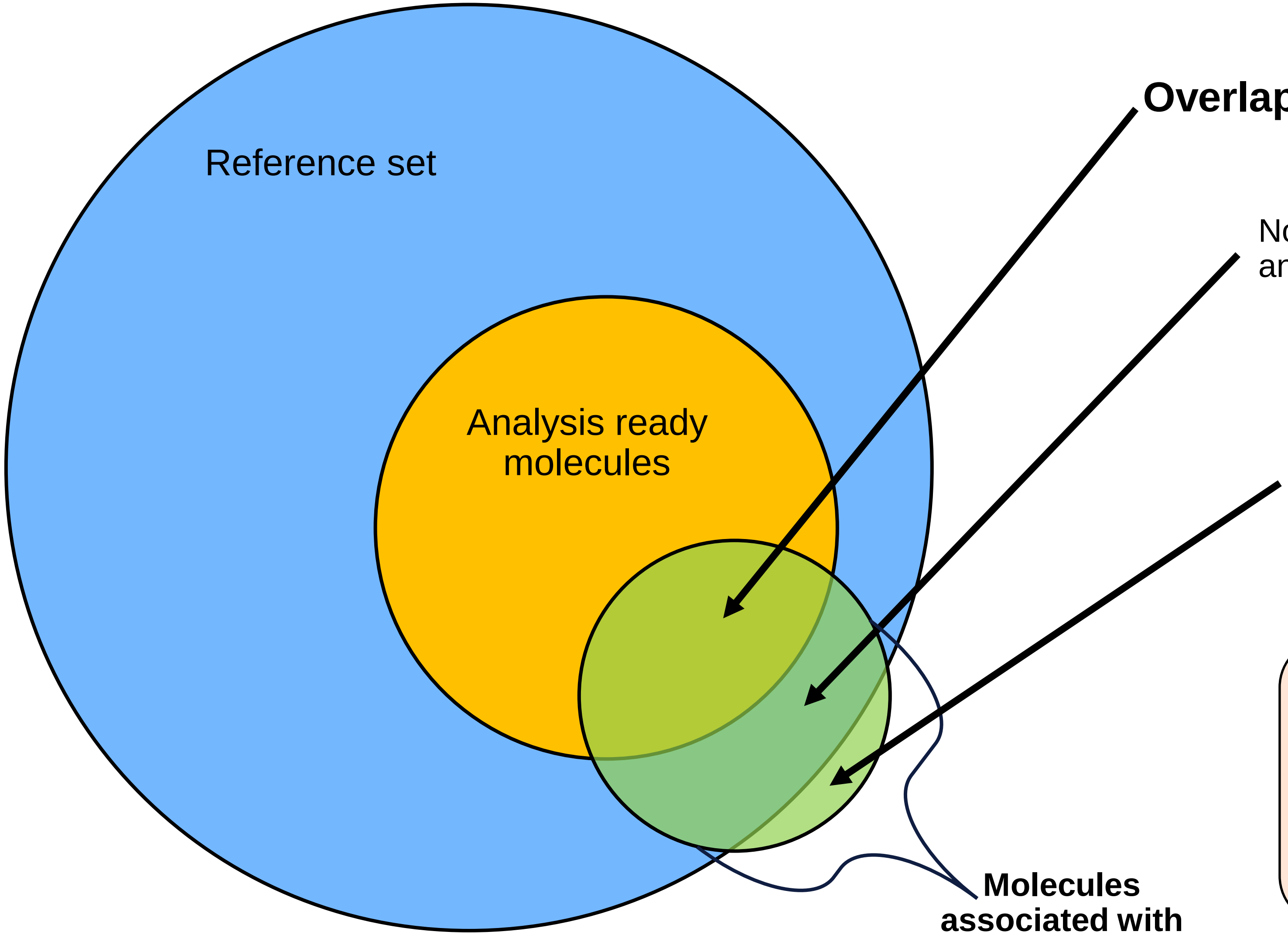


- **Reference set** is typically all genes or proteins that can be reliably detected by the ‘omics technology used

- **Most perturbed** is a subset of measured genes/proteins that were significantly different between experimental groups
  - Fold change cut offs and p-value cut offs used
  - IPA calls these “Analysis-ready molecules”

- **Molecules associated with a biological category** are a set of genes/proteins that the IPA knowledgebase has annotated to be important for a biological pathway, function, or disease.

Testing for Enrichment using the Fisher’s Exact Test



Reference set

Analysis ready molecules

Overlapping molecules

Non-analysis-ready molecules that have been annotated to a biological category

i.e. genes that did not pass cut offs

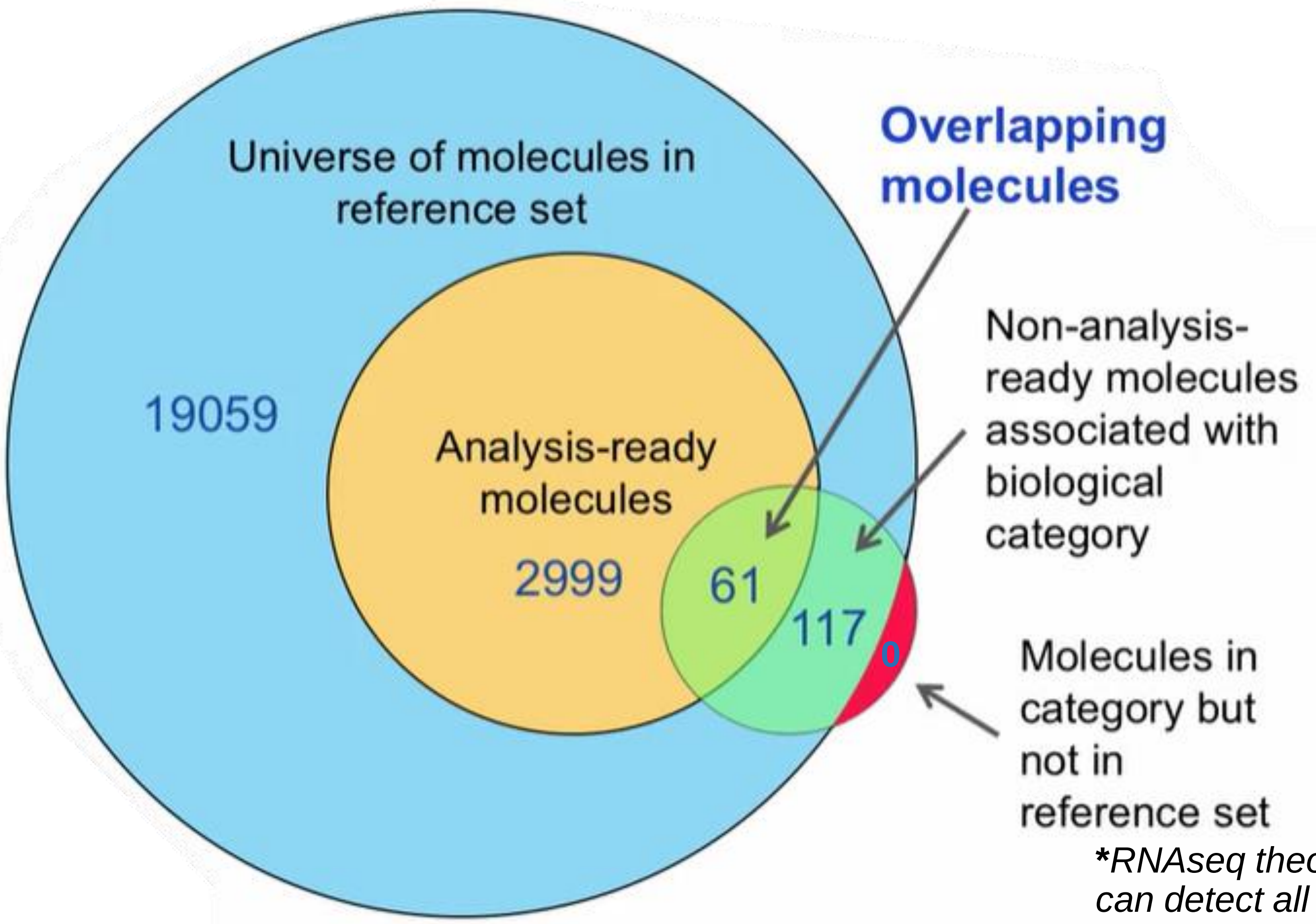
Genes not detected by the technology used and are annotated to a biological category

Molecules associated with a biological category

Is this overlap larger than expected by random sampling?

P-Value from the Right-tailed Fisher’s Exact Test

p-value: the probability of observing a result as extreme or more extreme, if the null hypothesis is true



Overlapping molecules

Non-analysis-ready molecules associated with biological category

Molecules in category but not in reference set

**RNAseq theoretically can detect all molecules*

H_o = Overlap of molecules for a particular biological category is due to chance

α (significance level) = 0.05

		Category 1		
		Group 1	Group 2	Total
Category 2	Group 1	a	b	a+b
	Group 2	c	d	c+d
	Total	a+c	b+d	a+b+c+d = n

$$\text{p-value} = \frac{(a+b)!(c+d)!(a+c)!(b+d)!}{n!a!b!c!d!}$$

P-value = 2.08 x 10^{-12}

We can reject the null hypothesis

Agenda

Refresher on QIAGEN Ingenuity Pathway Analysis

Interpreting your ′omics data using IPA

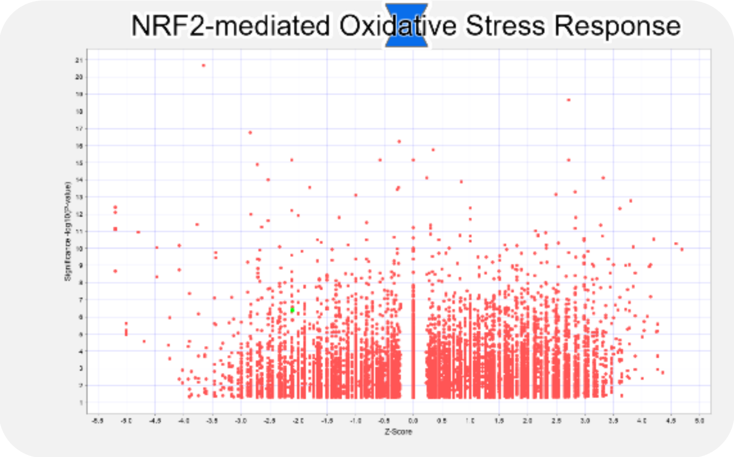
- Setting up a comparison analysis
- Upstream regulators
- Causal networks

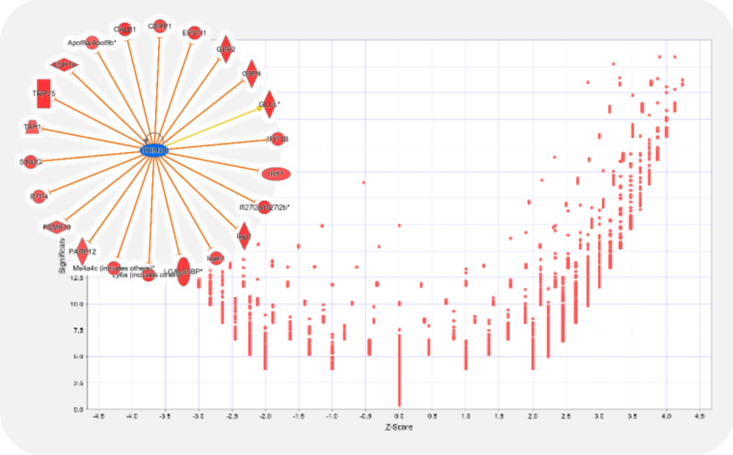
Exploring publicly available data

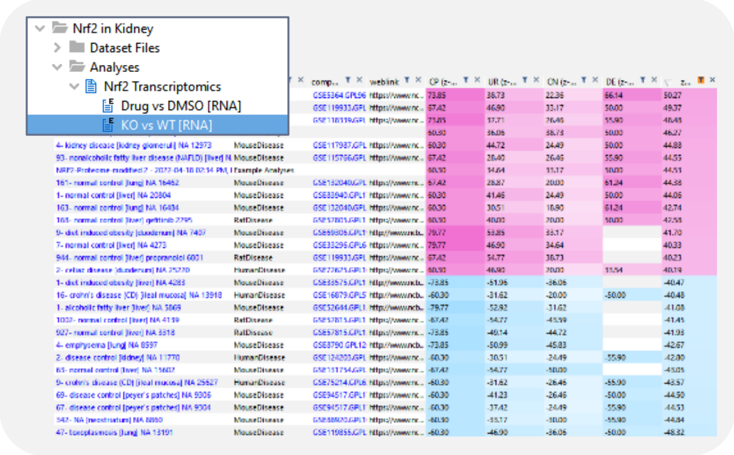
- Land Explorer
- Activity plot, pattern search, Analysis Match

Summary

Activity Plot, Pattern Search, and Analysis Match







		comp...	weblink	CP (z-...	UR (z-...	CN (z-...	DE (z-...	z...
		GSE5364.GPL96	https://www.nc...	73.85	38.73	22.36	66.14	50.27
		GSE119933.GPL	https://www.nc...	67.42	46.90	33.17	50.00	49.37
		GSE118339.GPL	https://www.nc...	73.85	17.71	26.46	55.90	48.48
				60.30	36.06	38.73	50.00	46.27
4- kidney disease [kidney glomeruli] NA 12973	MouseDisease	GSE117987.GPL	https://www.nc...	60.30	44.72	24.49	50.00	44.88
93- nonalcoholic fatty liver disease (NAFLD) [liver] N	MouseDisease	GSE115766.GPL	https://www.nc...	67.42	28.40	26.46	55.90	44.55
NRF2-Proteome-modified 2 - 2022-04-18 02:14 PM, I	Example Analyses			60.30	14.64	33.17	50.00	44.51
161- normal control [lung] NA 16462	MouseDisease	GSE132040.GPL	https://www.nc...	67.42	28.87	20.00	61.24	44.38
1- normal control [liver] NA 20804	MouseDisease	GSE83940.GPL1	https://www.nc...	60.30	41.46	24.49	50.00	44.06
163- normal control [lung] NA 16434	MouseDisease	GSE132040.GPL	https://www.nc...	60.30	30.51	18.90	61.24	42.74
168- normal control [liver] gefitinib 2295	RatDisease	GSE57805.GPL1	https://www.nc...	60.30	40.00	20.00	50.00	42.58
9- diet induced obesity [duodenum] NA 7407	MouseDisease	GSE69306.GPL1	http://www.ncb...	79.77	53.85	33.17		41.70
7- normal control [liver] NA 4273	MouseDisease	GSE33296.GPL6	https://www.nc...	79.77	46.90	34.64		40.33
944- normal control [liver] propranolol 6001	RatDisease	GSE119933.GPL	https://www.nc...	67.42	54.77	38.73		40.23
2- celiac disease [duodenum] NA 25220	HumanDisease	GSE72625.GPL1	https://www.nc...	60.30	46.90	20.00	33.54	40.19
1- diet induced obesity [liver] NA 4283	MouseDisease	GSE33575.GPL1	http://www.ncb...	-73.85	-51.96	-36.06		-40.47
16- crohn's disease (CD) [ileal mucosa] NA 13918	HumanDisease	GSE16879.GPL5	http://www.ncb...	-60.30	-31.62	-20.00	-50.00	-40.48
1- alcoholic fatty liver [liver] NA 5069	MouseDisease	GSE52644.GPL1	http://www.ncb...	-79.77	-52.92	-31.62		-41.08
1007- normal control [liver] NA 4119	RatDisease	GSE57815.GPL1	https://www.nc...	-67.42	-54.77	-43.59		-41.45
927- normal control [liver] NA 3318	RatDisease	GSE57815.GPL1	https://www.nc...	-73.85	-40.14	-44.72		-41.93
4- emphysema [lung] NA 8597	MouseDisease	GSE8790.GPL12	http://www.ncb...	-73.85	-50.99	-45.83		-42.67
2- disease control [kidney] NA 11770	HumanDisease	GSE124203.GPL	https://www.nc...	-60.30	-30.51	-24.49	-55.90	-42.80
65- normal control [liver] NA 15602	MouseDisease	GSE131754.GPL	https://www.nc...	-67.42	-54.77	-50.00		-43.05
9- crohn's disease (CD) [ileal mucosa] NA 25527	HumanDisease	GSE75214.GPL6	https://www.nc...	-60.30	-31.62	-26.46	-55.90	-43.57
69- disease control [peyer's patches] NA 9306	MouseDisease	GSE94517.GPL1	https://www.nc...	-60.30	-41.23	-26.46	-50.00	-44.50
67- disease control [peyer's patches] NA 9304	MouseDisease	GSE94517.GPL1	https://www.nc...	-60.30	-37.42	-24.49	-55.90	-44.53
342- NA [neostriatum] NA 8860	MouseDisease	GSE88820.GPL1	https://www.nc...	-60.30	-33.17	-30.00	-55.90	-44.84
47- toxoplasmosis [lung] NA 13191	MouseDisease	GSE119855.GPL	https://www.nc...	-60.30	-46.90	-36.06	-50.00	-48.32

Activity Plot: compare single entities

- Discover analyses with similar downstream activities of a particular node or entity
- Input: one gene, canonical pathway, or other “molecule” within IPA
- How: uses all downstream targets of the entity as a signature for comparison

Pattern Search: compare networks

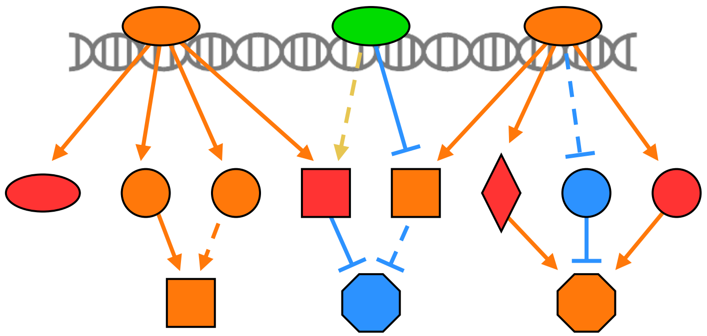
- Determine if your pattern of activity is seen among a massive collection of expression data
- Input: any network or pathway with multiple genes and a pattern
- How: uses the signature you provide to query our OmicSoft database

Analysis Match: compare entire studies

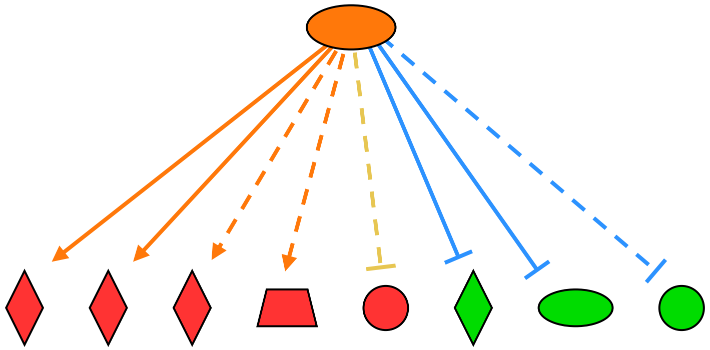
- Validate your biological model, find potential disease targets for drug repositioning, etc.
- Input: any IPA core analysis
- How: uses canonical pathways, upstream regulators, causal networks, and disease enrichment as signatures for comparison

Signatures used to match against other analyses

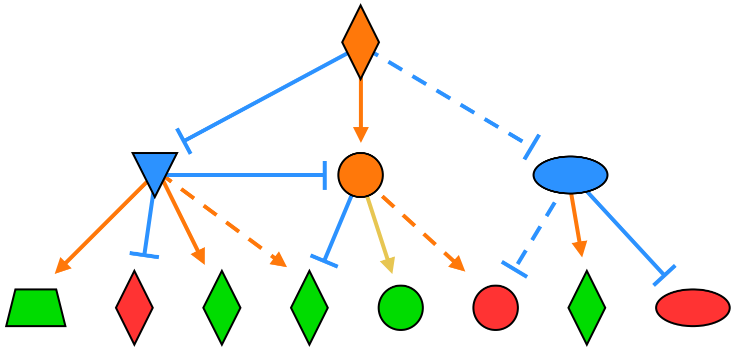
Canonical pathways



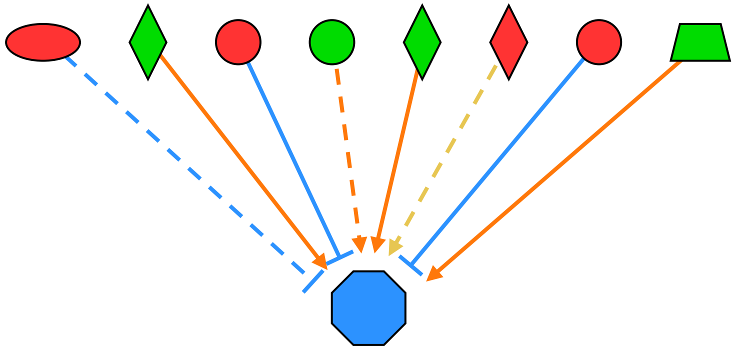
Upstream regulators



Causal networks



Disease enrichment



Agenda

Topics for today’s workshop

Interpreting your ′omics data using IPA Core Analysis

- Setting up a core analysis
- Canonical pathways
- Comparison analysis

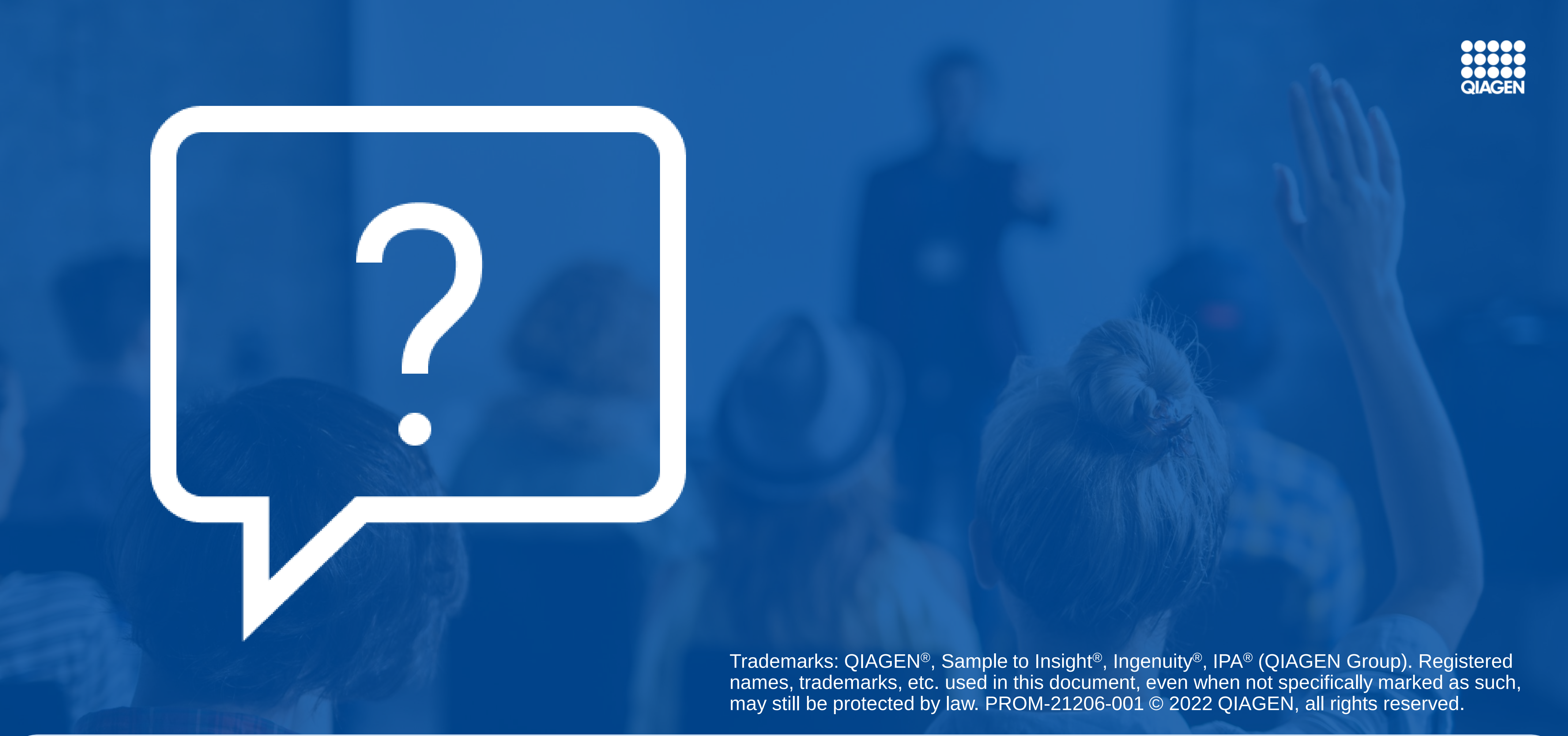
Creating networks from scratch

- Connecting genes in a network
- In silico testing
- Overlay drugs and biomarkers

Exploring publicly available data

- Activity plot, pattern search, Analysis Match
- Land Explorer

Summary



Feedback and contact information

Post-training survey:
https://www.surveymonkey.com/r/QLYLYK8

Software questions and support: ts-bioinformatics@qiagen.com
Sales and licensing questions: bioinformaticssales@qiagen.com
Additional feedback and training: devendra.mistry@qiagen.com

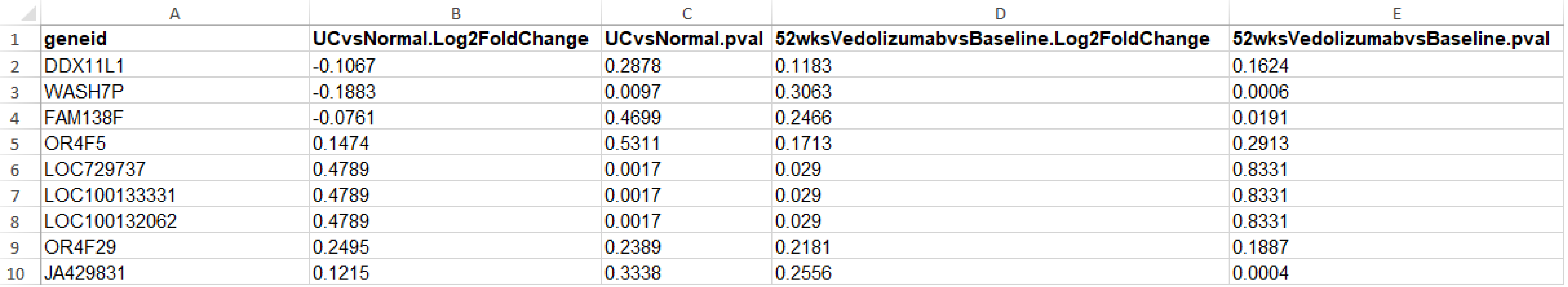
Data formatting

Formatting transcriptomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)



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

Observation 1

Observation 2

Common identifier types

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

Accepted file formats

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

IDs are the only **required** column

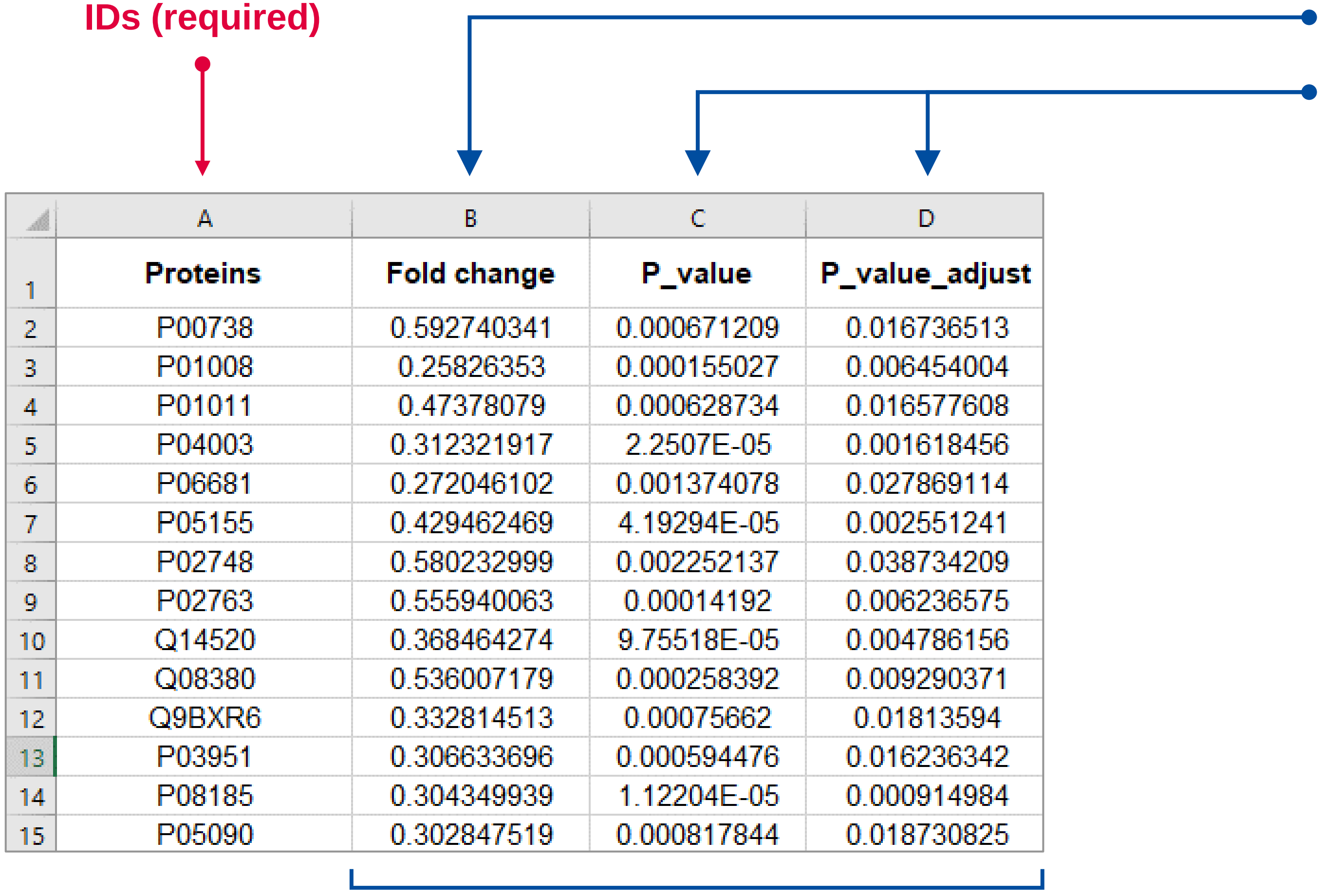
Change measurements are needed for IPA to make activity predictions

Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)



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

Observation 1

Common protein IDs

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

UniProt ID conversion tool:

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

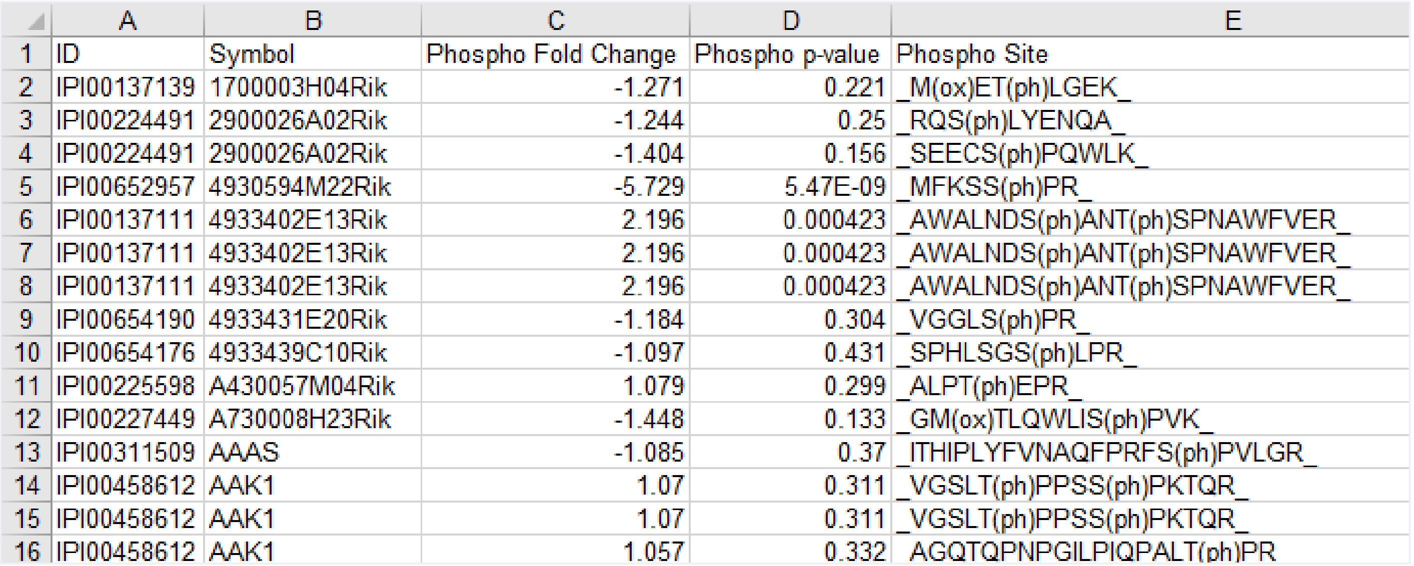
Phosphorylation changes (ratio, fold change, etc.) and sites are supported, but these columns **must be assigned**

Formatting proteomics data before uploading to IPA

IDs (required)

Ratio, fold change, etc. (recommended)

Significance (optional)



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

Observation 1

Common protein IDs

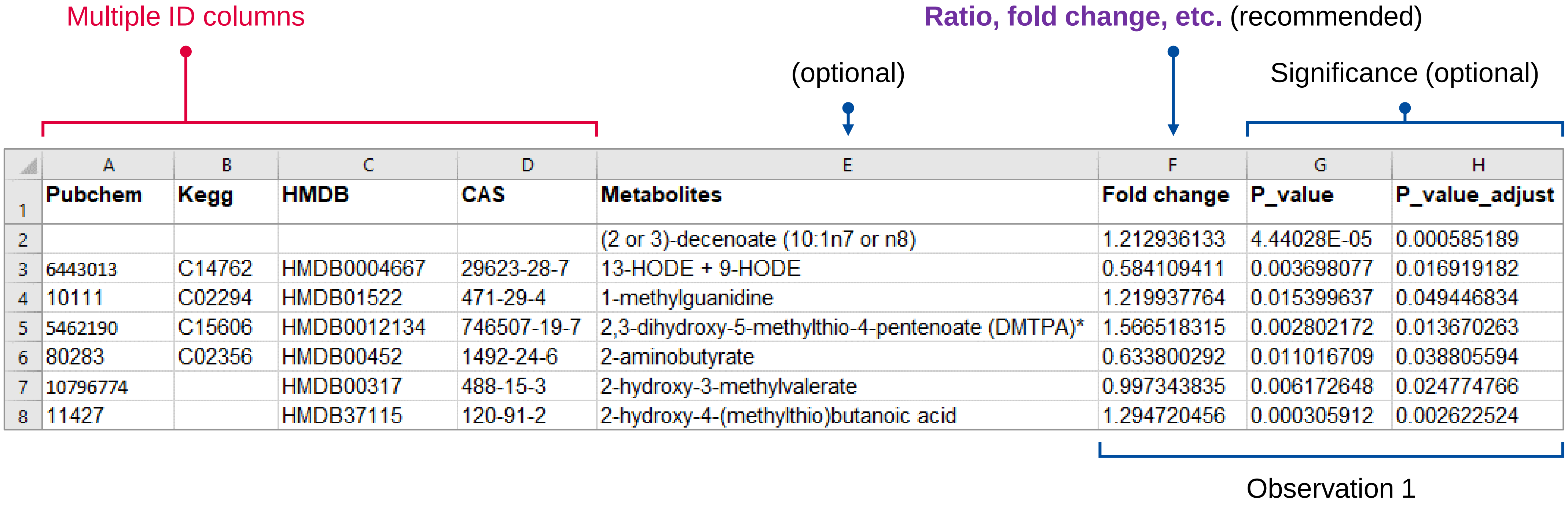
- Ensembl
- Gene symbols (Entrez or HUGO)
- GenPept and GenBank
- International Protein Index
- UniProt and SwissProt

UniProt ID conversion tool:

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

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

Formatting metabolomics data before uploading to IPA



Multiple ID columns

Ratio, fold change, etc. (recommended)

(optional)

Significance (optional)

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

Observation 1

Common metabolite IDs

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

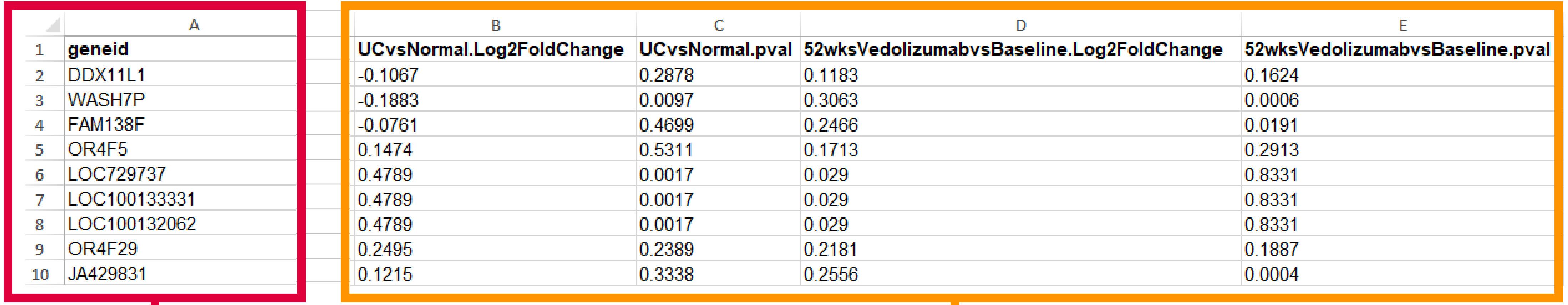
Metabolite ID conversion tools:

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

Formatting ‘omics data before uploading to IPA

Observation 1

Observation 2



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

Analyte identifier REQUIRED to explore enrichment

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

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

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

Change values needed to calculate activity predictions

Change value examples: fold changes, ratios, etc.

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

Accepted file formats:

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

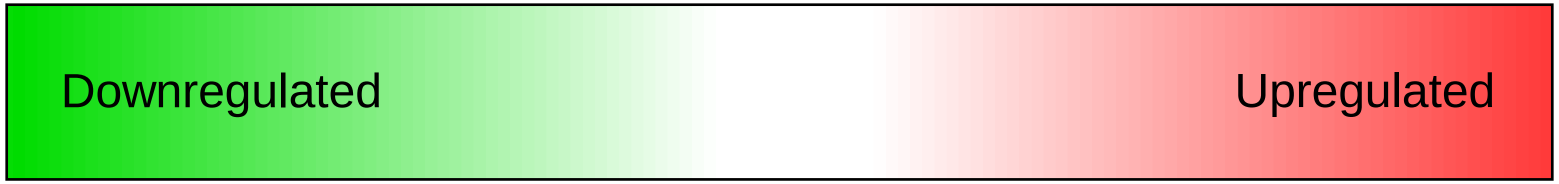
Multiple comparisons or observations may be uploaded in one file

IPA colors and z-scores

What do colors mean in IPA?

Pathway or gene activity predicted by IPA

Actual measurement of gene expression in your dataset

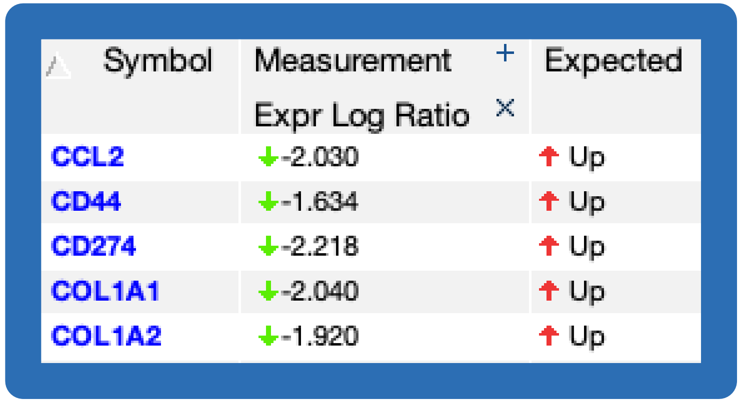


What do z-scores mean in IPA?

Actual dataset measurement

VS.

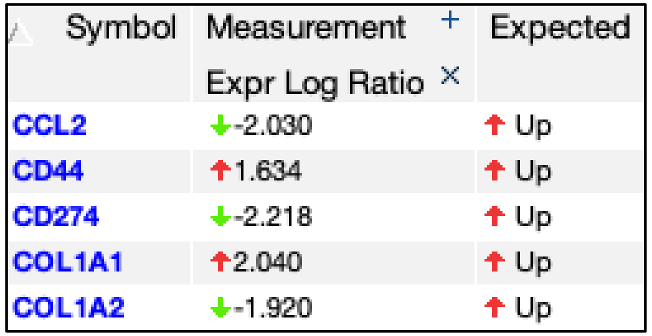
What IPA expects if pathway is activated



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

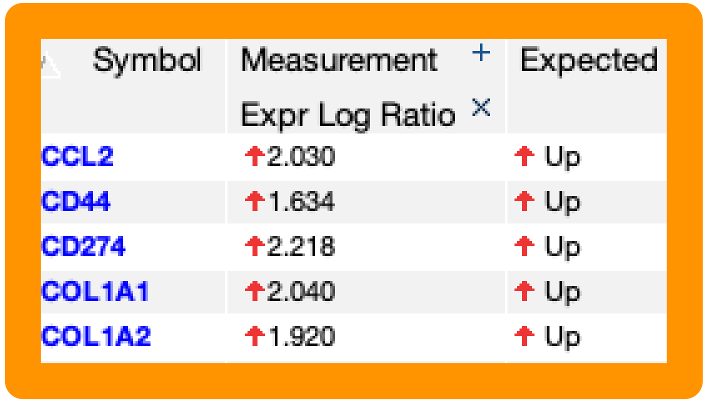
Pathway inhibited

- Z score



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

No clear signal for prediction Z score = 0



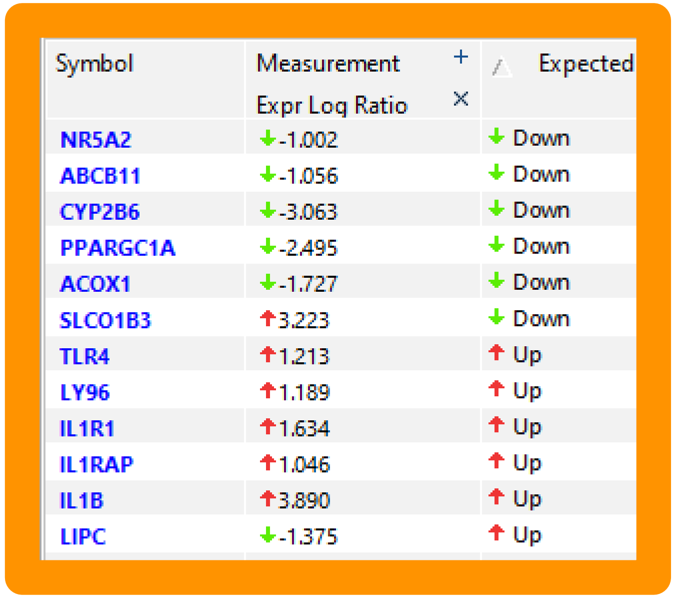
Symbol	Measurement + Expr Log Ratio ×	Expected
CCL2	↑2.030	↑ Up
CD44	↑1.634	↑ Up
CD274	↑2.218	↑ Up
COL1A1	↑2.040	↑ Up
COL1A2	↑1.920	↑ Up

Pathway activated

+ Z score

How well do the actual measurements match the expected measurements?

Examples of z-scores



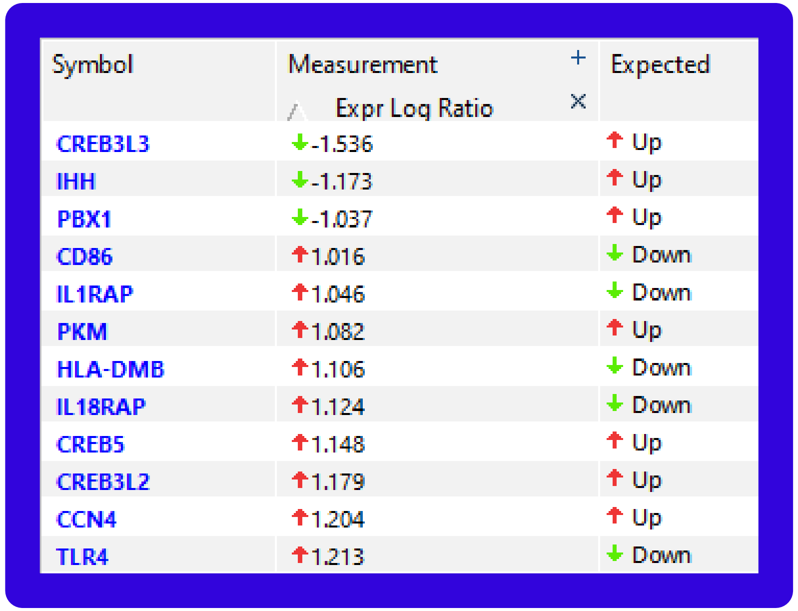
Symbol	Measurement Expr Log Ratio	Expected
NR5A2	↓-1.002	↓ Down
ABCB11	↓-1.056	↓ Down
CYP2B6	↓-3.063	↓ Down
PPARGC1A	↓-2.495	↓ Down
ACOX1	↓-1.727	↓ Down
SLCO1B3	↑3.223	↓ Down
TLR4	↑1.213	↑ Up
LY96	↑1.189	↑ Up
IL1R1	↑1.634	↑ Up
IL1RAP	↑1.046	↑ Up
IL1B	↑3.890	↑ Up
LIPC	↓-1.375	↑ Up

Z-score = 2.4

10/12 measurements match expected

Mostly matching

Signal predominantly points to predicted activation



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

Z-score = -2.236

4/12 measurements match expected

Mostly anti-matching

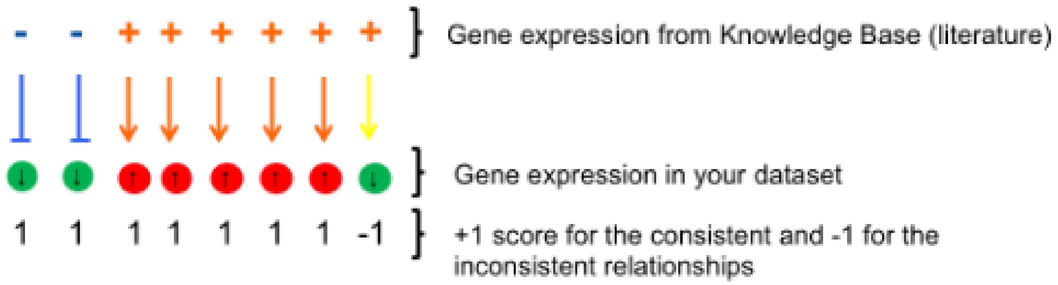
Signal predominantly points to predicted inhibition

Z-scores predict activity

Compares the EXPECTED gene expression pattern for activation in the knowledgebase to the ACTUAL gene expression measurements

Z-scores are used throughout IPA to predict activation or inhibition of:

- **Canonical pathways**
- **Upstream regulators**
- **Master regulators**
- **Diseases and functions**



Simplified z-score formula:

$$z = \frac{x}{\sigma_x} = \frac{\sum_i x_i}{\sqrt{N}} = \frac{N_+ - N_-}{\sqrt{N}}$$

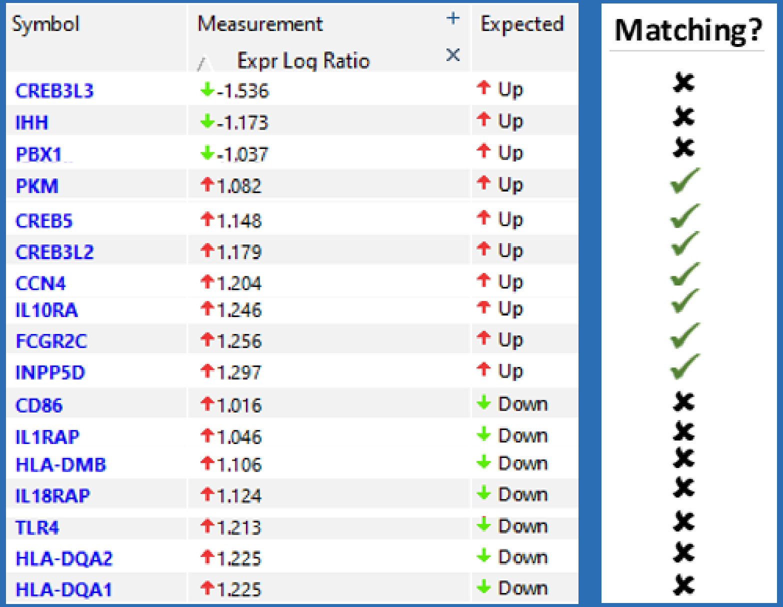
Z-score calculation summary

Compares the EXPECTED gene expression pattern for activation in the knowledgebase to the ACTUAL data set gene expression measurements

Does the expected pattern of activation *mostly* match the actual gene expression measurements?

NO! a NEGATIVE Z-score is calculated indicating predicted inhibition

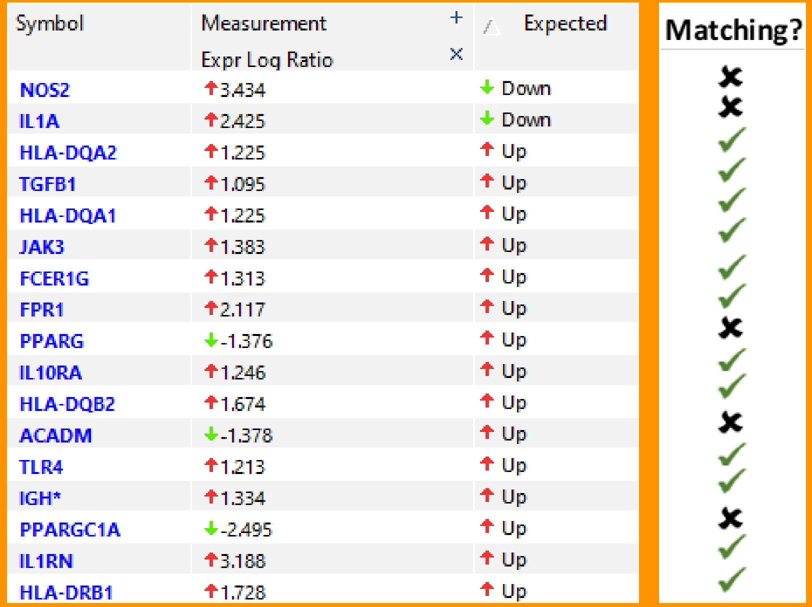
Z-score= -2.236



Symbol	Measurement Expr Log Ratio	Expected	Matching?
CREB3L3	↓-1.536	↑ Up	✗
IHH	↓-1.173	↑ Up	✗
PBX1	↓-1.037	↑ Up	✗
PKM	↑1.082	↑ Up	✓
CREB5	↑1.148	↑ Up	✓
CREB3L2	↑1.179	↑ Up	✓
CCN4	↑1.204	↑ Up	✓
IL10RA	↑1.246	↑ Up	✓
FCGR2C	↑1.256	↑ Up	✓
INPP5D	↑1.297	↑ Up	✓
CD86	↑1.016	↓ Down	✗
IL1RAP	↑1.046	↓ Down	✗
HLA-DMB	↑1.106	↓ Down	✗
IL18RAP	↑1.124	↓ Down	✗
TLR4	↑1.213	↓ Down	✗
HLA-DQA2	↑1.225	↓ Down	✗
HLA-DQA1	↑1.225	↓ Down	✗

YES! a POSITIVE Z-score is calculated indicating predicted activation

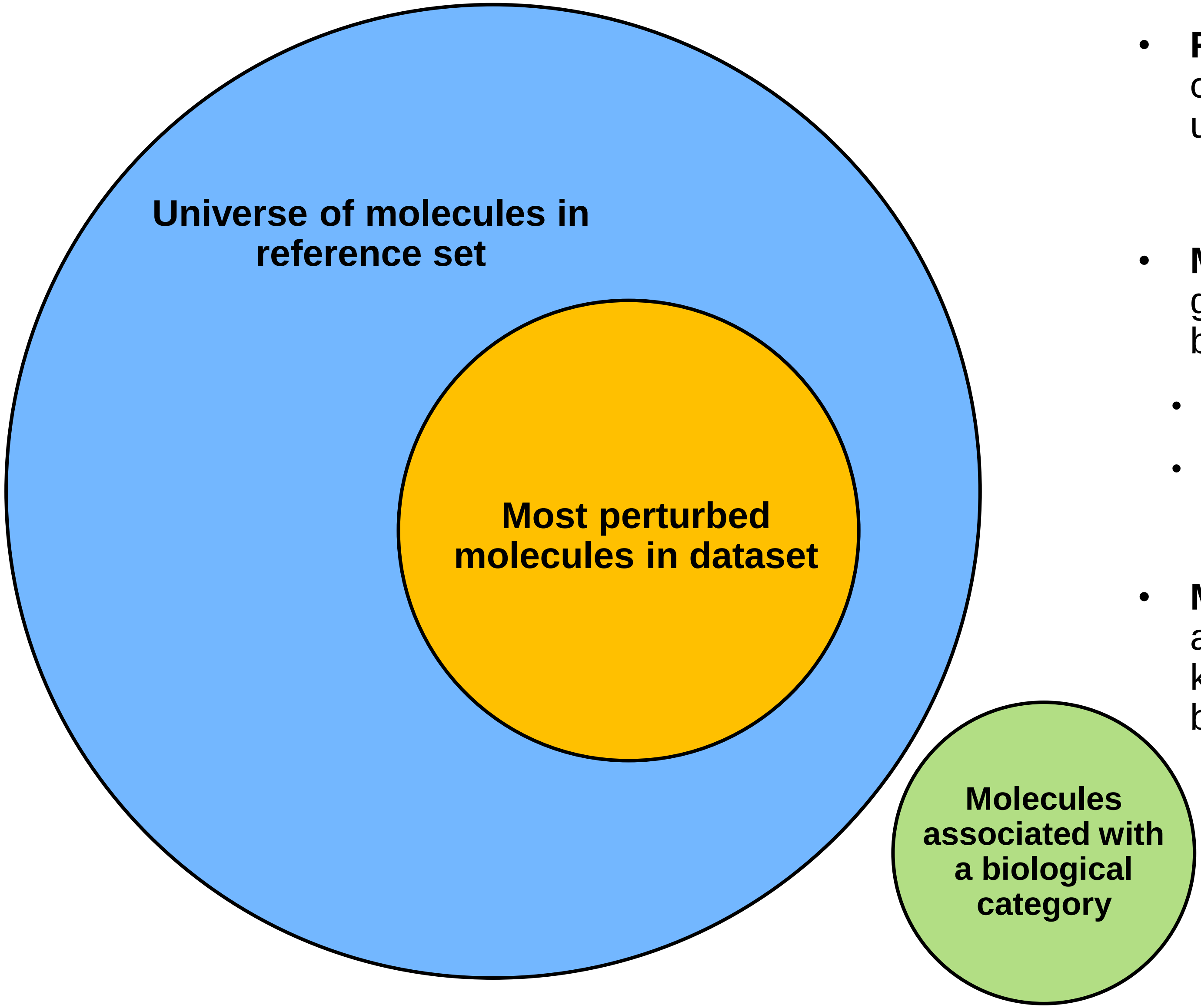
Z-score= 2.427



Symbol	Measurement Expr Log Ratio	Expected	Matching?
NOS2	↑3.434	↓ Down	✗
IL1A	↑2.425	↓ Down	✗
HLA-DQA2	↑1.225	↑ Up	✓
TGFB1	↑1.095	↑ Up	✓
HLA-DQA1	↑1.225	↑ Up	✓
JAK3	↑1.383	↑ Up	✓
FCER1G	↑1.313	↑ Up	✓
FPR1	↑2.117	↑ Up	✓
PPARG	↓-1.376	↑ Up	✗
IL10RA	↑1.246	↑ Up	✓
HLA-DQB2	↑1.674	↑ Up	✓
ACADM	↓-1.378	↑ Up	✗
TLR4	↑1.213	↑ Up	✓
IGH*	↑1.334	↑ Up	✓
PPARGC1A	↓-2.495	↑ Up	✗
IL1RN	↑3.188	↑ Up	✓
HLA-DRB1	↑1.728	↑ Up	✓

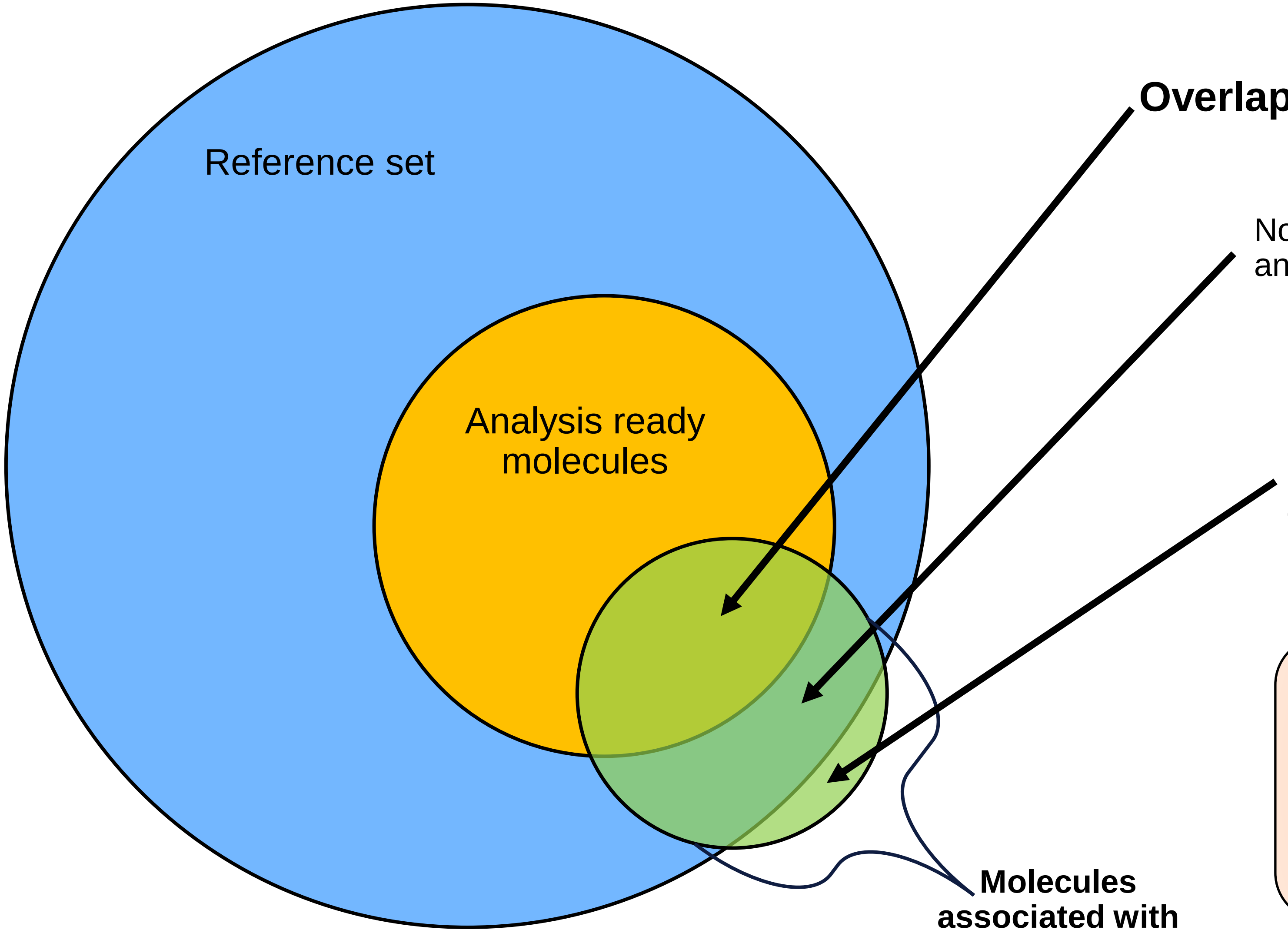
Enrichment in IPA

Pathway enrichment: P-value of overlap



- **Reference set** is typically all genes or proteins that can be reliably detected by the ‘omics technology used
- **Most perturbed** is a subset of measured genes/proteins that were significantly different between experimental groups
  - Fold change cut offs and p-value cut offs used
  - IPA calls these “Analysis-ready molecules”
- **Molecules associated with a biological category** are a set of genes/proteins that the IPA knowledgebase has annotated to be important for a biological pathway, function, or disease.

Testing for Enrichment using the Fisher's Exact Test



Overlapping molecules

Non-analysis-ready molecules that have been annotated to a biological category

i.e. genes that did not pass cut offs

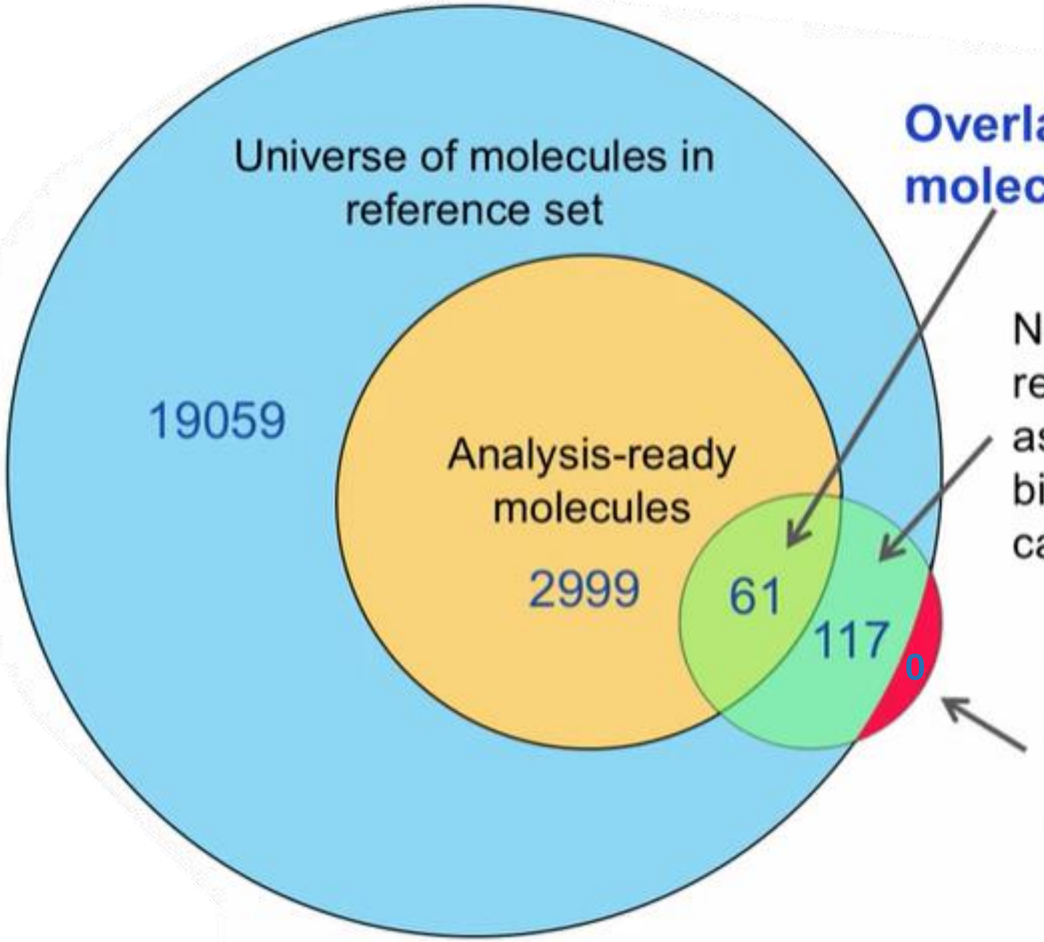
Genes not detected by the technology used and are annotated to a biological category

Molecules associated with a biological category

Is this overlap larger than expected by random sampling?

P-Value from the Right-tailed Fisher's Exact Test

p-value: the probability of observing a result as extreme or more extreme, if the null hypothesis is true



Overlapping molecules

Non-analysis-ready molecules associated with biological category

Molecules in category but not in reference set

**RNAseq theoretically can detect all molecules*

H_o = Overlap of molecules for a particular biological category is due to chance

α (significance level) = 0.05

		Category 1		
		Group 1	Group 2	Total
Category 2	Group 1	a	b	a+b
	Group 2	c	d	c+d
	Total	a+c	b+d	a+b+c+d = n

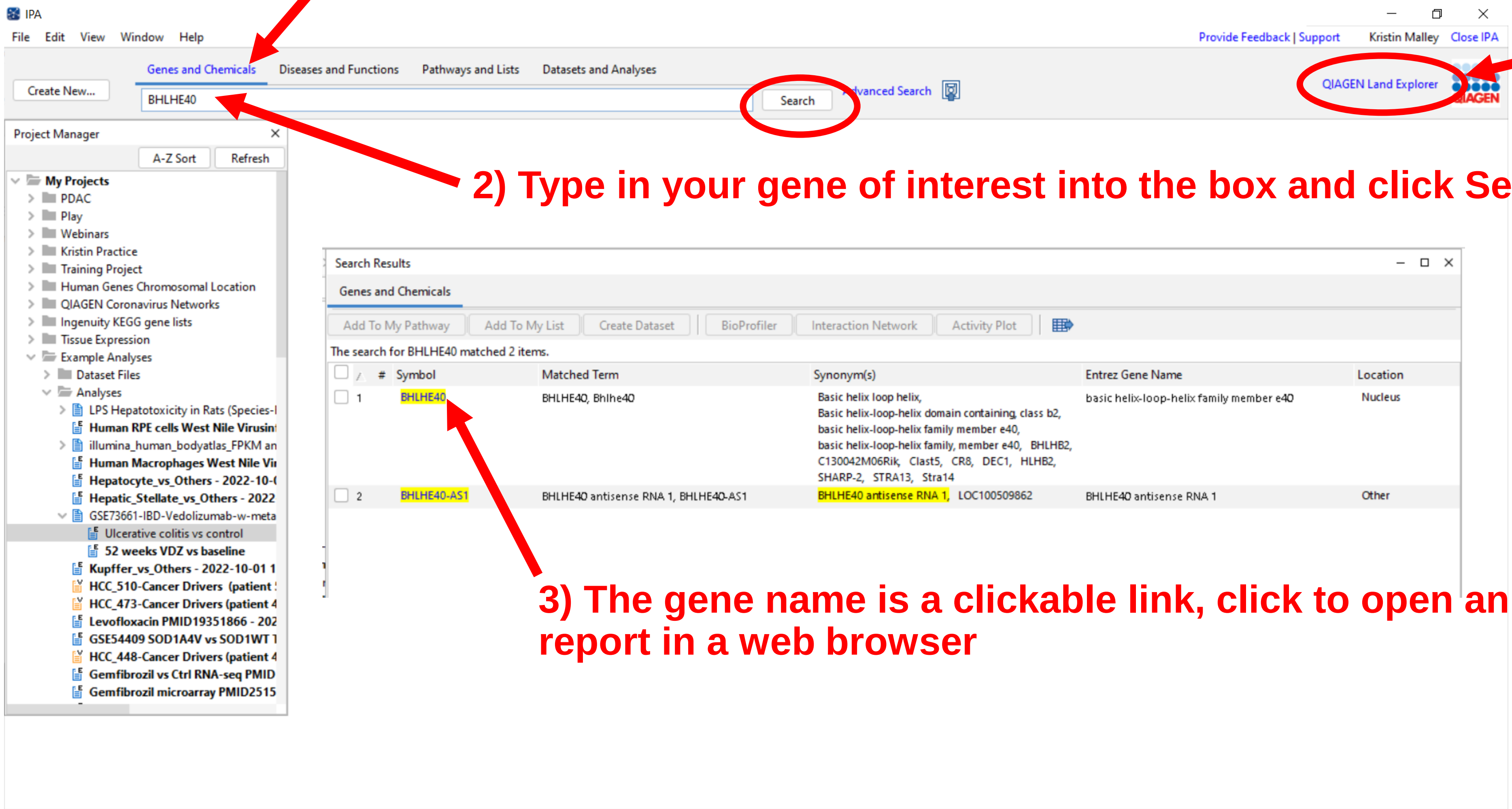
$$\text{p-value} = \frac{(a+b)!(c+d)!(a+c)!(b+d)!}{n!a!b!c!d!}$$

P-value = 2.08×10^{-12}

We can reject the null hypothesis

Land explorer

How to access Land Explorer data



1) Click on Genes and Chemicals

Link to Land Explorer home page

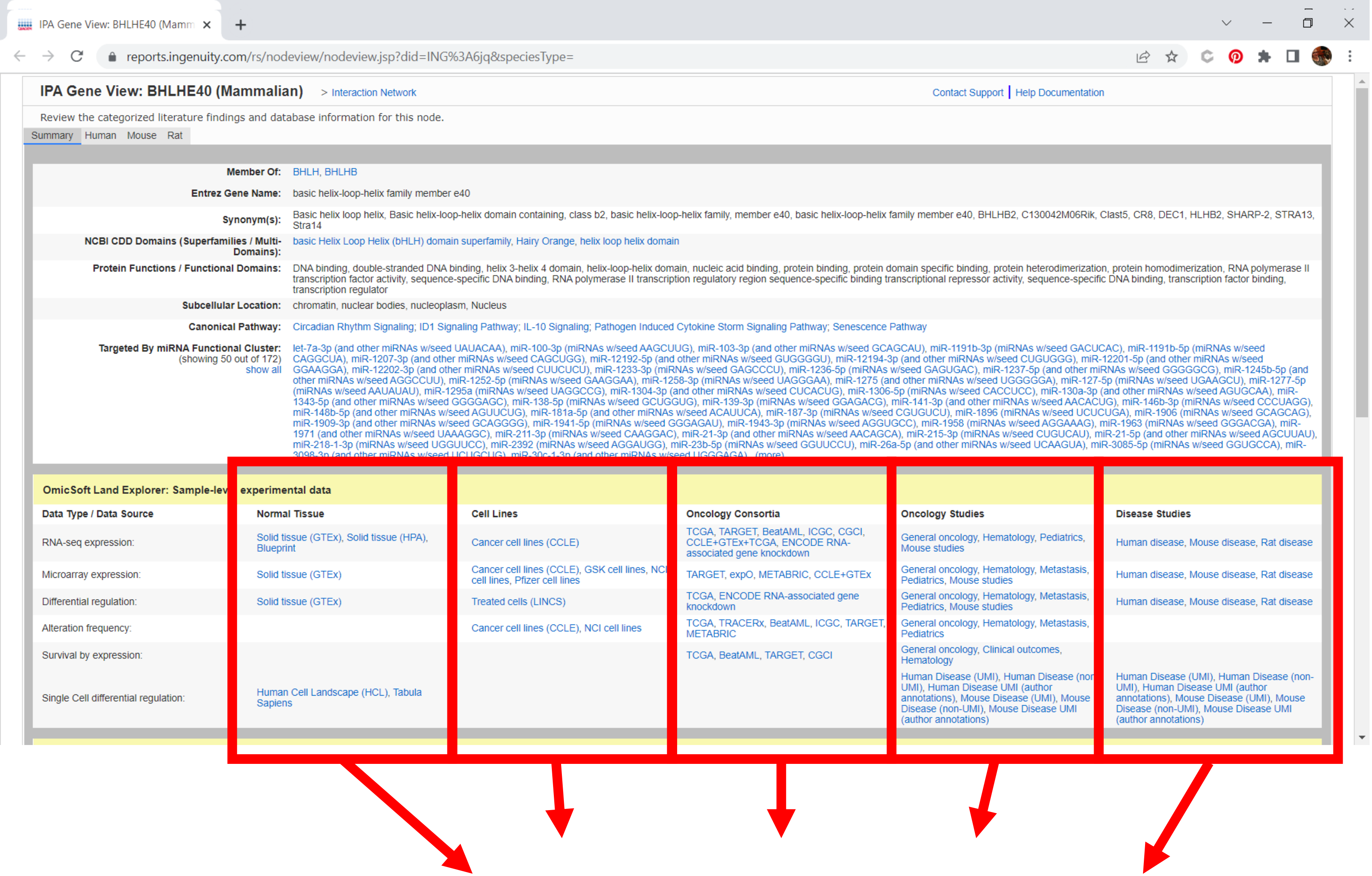
2) Type in your gene of interest into the box and click Search

The search for BHLHE40 matched 2 items.

☐	#	Symbol	Matched Term	Synonym(s)	Entrez Gene Name	Location
☐	1	BHLHE40	BHLHE40, Bhlhe40	Basic helix loop helix, Basic helix-loop-helix domain containing, class b2, basic helix-loop-helix family member e40, basic helix-loop-helix family, member e40, BHLHB2, C130042M06Rik, Clast5, CR8, DEC1, HLHB2, SHARP-2, STRA13, Stra14	basic helix-loop-helix family member e40	Nucleus
☐	2	BHLHE40-AS1	BHLHE40 antisense RNA 1, BHLHE40-AS1	BHLHE40 antisense RNA 1, LOC100509862	BHLHE40 antisense RNA 1	Other

3) The gene name is a clickable link, click to open an IPA gene view report in a web browser

IPA Gene View report



reports.ingenuity.com/rs/nodeview/nodeview.jsp?did=ING%3A6jq&speciesType=

IPA Gene View: BHLHE40 (Mammalian) > Interaction Network

Contact Support | Help Documentation

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

Member Of:	BHLH, BHLHB
Entrez Gene Name:	basic helix-loop-helix family member e40
Synonym(s):	Basic helix loop helix, Basic helix-loop-helix domain containing, class b2, basic helix-loop-helix family, member e40, basic helix-loop-helix family member e40, BHLHB2, C130042M06Rik, Clast5, CR8, DEC1, HLHB2, SHARP-2, STRA13, Stra14
NCBI CDD Domains (Superfamilies / Multi-Domains):	basic Helix Loop Helix (bHLH) domain superfamily, Hairy Orange, helix loop helix domain
Protein Functions / Functional Domains:	DNA binding, double-stranded DNA binding, helix 3-helix 4 domain, helix-loop-helix domain, nucleic acid binding, protein binding, protein domain specific binding, protein heterodimerization, protein homodimerization, RNA polymerase II transcription factor activity, sequence-specific DNA binding, RNA polymerase II transcription regulatory region sequence-specific binding transcriptional repressor activity, sequence-specific DNA binding, transcription factor binding, transcription regulator
Subcellular Location:	chromatin, nuclear bodies, nucleoplasm, Nucleus
Canonical Pathway:	Circadian Rhythm Signaling; ID1 Signaling Pathway; IL-10 Signaling; Pathogen Induced Cytokine Storm Signaling Pathway; Senescence Pathway
Targeted By miRNA Functional Cluster: (showing 50 out of 172) show all	let-7a-3p (and other miRNAs w/seed UAUACAA), miR-100-3p (miRNAs w/seed AAGCUUG), miR-103-3p (and other miRNAs w/seed GCAGCAU), miR-1191b-3p (miRNAs w/seed GACUCAC), miR-1191b-5p (miRNAs w/seed CAGGCUA), miR-1207-3p (and other miRNAs w/seed CAGCUGG), miR-12192-5p (and other miRNAs w/seed GUGGGGU), miR-12194-3p (and other miRNAs w/seed CUGUGGG), miR-12201-5p (and other miRNAs w/seed GGAAGGA), miR-12202-3p (and other miRNAs w/seed CUUCUCU), miR-1233-3p (miRNAs w/seed GAGCCCU), miR-1236-5p (miRNAs w/seed GAGUGAC), miR-1237-5p (and other miRNAs w/seed GGGGGCG), miR-1245b-5p (and other miRNAs w/seed AGGCCUU), miR-1252-5p (miRNAs w/seed GAAGGAA), miR-1258-3p (miRNAs w/seed UAGGGAA), miR-1275 (and other miRNAs w/seed UGGGGGA), miR-127-5p (miRNAs w/seed UGAAGCU), miR-1277-5p (miRNAs w/seed AAUAUAU), miR-1295a (miRNAs w/seed UAGGCCG), miR-1304-3p (and other miRNAs w/seed CUCACUG), miR-1306-5p (miRNAs w/seed CACCUCC), miR-130a-3p (and other miRNAs w/seed AGUGCAA), miR-1343-5p (and other miRNAs w/seed GGGGAGC), miR-138-5p (miRNAs w/seed GCUGGUG), miR-139-3p (miRNAs w/seed GGAGACG), miR-141-3p (and other miRNAs w/seed AACACUG), miR-146b-3p (miRNAs w/seed CCCUAGG), miR-148b-5p (and other miRNAs w/seed AGUUCUG), miR-181a-5p (and other miRNAs w/seed ACAUUCA), miR-187-3p (miRNAs w/seed CGUGUCU), miR-1896 (miRNAs w/seed UCUCUGA), miR-1906 (miRNAs w/seed GCAGCAG), miR-1909-3p (and other miRNAs w/seed GCAGGGG), miR-1941-5p (miRNAs w/seed GGGAGAU), miR-1943-3p (miRNAs w/seed AGGUGCC), miR-1958 (miRNAs w/seed AGGAAAG), miR-1963 (miRNAs w/seed GGGACGA), miR-1971 (and other miRNAs w/seed UAAAGGC), miR-211-3p (miRNAs w/seed CAAGGAC), miR-21-3p (and other miRNAs w/seed AACAGCA), miR-215-3p (miRNAs w/seed CUGUCAU), miR-21-5p (and other miRNAs w/seed AGCUUAU), miR-218-1-3p (miRNAs w/seed UGGUUCC), miR-2392 (miRNAs w/seed AGGAUGG), miR-23b-5p (miRNAs w/seed GGUUCCU), miR-26a-5p (and other miRNAs w/seed UCAAGUA), miR-3085-5p (miRNAs w/seed GGUGCCA), miR-3098-3p (and other miRNAs w/seed UCUGCUG), miR-30c-1-3p (and other miRNAs w/seed UGGGAGA) ...(more)

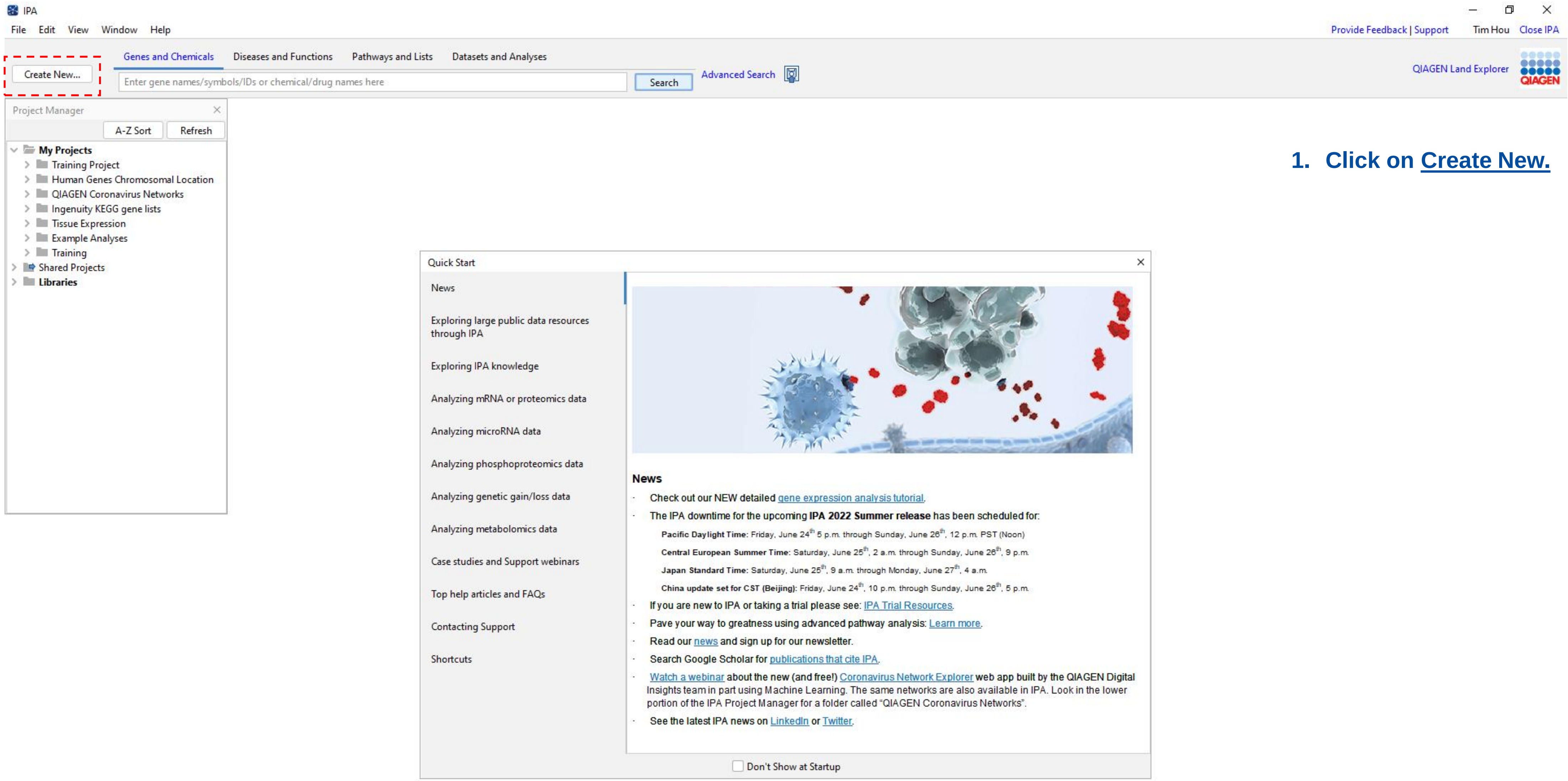
OmicSoft Land Explorer: Sample-lev experimental data

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

Click these links to view publicly available data in Land Explorer!

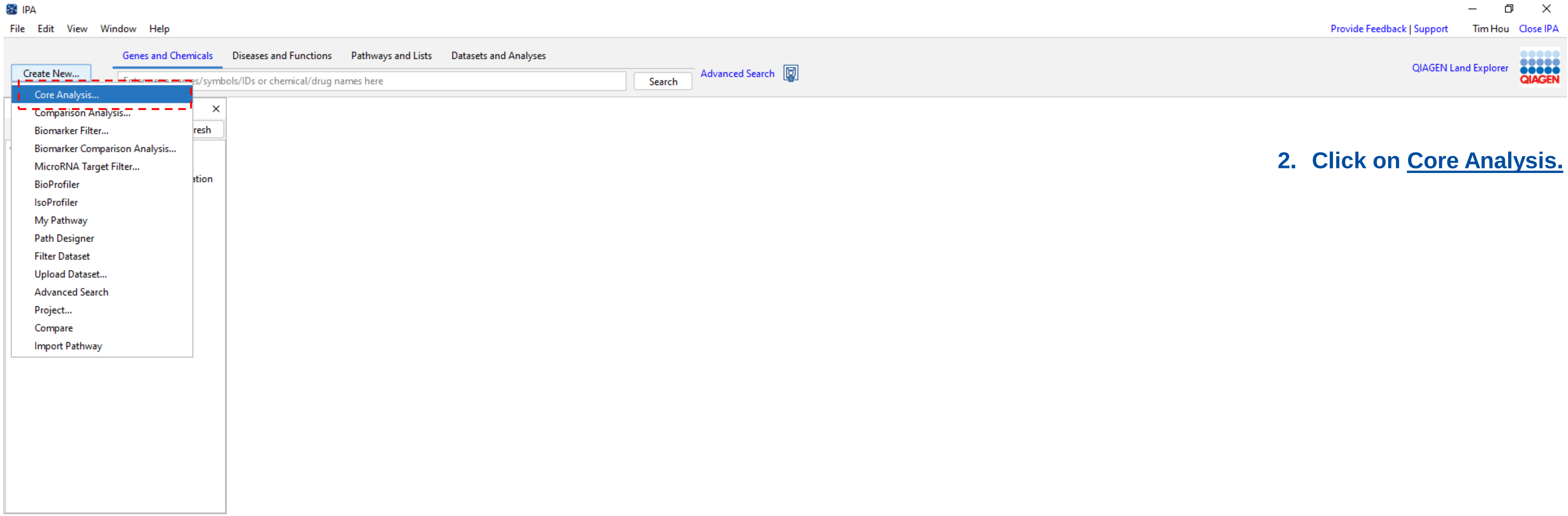
Data upload step by step

1. Click on <u>Create New.</u>

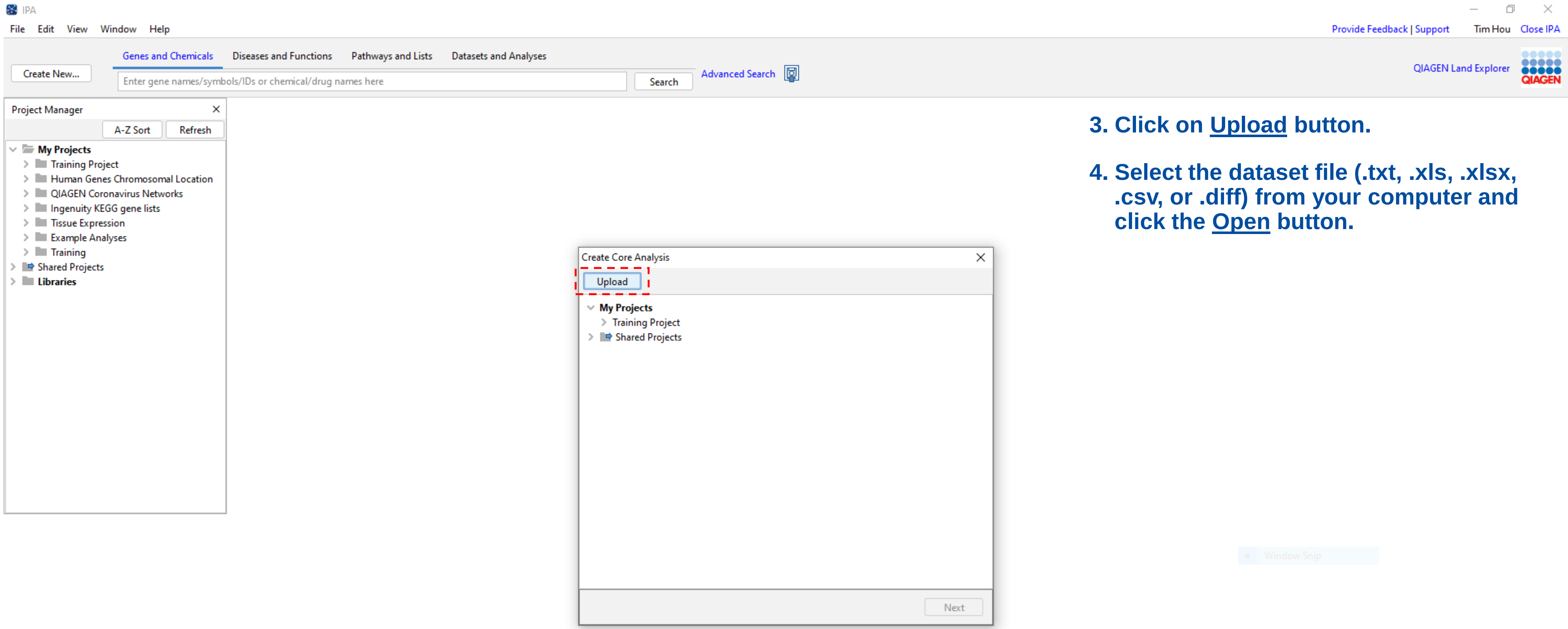


News

- Check out our NEW detailed gene expression analysis tutorial.
- The IPA downtime for the upcoming **IPA 2022 Summer release** has been scheduled for:
  - **Pacific Daylight Time:** Friday, June 24th 5 p.m. through Sunday, June 26th, 12 p.m. PST (Noon)
  - **Central European Summer Time:** Saturday, June 25th, 2 a.m. through Sunday, June 26th, 9 p.m.
  - **Japan Standard Time:** Saturday, June 25th, 9 a.m. through Monday, June 27th, 4 a.m.
  - **China update set for CST (Beijing):** Friday, June 24th, 10 p.m. through Sunday, June 26th, 5 p.m.
- 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.
- Watch a webinar about the new (and free!) Coronavirus Network Explorer web app built by the QIAGEN Digital Insights team in part using Machine Learning. The same networks are also available in IPA. Look in the lower portion of the IPA Project Manager for a folder called "QIAGEN Coronavirus Networks".
- See the latest IPA news on LinkedIn or Twitter.

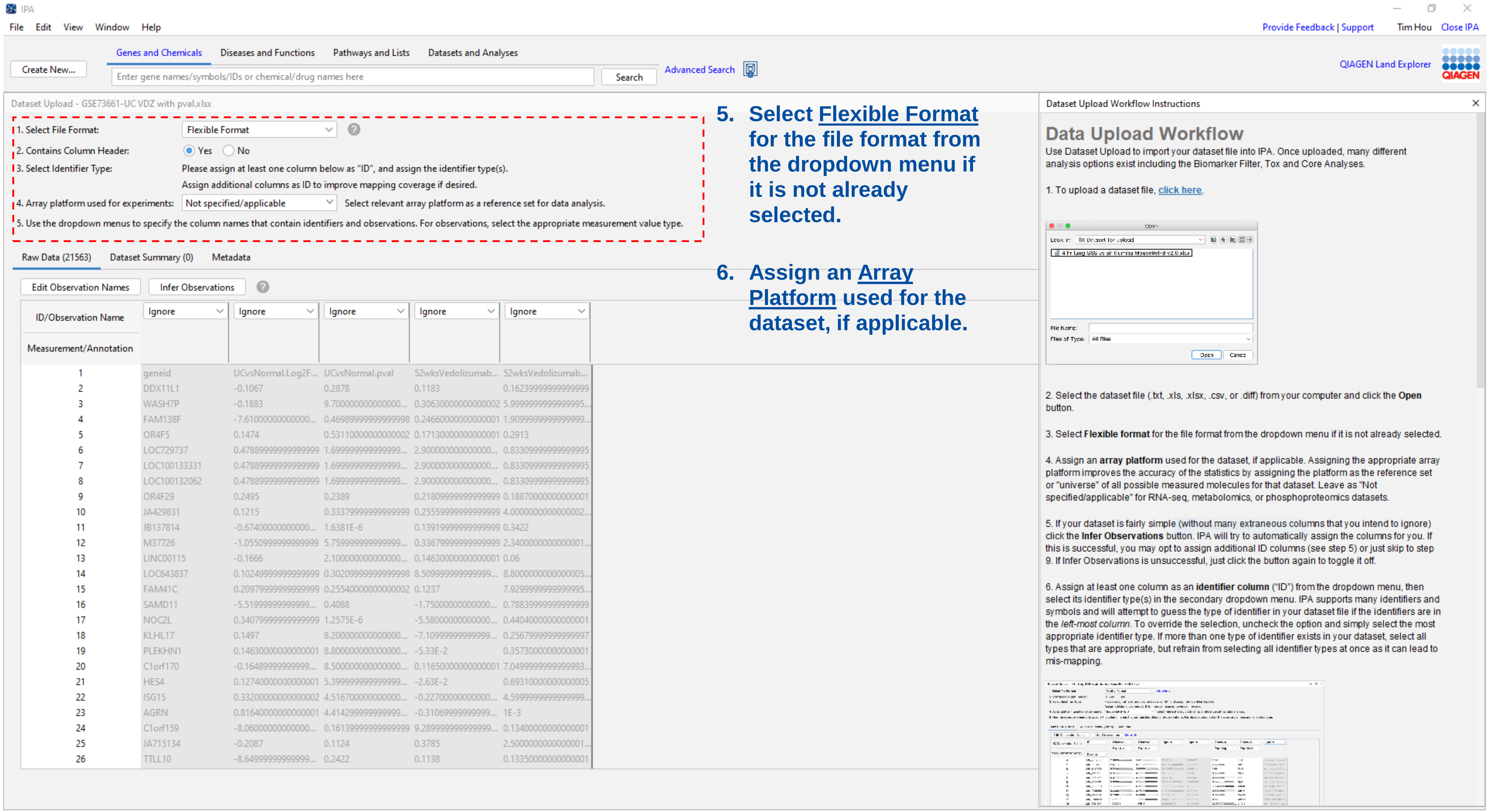


2. Click on Core Analysis.



3. **Click on <u>Upload</u> button.**

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



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

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

ID/Observation Name Measurement/Annotation	Ignore	Ignore	Ignore	Ignore	Ignore
1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999999999
3	WASH7P	-0.1883	9.70000000000000...	0.30630000000000002	5.9999999999999995...
4	FAM138F	-7.61000000000000...	0.46989999999999998	0.24660000000000001	1.9099999999999999...
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.90000000000000...	0.83309999999999995
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.90000000000000...	0.83309999999999995
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.90000000000000...	0.83309999999999995
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000001
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.0000000000000002...
11	JB137814	-0.67400000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.10000000000000...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999999...	0.4088	-1.75000000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.58000000000000...	0.44040000000000001
18	KLHL17	0.1497	8.20000000000000...	-7.1099999999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.80000000000000...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999999...	8.50000000000000...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.51670000000000...	-0.22700000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999999...	1E-3
24	C1orf159	-8.06000000000000...	0.16139999999999999	9.2899999999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999999...	0.2422	0.1138	0.13350000000000001

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

6. Assign an Array Platform used for the dataset, if applicable.

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.

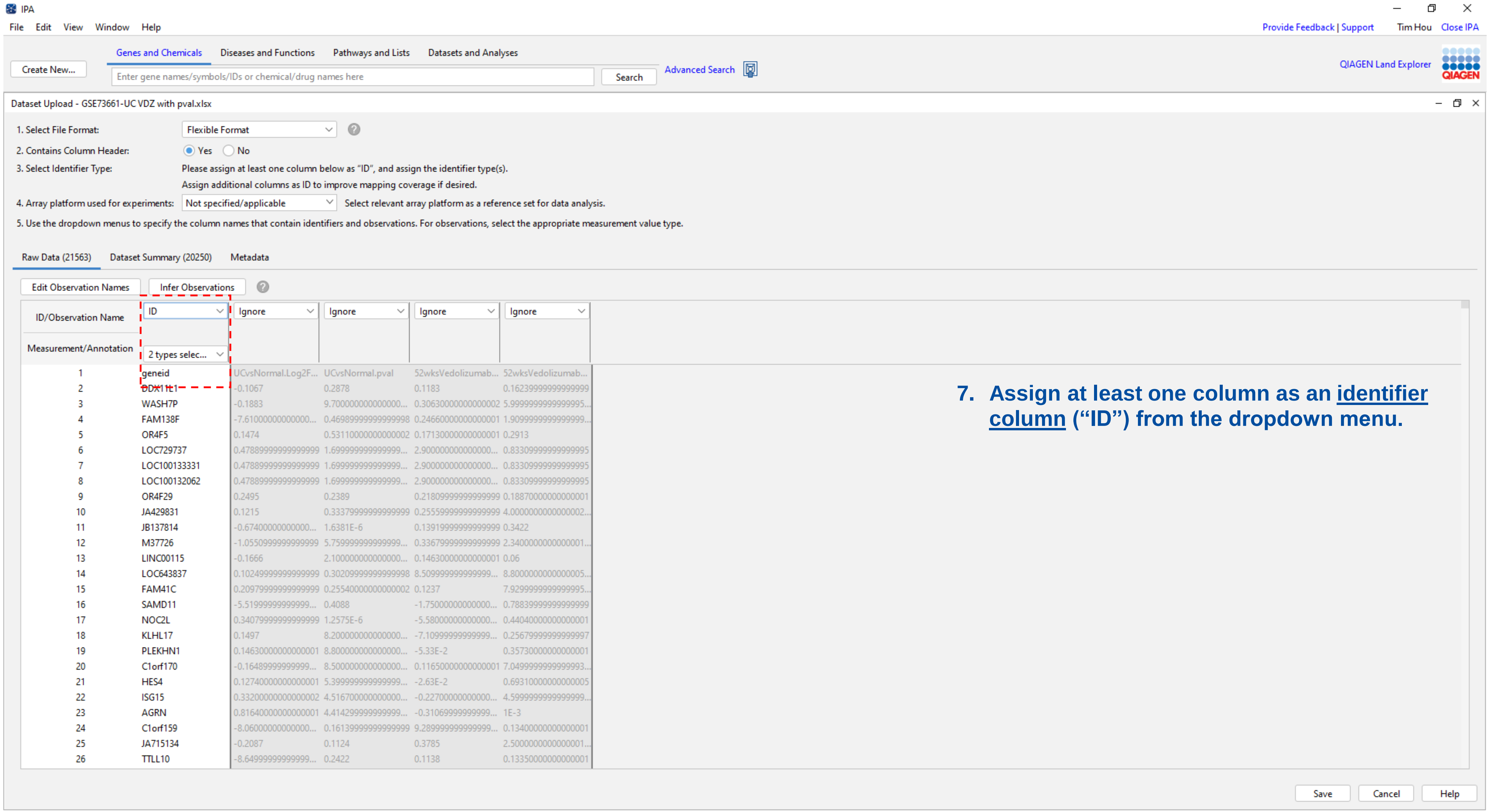
2. Select the dataset file (.txt, .xls, .xlsx, .csv, or .diff) from your computer and click the **Open** button.

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 supports many identifiers and symbols and will attempt to guess the type of identifier in your dataset file if the identifiers are in the *left-most column*. To override the selection, uncheck the option and simply select the most appropriate identifier type. If more than one type of identifier exists in your dataset, select all types that are appropriate, but refrain from selecting all identifier types at once as it can lead to mis-mapping.



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

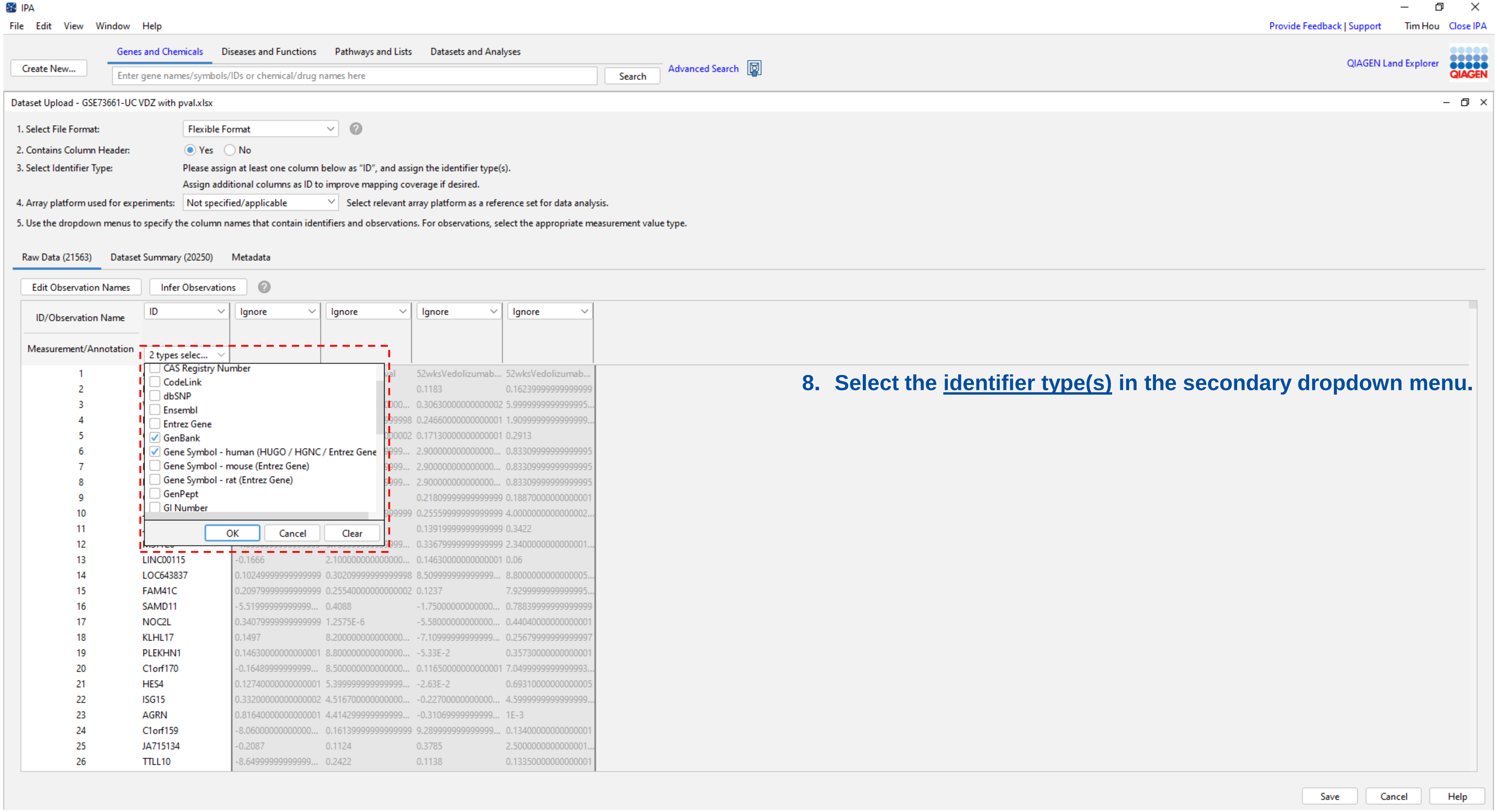
3. Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s).
Assign additional columns as ID to improve mapping coverage if desired.

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

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

ID/Observation Name	ID	Ignore	Ignore	Ignore	Ignore
Measurement/Annotation	2 types selec...				
1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999999999
3	WASH7P	-0.1883	9.700000000000000...	0.30630000000000002	5.9999999999999995...
4	FAM138F	-7.6100000000000...	0.46989999999999998	0.24660000000000001	1.9099999999999999...
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.9000000000000000...	0.83309999999999995
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.9000000000000000...	0.83309999999999995
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.9000000000000000...	0.83309999999999995
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000001
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.0000000000000002...
11	JB137814	-0.6740000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000000...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999...	0.4088	-1.7500000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000000...	-7.1099999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000000...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999...	8.5000000000000000...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000000...	-0.2270000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999...	1E-3
24	C1orf159	-8.0600000000000...	0.16139999999999999	9.2899999999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999...	0.2422	0.1138	0.13350000000000001

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



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

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

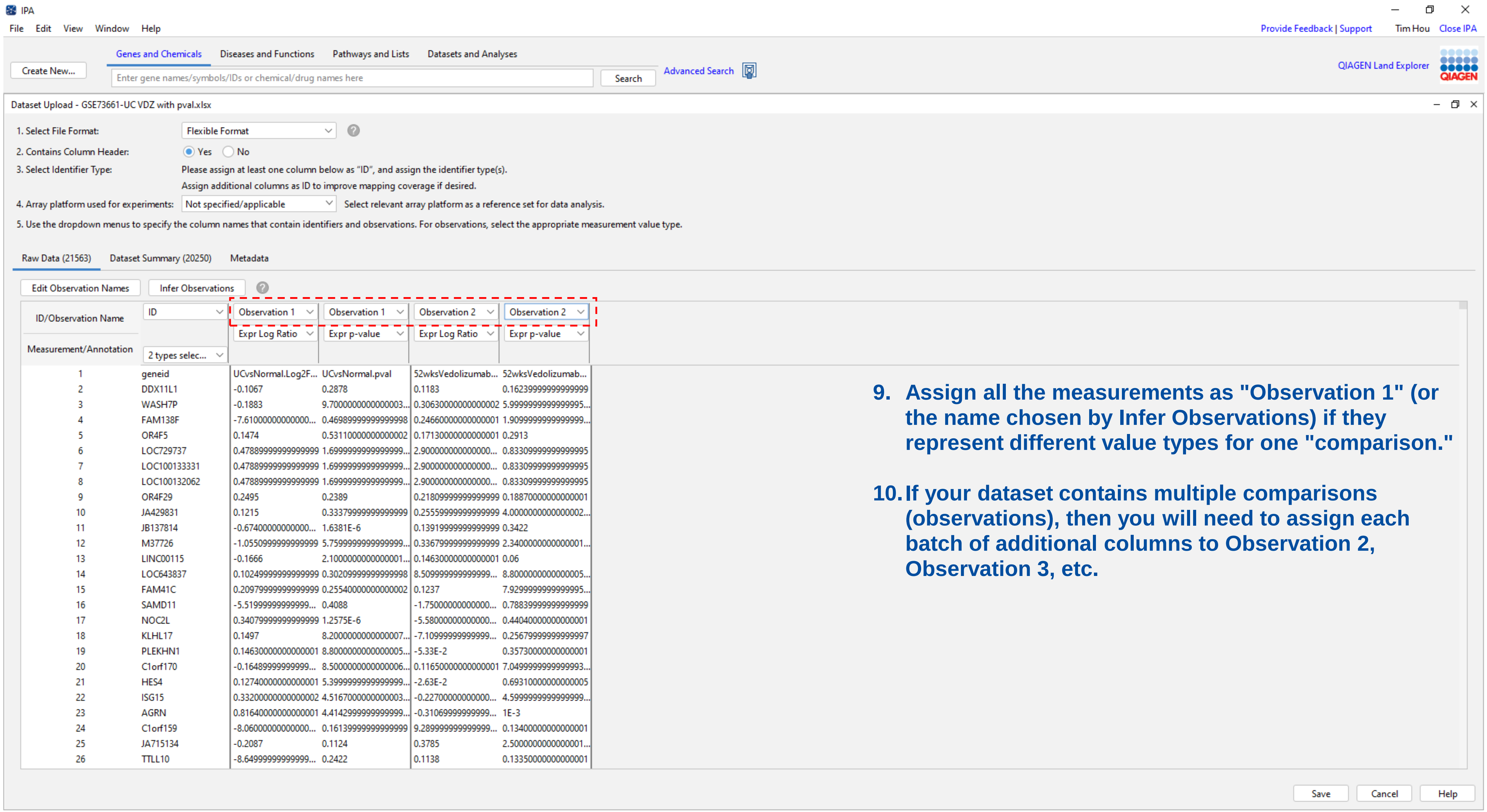
4. Array platform used for experiments: Not specified/applicable — Select relevant array platform as a reference set for data analysis.

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

ID/Observation Name	ID	Ignore	Ignore	Ignore	Ignore
Measurement/Annotation	2 types selec...				
1				52wksVedolizumab...	52wksVedolizumab...
2				0.1183	0.16239999999999999
3				0.30630000000000002	5.9999999999999995...
4				0.24660000000000001	1.9099999999999999...
5				0.17130000000000001	0.2913
6				2.9000000000000000...	0.83309999999999995
7				2.9000000000000000...	0.83309999999999995
8				2.9000000000000000...	0.83309999999999995
9				0.21809999999999999	0.18870000000000001
10				0.25559999999999999	4.0000000000000002...
11				0.13919999999999999	0.3422
12				0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000000...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999...	0.4088	-1.7500000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000...	-7.1099999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999...	8.5000000000000...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000...	-0.2270000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999...	-0.3106999999999...	1E-3
24	C1orf159	-8.0600000000000...	0.16139999999999999	9.2899999999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999...	0.2422	0.1138	0.13350000000000001

- ☐ CAS Registry Number
- ☐ CodeLink
- ☐ dbSNP
- ☐ Ensembl
- ☐ Entrez Gene
- ☑ GenBank
- ☑ Gene Symbol - human (HUGO / HGNC / Entrez Gene
- ☐ Gene Symbol - mouse (Entrez Gene)
- ☐ Gene Symbol - rat (Entrez Gene)
- ☐ GenPept
- ☐ GI Number

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



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

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

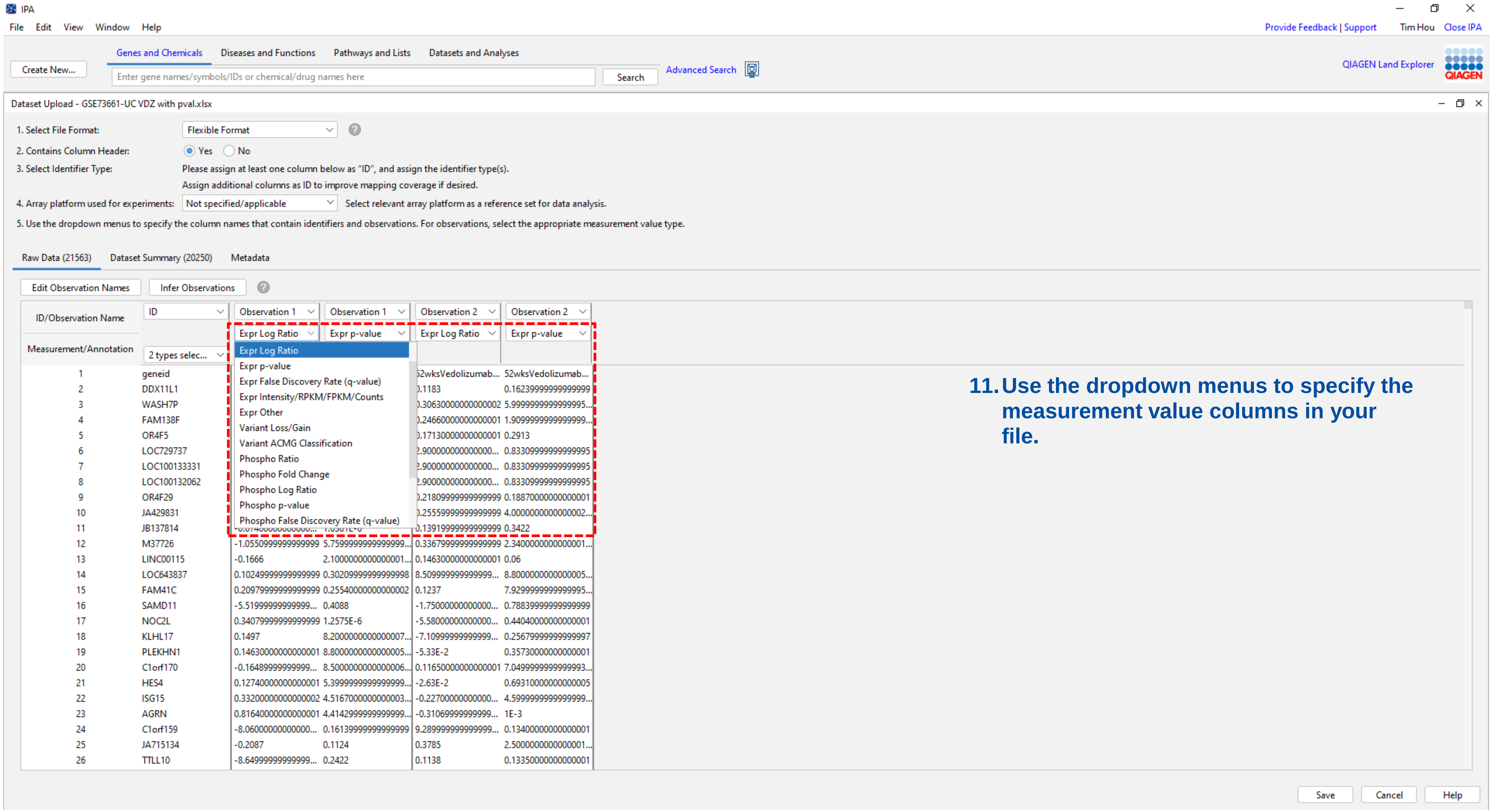
Raw Data (21563) | Dataset Summary (20250) | Metadata

Edit Observation Names | Infer Observations

ID/Observation Name	ID	Observation 1	Observation 1	Observation 2	Observation 2
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999999999
3	WASH7P	-0.1883	9.7000000000000003...	0.30630000000000002	5.9999999999999995...
4	FAM138F	-7.6100000000000...	0.46989999999999998	0.24660000000000001	1.9099999999999999...
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000001
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.0000000000000002...
11	JB137814	-0.6740000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999...	0.4088	-1.7500000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000007...	-7.1099999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999...	8.5000000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000003...	-0.2270000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999...	1E-3
24	C1orf159	-8.0600000000000...	0.16139999999999999	9.2899999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999...	0.2422	0.1138	0.13350000000000001

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

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

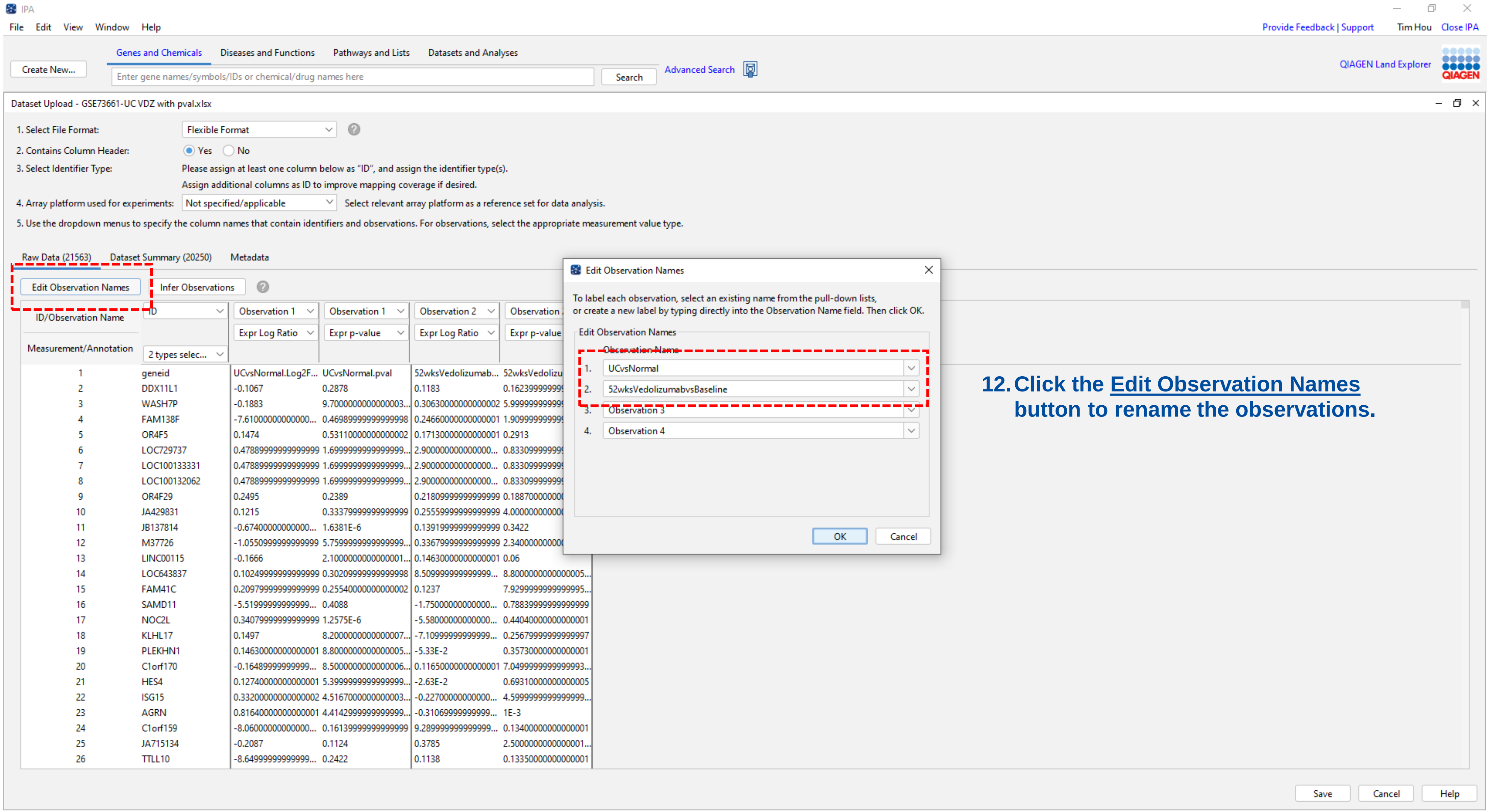


Dataset Upload - GSE73661-UC VDZ with pval.xlsx

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

ID/Observation Name	ID	Observation 1	Observation 1	Observation 2	Observation 2
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid			52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1			0.1183	0.16239999999999999
3	WASH7P			0.30630000000000002	5.9999999999999995...
4	FAM138F			0.24660000000000001	1.9099999999999999...
5	OR4F5			0.17130000000000001	0.2913
6	LOC729737			2.900000000000000...	0.83309999999999995
7	LOC100133331			2.900000000000000...	0.83309999999999995
8	LOC100132062			2.900000000000000...	0.83309999999999995
9	OR4F29			0.21809999999999999	0.18870000000000001
10	JA429831			0.25559999999999999	4.0000000000000002...
11	JB137814			0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999999...	0.4088	-1.7500000000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000007...	-7.1099999999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.16489999999999999...	8.5000000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000003...	-0.22700000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.31069999999999...	1E-3
24	C1orf159	-8.0600000000000000...	0.16139999999999999	9.2899999999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999999...	0.2422	0.1138	0.13350000000000001

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



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

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

ID/Observation Name	ID	Observation 1	Observation 1	Observation 2	Observation
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizu
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999
3	WASH7P	-0.1883	9.7000000000000003...	0.30630000000000002	5.99999999999
4	FAM138F	-7.6100000000000...	0.46989999999999998	0.24660000000000001	1.90999999999
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.00000000000
11	JB137814	-0.6740000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.34000000000
13	LINC00115	-0.1666	2.1000000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999...	0.4088	-1.7500000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000007...	-7.1099999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999...	8.5000000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000003...	-0.2270000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999...	1E-3
24	C1orf159	-8.0600000000000...	0.16139999999999999	9.2899999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999...	0.2422	0.1138	0.13350000000000001

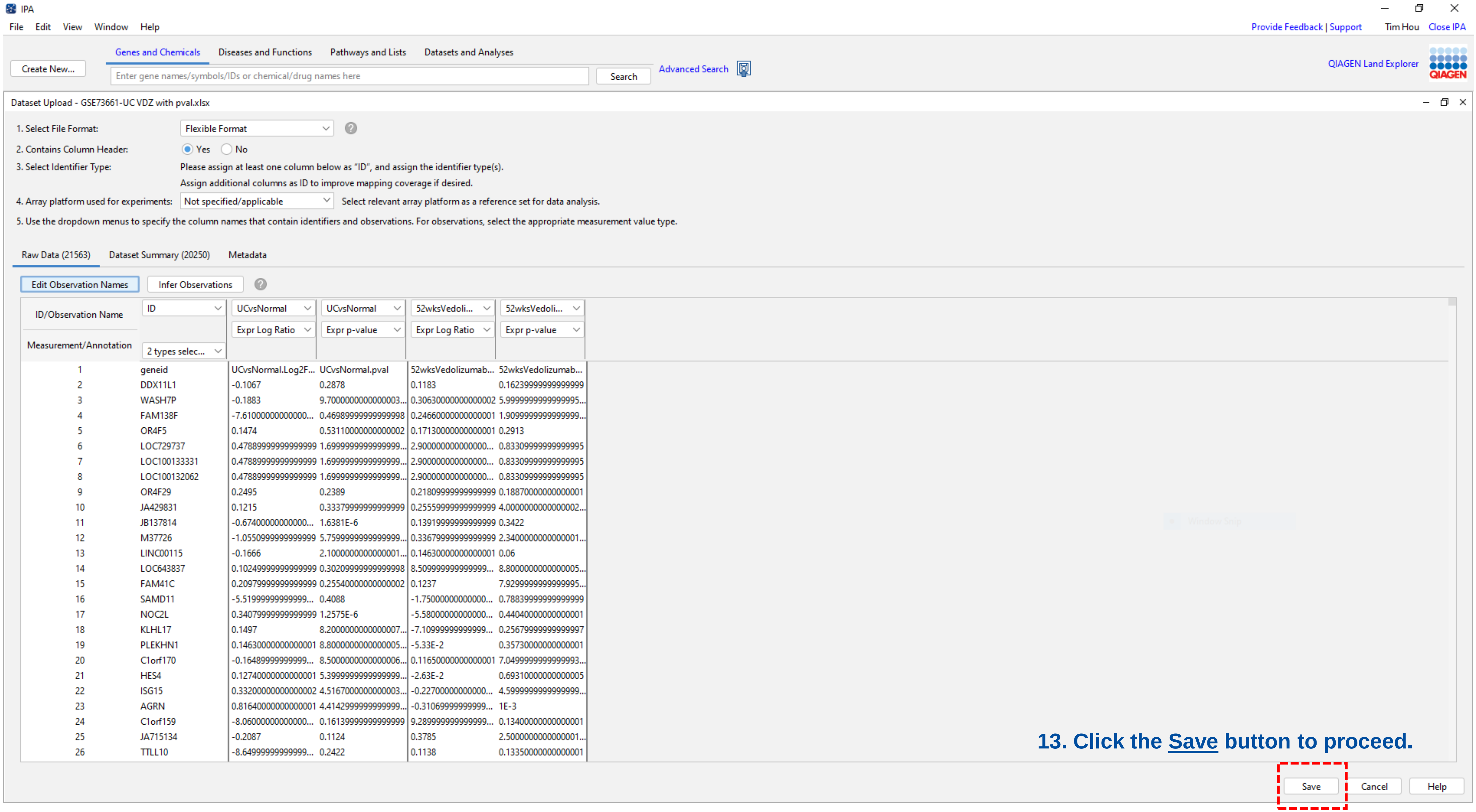
Edit Observation Names

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

Edit Observation Names

Observation Name
1. UCvsNormal
2. 52wksVedolizumabvsBaseline
3. Observation 3
4. Observation 4

12. Click the Edit Observation Names button to rename the observations.



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

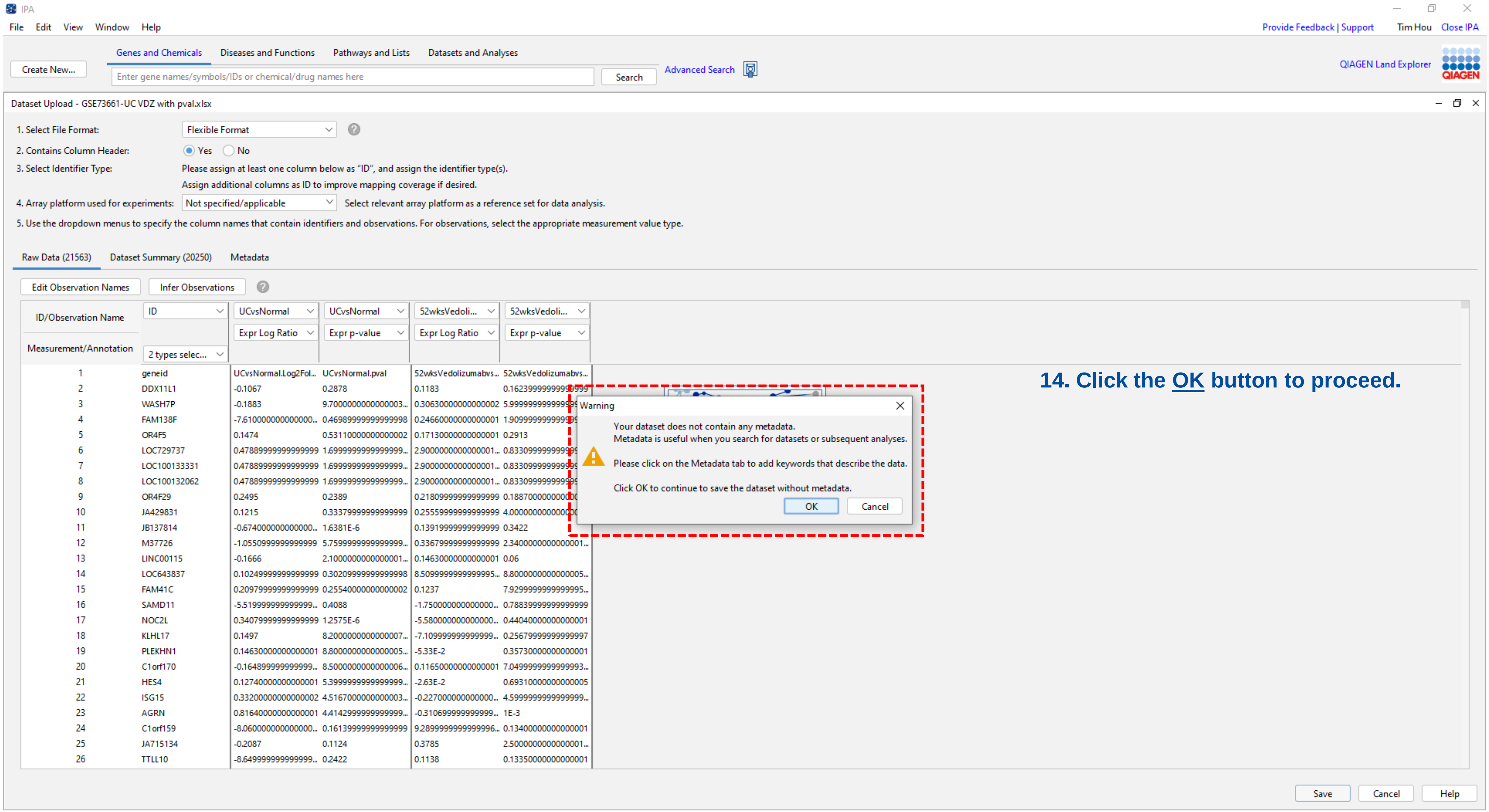
3. Select Identifier Type: Please assign at least one column below as "ID", and assign the identifier type(s).
Assign additional columns as ID to improve mapping coverage if desired.

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

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

ID/Observation Name	ID	UCvsNormal	UCvsNormal	52wksVedoli...	52wksVedoli...
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid	UCvsNormal.Log2F...	UCvsNormal.pval	52wksVedolizumab...	52wksVedolizumab...
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999999999
3	WASH7P	-0.1883	9.7000000000000003...	0.30630000000000002	5.9999999999999995...
4	FAM138F	-7.6100000000000...	0.46989999999999998	0.24660000000000001	1.9099999999999999...
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.9000000000000...	0.83309999999999995
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000001
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.0000000000000002...
11	JB137814	-0.6740000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999999...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999...	0.4088	-1.7500000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000007...	-7.1099999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999...	8.5000000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000003...	-0.2270000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999...	1E-3
24	C1orf159	-8.0600000000000...	0.16139999999999999	9.2899999999999999...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999...	0.2422	0.1138	0.13350000000000001

13. Click the Save button to proceed.



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

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

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

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

ID/Observation Name	ID	UCvsNormal	UCvsNormal	52wksVedoli...	52wksVedoli...
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid	UCvsNormal.Log2Fol...	UCvsNormal.pval	52wksVedolizumabvs...	52wksVedolizumabvs...
2	DDX11L1	-0.1067	0.2878	0.1183	0.16239999999999999
3	WASH7P	-0.1883	9.7000000000000003...	0.30630000000000002	5.999999999999
4	FAM138F	-7.6100000000000000...	0.46989999999999998	0.24660000000000001	1.909999999999
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.6999999999999999...	2.9000000000000001...	0.83309999999999
7	LOC100133331	0.47889999999999999	1.6999999999999999...	2.9000000000000001...	0.83309999999999
8	LOC100132062	0.47889999999999999	1.6999999999999999...	2.9000000000000001...	0.83309999999999
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.00000000000000
11	JB137814	-0.6740000000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.7599999999999999...	0.33679999999999999	2.3400000000000001...
13	LINC00115	-0.1666	2.1000000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.5099999999999995...	8.8000000000000005...
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.9299999999999995...
16	SAMD11	-5.5199999999999999...	0.4088	-1.7500000000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.5800000000000000...	0.44040000000000001
18	KLHL17	0.1497	8.2000000000000007...	-7.1099999999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.8000000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.1648999999999999...	8.5000000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.3999999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.5167000000000003...	-0.2270000000000000...	4.5999999999999999...
23	AGRN	0.81640000000000001	4.4142999999999999...	-0.3106999999999999...	1E-3
24	C1orf159	-8.0600000000000000...	0.16139999999999999	9.2899999999999996...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.5000000000000001...
26	TTLL10	-8.6499999999999999...	0.2422	0.1138	0.13350000000000001

Warning

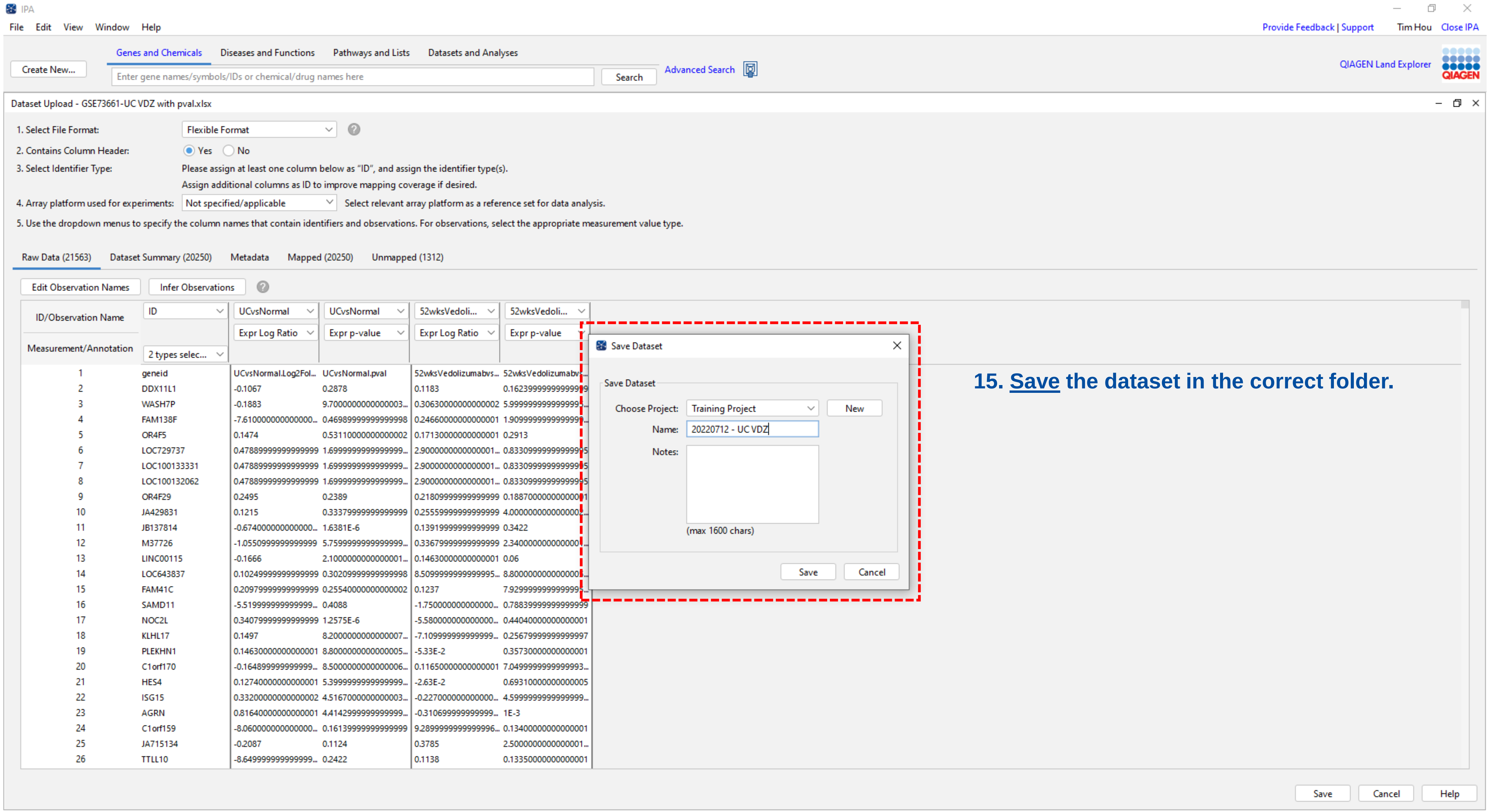
Your dataset does not contain any metadata.
Metadata is useful when you search for datasets or subsequent analyses.

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

14. Click the OK button to proceed.



Dataset Upload - GSE73661-UC VDZ with pval.xlsx

1. Select File Format: Flexible Format

2. Contains Column Header: ● Yes ○ No

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

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

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

ID/Observation Name	ID	UCvsNormal	UCvsNormal	52wksVedoli...	52wksVedoli...
Measurement/Annotation	2 types selec...	Expr Log Ratio	Expr p-value	Expr Log Ratio	Expr p-value
1	geneid	UCvsNormal.Log2Fol...	UCvsNormal.pval	52wksVedolizumabvs...	52wksVedolizumabv
2	DDX11L1	-0.1067	0.2878	0.1183	0.162399999999999
3	WASH7P	-0.1883	9.700000000000003...	0.30630000000000002	5.99999999999999
4	FAM138F	-7.610000000000000...	0.46989999999999998	0.24660000000000001	1.90999999999999
5	OR4F5	0.1474	0.53110000000000002	0.17130000000000001	0.2913
6	LOC729737	0.47889999999999999	1.699999999999999...	2.900000000000001...	0.833099999999999
7	LOC100133331	0.47889999999999999	1.699999999999999...	2.900000000000001...	0.833099999999999
8	LOC100132062	0.47889999999999999	1.699999999999999...	2.900000000000001...	0.833099999999999
9	OR4F29	0.2495	0.2389	0.21809999999999999	0.18870000000000
10	JA429831	0.1215	0.33379999999999999	0.25559999999999999	4.00000000000000
11	JB137814	-0.674000000000000...	1.6381E-6	0.13919999999999999	0.3422
12	M37726	-1.0550999999999999	5.759999999999999...	0.33679999999999999	2.34000000000000
13	LINC00115	-0.1666	2.100000000000001...	0.14630000000000001	0.06
14	LOC643837	0.10249999999999999	0.30209999999999998	8.509999999999995...	8.80000000000000
15	FAM41C	0.20979999999999999	0.25540000000000002	0.1237	7.92999999999999
16	SAMD11	-5.519999999999999...	0.4088	-1.750000000000000...	0.78839999999999999
17	NOC2L	0.34079999999999999	1.2575E-6	-5.580000000000000...	0.44040000000000001
18	KLHL17	0.1497	8.200000000000007...	-7.109999999999999...	0.25679999999999997
19	PLEKHN1	0.14630000000000001	8.800000000000005...	-5.33E-2	0.35730000000000001
20	C1orf170	-0.164899999999999...	8.500000000000006...	0.11650000000000001	7.0499999999999993...
21	HES4	0.12740000000000001	5.399999999999999...	-2.63E-2	0.69310000000000005
22	ISG15	0.33200000000000002	4.516700000000003...	-0.227000000000000...	4.599999999999999...
23	AGRN	0.81640000000000001	4.414299999999999...	-0.310699999999999...	1E-3
24	C1orf159	-8.060000000000000...	0.16139999999999999	9.289999999999996...	0.13400000000000001
25	JA715134	-0.2087	0.1124	0.3785	2.500000000000001...
26	TTLL10	-8.649999999999999...	0.2422	0.1138	0.13350000000000001

Save Dataset

Save Dataset

Choose Project: Training Project [New]

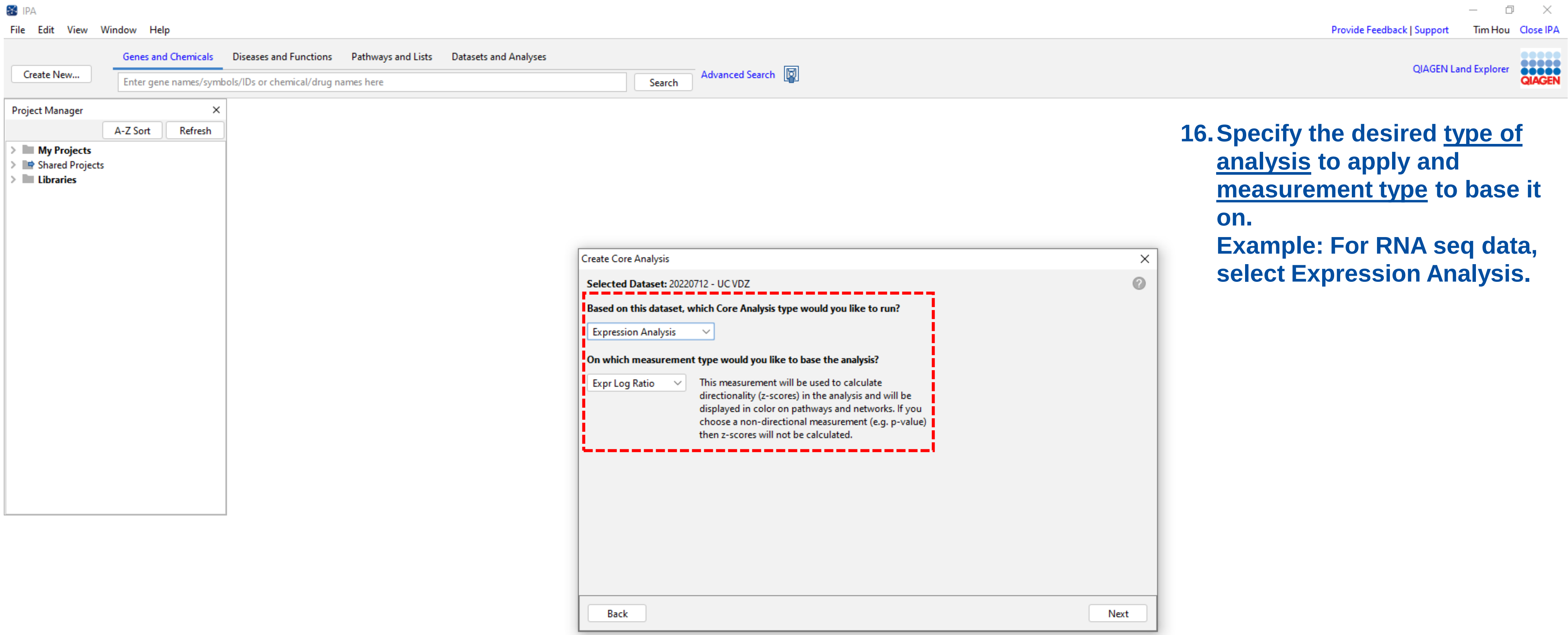
Name: 20220712 - UC VDZ

Notes:

(max 1600 chars)

[Save] [Cancel]

15. Save the dataset in the correct folder.



Selected Dataset: 20220712 - UC VDZ

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

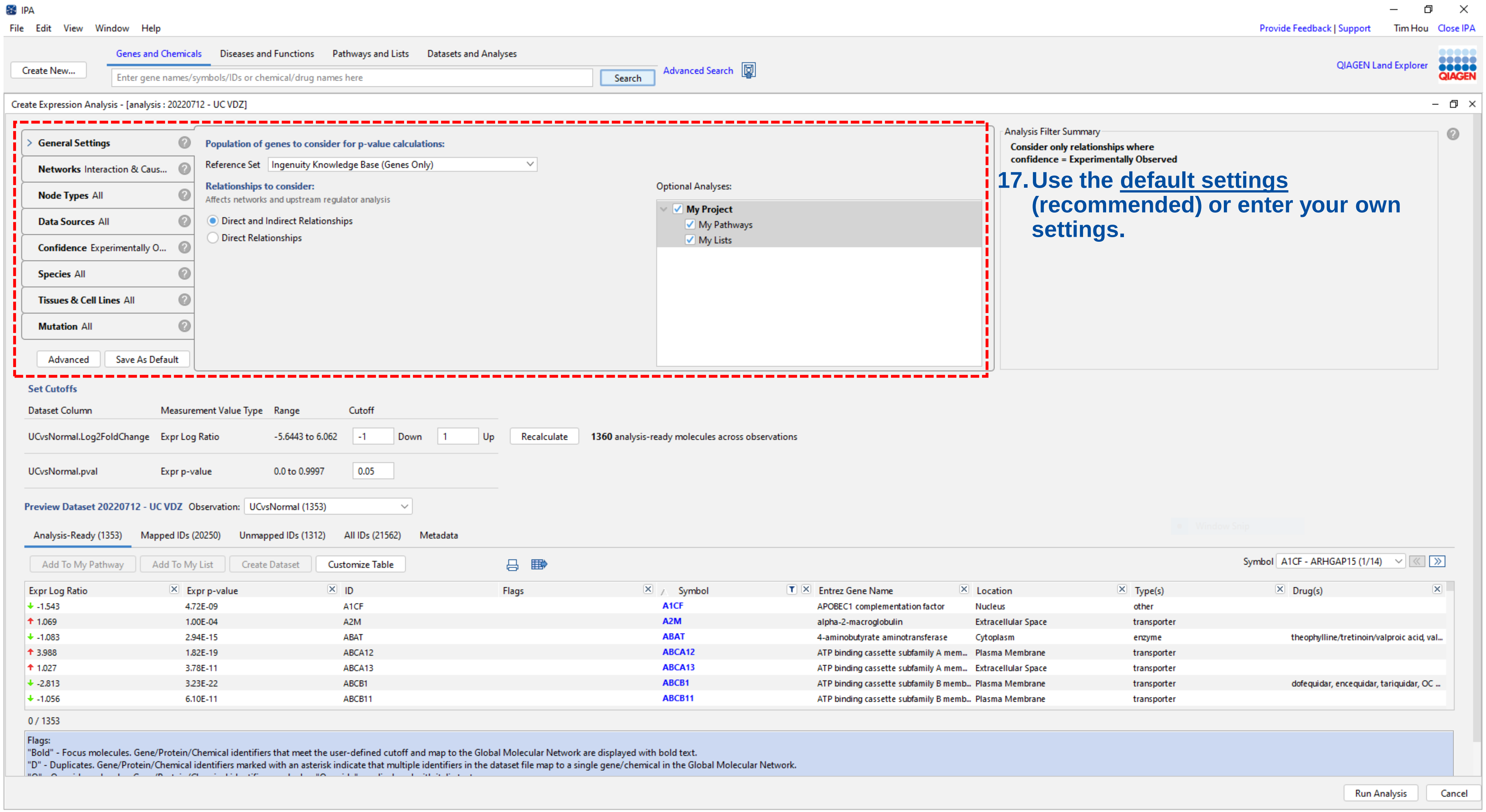
Expression Analysis

On which measurement type would you like to base the analysis?

Expr Log Ratio

This measurement will be used to calculate directionality (z-scores) in the analysis and will be displayed in color on pathways and networks. If you choose a non-directional measurement (e.g. p-value) then z-scores will not be calculated.

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



Create Expression Analysis - [analysis : 20220712 - UC VDZ]

- **General Settings**
- **Networks** Interaction & Caus...
- **Node Types** All
- **Data Sources** All
- **Confidence** Experimentally O...
- **Species** All
- **Tissues & Cell Lines** All
- **Mutation** All

Population of genes to consider for p-value calculations:

Reference Set: Ingenuity Knowledge Base (Genes Only)

Relationships to consider:

Affects networks and upstream regulator analysis

● Direct and Indirect Relationships

○ Direct Relationships

Optional Analyses:

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

Analysis Filter Summary

Consider only relationships where confidence = Experimentally Observed

17. Use the default settings (recommended) or enter your own settings.

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff			
UCvsNormal.Log2FoldChange	Expr Log Ratio	-5.6443 to 6.062	-1	Down	1	Up
UCvsNormal.pval	Expr p-value	0.0 to 0.9997	0.05			

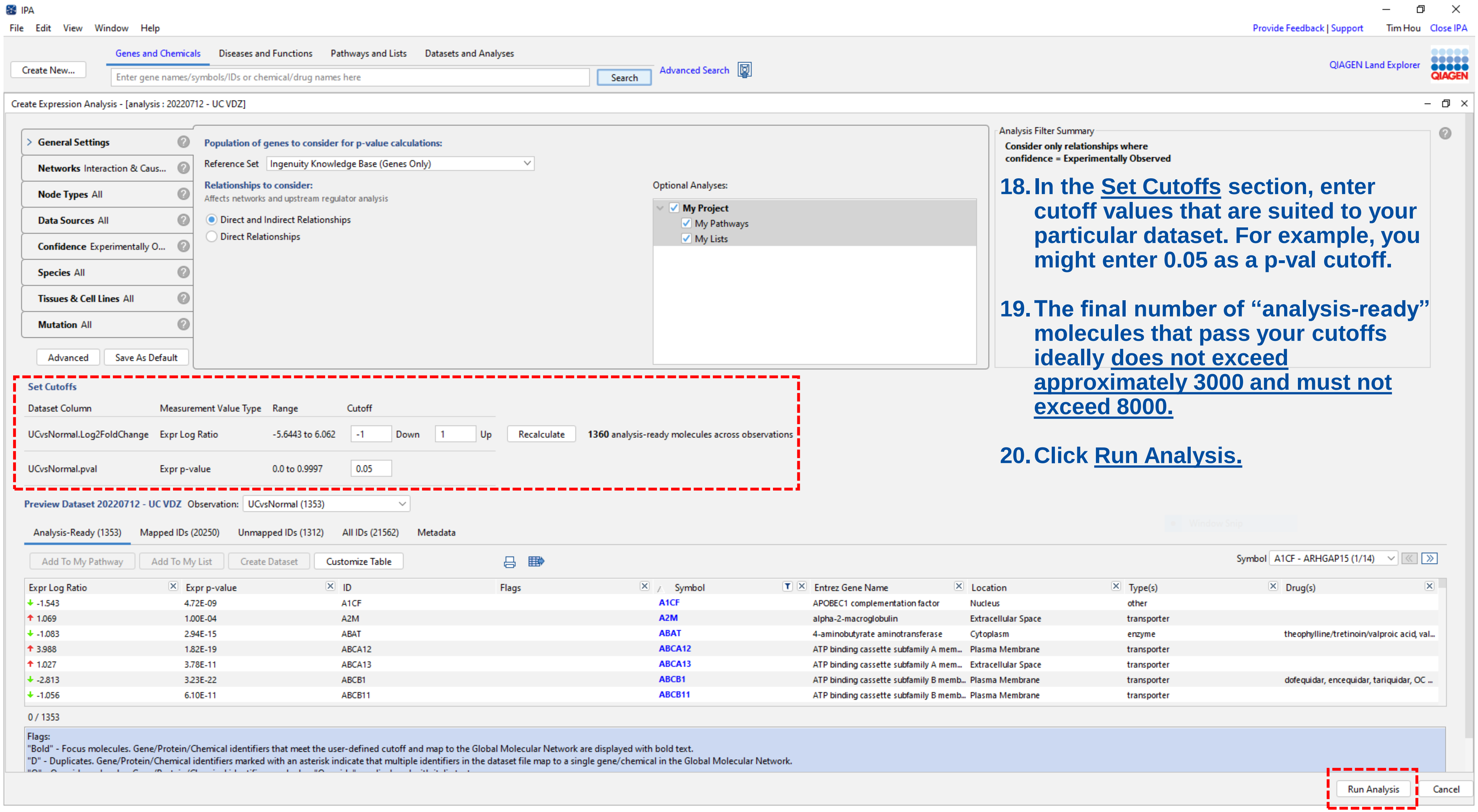
1360 analysis-ready molecules across observations

Preview Dataset 20220712 - UC VDZ Observation: UCvsNormal (1353)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
↓ -1.543	4.72E-09	A1CF		A1CF	APOBEC1 complementation factor	Nucleus	other	
↑ 1.069	1.00E-04	A2M		A2M	alpha-2-macroglobulin	Extracellular Space	transporter	
↓ -1.083	2.94E-15	ABAT		ABAT	4-aminobutyrate aminotransferase	Cytoplasm	enzyme	theophylline/tretinoin/valproic acid, val...
↑ 3.988	1.82E-19	ABCA12		ABCA12	ATP binding cassette subfamily A mem...	Plasma Membrane	transporter	
↑ 1.027	3.78E-11	ABCA13		ABCA13	ATP binding cassette subfamily A mem...	Extracellular Space	transporter	
↓ -2.813	3.23E-22	ABCB1		ABCB1	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	dofequidar, encequidar, tariquidar, OC ...
↓ -1.056	6.10E-11	ABCB11		ABCB11	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	

0 / 1353

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



Create Expression Analysis - [analysis : 20220712 - UC VDZ]

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

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff			
UCvsNormal.Log2FoldChange	Expr Log Ratio	-5.6443 to 6.062	-1 Down	1 Up	Recalculate	**1360** analysis-ready molecules across observations
UCvsNormal.pval	Expr p-value	0.0 to 0.9997	0.05			

Preview Dataset 20220712 - UC VDZ Observation: UCvsNormal (1353)

Analysis-Ready (1353) | Mapped IDs (20250) | Unmapped IDs (1312) | All IDs (21562) | Metadata

Symbol: A1CF - ARHGAP15 (1/14)

Expr Log Ratio	Expr p-value	ID	Flags	Symbol	Entrez Gene Name	Location	Type(s)	Drug(s)
↓ -1.543	4.72E-09	A1CF		**A1CF**	APOBEC1 complementation factor	Nucleus	other	
↑ 1.069	1.00E-04	A2M		**A2M**	alpha-2-macroglobulin	Extracellular Space	transporter	
↓ -1.083	2.94E-15	ABAT		**ABAT**	4-aminobutyrate aminotransferase	Cytoplasm	enzyme	theophylline/tretinoin/valproic acid, val...
↑ 3.988	1.82E-19	ABCA12		**ABCA12**	ATP binding cassette subfamily A mem...	Plasma Membrane	transporter	
↑ 1.027	3.78E-11	ABCA13		**ABCA13**	ATP binding cassette subfamily A mem...	Extracellular Space	transporter	
↓ -2.813	3.23E-22	ABCB1		**ABCB1**	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	dofequidar, encequidar, tariquidar, OC ...
↓ -1.056	6.10E-11	ABCB11		**ABCB11**	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	

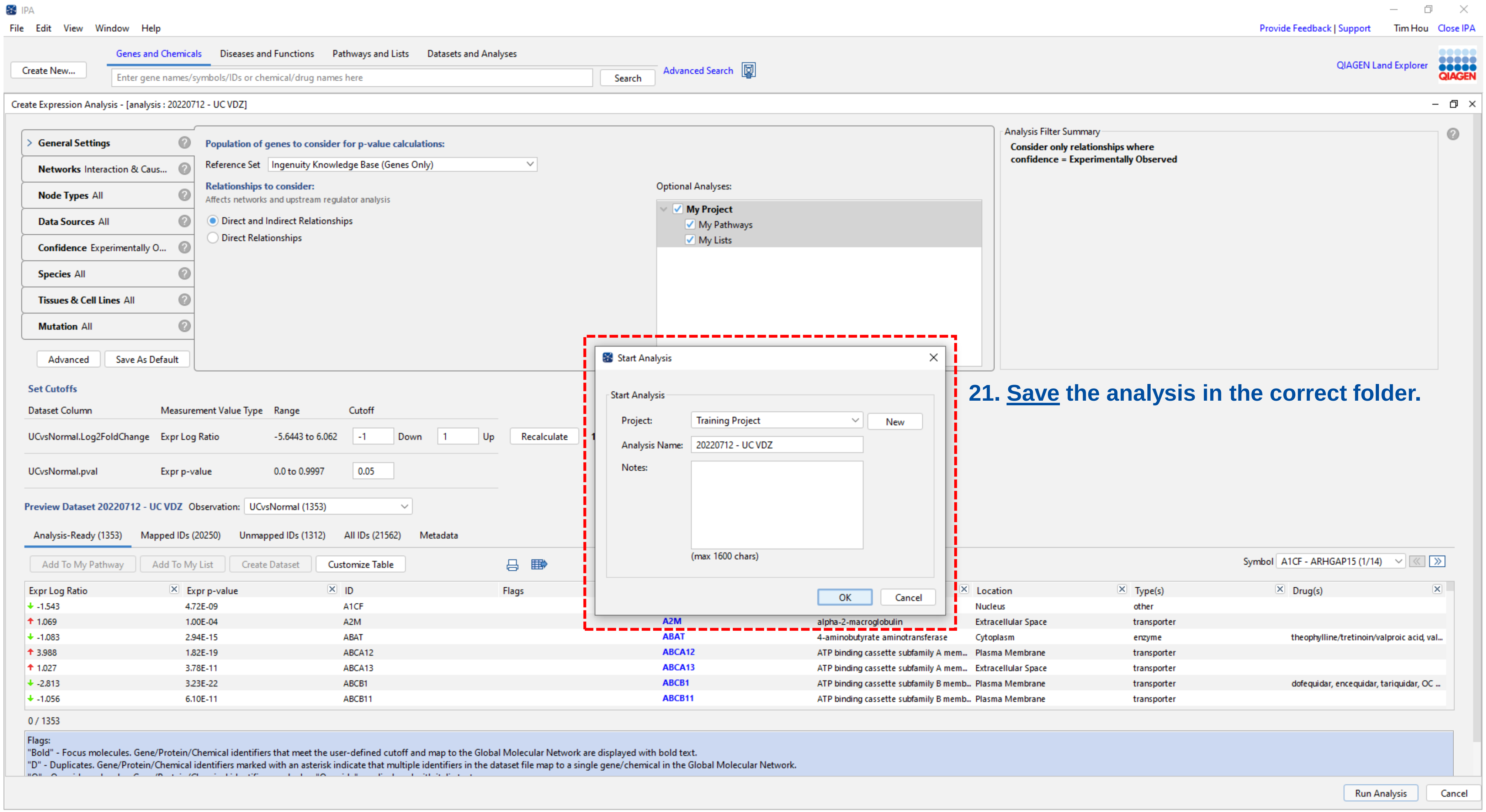
0 / 1353

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

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

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

20. Click Run Analysis.



Create Expression Analysis - [analysis : 20220712 - UC VDZ]

- **General Settings**
- **Networks** Interaction & Caus...
- **Node Types** All
- **Data Sources** All
- **Confidence** Experimentally O...
- **Species** All
- **Tissues & Cell Lines** All
- **Mutation** All

Population of genes to consider for p-value calculations:

Reference Set: Ingenuity Knowledge Base (Genes Only)

Relationships to consider:

Affects networks and upstream regulator analysis

● Direct and Indirect Relationships
○ Direct Relationships

Optional Analyses:

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

Analysis Filter Summary

Consider only relationships where confidence = Experimentally Observed

Set Cutoffs

Dataset Column	Measurement Value Type	Range	Cutoff
UCvsNormal.Log2FoldChange	Expr Log Ratio	-5.6443 to 6.062	-1 Down 1 Up
UCvsNormal.pval	Expr p-value	0.0 to 0.9997	0.05

Preview Dataset 20220712 - UC VDZ Observation: UCvsNormal (1353)

Analysis-Ready (1353) | Mapped IDs (20250) | Unmapped IDs (1312) | All IDs (21562) | Metadata

Symbol: A1CF - ARHGAP15 (1/14)

Expr Log Ratio	Expr p-value	ID	Flags			Location	Type(s)	Drug(s)
↓ -1.543	4.72E-09	A1CF				Nucleus	other	
↑ 1.069	1.00E-04	A2M		**A2M**	alpha-2-macroglobulin	Extracellular Space	transporter	
↓ -1.083	2.94E-15	ABAT		**ABAT**	4-aminobutyrate aminotransferase	Cytoplasm	enzyme	theophylline/tretinoin/valproic acid, val...
↑ 3.988	1.82E-19	ABCA12		**ABCA12**	ATP binding cassette subfamily A mem...	Plasma Membrane	transporter	
↑ 1.027	3.78E-11	ABCA13		**ABCA13**	ATP binding cassette subfamily A mem...	Extracellular Space	transporter	
↓ -2.813	3.23E-22	ABCB1		**ABCB1**	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	dofequidar, encequidar, tariquidar, OC ...
↓ -1.056	6.10E-11	ABCB11		**ABCB11**	ATP binding cassette subfamily B memb...	Plasma Membrane	transporter	

0 / 1353

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

Start Analysis

Start Analysis

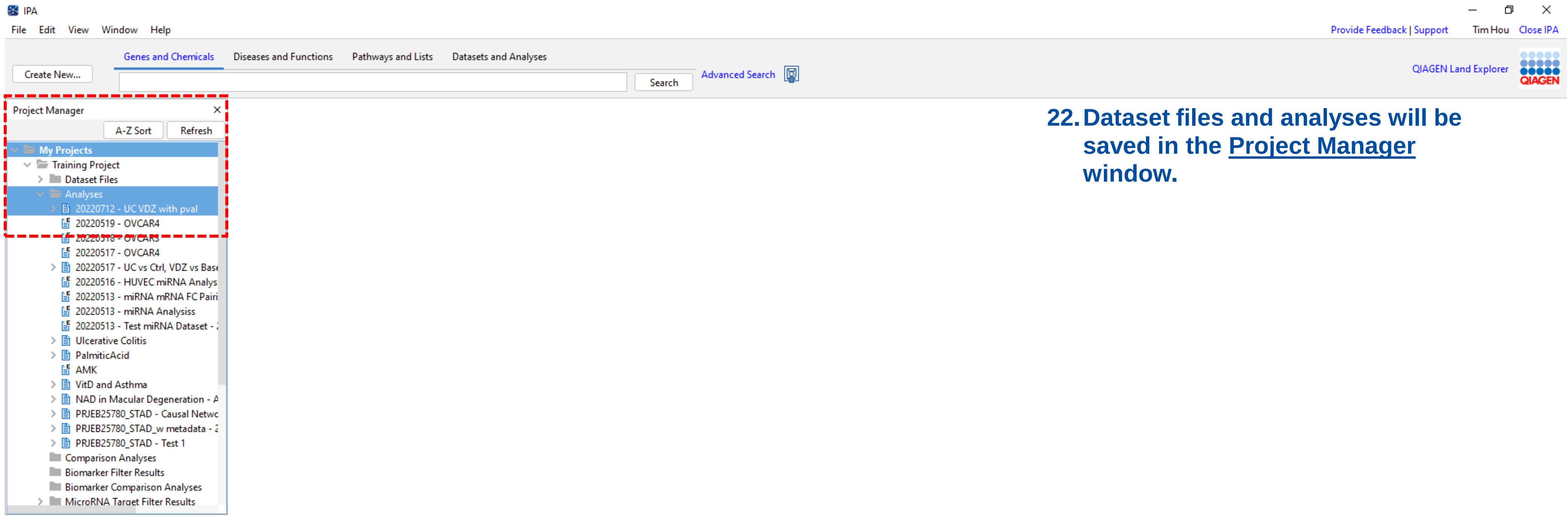
Project: Training Project

Analysis Name: 20220712 - UC VDZ

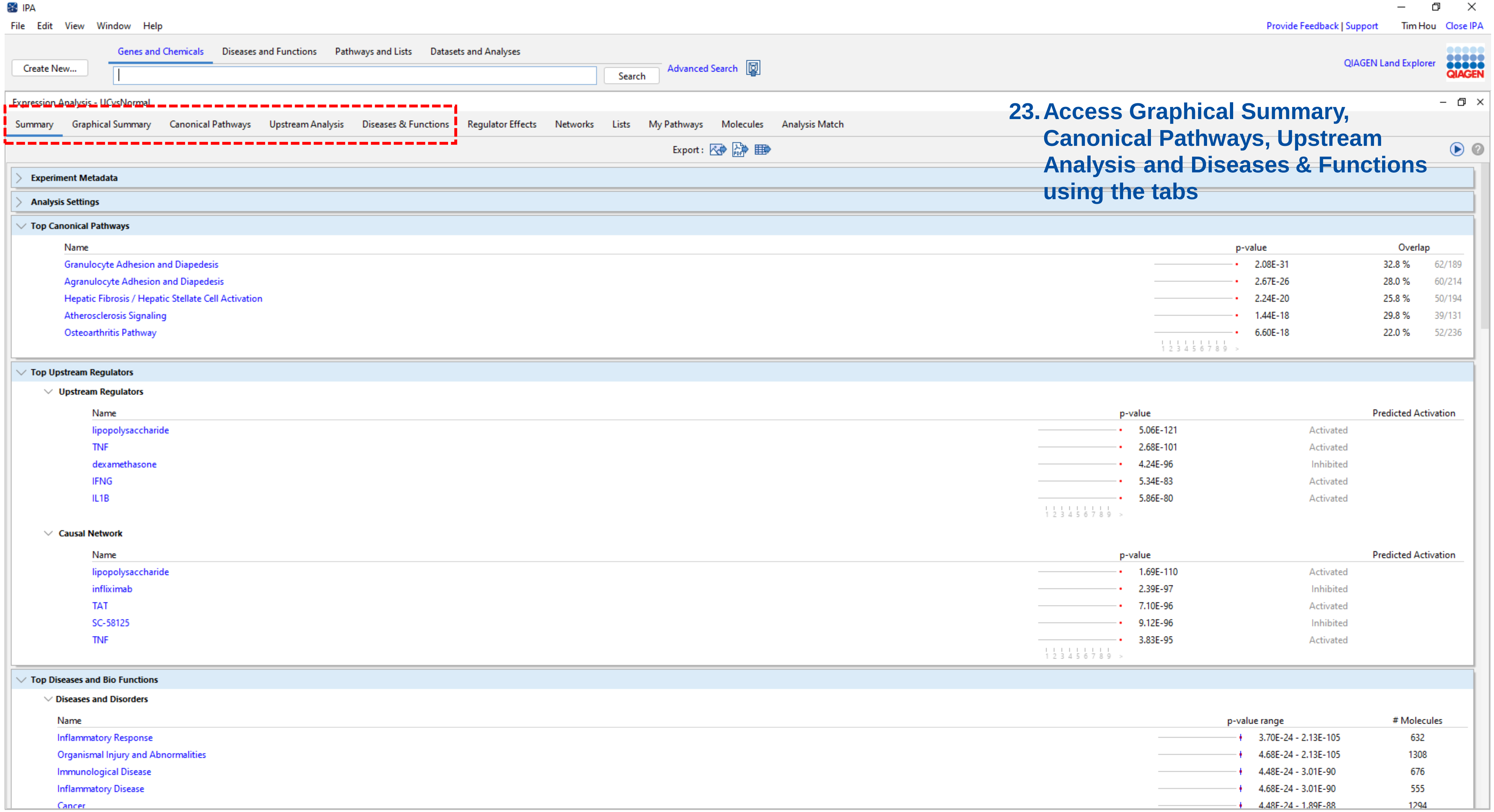
Notes:

(max 1600 chars)

21. Save the analysis in the correct folder.



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



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

Top Canonical Pathways

Name	p-value	Overlap	
Granulocyte Adhesion and Diapedesis	2.08E-31	32.8 %	62/189
Agranulocyte Adhesion and Diapedesis	2.67E-26	28.0 %	60/214
Hepatic Fibrosis / Hepatic Stellate Cell Activation	2.24E-20	25.8 %	50/194
Atherosclerosis Signaling	1.44E-18	29.8 %	39/131
Osteoarthritis Pathway	6.60E-18	22.0 %	52/236

Top Upstream Regulators

Upstream Regulators

Name	p-value	Predicted Activation
lipopolysaccharide	5.06E-121	Activated
TNF	2.68E-101	Activated
dexamethasone	4.24E-96	Inhibited
IFNG	5.34E-83	Activated
IL1B	5.86E-80	Activated

Causal Network

Name	p-value	Predicted Activation
lipopolysaccharide	1.69E-110	Activated
infliximab	2.39E-97	Inhibited
TAT	7.10E-96	Activated
SC-58125	9.12E-96	Inhibited
TNF	3.83E-95	Activated

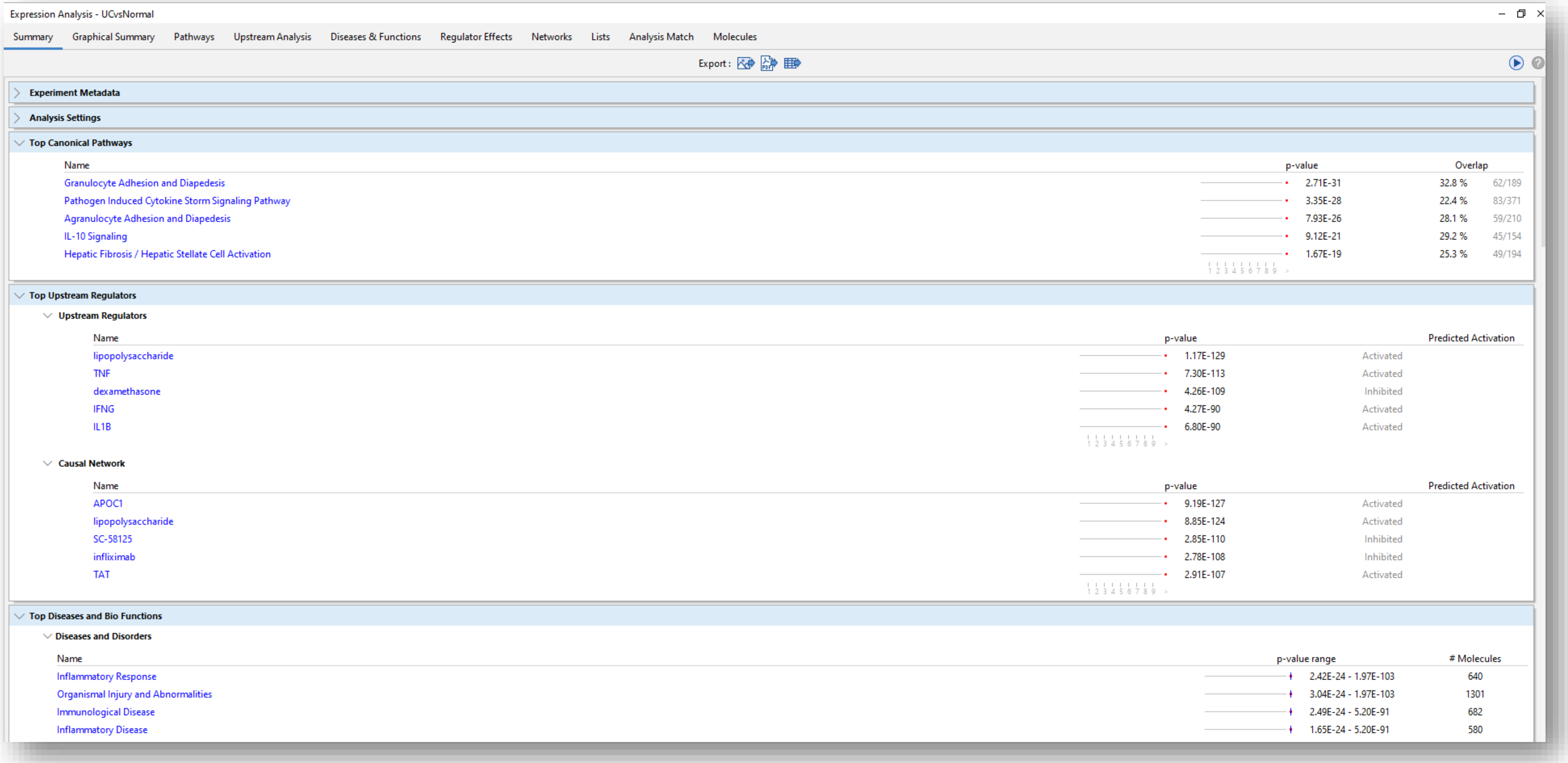
Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value range	# Molecules
Inflammatory Response	3.70E-24 - 2.13E-105	632
Organismal Injury and Abnormalities	4.68E-24 - 2.13E-105	1308
Immunological Disease	4.48E-24 - 3.01E-90	676
Inflammatory Disease	4.68E-24 - 3.01E-90	555
Cancer	4.48E-24 - 1.89E-88	1294

IPA Analysis Tabs

Summary Tab



Experiment Metadata

Analysis Settings

Top Canonical Pathways

Name	p-value	Overlap	
Granulocyte Adhesion and Diapedesis	2.71E-31	32.8 %	62/189
Pathogen Induced Cytokine Storm Signaling Pathway	3.35E-28	22.4 %	83/371
Agranulocyte Adhesion and Diapedesis	7.93E-26	28.1 %	59/210
IL-10 Signaling	9.12E-21	29.2 %	45/154
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.67E-19	25.3 %	49/194

Top Upstream Regulators

Upstream Regulators

Name	p-value	Predicted Activation
lipopolysaccharide	1.17E-129	Activated
TNF	7.30E-113	Activated
dexamethasone	4.26E-109	Inhibited
IFNG	4.27E-90	Activated
IL1B	6.80E-90	Activated

Causal Network

Name	p-value	Predicted Activation
APOC1	9.19E-127	Activated
lipopolysaccharide	8.85E-124	Activated
SC-58125	2.85E-110	Inhibited
infliximab	2.78E-108	Inhibited
TAT	2.91E-107	Activated

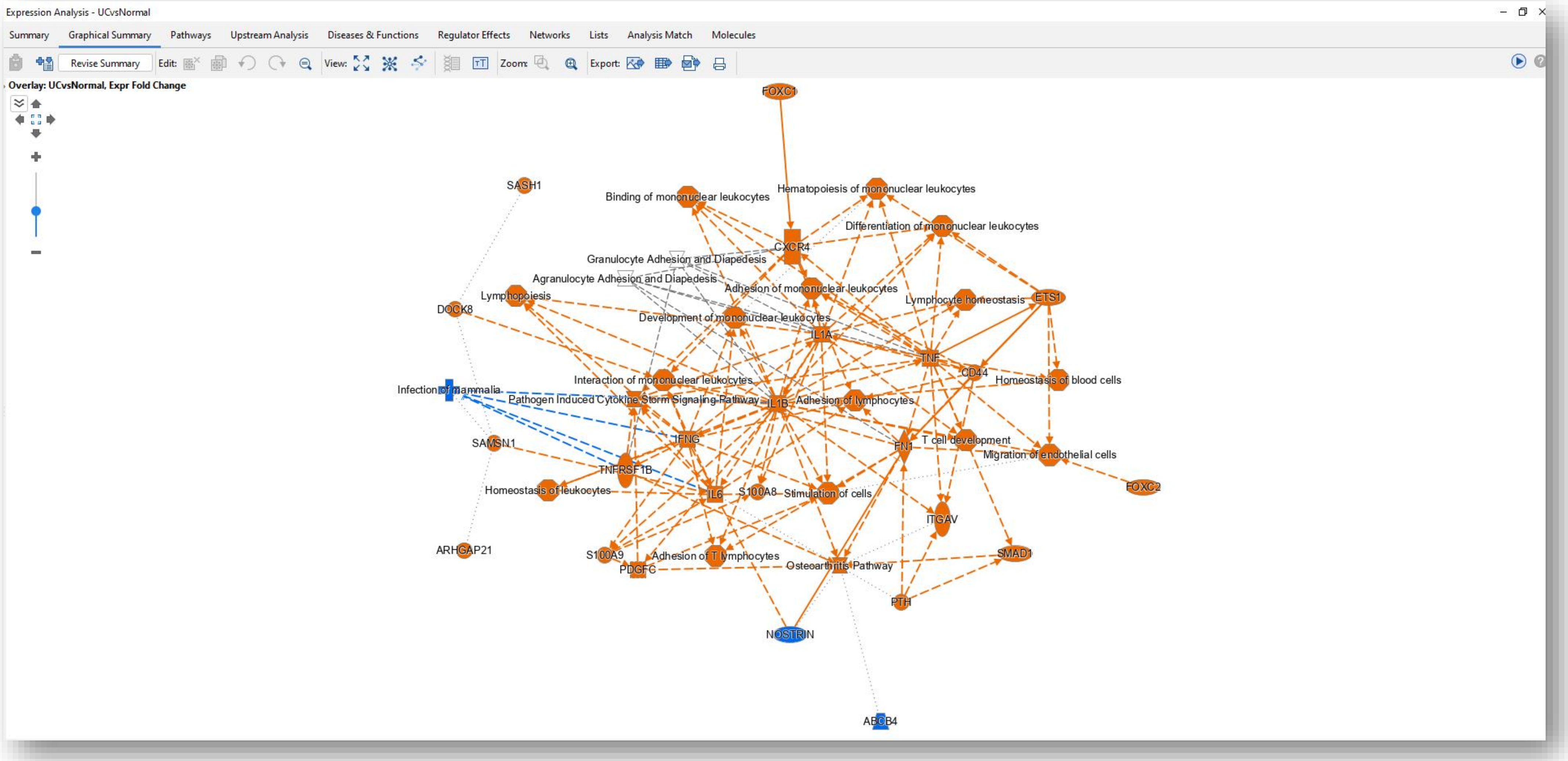
Top Diseases and Bio Functions

Diseases and Disorders

Name	p-value range	# Molecules
Inflammatory Response	2.42E-24 - 1.97E-103	640
Organismal Injury and Abnormalities	3.04E-24 - 1.97E-103	1301
Immunological Disease	2.49E-24 - 5.20E-91	682
Inflammatory Disease	1.65E-24 - 5.20E-91	580

Top 5 for all analysis modules and a quick high-level look at your data

Graphical Summary Tab



Overlay: UCvsNormal, Expr Fold Change

Graphical display of the top biological themes and features within your data with added AI inferences (dotted lines)

Pathways Tab

Change chart characteristics

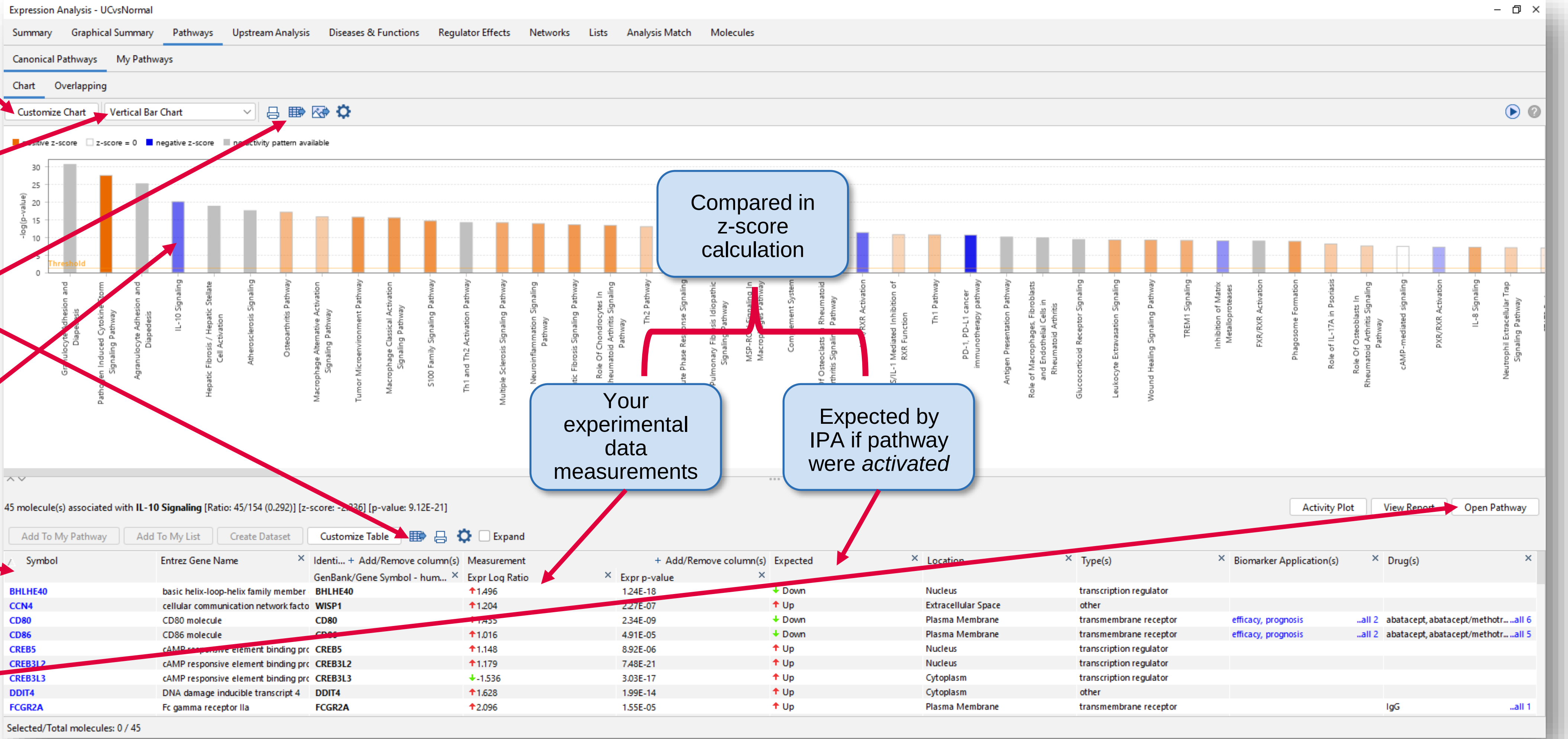
Change chart view

Export data or picture

Click on bar to display chart below

Genes in data set annotated to selected pathway

View network map of pathway



Compared in z-score calculation

Your experimental data measurements

Expected by IPA if pathway were *activated*

45 molecule(s) associated with **IL-10 Signaling** [Ratio: 45/154 (0.292)] [z-score: -2.236] [p-value: 9.12E-21]

Symbol	Entrez Gene Name	Identi... GenBank/Gene Symbol - hum...	Measurement Expr Log Ratio	Expr p-value	Expected	Location	Type(s)	Biomarker Application(s)	Drug(s)
BHLHE40	basic helix-loop-helix family member	BHLHE40	↑1.496	1.24E-18	↓ Down	Nucleus	transcription regulator		
CCN4	cellular communication network facto	WISP1	↑1.204	2.27E-07	↑ Up	Extracellular Space	other		
CD80	CD80 molecule	CD80	↑1.435	2.34E-09	↓ Down	Plasma Membrane	transmembrane receptor	efficacy, prognosis ...all 2	abatacept, abatacept/methotr... ...all 6
CD86	CD86 molecule	CD86	↑1.016	4.91E-05	↓ Down	Plasma Membrane	transmembrane receptor	efficacy, prognosis ...all 2	abatacept, abatacept/methotr... ...all 5
CREB5	cAMP responsive element binding prc	CREB5	↑1.148	8.92E-06	↑ Up	Nucleus	transcription regulator		
CREB3L2	cAMP responsive element binding prc	CREB3L2	↑1.179	7.48E-21	↑ Up	Nucleus	transcription regulator		
CREB3L3	cAMP responsive element binding prc	CREB3L3	↓-1.536	3.03E-17	↑ Up	Cytoplasm	transcription regulator		
DDIT4	DNA damage inducible transcript 4	DDIT4	↑1.628	1.99E-14	↑ Up	Cytoplasm	other		
FCGR2A	Fc gamma receptor IIa	FCGR2A	↑2.096	1.55E-05	↑ Up	Plasma Membrane	transmembrane receptor		IgG ...all 1

Selected/Total molecules: 0 / 45

Metabolic and cell signaling pathways that are enriched in your data with activity prediction

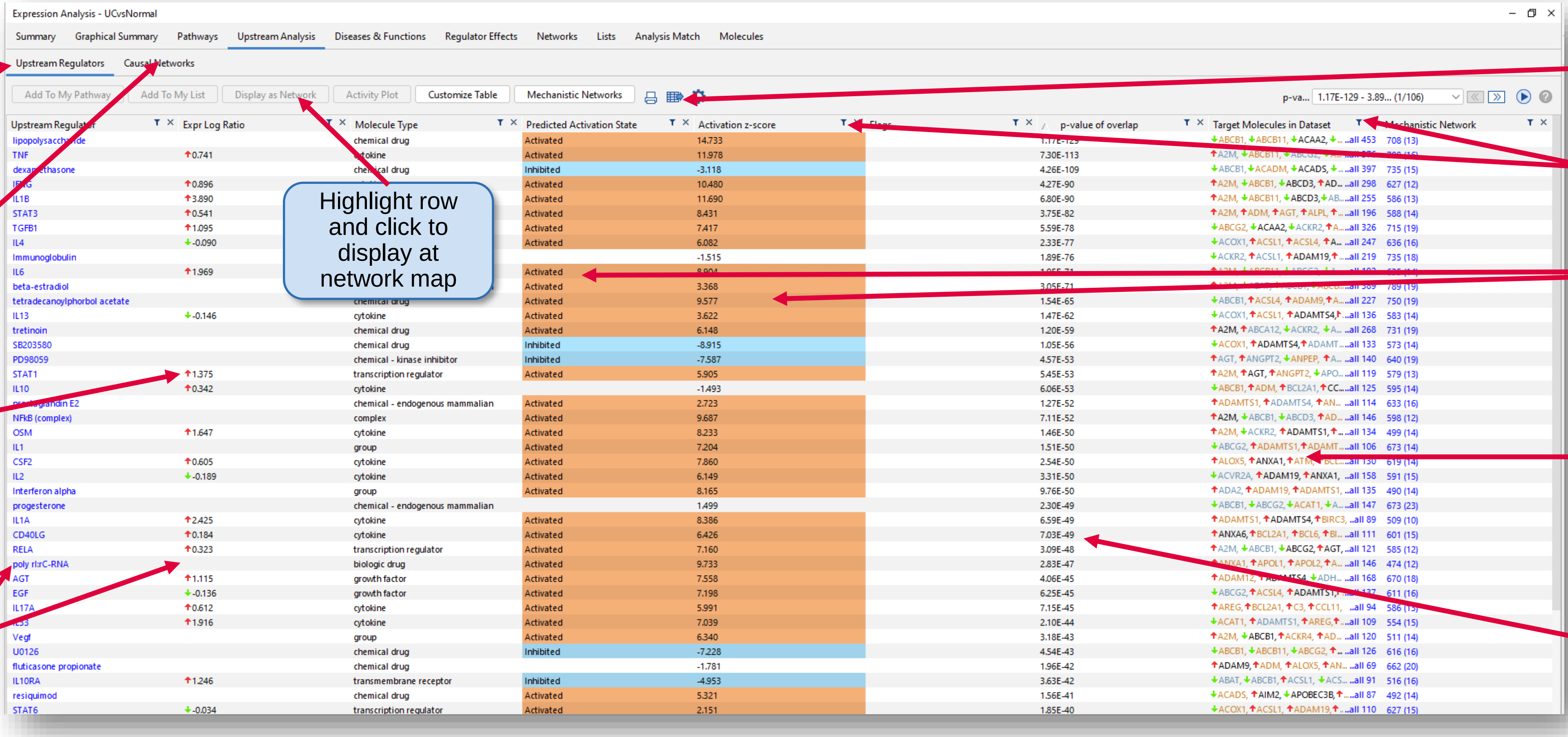
Upstream Analysis Tab

Immediately upstream of dataset genes regulators

One additional level upstream of regulatory networks

Measurement from your dataset for this regulator

Regulator predicted by IPA using patterns seen in your data (no measurement)



Upstream Regulator	Expr Log Ratio	Molecule Type	Predicted Activation State	Activation z-score	Flags	p-value of overlap	Target Molecules in Dataset	Mechanistic Network
lipopolysaccharide		chemical drug	Activated	14.733		1.17E-129	↓ABCB1, ↓ABCB11, ↓ACAA2, ↓... ...all 453	708 (13)
TNF	↑0.741	cytokine	Activated	11.978		7.30E-113	↑A2M, ↓ABCB11, ↓ABCG2, ↓A... ...all 376	708 (16)
dexamethasone		chemical drug	Inhibited	-3.118		4.26E-109	↓ABCB1, ↓ACADM, ↓ACADS, ↓... ...all 397	735 (15)
IFNG	↑0.896		Activated	10.480		4.27E-90	↑A2M, ↓ABCB1, ↓ABCD3, ↑AD... ...all 298	627 (12)
IL1B	↑3.890		Activated	11.690		6.80E-90	↑A2M, ↓ABCB11, ↓ABCD3, ↓AB... ...all 255	586 (13)
STAT3	↑0.541		Activated	8.431		3.75E-82	↑A2M, ↑ADM, ↑AGT, ↑ALPL, ↑... ...all 196	588 (14)
TGFB1	↑1.095		Activated	7.417		5.59E-78	↓ABCG2, ↓ACAA2, ↓ACKR2, ↑A... ...all 326	715 (19)
IL4	↓-0.090		Activated	6.082		2.33E-77	↓ACOX1, ↑ACSL1, ↑ACSL4, ↑A... ...all 247	636 (16)
Immunoglobulin				-1.515		1.89E-76	↓ACKR2, ↑ACSL1, ↑ADAM19, ↑... ...all 219	735 (18)
IL6	↑1.969		Activated	8.904		1.05E-71	↑A2M, ↓ABCB11, ↓ABCG2, ↓A... ...all 192	635 (14)
beta-estradiol			Activated	3.368		3.05E-71	↑A2M, ↓ABAT, ↓ABCB1, ↓ABCB... ...all 389	789 (19)
tetradecanoylphorbol acetate		chemical drug	Activated	9.577		1.54E-65	↓ABCB1, ↑ACSL4, ↑ADAM9, ↑A... ...all 227	750 (19)
IL13	↓-0.146	cytokine	Activated	3.622		1.47E-62	↓ACOX1, ↑ACSL1, ↑ADAMTS4, ↑... ...all 136	583 (14)
tretinoin		chemical drug	Activated	6.148		1.20E-59	↑A2M, ↑ABCA12, ↓ACKR2, ↓A... ...all 268	731 (19)
SB203580		chemical drug	Inhibited	-8.915		1.05E-56	↓ACOX1, ↑ADAMTS4, ↑ADAMT... ...all 133	573 (14)
PD98059		chemical - kinase inhibitor	Inhibited	-7.587		4.57E-53	↑AGT, ↑ANGPT2, ↓ANPEP, ↑A... ...all 140	640 (19)
STAT1	↑1.375	transcription regulator	Activated	5.905		5.45E-53	↑A2M, ↑AGT, ↑ANGPT2, ↓APO... ...all 119	579 (13)
IL10	↑0.342	cytokine		-1.493		6.06E-53	↓ABCB1, ↑ADM, ↑BCL2A1, ↑CC... ...all 125	595 (14)
prostaglandin E2		chemical - endogenous mammalian	Activated	2.723		1.27E-52	↑ADAMTS1, ↑ADAMTS4, ↑AN... ...all 114	633 (16)
NFkB (complex)		complex	Activated	9.687		7.11E-52	↑A2M, ↓ABCB1, ↓ABCD3, ↑AD... ...all 146	598 (12)
OSM	↑1.647	cytokine	Activated	8.233		1.46E-50	↑A2M, ↓ACKR2, ↑ADAMTS1, ↑... ...all 134	499 (14)
IL1		group	Activated	7.204		1.51E-50	↓ABCG2, ↑ADAMTS1, ↑ADAMT... ...all 106	673 (14)
CSF2	↑0.605	cytokine	Activated	7.860		2.54E-50	↑ALOX5, ↑ANXA1, ↑ATM, ↑BCL... ...all 130	619 (14)
IL2	↓-0.189	cytokine	Activated	6.149		3.31E-50	↓ACVR2A, ↑ADAM19, ↑ANXA1, ...all 158	591 (15)
Interferon alpha		group	Activated	8.165		9.76E-50	↑ADA2, ↑ADAM19, ↑ADAMTS1, ...all 135	490 (14)
progesterone		chemical - endogenous mammalian		1.499		2.30E-49	↓ABCB1, ↓ABCG2, ↓ACAT1, ↓A... ...all 147	673 (23)
IL1A	↑2.425	cytokine	Activated	8.386		6.59E-49	↑ADAMTS1, ↑ADAMTS4, ↑BIRC3, ...all 89	509 (10)
CD40LG	↑0.184	cytokine	Activated	6.426		7.03E-49	↑ANXA6, ↑BCL2A1, ↑BCL6, ↑BI... ...all 111	601 (15)
RELA	↑0.323	transcription regulator	Activated	7.160		3.09E-48	↑A2M, ↓ABCB1, ↓ABCG2, ↑AGT, ...all 121	585 (12)
poly rI:rC-RNA		biologic drug	Activated	9.733		2.83E-47	↑ANXA1, ↑APOL1, ↑APOL2, ↑A... ...all 146	474 (12)
AGT	↑1.115	growth factor	Activated	7.558		4.06E-45	↑ADAM12, ↑ADAMTS4, ↓ADH... ...all 168	670 (18)
EGF	↓-0.136	growth factor	Activated	7.198		6.25E-45	↓ABCG2, ↑ACSL4, ↑ADAMTS1, ↑... ...all 137	611 (16)
IL17A	↑0.612	cytokine	Activated	5.991		7.15E-45	↑AREG, ↑BCL2A1, ↑C3, ↑CCL11, ...all 94	586 (13)
IL33	↑1.916	cytokine	Activated	7.039		2.10E-44	↓ACAT1, ↑ADAMTS1, ↑AREG, ↑... ...all 109	554 (15)
Vegf		group	Activated	6.340		3.18E-43	↑A2M, ↓ABCB1, ↑ACKR4, ↑AD... ...all 120	511 (14)
U0126		chemical drug	Inhibited	-7.228		4.54E-43	↓ABCB1, ↓ABCB11, ↓ABCG2, ↑... ...all 126	616 (16)
fluticasone propionate		chemical drug		-1.781		1.96E-42	↑ADAM9, ↑ADM, ↑ALOX5, ↑AN... ...all 69	662 (20)
IL10RA	↑1.246	transmembrane receptor	Inhibited	-4.953		3.63E-42	↓ABAT, ↓ABCB1, ↑ACSL1, ↓ACS... ...all 91	516 (16)
resiquimod		chemical drug	Activated	5.321		1.56E-41	↓ACADS, ↑AIM2, ↓APOBEC3B, ↑... ...all 87	492 (14)
STAT6	↓-0.034	transcription regulator	Activated	2.151		1.85E-40	↓ACOX1, ↑ACSL1, ↑ADAM19, ↑... ...all 110	627 (15)

Highlight row and click to display at network map

Export

Filter icons

Activity prediction

Genes that this regulator targets present in your filtered dataset

P-value of significance

Regulators that may be contributing to the signal observed in your data. Some have been measured in your dataset and some have been predicted by IPA

**** ALL COLUMNS ARE FILTERABLE****

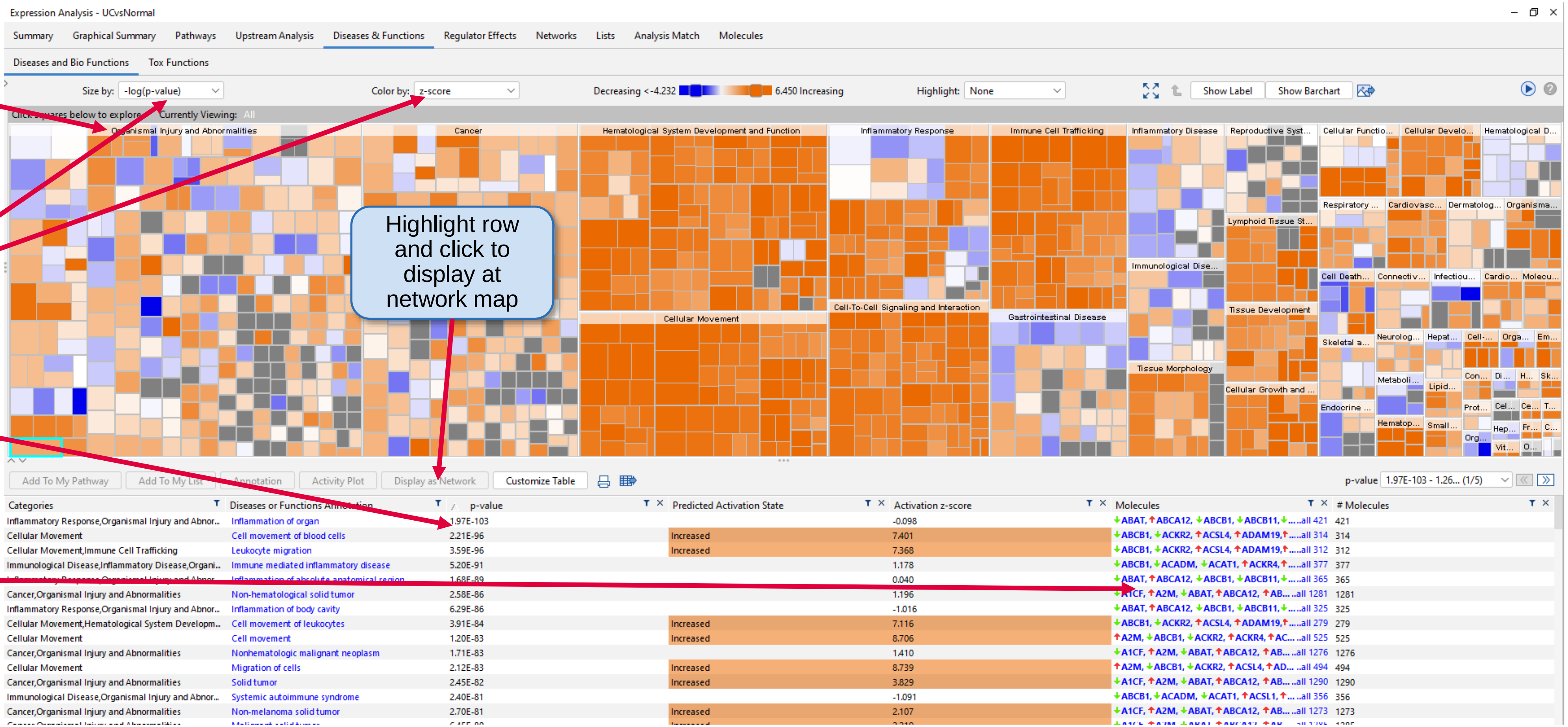
Diseases & Functions Tab

Color is activity prediction; size of square is p-value but can be changed

Organized by biological themes

Significance of enrichment

Genes from dataset involved in disease or function



Size by: -log(p-value)

Color by: z-score

Decreasing <-4.232 6.450 Increasing

Highlight: None

Currently Viewing: All

p-value 1.97E-103 - 1.26... (1/5)

Highlight row and click to display at network map

Categories	Diseases or Functions Annotation	p-value	Predicted Activation State	Activation z-score	Molecules	# Molecules
Inflammatory Response,Organismal Injury and Abnor...	Inflammation of organ	1.97E-103		-0.098	↓ABAT, ↑ABCA12, ↓ABCB1, ↓ABCB11,↓... ...all 421	421
Cellular Movement	Cell movement of blood cells	2.21E-96	Increased	7.401	↓ABCB1, ↓ACKR2, ↑ACSL4, ↑ADAM19,↑... ...all 314	314
Cellular Movement,Immune Cell Trafficking	Leukocyte migration	3.59E-96	Increased	7.368	↓ABCB1, ↓ACKR2, ↑ACSL4, ↑ADAM19,↑... ...all 312	312
Immunological Disease,Inflammatory Disease,Organi...	Immune mediated inflammatory disease	5.20E-91		1.178	↓ABCB1, ↓ACADM, ↓ACAT1, ↑ACKR4,↑... ...all 377	377
Inflammatory Response,Organismal Injury and Abnor...	Inflammation of absolute anatomical region	1.68E-89		0.040	↓ABAT, ↑ABCA12, ↓ABCB1, ↓ABCB11,↓... ...all 365	365
Cancer,Organismal Injury and Abnormalities	Non-hematological solid tumor	2.58E-86		1.196	↓A1CF, ↑A2M, ↓ABAT, ↑ABCA12, ↑AB... ...all 1281	1281
Inflammatory Response,Organismal Injury and Abnor...	Inflammation of body cavity	6.29E-86		-1.016	↓ABAT, ↑ABCA12, ↓ABCB1, ↓ABCB11,↓... ...all 325	325
Cellular Movement,Hematological System Developm...	Cell movement of leukocytes	3.91E-84	Increased	7.116	↓ABCB1, ↓ACKR2, ↑ACSL4, ↑ADAM19,↑... ...all 279	279
Cellular Movement	Cell movement	1.20E-83	Increased	8.706	↑A2M, ↓ABCB1, ↓ACKR2, ↑ACKR4, ↑AC... ...all 525	525
Cancer,Organismal Injury and Abnormalities	Nonhematologic malignant neoplasm	1.71E-83		1.410	↓A1CF, ↑A2M, ↓ABAT, ↑ABCA12, ↑AB... ...all 1276	1276
Cellular Movement	Migration of cells	2.12E-83	Increased	8.739	↑A2M, ↓ABCB1, ↓ACKR2, ↑ACSL4, ↑AD... ...all 494	494
Cancer,Organismal Injury and Abnormalities	Solid tumor	2.45E-82	Increased	3.829	↓A1CF, ↑A2M, ↓ABAT, ↑ABCA12, ↑AB... ...all 1290	1290
Immunological Disease,Organismal Injury and Abnor...	Systemic autoimmune syndrome	2.40E-81		-1.091	↓ABCB1, ↓ACADM, ↓ACAT1, ↑ACSL1, ↑... ...all 356	356
Cancer,Organismal Injury and Abnormalities	Non-melanoma solid tumor	2.70E-81	Increased	2.107	↓A1CF, ↑A2M, ↓ABAT, ↑ABCA12, ↑AB... ...all 1273	1273

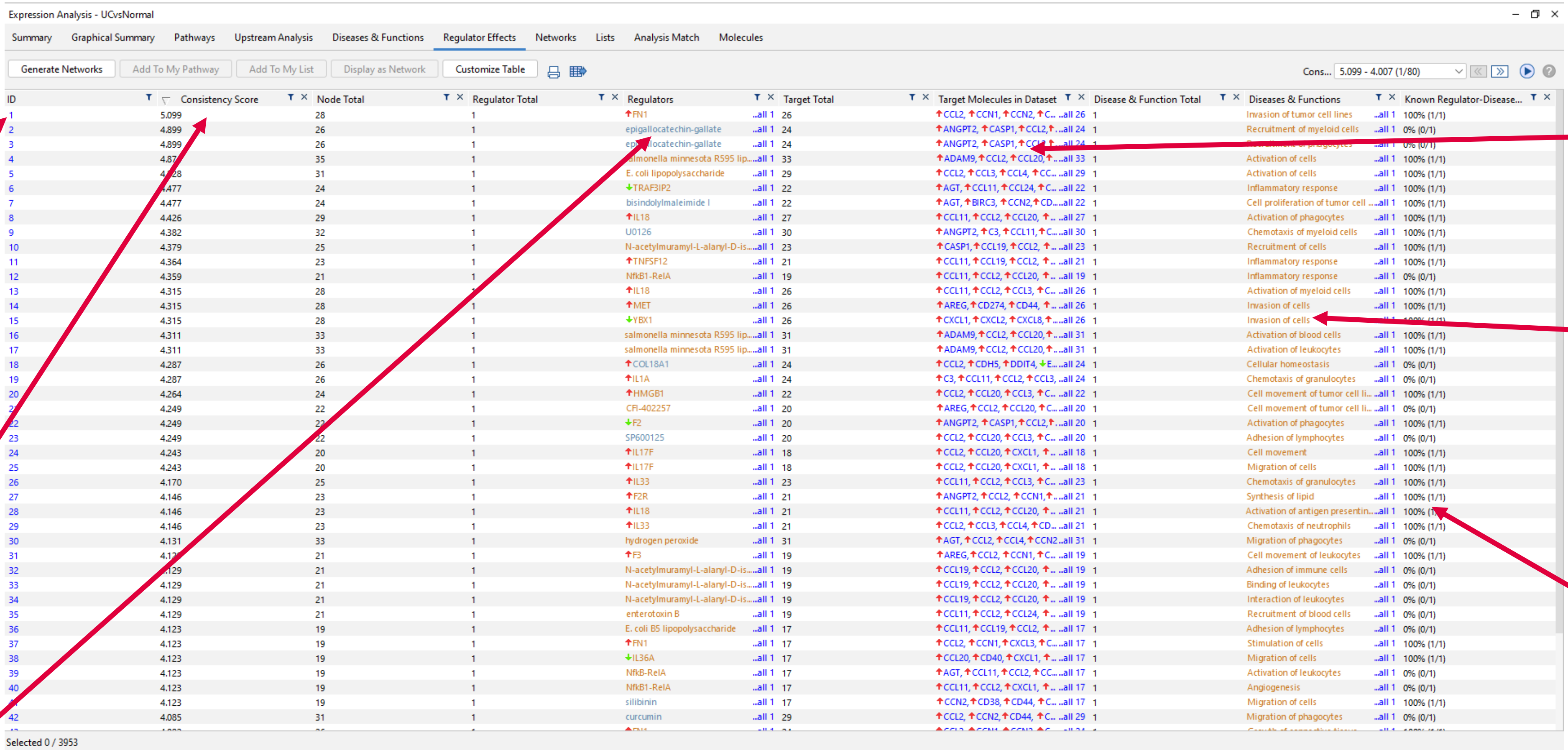
Diseases and functions that may be key to the biology in your experimental data based on patterns of expression observed

Regulator Effects Tab

Network of molecules and regulators that are predicted to be involved in diseases & functions

How matching your data is with the expected directions in IPA for the diseases & functions they're predicted to effect

Regulators involved in network



Expression Analysis - UCvsNormal

Cons... 5.099 - 4.007 (1/80)

ID	Consistency Score	Node Total	Regulator Total	Regulators	Target Total	Target Molecules in Dataset	Disease & Function Total	Diseases & Functions	Known Regulator-Disease...
1	5.099	28	1	↑FN1 …all 1	26	↑CCL2, ↑CCN1, ↑CCN2, ↑C… …all 26	1	Invasion of tumor cell lines …all 1	100% (1/1)
2	4.899	26	1	epigallocatechin-gallate …all 1	24	↑ANGPT2, ↑CASP1, ↑CCL2, ↑. …all 24	1	Recruitment of myeloid cells …all 1	0% (0/1)
3	4.899	26	1	epigallocatechin-gallate …all 1	24	↑ANGPT2, ↑CASP1, ↑CC[illegible] …all 24	1	Recruitment of phagocytes …all 1	0% (0/1)
4	4.87[illegible]	35	1	salmonella minnesota R595 lip… …all 1	33	↑ADAM9, ↑CCL2, ↑CCL20, ↑.. …all 33	1	Activation of cells …all 1	100% (1/1)
5	4.[illegible]28	31	1	E. coli lipopolysaccharide …all 1	29	↑CCL2, ↑CCL3, ↑CCL4, ↑CC… …all 29	1	Activation of cells …all 1	100% (1/1)
6	4.477	24	1	↓TRAF3IP2 …all 1	22	↑AGT, ↑CCL11, ↑CCL24, ↑C… …all 22	1	Inflammatory response …all 1	100% (1/1)
7	4.477	24	1	bisindolylmaleimide I …all 1	22	↑AGT, ↑BIRC3, ↑CCN2, ↑CD… …all 22	1	Cell proliferation of tumor cell … …all 1	100% (1/1)
8	4.426	29	1	↑IL18 …all 1	27	↑CCL11, ↑CCL2, ↑CCL20, ↑… …all 27	1	Activation of phagocytes …all 1	100% (1/1)
9	4.382	32	1	U0126 …all 1	30	↑ANGPT2, ↑C3, ↑CCL11, ↑C… …all 30	1	Chemotaxis of myeloid cells …all 1	100% (1/1)
10	4.379	25	1	N-acetylmuramyl-L-alanyl-D-is… …all 1	23	↑CASP1, ↑CCL19, ↑CCL2, ↑… …all 23	1	Recruitment of cells …all 1	100% (1/1)
11	4.364	23	1	↑TNFSF12 …all 1	21	↑CCL11, ↑CCL19, ↑CCL2, ↑… …all 21	1	Inflammatory response …all 1	100% (1/1)
12	4.359	21	1	NfkB1-RelA …all 1	19	↑CCL11, ↑CCL2, ↑CCL20, ↑… …all 19	1	Inflammatory response …all 1	0% (0/1)
13	4.315	28	1	↑IL18 …all 1	26	↑CCL11, ↑CCL2, ↑CCL3, ↑C… …all 26	1	Activation of myeloid cells …all 1	100% (1/1)
14	4.315	28	1	↑MET …all 1	26	↑AREG, ↑CD274, ↑CD44, ↑… …all 26	1	Invasion of cells …all 1	100% (1/1)
15	4.315	28	1	↓YBX1 …all 1	26	↑CXCL1, ↑CXCL2, ↑CXCL8, ↑… …all 26	1	Invasion of cells …all 1	100% (1/1)
16	4.311	33	1	salmonella minnesota R595 lip… …all 1	31	↑ADAM9, ↑CCL2, ↑CCL20, ↑.. …all 31	1	Activation of blood cells …all 1	100% (1/1)
17	4.311	33	1	salmonella minnesota R595 lip… …all 1	31	↑ADAM9, ↑CCL2, ↑CCL20, ↑.. …all 31	1	Activation of leukocytes …all 1	100% (1/1)
18	4.287	26	1	↑COL18A1 …all 1	24	↑CCL2, ↑CDH5, ↑DDIT4, ↓E… …all 24	1	Cellular homeostasis …all 1	0% (0/1)
19	4.287	26	1	↑IL1A …all 1	24	↑C3, ↑CCL11, ↑CCL2, ↑CCL3, …all 24	1	Chemotaxis of granulocytes …all 1	0% (0/1)
20	4.264	24	1	↑HMGB1 …all 1	22	↑CCL2, ↑CCL20, ↑CCL3, ↑C… …all 22	1	Cell movement of tumor cell li… …all 1	100% (1/1)
21	4.249	22	1	CFI-402257 …all 1	20	↑AREG, ↑CCL2, ↑CCL20, ↑C… …all 20	1	Cell movement of tumor cell li… …all 1	0% (0/1)
22	4.249	22	1	↓F2 …all 1	20	↑ANGPT2, ↑CASP1, ↑CCL2, ↑. …all 20	1	Activation of phagocytes …all 1	100% (1/1)
23	4.249	22	1	SP600125 …all 1	20	↑CCL2, ↑CCL20, ↑CCL3, ↑C… …all 20	1	Adhesion of lymphocytes …all 1	0% (0/1)
24	4.243	20	1	↑IL17F …all 1	18	↑CCL2, ↑CCL20, ↑CXCL1, ↑… …all 18	1	Cell movement …all 1	100% (1/1)
25	4.243	20	1	↑IL17F …all 1	18	↑CCL2, ↑CCL20, ↑CXCL1, ↑… …all 18	1	Migration of cells …all 1	100% (1/1)
26	4.170	25	1	↑IL33 …all 1	23	↑CCL11, ↑CCL2, ↑CCL3, ↑C… …all 23	1	Chemotaxis of granulocytes …all 1	100% (1/1)
27	4.146	23	1	↑F2R …all 1	21	↑ANGPT2, ↑CCL2, ↑CCN1, ↑.. …all 21	1	Synthesis of lipid …all 1	100% (1/1)
28	4.146	23	1	↑IL18 …all 1	21	↑CCL11, ↑CCL2, ↑CCL20, ↑… …all 21	1	Activation of antigen presentin… …all 1	100% (1/1)
29	4.146	23	1	↑IL33 …all 1	21	↑CCL2, ↑CCL3, ↑CCL4, ↑CD… …all 21	1	Chemotaxis of neutrophils …all 1	100% (1/1)
30	4.131	33	1	hydrogen peroxide …all 1	31	↑AGT, ↑CCL2, ↑CCL4, ↑CCN2 …all 31	1	Migration of phagocytes …all 1	0% (0/1)
31	4.12[illegible]	21	1	↑F3 …all 1	19	↑AREG, ↑CCL2, ↑CCN1, ↑C… …all 19	1	Cell movement of leukocytes …all 1	100% (1/1)
32	4.129	21	1	N-acetylmuramyl-L-alanyl-D-is… …all 1	19	↑CCL19, ↑CCL2, ↑CCL20, ↑… …all 19	1	Adhesion of immune cells …all 1	0% (0/1)
33	4.129	21	1	N-acetylmuramyl-L-alanyl-D-is… …all 1	19	↑CCL19, ↑CCL2, ↑CCL20, ↑… …all 19	1	Binding of leukocytes …all 1	0% (0/1)
34	4.129	21	1	N-acetylmuramyl-L-alanyl-D-is… …all 1	19	↑CCL19, ↑CCL2, ↑CCL20, ↑… …all 19	1	Interaction of leukocytes …all 1	0% (0/1)
35	4.129	21	1	enterotoxin B …all 1	19	↑CCL11, ↑CCL2, ↑CCL24, ↑… …all 19	1	Recruitment of blood cells …all 1	0% (0/1)
36	4.123	19	1	E. coli B5 lipopolysaccharide …all 1	17	↑CCL11, ↑CCL19, ↑CCL2, ↑… …all 17	1	Adhesion of lymphocytes …all 1	0% (0/1)
37	4.123	19	1	↑FN1 …all 1	17	↑CCL2, ↑CCN1, ↑CXCL3, ↑C… …all 17	1	Stimulation of cells …all 1	100% (1/1)
38	4.123	19	1	↓IL36A …all 1	17	↑CCL20, ↑CD40, ↑CXCL1, ↑… …all 17	1	Migration of cells …all 1	100% (1/1)
39	4.123	19	1	NfkB-RelA …all 1	17	↑AGT, ↑CCL11, ↑CCL2, ↑CC… …all 17	1	Activation of leukocytes …all 1	0% (0/1)
40	4.123	19	1	NfkB1-RelA …all 1	17	↑CCL11, ↑CCL2, ↑CXCL1, ↑… …all 17	1	Angiogenesis …all 1	0% (0/1)
41	4.123	19	1	silibinin …all 1	17	↑CCN2, ↑CD38, ↑CD44, ↑C… …all 17	1	Migration of cells …all 1	100% (1/1)
42	4.085	31	1	curcumin …all 1	29	↑CCL2, ↑CCN2, ↑CD44, ↑C… …all 29	1	Migration of phagocytes …all 1	0% (0/1)

Selected 0 / 3953

Genes from dataset involved in disease or function

Disease or function

Known connections in IPA between regulator and disease & function-discover novel relationships

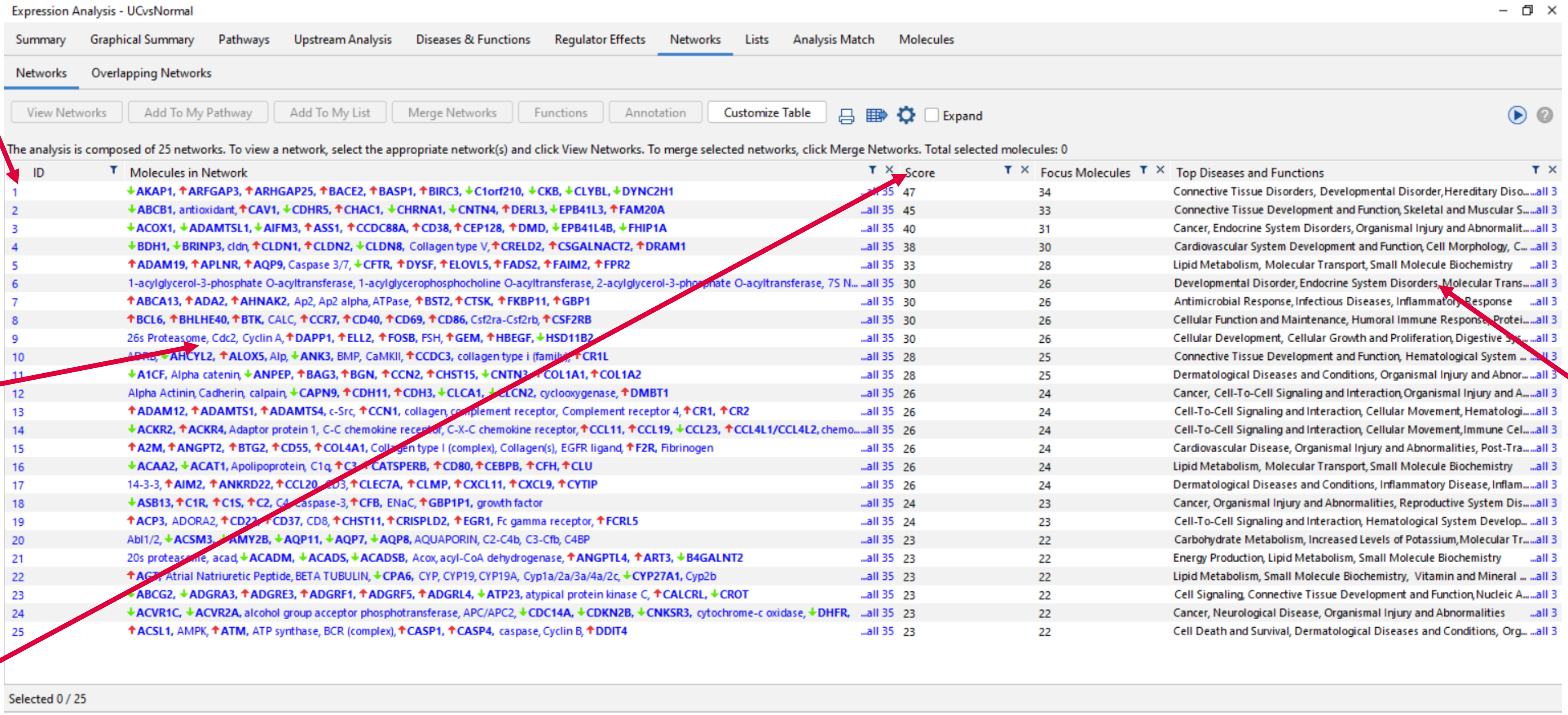
Ties dataset molecules and regulators to a predicted phenotypic outcome

Networks Tab

Network of highly connected molecules, click to open network map

Molecule in **bold** is in your dataset; unbolded have been added to maximize connectivity

Based on a p-value calculation how likely molecules exist as part of a network than chance alone



The analysis is composed of 25 networks. To view a network, select the appropriate network(s) and click View Networks. To merge selected networks, click Merge Networks. Total selected molecules: 0

ID	Molecules in Network	Score	Focus Molecules	Top Diseases and Functions
1	↓**AKAP1**, ↑**ARFGAP3**, ↑**ARHGAP25**, ↑**BACE2**, ↑**BASP1**, ↑**BIRC3**, ↓**C1orf210**, ↓**CKB**, ↓**CLYBL**, ↓**DYNC2H1** ...all 35	47	34	Connective Tissue Disorders, Developmental Disorder, Hereditary Diso... ...all 3
2	↓**ABCB1**, antioxidant, ↑**CAV1**, ↓**CDHR5**, ↑**CHAC1**, ↓**CHRNA1**, ↓**CNTN4**, ↑**DERL3**, ↓**EPB41L3**, ↑**FAM20A** ...all 35	45	33	Connective Tissue Development and Function, Skeletal and Muscular S... ...all 3
3	↓**ACOX1**, ↓**ADAMTSL1**, ↓**AIFM3**, ↑**ASS1**, ↑**CCDC88A**, ↑**CD38**, ↑**CEP128**, ↑**DMD**, ↓**EPB41L4B**, ↓**FHIP1A** ...all 35	40	31	Cancer, Endocrine System Disorders, Organismal Injury and Abnormalit... ...all 3
4	↓**BDH1**, ↓**BRINP3**, cldn, ↑**CLDN1**, ↑**CLDN2**, ↓**CLDN8**, Collagen type V, ↑**CRELD2**, ↑**CSGALNACT2**, ↑**DRAM1** ...all 35	38	30	Cardiovascular System Development and Function, Cell Morphology, C... ...all 3
5	↑**ADAM19**, ↑**APLNR**, ↑**AQP9**, Caspase 3/7, ↓**CFTR**, ↑**DYSF**, ↑**ELOVL5**, ↑**FADS2**, ↑**FAIM2**, ↑**FPR2** ...all 35	33	28	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry ...all 3
6	1-acylglycerol-3-phosphate O-acyltransferase, 1-acylglycerophosphocholine O-acyltransferase, 2-acylglycerol-3-phosphate O-acyltransferase, 7S N... ...all 35	30	26	Developmental Disorder, Endocrine System Disorders, Molecular Trans... ...all 3
7	↑**ABCA13**, ↑**ADA2**, ↑**AHNAK2**, Ap2, Ap2 alpha, ATPase, ↑**BST2**, ↑**CTSK**, ↑**FKBP11**, ↑**GBP1** ...all 35	30	26	Antimicrobial Response, Infectious Diseases, Inflammatory Response ...all 3
8	↑**BCL6**, ↑**BHLHE40**, ↑**BTK**, CALC, ↑**CCR7**, ↑**CD40**, ↑**CD69**, ↑**CD86**, Csf2ra-Csf2rb, ↑**CSF2RB** ...all 35	30	26	Cellular Function and Maintenance, Humoral Immune Response, Protei... ...all 3
9	26s Proteasome, Cdc2, Cyclin A, ↑**DAPP1**, ↑**ELL2**, ↑**FOSB**, FSH, ↑**GEM**, ↑**HBEGF**, ↓**HSD11B2** ...all 35	30	26	Cellular Development, Cellular Growth and Proliferation, Digestive Sys... ...all 3
10	ADRB, ↓**AHCYL2**, ↑**ALOX5**, Alp, ↓**ANK3**, BMP, CaMKII, ↑**CCDC3**, collagen type i (family), ↑**CR1L** ...all 35	28	25	Connective Tissue Development and Function, Hematological System ... ...all 3
11	↓**A1CF**, Alpha catenin, ↓**ANPEP**, ↑**BAG3**, ↑**BGN**, ↑**CCN2**, ↑**CHST15**, ↓**CNTN3**, ↑**COL1A1**, ↑**COL1A2** ...all 35	28	25	Dermatological Diseases and Conditions, Organismal Injury and Abnor... ...all 3
12	Alpha Actinin, Cadherin, calpain, ↓**CAPN9**, ↑**CDH11**, ↑**CDH3**, ↓**CLCA1**, ↓**CLCN2**, cyclooxygenase, ↑**DMBT1** ...all 35	26	24	Cancer, Cell-To-Cell Signaling and Interaction, Organismal Injury and A... ...all 3
13	↑**ADAM12**, ↑**ADAMTS1**, ↑**ADAMTS4**, c-Src, ↑**CCN1**, collagen, complement receptor, Complement receptor 4, ↑**CR1**, ↑**CR2** ...all 35	26	24	Cell-To-Cell Signaling and Interaction, Cellular Movement, Hematologi... ...all 3
14	↓**ACKR2**, ↑**ACKR4**, Adaptor protein 1, C-C chemokine receptor, C-X-C chemokine receptor, ↑**CCL11**, ↑**CCL19**, ↓**CCL23**, ↑**CCL4L1/CCL4L2**, chemo... ...all 35	26	24	Cell-To-Cell Signaling and Interaction, Cellular Movement, Immune Cel... ...all 3
15	↑**A2M**, ↑**ANGPT2**, ↑**BTG2**, ↑**CD55**, ↑**COL4A1**, Collagen type I (complex), Collagen(s), EGFR ligand, ↑**F2R**, Fibrinogen ...all 35	26	24	Cardiovascular Disease, Organismal Injury and Abnormalities, Post-Tra... ...all 3
16	↓**ACAA2**, ↓**ACAT1**, Apolipoprotein, C1q, ↑**C3**, ↑**CATSPERB**, ↑**CD80**, ↑**CEBPB**, ↑**CFH**, ↑**CLU** ...all 35	26	24	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry ...all 3
17	14-3-3, ↑**AIM2**, ↑**ANKRD22**, ↑**CCL20**, CD3, ↑**CLEC7A**, ↑**CLMP**, ↑**CXCL11**, ↑**CXCL9**, ↑**CYTIP** ...all 35	26	24	Dermatological Diseases and Conditions, Inflammatory Disease, Inflam... ...all 3
18	↓**ASB13**, ↑**C1R**, ↑**C1S**, ↑**C2**, C4, Caspase-3, ↑**CFB**, ENaC, ↑**GBP1P1**, growth factor ...all 35	24	23	Cancer, Organismal Injury and Abnormalities, Reproductive System Dis... ...all 3
19	↑**ACP3**, ADORA2, ↑**CD22**, ↑**CD37**, CD8, ↑**CHST11**, ↑**CRISPLD2**, ↑**EGR1**, Fc gamma receptor, ↑**FCRL5** ...all 35	24	23	Cell-To-Cell Signaling and Interaction, Hematological System Develop... ...all 3
20	Abl1/2, ↓**ACSM3**, ↓**AMY2B**, ↓**AQP11**, ↓**AQP7**, ↓**AQP8**, AQUAPORIN, C2-C4b, C3-Cfb, C4BP ...all 35	23	22	Carbohydrate Metabolism, Increased Levels of Potassium, Molecular Tr... ...all 3
21	20s proteasome, acad, ↓**ACADM**, ↓**ACADS**, ↓**ACADSB**, Acox, acyl-CoA dehydrogenase, ↑**ANGPTL4**, ↑**ART3**, ↓**B4GALNT2** ...all 35	23	22	Energy Production, Lipid Metabolism, Small Molecule Biochemistry ...all 3
22	↑**AGT**, Atrial Natriuretic Peptide, BETA TUBULIN, ↓**CPA6**, CYP, CYP19, CYP19A, Cyp1a/2a/3a/4a/2c, ↓**CYP27A1**, Cyp2b ...all 35	23	22	Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral ... ...all 3
23	↓**ABCG2**, ↓**ADGRA3**, ↑**ADGRE3**, ↑**ADGRF1**, ↑**ADGRF5**, ↑**ADGRL4**, ↓**ATP23**, atypical protein kinase C, ↑**CALCRL**, ↓**CROT** ...all 35	23	22	Cell Signaling, Connective Tissue Development and Function, Nucleic A... ...all 3
24	↓**ACVR1C**, ↓**ACVR2A**, alcohol group acceptor phosphotransferase, APC/APC2, ↓**CDC14A**, ↓**CDKN2B**, ↓**CNKSR3**, cytochrome-c oxidase, ↓**DHFR**, ...all 35	23	22	Cancer, Neurological Disease, Organismal Injury and Abnormalities ...all 3
25	↑**ACSL1**, AMPK, ↑**ATM**, ATP synthase, BCR (complex), ↑**CASP1**, ↑**CASP4**, caspase, Cyclin B, ↑**DDIT4** ...all 35	23	22	Cell Death and Survival, Dermatological Diseases and Conditions, Org... ...all 3

Selected 0 / 25

Disease or function predicted to be an outcome

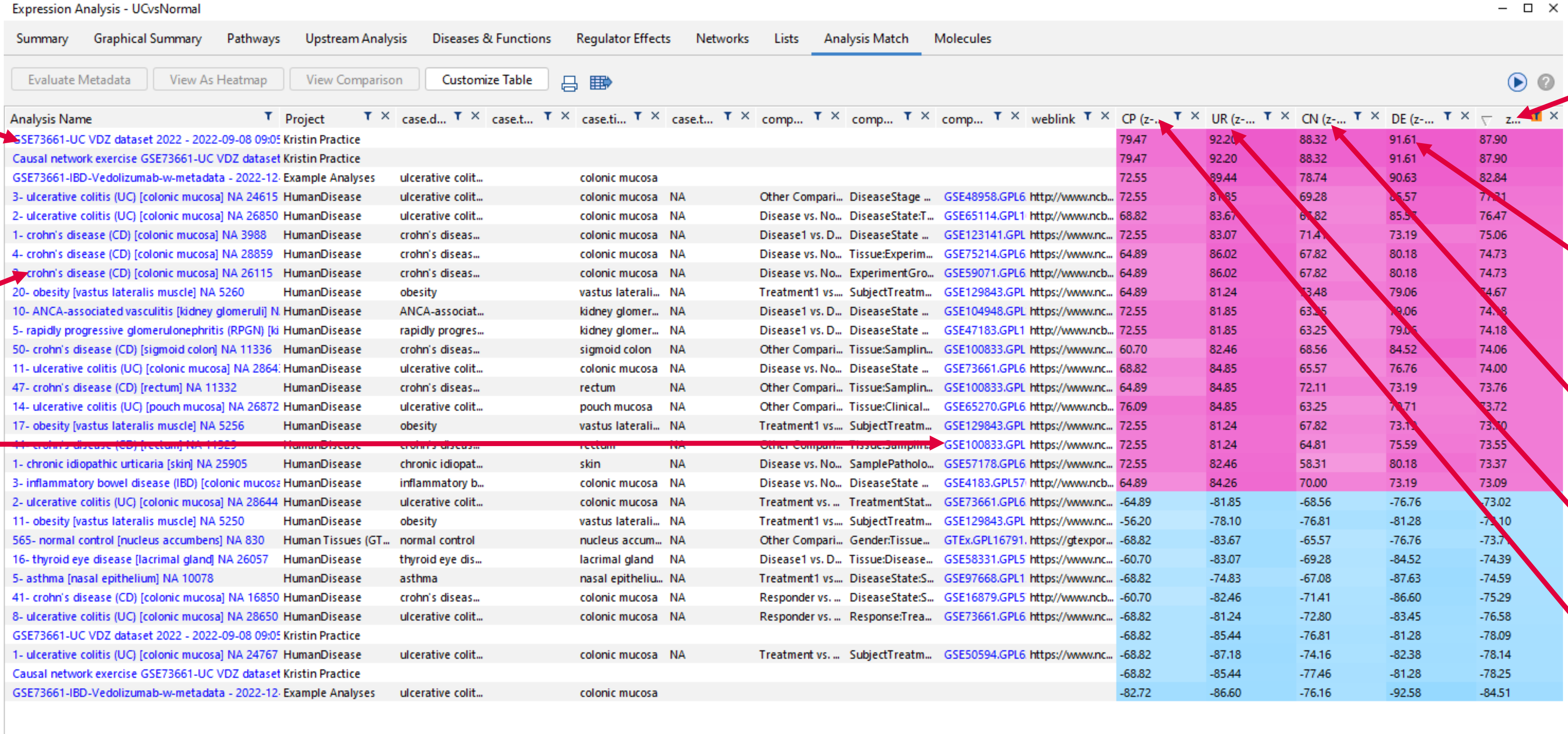
Networks constructed from your dataset with level of connectivity prioritized

Analysis Match Tab

Public and previously run analyses with matching or antimatching results

Double click to open core analysis

Link to Land Explorer to view volcano plot of comparison



Analysis Name	Project	case.d...	case.t...	case.ti...	case.t...	comp...	comp...	comp...	weblink	CP (z-...	UR (z-...	CN (z-...	DE (z-...	z...
GSE73661-UC VDZ dataset 2022 - 2022-09-08 09:05	Kristin Practice									79.47	92.20	88.32	91.61	87.90
Causal network exercise GSE73661-UC VDZ dataset	Kristin Practice									79.47	92.20	88.32	91.61	87.90
GSE73661-IBD-Vedolizumab-w-metadata - 2022-12-	Example Analyses	ulcerative colit...		colonic mucosa						72.55	89.44	78.74	90.63	82.84
3- ulcerative colitis (UC) [colonic mucosa] NA 24615	HumanDisease	ulcerative colit...		colonic mucosa	NA	Other Compari...	DiseaseStage ...	GSE48958.GPL6	http://www.ncb...	72.55	81.85	69.28	85.57	77.31
2- ulcerative colitis (UC) [colonic mucosa] NA 26850	HumanDisease	ulcerative colit...		colonic mucosa	NA	Disease vs. No...	DiseaseState:T...	GSE65114.GPL1	http://www.ncb...	68.82	83.67	67.82	85.57	76.47
1- crohn's disease (CD) [colonic mucosa] NA 3988	HumanDisease	crohn's diseas...		colonic mucosa	NA	Disease1 vs. D...	DiseaseState ...	GSE123141.GPL	https://www.nc...	72.55	83.07	71.41	73.19	75.06
4- crohn's disease (CD) [colonic mucosa] NA 28859	HumanDisease	crohn's diseas...		colonic mucosa	NA	Disease vs. No...	Tissue:Experim...	GSE75214.GPL6	https://www.nc...	64.89	86.02	67.82	80.18	74.73
2- crohn's disease (CD) [colonic mucosa] NA 26115	HumanDisease	crohn's diseas...		colonic mucosa	NA	Disease vs. No...	ExperimentGro...	GSE59071.GPL6	http://www.ncb...	64.89	86.02	67.82	80.18	74.73
20- obesity [vastus lateralis muscle] NA 5260	HumanDisease	obesity		vastus laterali...	NA	Treatment1 vs....	SubjectTreatm...	GSE129843.GPL	https://www.nc...	64.89	81.24	73.48	79.06	74.67
10- ANCA-associated vasculitis [kidney glomeruli] N.	HumanDisease	ANCA-associat...		kidney glomer...	NA	Disease1 vs. D...	DiseaseState ...	GSE104948.GPL	https://www.nc...	72.55	81.85	63.25	79.06	74.18
5- rapidly progressive glomerulonephritis (RPGN) [ki	HumanDisease	rapidly progres...		kidney glomer...	NA	Disease1 vs. D...	DiseaseState ...	GSE47183.GPL1	http://www.ncb...	72.55	81.85	63.25	79.06	74.18
50- crohn's disease (CD) [sigmoid colon] NA 11336	HumanDisease	crohn's diseas...		sigmoid colon	NA	Other Compari...	Tissue:Samplin...	GSE100833.GPL	https://www.nc...	60.70	82.46	68.56	84.52	74.06
11- ulcerative colitis (UC) [colonic mucosa] NA 2864:	HumanDisease	ulcerative colit...		colonic mucosa	NA	Disease vs. No...	DiseaseState ...	GSE73661.GPL6	https://www.nc...	68.82	84.85	65.57	76.76	74.00
47- crohn's disease (CD) [rectum] NA 11332	HumanDisease	crohn's diseas...		rectum	NA	Other Compari...	Tissue:Samplin...	GSE100833.GPL	https://www.nc...	64.89	84.85	72.11	73.19	73.76
14- ulcerative colitis (UC) [pouch mucosa] NA 26872	HumanDisease	ulcerative colit...		pouch mucosa	NA	Other Compari...	Tissue:Clinical...	GSE65270.GPL6	http://www.ncb...	76.09	84.85	63.25	78.71	73.72
17- obesity [vastus lateralis muscle] NA 5256	HumanDisease	obesity		vastus laterali...	NA	Treatment1 vs....	SubjectTreatm...	GSE129843.GPL	https://www.nc...	72.55	81.24	67.82	73.19	73.70
44- crohn's disease (CD) [rectum] NA 11329	HumanDisease	crohn's diseas...		rectum	NA	Other Compari...	Tissue:Samplin...	GSE100833.GPL	https://www.nc...	72.55	81.24	64.81	75.59	73.55
1- chronic idiopathic urticaria [skin] NA 25905	HumanDisease	chronic idiopat...		skin	NA	Disease vs. No...	SamplePatholo...	GSE57178.GPL6	https://www.nc...	72.55	82.46	58.31	80.18	73.37
3- inflammatory bowel disease (IBD) [colonic mucosa	HumanDisease	inflammatory b...		colonic mucosa	NA	Disease vs. No...	DiseaseState ...	GSE4183.GPL57	http://www.ncb...	64.89	84.26	70.00	73.19	73.09
2- ulcerative colitis (UC) [colonic mucosa] NA 28644	HumanDisease	ulcerative colit...		colonic mucosa	NA	Treatment vs. ...	TreatmentStat...	GSE73661.GPL6	https://www.nc...	-64.89	-81.85	-68.56	-76.76	-73.02
11- obesity [vastus lateralis muscle] NA 5250	HumanDisease	obesity		vastus laterali...	NA	Treatment1 vs....	SubjectTreatm...	GSE129843.GPL	https://www.nc...	-56.20	-78.10	-76.81	-81.28	-73.10
565- normal control [nucleus accumbens] NA 830	Human Tissues (GT...	normal control		nucleus accum...	NA	Other Compari...	Gender:Tissue...	GTEx.GPL16791.	https://gtexpor...	-68.82	-83.67	-65.57	-76.76	-73.71
16- thyroid eye disease [lacrimal gland] NA 26057	HumanDisease	thyroid eye dis...		lacrimal gland	NA	Disease1 vs. D...	Tissue:Disease...	GSE58331.GPL5	https://www.nc...	-60.70	-83.07	-69.28	-84.52	-74.39
5- asthma [nasal epithelium] NA 10078	HumanDisease	asthma		nasal epitheliu...	NA	Treatment1 vs....	DiseaseState:S...	GSE97668.GPL1	https://www.nc...	-68.82	-74.83	-67.08	-87.63	-74.59
41- crohn's disease (CD) [colonic mucosa] NA 16850	HumanDisease	crohn's diseas...		colonic mucosa	NA	Responder vs. ...	DiseaseState:S...	GSE16879.GPL5	http://www.ncb...	-60.70	-82.46	-71.41	-86.60	-75.29
8- ulcerative colitis (UC) [colonic mucosa] NA 28650	HumanDisease	ulcerative colit...		colonic mucosa	NA	Responder vs. ...	Response:Trea...	GSE73661.GPL6	https://www.nc...	-68.82	-81.24	-72.80	-83.45	-76.58
GSE73661-UC VDZ dataset 2022 - 2022-09-08 09:05	Kristin Practice									-68.82	-85.44	-76.81	-81.28	-78.09
1- ulcerative colitis (UC) [colonic mucosa] NA 24767	HumanDisease	ulcerative colit...		colonic mucosa	NA	Treatment vs. ...	SubjectTreatm...	GSE50594.GPL6	https://www.nc...	-68.82	-87.18	-74.16	-82.38	-78.14
Causal network exercise GSE73661-UC VDZ dataset	Kristin Practice									-68.82	-85.44	-77.46	-81.28	-78.25
GSE73661-IBD-Vedolizumab-w-metadata - 2022-12-	Example Analyses	ulcerative colit...		colonic mucosa						-82.72	-86.60	-76.16	-92.58	-84.51

Average z-score from all 4 analysis features

DE: Downstream effects (i.e. diseases and functions

CN: Causal Networks

UR: Upstream Regulators

CP: Canonical Pathways

Matches your core analysis against public datasets in IPA as well as previously run core analyses and returns similar and dissimilar datasets based on 4 core analysis features: CP, UR, CN, DE

****All columns are filterable****

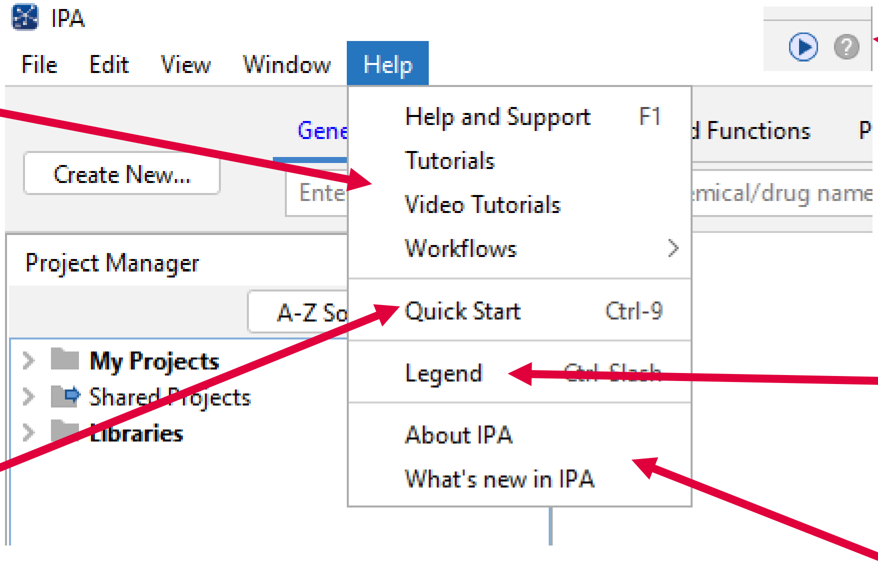
Positive z-score: Pink: matching ***Negative z-score: Blue: antimatching***

IPA Help

IPA Help Resources

Online help, videos, and tutorials

Returns Quick Start menu to your screen with helpful workflow guides



Video and help page tailored to the topic currently visualized

Detailed legend for all colors, shapes, symbols, lines, etc in IPA

Latest news and updates in IPA

Previous webinar and training recordings

https://tv.qiagenbioinformatics.com/

Technical support: ts-bioinformatics@qiagen.com