IPA Introduction and Analysis Match:

Understanding biological mechanisms in transcriptomics or proteomics datasets

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Agenda

What is Ingenuity Pathway Analysis?

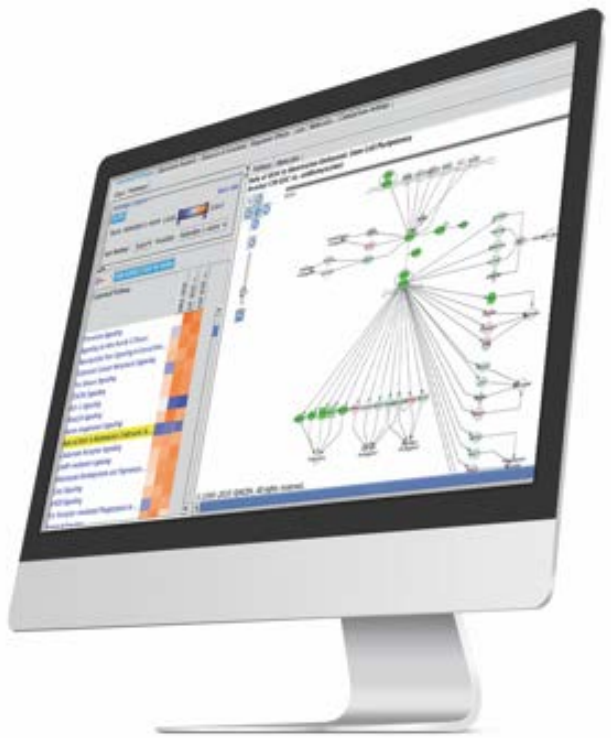
The QIAGEN Knowledge Base powers IPA

How can you find analyses similar or different to yours?

Case Study: Biological effects of gemfibrozil in liver (of rat)

Land Explorer for IPA

Conclusions



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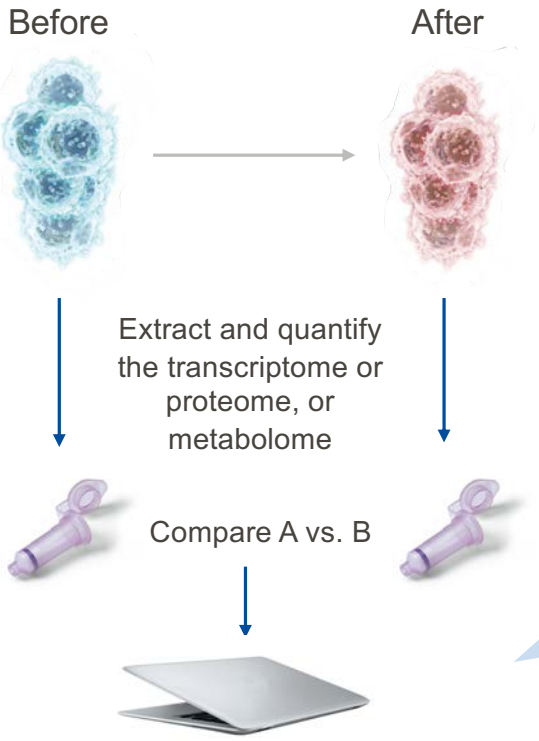
What is Ingenuity Pathway Analysis?

IPA was built to understand the biology of living systems

How do two samples differ from one another biologically?

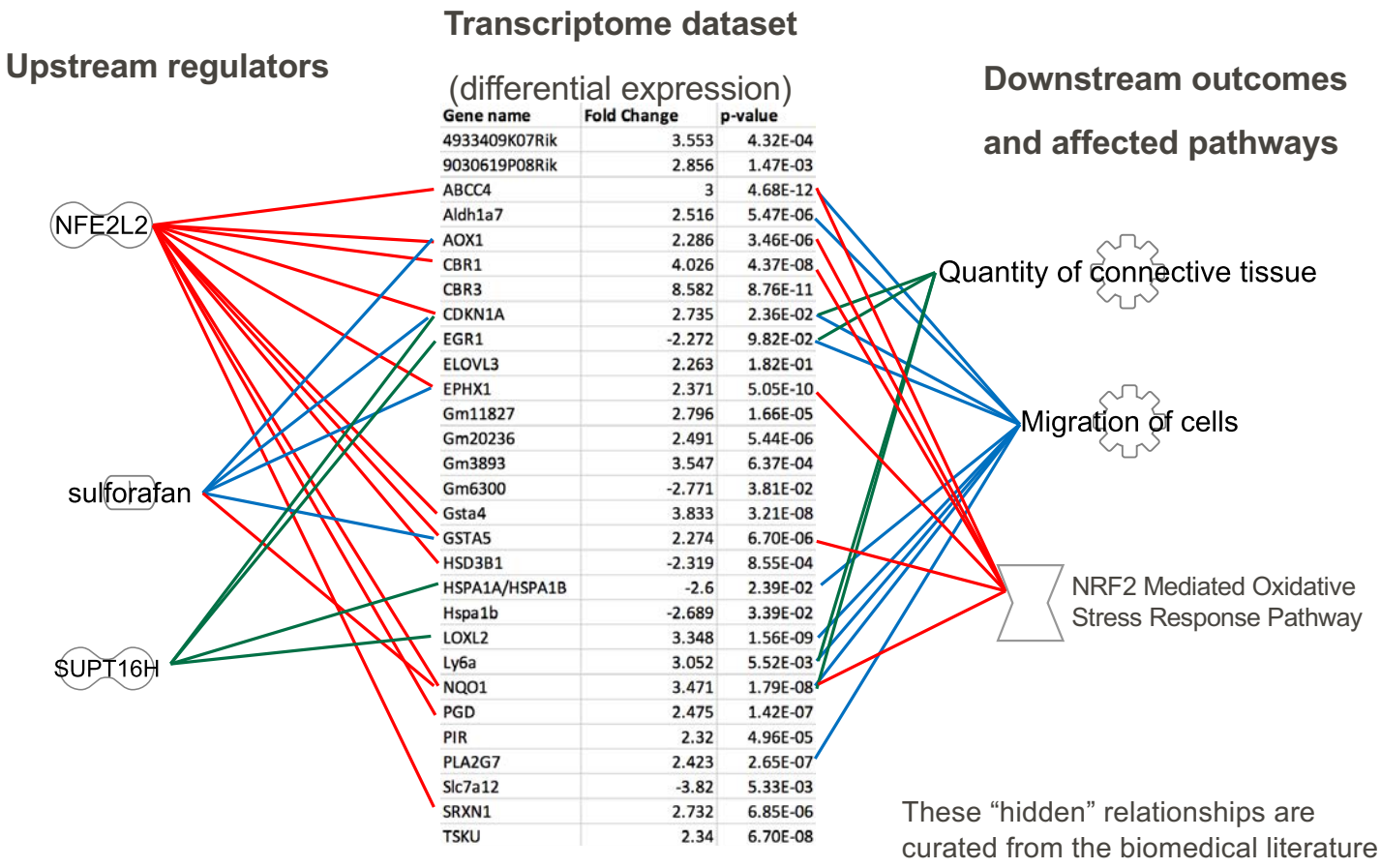


What is the cause and what is the effect?

- What drives the expression changes?
- What effect does that have?
- What well-understood pathways are involved?

- Do I see the biological changes I expect?
- Do the results suggest new hypotheses?
- Are these results unusual or fairly common?

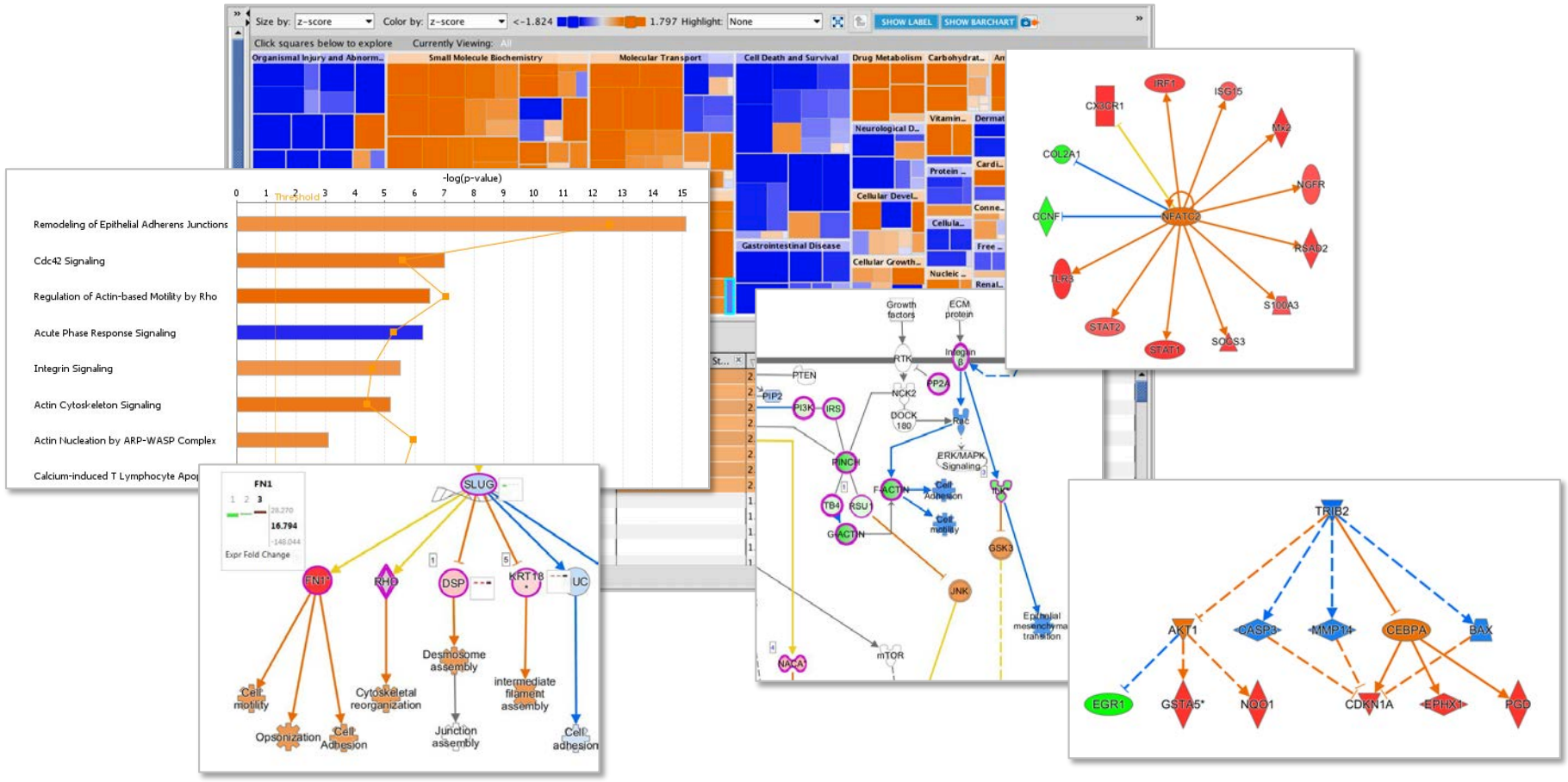
IPA's Knowledge Base identifies the "hidden" information in datasets



Gene name	Fold Change	p-value
4933409K07Rik	3.553	4.32E-04
9030619P08Rik	2.856	1.47E-03
ABCC4	3	4.68E-12
Aldh1a7	2.516	5.47E-06
AOX1	2.286	3.46E-06
CBR1	4.026	4.37E-08
CBR3	8.582	8.76E-11
CDKN1A	2.735	2.36E-02
EGR1	-2.272	9.82E-02
ELOVL3	2.263	1.82E-01
EPHX1	2.371	5.05E-10
Gm11827	2.796	1.66E-05
Gm20236	2.491	5.44E-06
Gm3893	3.547	6.37E-04
Gm6300	-2.771	3.81E-02
Gsta4	3.833	3.21E-08
GSTA5	2.274	6.70E-06
HSD3B1	-2.319	8.55E-04
HSPA1A/HSPA1B	-2.6	2.39E-02
Hspa1b	-2.689	3.39E-02
LOXL2	3.348	1.56E-09
Ly6a	3.052	5.52E-03
NQO1	3.471	1.79E-08
PGD	2.475	1.42E-07
PIR	2.32	4.96E-05
PLA2G7	2.423	2.65E-07
Slc7a12	-3.82	5.33E-03
SRXN1	2.732	6.85E-06
TSKU	2.34	6.70E-08

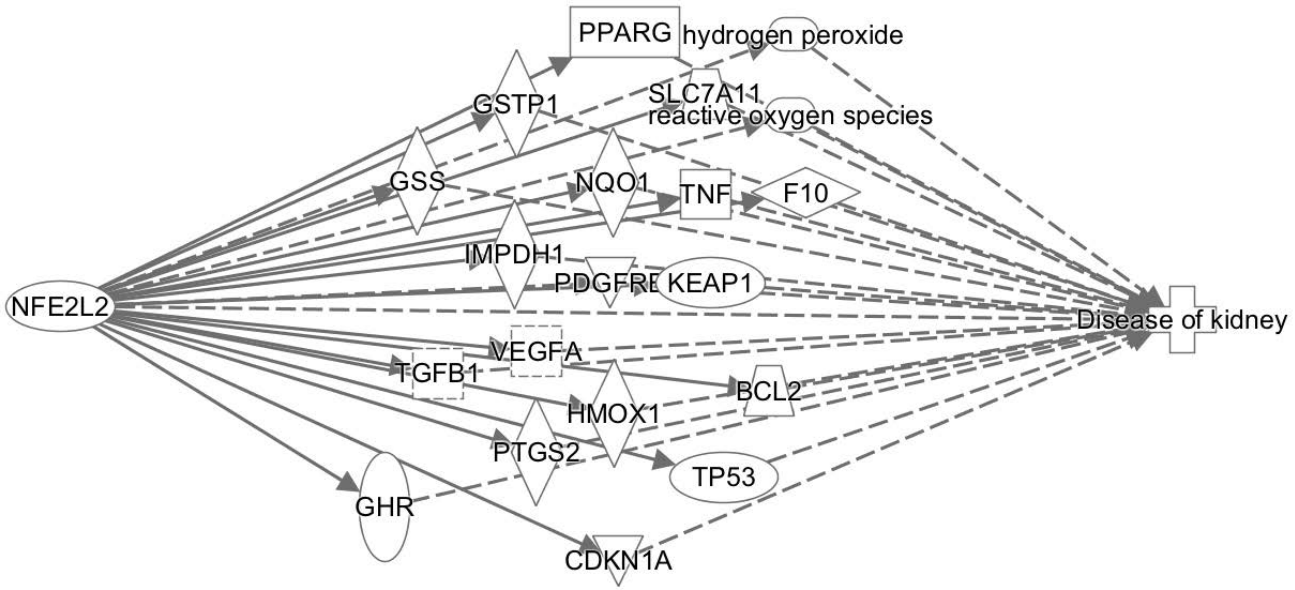
These "hidden" relationships are curated from the biomedical literature

IPA visualizes the hidden biology in a dataset

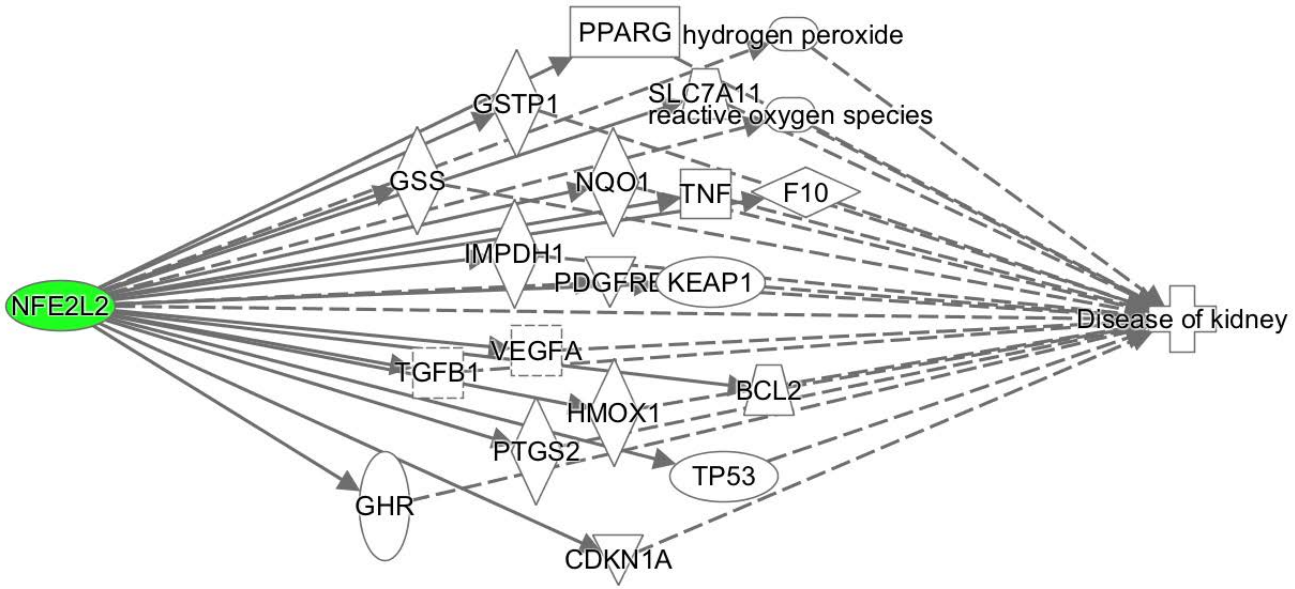


But you don't *need* a dataset to use IPA…

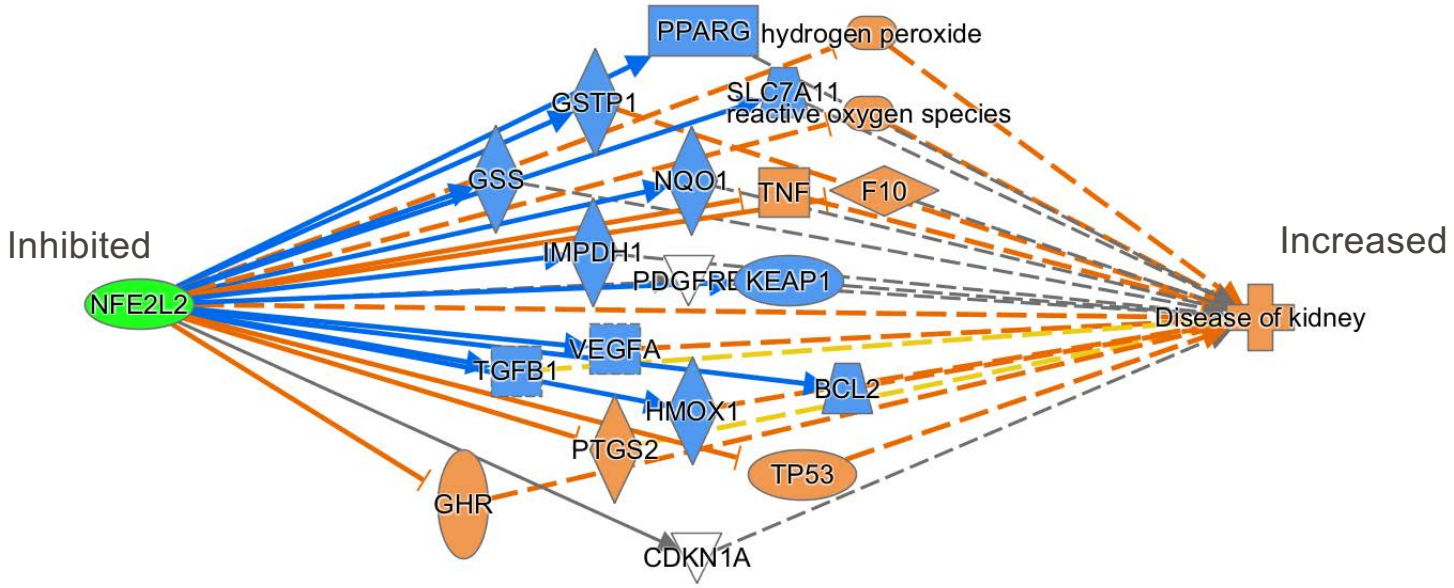
Search and explore (no dataset)



Search and explore (no dataset)

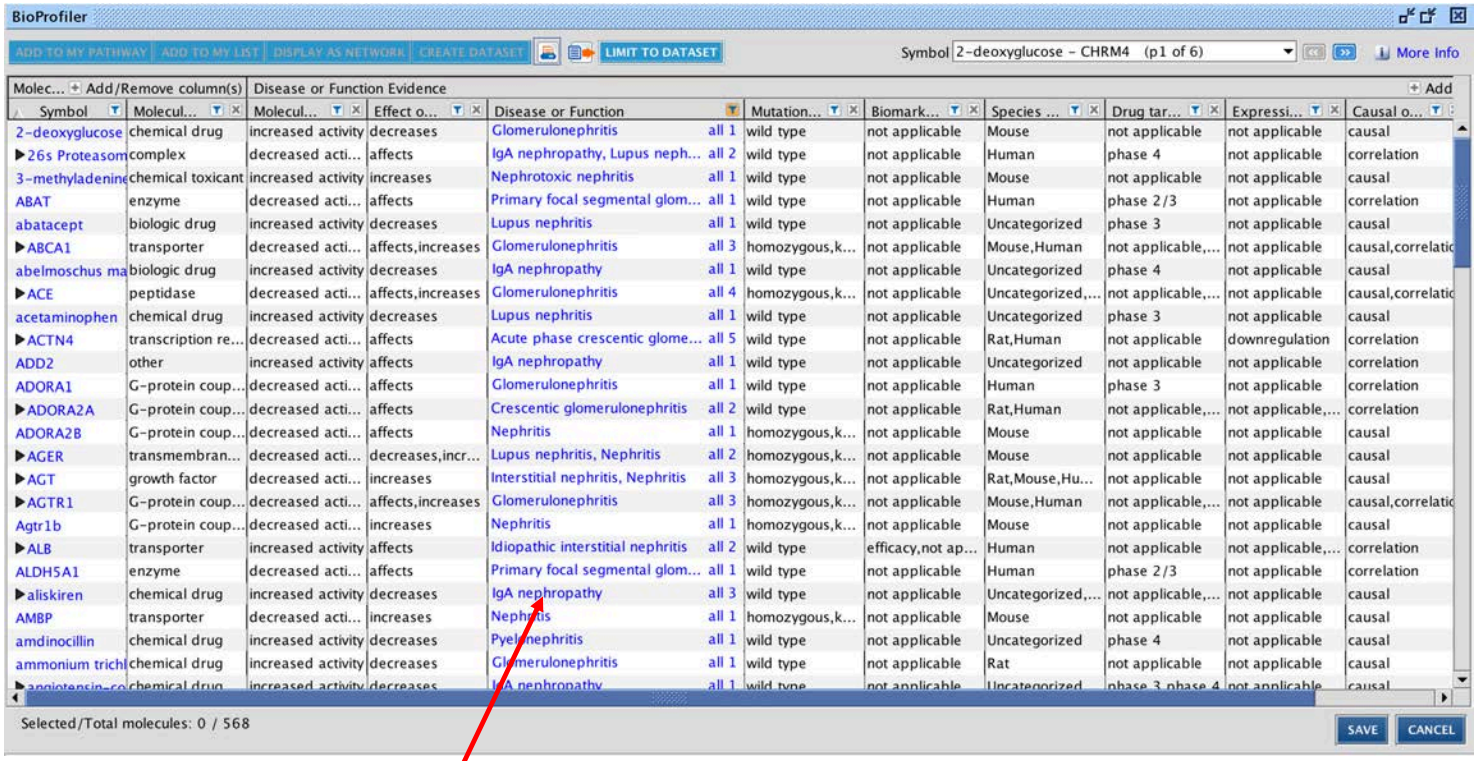


MAP (overlay) predicts effects based on literature



BioProfiler can be used to explore hypotheses

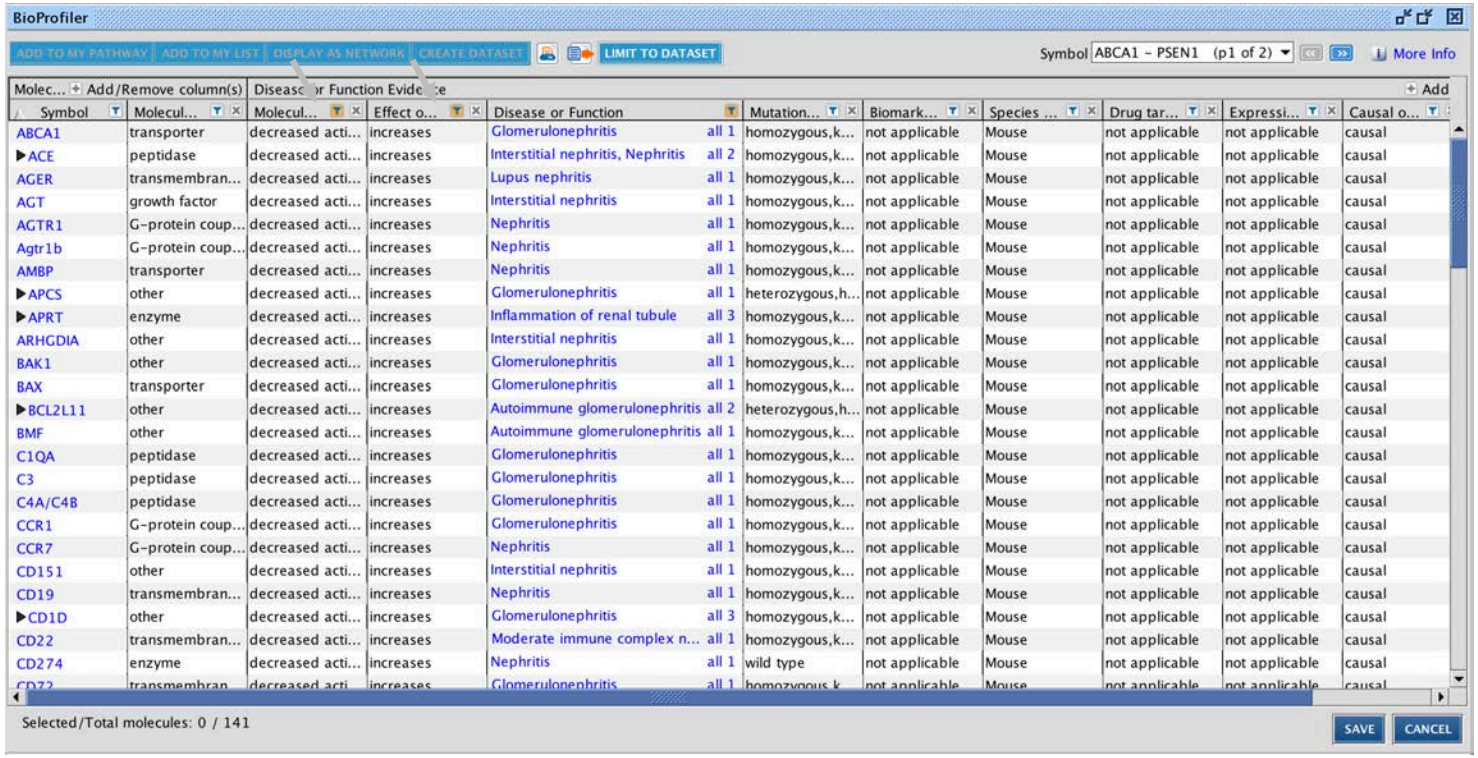
All molecules (genes, drugs, etc.) known to connect to nephritis



Note how the Ingenuity Ontology is used to gather all nephritis subtypes

BioProfiler can be used to explore hypotheses

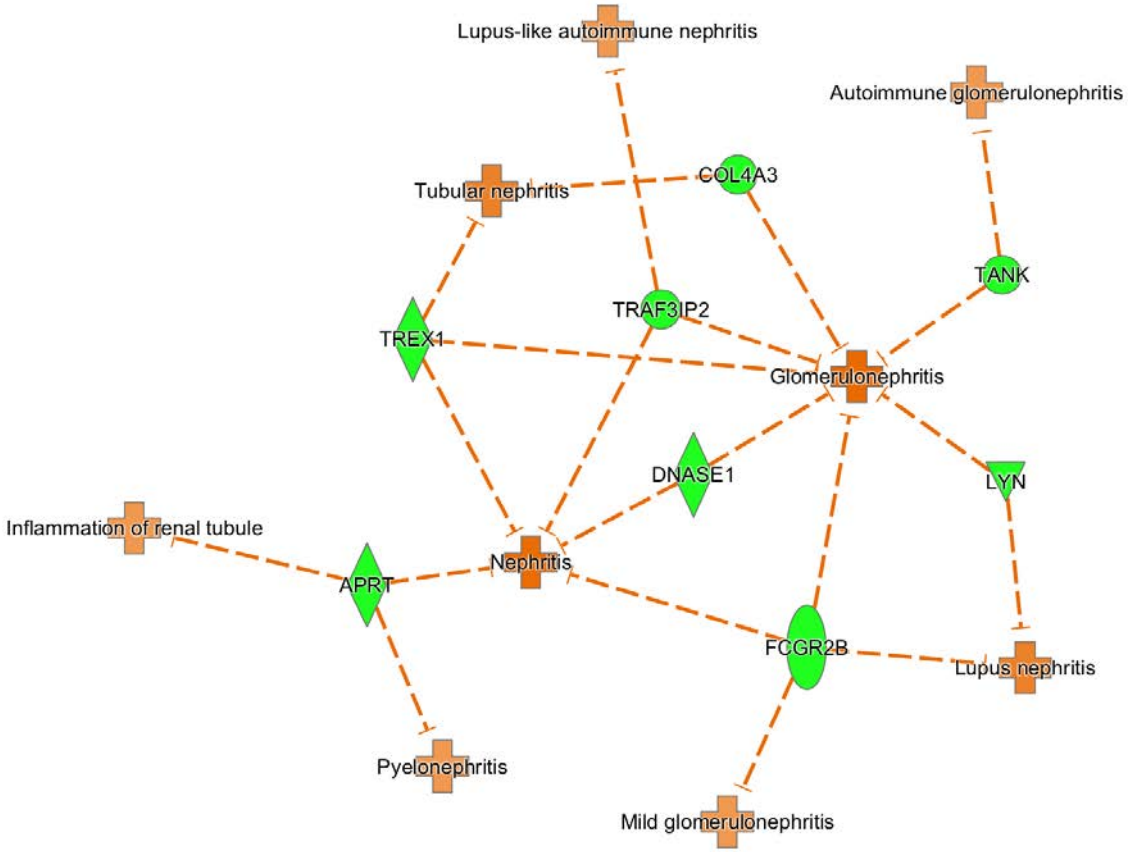
Filtering: All molecules when DECREASED in activity, INCREASE nephritis



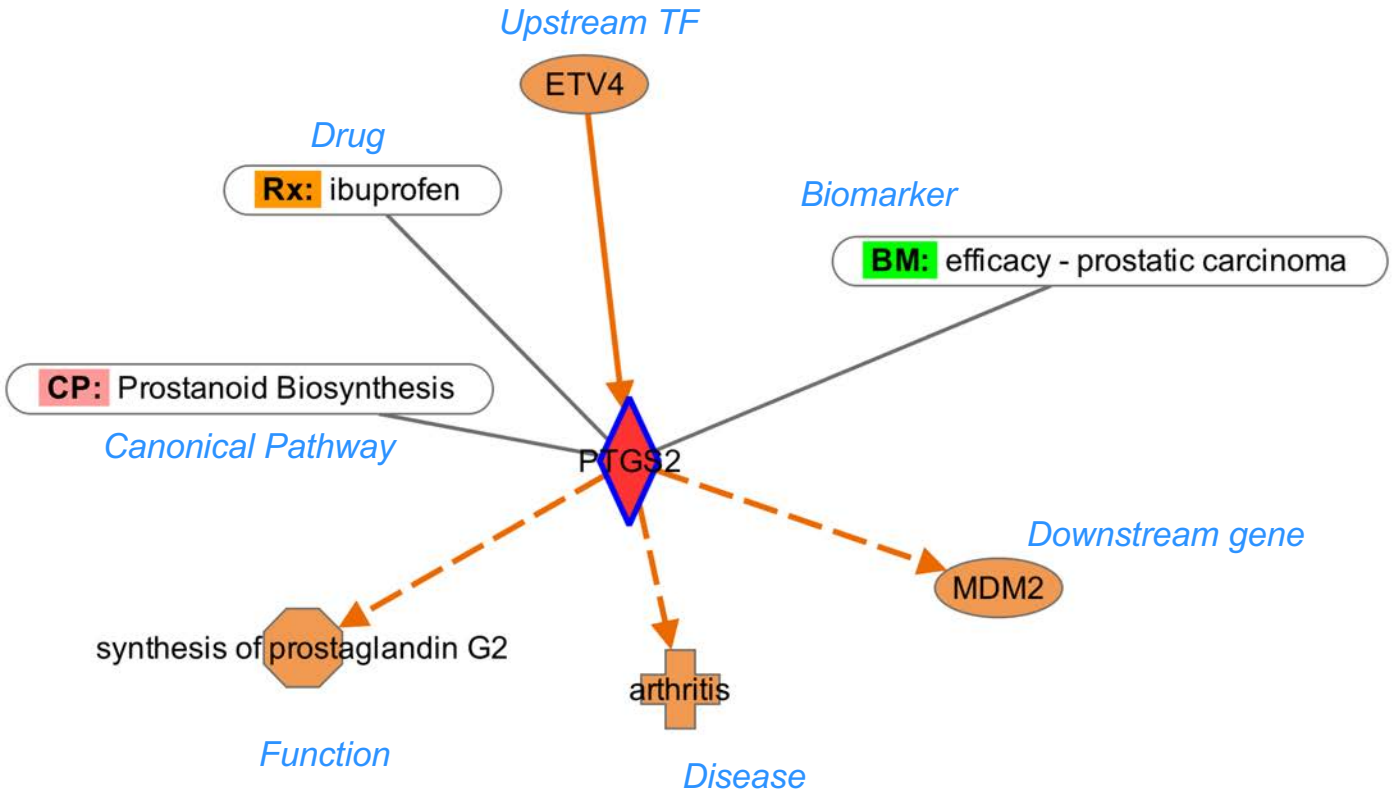
Visualize several on a network →

Visualizing BioProfiler results as a network

Specific subtypes of nephritis are carried over to the network



The basis of IPA: molecular information curated from the literature



Gather this information for nearly every gene. Inferences can be made from the resulting networks.

The QIAGEN Knowledge Base powers IPA

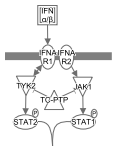
A massive, manually curated Knowledge Base

Ingenuity Literature Findings

Ingenuity® Expert Findings –
Manually curated Findings from the full-text, with contextual details, from top journals.

Ingenuity® ExpertAssist Findings –
Automated text Findings that are manually reviewed, from abstracts covering a broader range of publications. Comprise a small % of IPA's findings.

Ingenuity Modeled Knowledge



- COSMIC
- Clinical Trials
- OMIM
- BioGRID
- MGD
- HumanCyc
- And more

Ingenuity® Expert Knowledge – Content we model such as Canonical Pathways, toxicity lists, etc.

Ingenuity® Supported Third Party Information –
Content areas include Protein-Protein, miRNA, biomarker, clinical trial information, and others

Update weekly for last ~20 years

>6.7 M findings

INGENUITY PATHWAY ANALYSIS

How IPA content is different: context and direction of effect

Homozygous mutant mouse Nrf2 [Nfe2l2] gene (knockout) in mouse decreases constitutive expression of mouse Gstm3 mRNA in mouse liver.

11991805 Chanas SA, Jiang Q, McMahon M, McWalter GK, McLellan LI, Elcombe CR, Henderson CJ, Wolf CR, Moffat GJ, Itoh K, Yamamoto M, Hayes JD. Loss of the Nrf2 transcription factor causes a marked reduction in constitutive and inducible expression of the glutathione S-transferase Gsta1, Gsta2, Gstm1, Gstm2, Gstm3 and Gstm4 genes in the livers of male and female mice. Biochem J. 2002 Jul 15;365(Pt 2):405-16.

Source: Ingenuity Expert Findings

species

downstream gene

tissue

upstream gene

mutation type

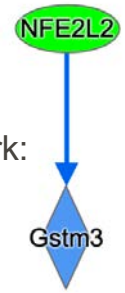
Activity of the molecule in this finding (decreased)

Direction of effect on gene expression

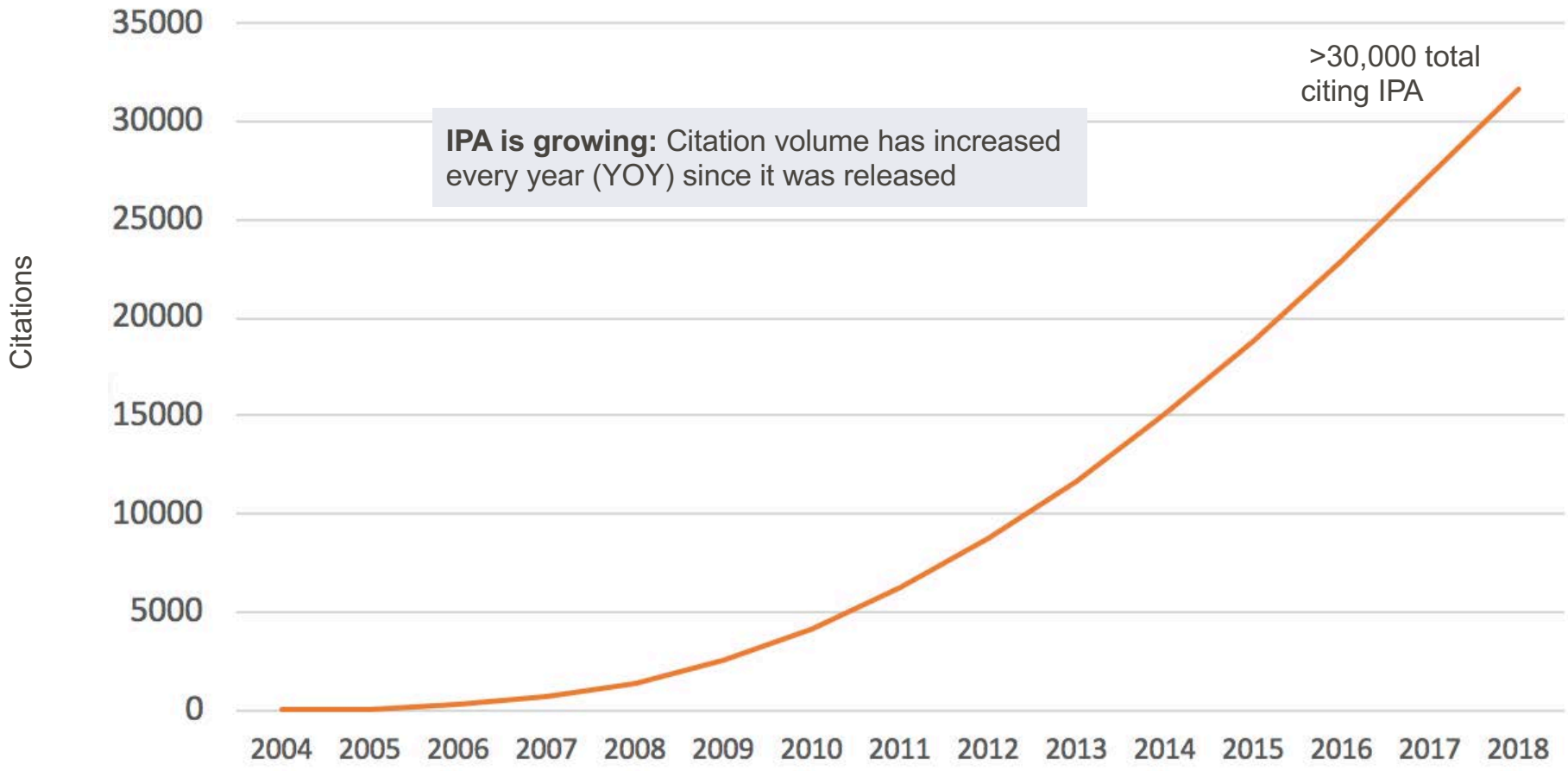
This structure provides

rich contextual detail and causality and can be used **computationally**

As represented in an IPA network:

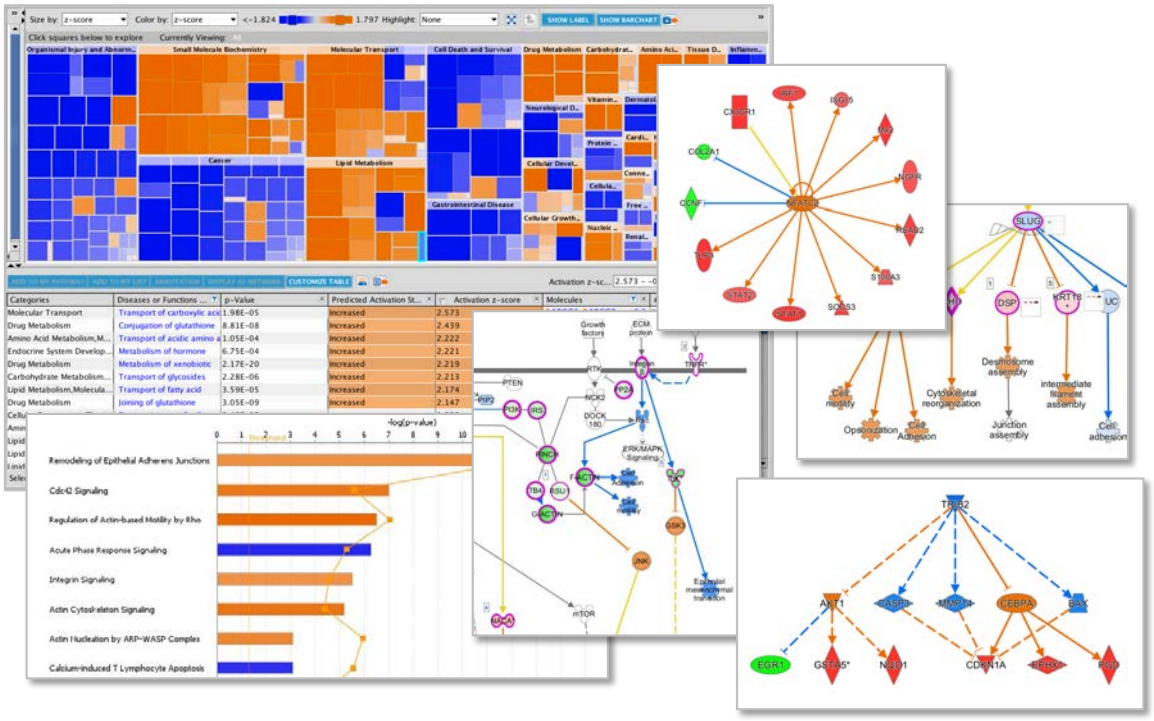


IPA cumulative citation volume. IPA was released in late 2003



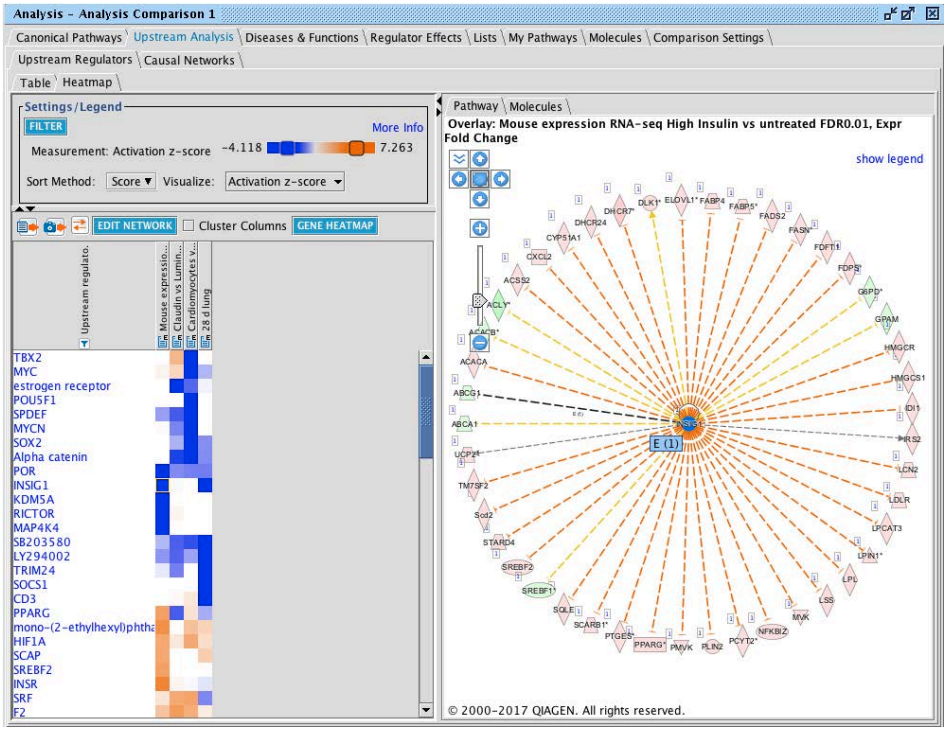
IPA visualizes the hidden biology in a dataset

But how do you find other analyses that resemble yours?



How can you find analyses similar or different to yours?

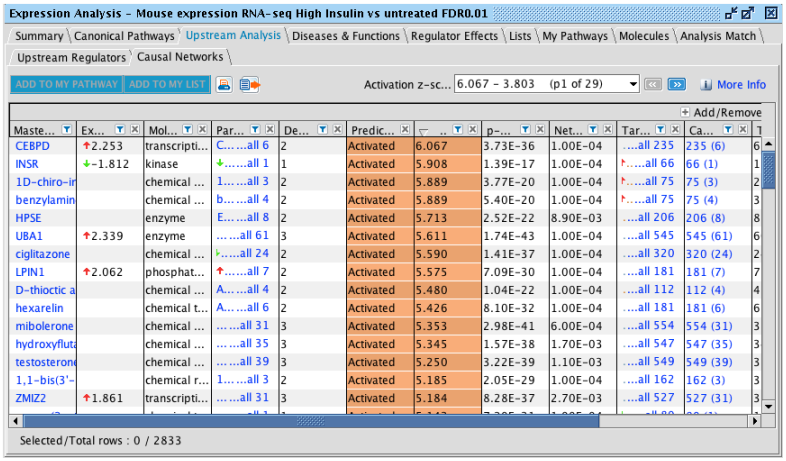
Until now, manually create a Comparison Analysis



(up to 20 analyses)

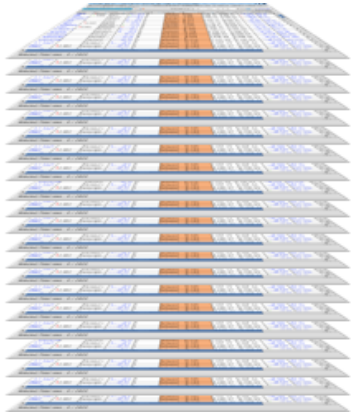
Analysis Match makes it easy to find insights

Discover which analyses resemble yours, to uncover insights from mechanistic similarities and differences



Match against your own analyses and

>56,000 other curated analyses



Which analyses have similar Upstream Regulators, Canonical Pathways, Diseases & Functions, etc?

Unprecedented Discovery with Analysis Match

Build confidence in your results

- Identifying shared biology across disparate diseases, tissues, treatments and more.

Develop greater insights

- Upstream drivers, downstream phenotypes and biological pathways.

Identify key regulators/pathways

- Similarly activated/inhibited across the groups

Easily evaluate critical hypotheses

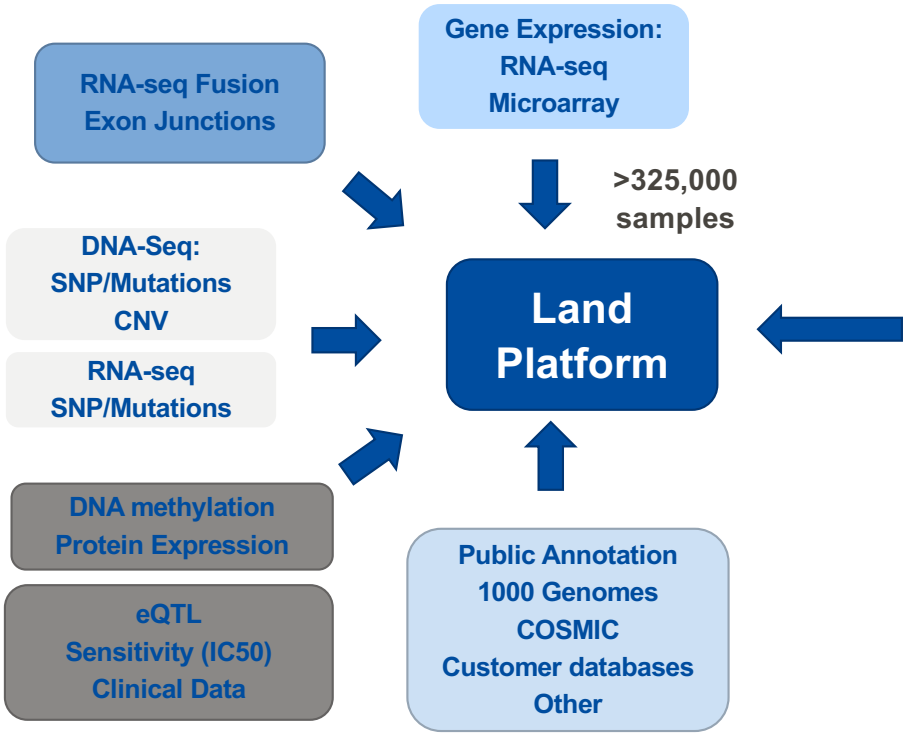
- Across an extensive collection of public data

Applications

- Biomarker discovery through comparison analysis
- Mechanism of action
- Target discovery/validation
- Drug repurposing

>56,000 comparison datasets from OmicSoft Lands in IPA

OmicSoft Lands, expression data in IPA



Analysis Match combines knowledge with data

Array Express
GEO
SRA
TCGA
LINCS
Etc.

Journal articles
Clinical Trials
COSMIC
OMIM
MGD
Etc.

>6.7 million curated Findings

Curation & QA

Reprocessed using the same pipeline

OmicSoft Array Studio

>56,000 comparison datasets

Built from >325,000 samples

INGENUITY PATHWAY ANALYSIS

- Biological analyses of each dataset
- Compare your analysis to all OmicSoft analyses

What the >57,000 Land Comparisons represent (End of Sept. 2019)

DiseaseLand

HumanDisease (8891)
- 519 diseases
- 259 tissues
- 66 expression platforms
- 1577 RNA-seq datasets

MouseDisease (10,326)
- 332 diseases
- 223 tissues
- 55 expression platforms
- 4078 RNA-seq datasets

RatDisease (846)
- 37 diseases
- 62 tissues
- 329 RNA-seq datasets

LINCS (28,234)
- 23 cell lines
- 374 chemical treatments or gene overexpression
- 226 different targets (or groups of target genes)

OncoLand

OncoGeo (2859)
- 141 cancers
- 73 tissues
- 42 expression platforms
- 944 RNA-seq datasets

TCGA (4789)
- 33 cancers
- 27 tissues
- 385 different mutational status / clinical signs

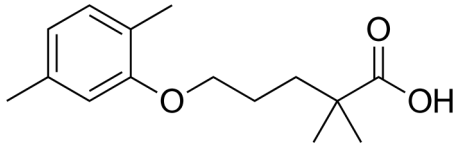
Pediatrics (444)
- 47 cancers
- 23 tissues

Metastatic Cancer (81)
- 27 cancers
- 18 tissues

Hematology (1387)
- 46 cancers
- 73 cell types
- 196 RNA-seq datasets

Case Study: Biological effects of gemfibrozil in liver (of rat)

\+

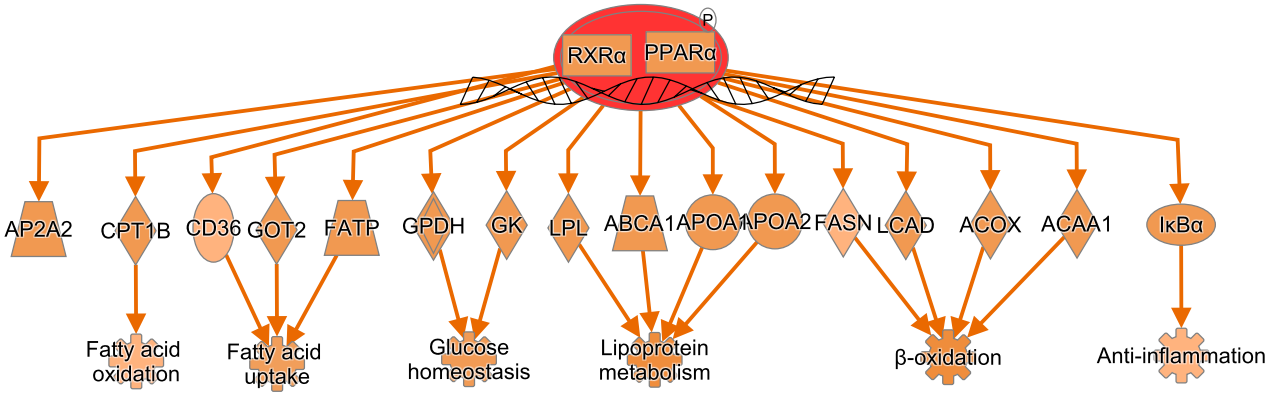


gemfibrozil

Liver transcriptome

- Lipid-lowering drug
- Agonist of the Peroxisome Proliferator-Activated Receptor alpha (PPARα), a ligand-dependent transcription factor

What we expect to see:



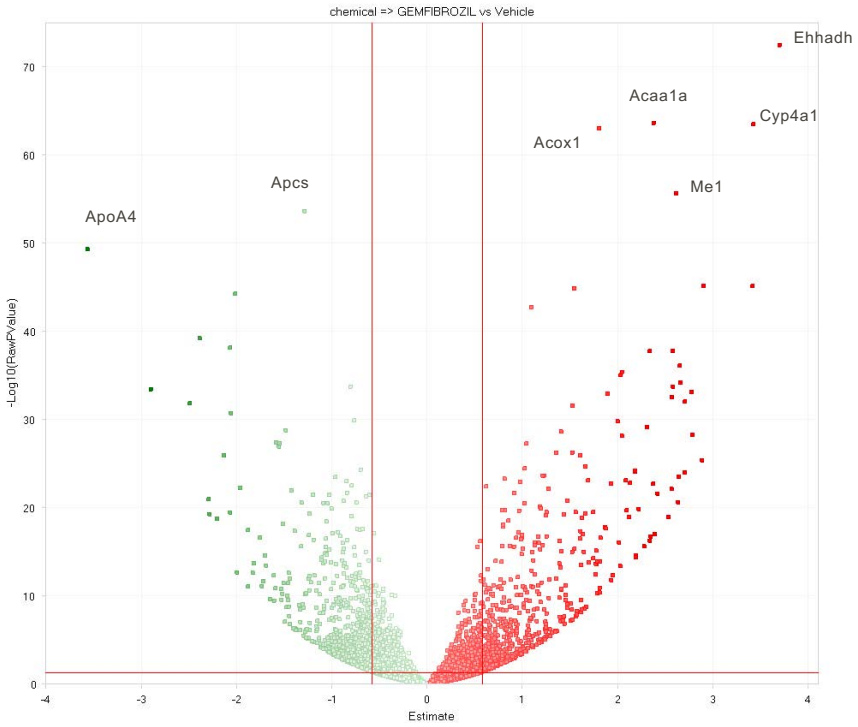
Using IPA to explore the biology of gemfibrozil in rat liver

Analysis of liver expression of gemfibrozil-treated rats for 7 days compared to control

Series GSE47875	Query DataSets for GSE47875
Status	Public on Aug 08, 2014
Title	SEQC Toxicogenomics Study: microarray data set
Organism	Rattus norvegicus
Experiment type	Expression profiling by array
Summary	The comparative advantages of RNA-Seq and microarrays in transcriptome profiling were evaluated in the context of a comprehensive study design. Gene expression data from Illumina RNA-Seq and Affymetrix microarrays were obtained from livers of rats exposed to 27 agents that comprised of seven modes of action (MOAs); they were split into training and test sets and verified with real time PCR. contributor: DrugMatrix, National Toxicology program (NTP)

GSE47875

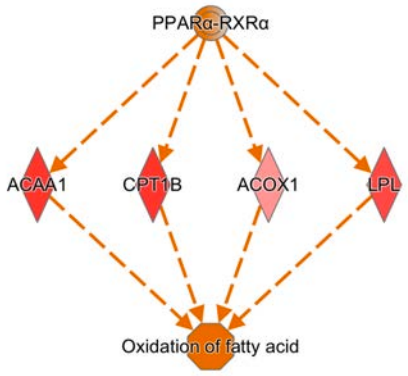
- 3 rats treated w/ 700 mg/kg for 7 days vs. 6 rats with corn oil control
- Illumina HiScanSQ FASTQ processed in OmicSoft Array Studio
- Analysis cutoffs in IPA:
  - Fold change <-1.5 or >1.5
  - Adjusted p-value <0.01
  - Max of group means > 10 FPKM
- Analyzed 503 down-regulated and 461 upregulated genes



IPA summary: Confirmation of known biology + new insights

Effects on regulators and pathways (IPA Core Analysis)

- ↑ PPARα upstream regulator
- ↑ Cholesterol biosynthesis
- ↑ Fatty acid β-oxidation
- ↑ Ketogenesis
- ↓ LXR/RXR pathway
- ↓ Cholesterol transport

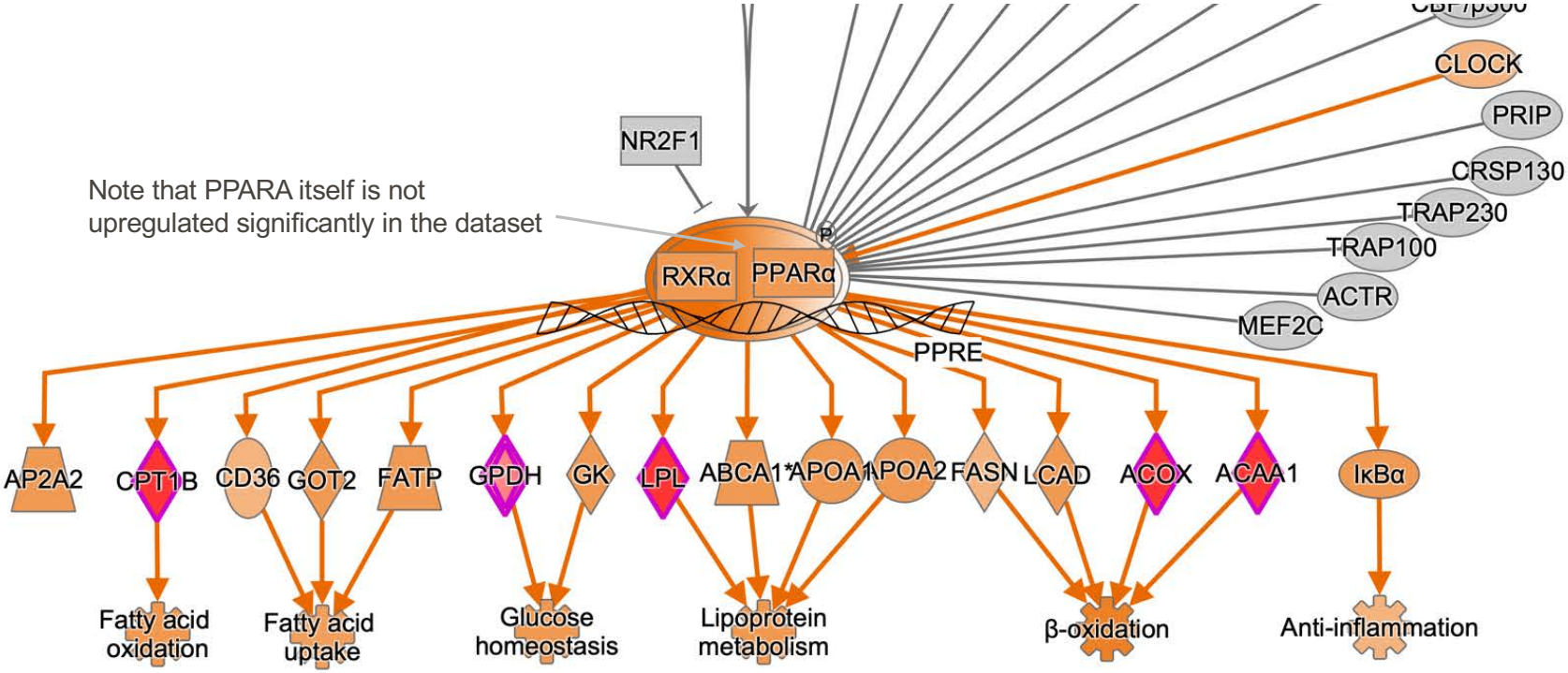


Similarities and differences to other analyses (Analysis Match)

- Confirm known effects
  - Matches to well-known PPAR agonists such as fenofibrate, tesaglitazar, rosiglitazone, and amorfrutin (mouse, rat, and human and in liver and adipose tissue).
- Insights into related biology
  - Weaker but significant matches with conditions which (like gemfibrozil) appear to activate the key cholesterol regulators SREBF1, SREBF2, and SCAP but (unlike gemfibrozil) *don't* activate PPARα.
  - Anti-match to siRNA knockdown of Prdm16 in mouse white adipose. Prdm16 regulates PPAR activity in adipose tissue and is a master transcriptional coregulator in brown adipocytes, promoting expression of brown fat-selective genes and repression of white-selective genes.
- Potential for drug discovery
  - Anti-match to severe atopic dermatitis samples (where PPARα is "inhibited"). Possible treatment with PPARα agonists.

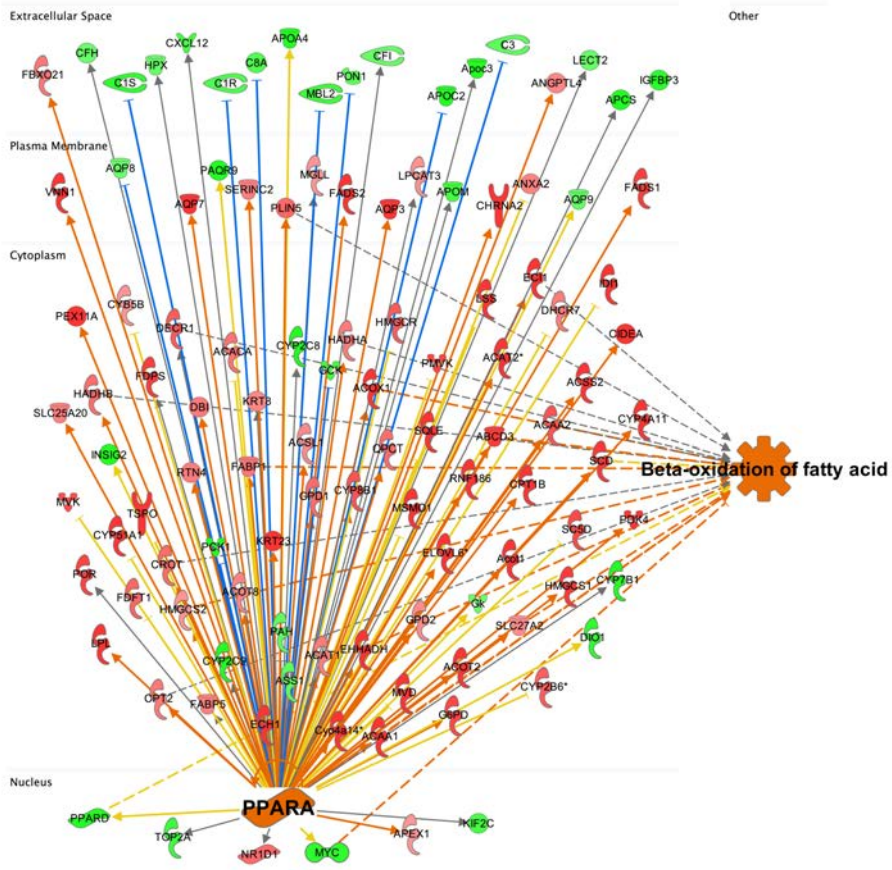
Confirm known biology (we see the expected target activation)

Activation of RXRα/PPARα by gemfibrozil (predicted from the gemfibrozil RNA-seq data)



(zoomed in to show detail)

Confirm known biology (expected drug target, pathways, and functional effects)



Examples of pathway impacts

Canonical Pathway	B-H p-value	z-score
Superpathway of Cholesterol Biosynthesis	3.14E-14	**4.796**
Ketogenesis	7.05E-08	**2.646**
Acyl-CoA Hydrolysis	3.33E-06	**2.449**
Fatty Acid Beta oxidation I	4.84E-06	**3**
Isoleucine Degradation I	8.01E-04	**2.236**
LXR/RXR Activation	2.47E-11	**-3.674**

Examples of functional impacts

Disease or Function	p-value	z-score
Oxidation of fatty acid	2.30E-11	2.577
Synthesis of cholesterol	1.05E-17	2.109
Vascularization	3.50E-04	-2.067
Invasion of cells	3.43E-04	-2.181
Cholesterol transport	9.87E-05	-3.204

What other conditions have predictions similar to these?

How can we find matches to other analyses?

Conceptually, create *signatures* of the predicted "entities" for every analysis and compare them:

Query signature

Upstream Regulator	Predicted Activation
PPARA	Activated
ACSL3	Activated
INSR	Activated
RPE65	Activated
SREBF1	Activated
SCAP	Activated
SREBF2	Activated
ZNF423	Activated
PPARG	Activated
POR	Inhibited
ASXL1	Inhibited
NR1D2	Inhibited
ST3GAL5	Inhibited
CREB3L3	Inhibited
ACOX1	Inhibited
GRB14	Inhibited
PDE8A	Inhibited

Compare

Signature from another analysis

Does it Match?	Upstream Regulator	Predicted Activation
YES	**PPARA**	**Activated**
	ABDH5	Activated
	ASXL2	Activated
YES	**RPE65**	**Activated**
YES	**SREBF1**	**Activated**
	KLF15	Activated
YES	**SREBF2**	**Activated**
	BTN2A2	Activated
	ACSBG1	Activated
	NR1I3	Inhibited
	CR1	Inhibited
	ASXL1	Inhibited
	DUT	Inhibited
YES	**ACOX1**	**Inhibited**
	NR1I3	Inhibited
YES	**GRB14**	**Inhibited**
YES	**PDE8A**	**Inhibited**

Create and score signatures for

- Upstream Regulators
- Causal Networks
- Canonical Pathways
- Diseases & Functions

The *sign* of the entity (activated or inhibited) is important, but not its *order* in the signature

Analysis Match results for gemfibrozil in rat liver

Filtered to show top matching (>45% match) or top anti-matching (< -45% match)

Filtered to mostly exclude matches to own analyses

Examples of available metadata

Brief description of the comparison

Upstream Regulators

Diseases & Functions

Canonical Pathways

Master Regulators

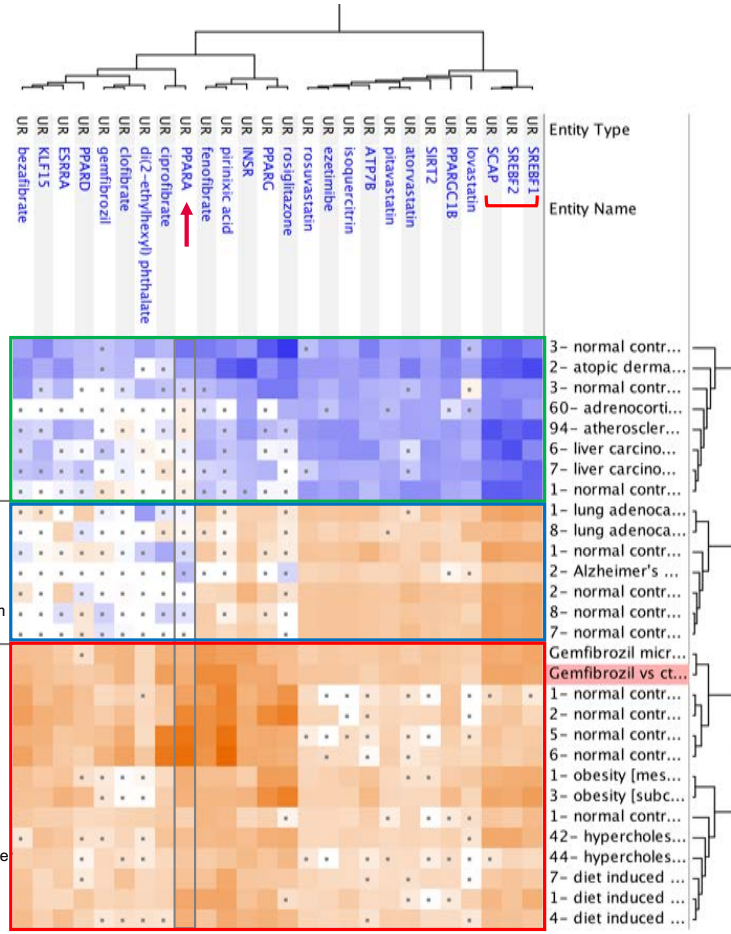
Overall average

Analysis Name	Project	case.diseas...	case.tissue	comparisoncategory	comparisoncontrast	CP	UR	CN	DE	
Gemfibrozil microarray PM	Microarray Gem...					78.45	72.11	61.64	56.41	67.15
6- normal control [liver] N	MouseDisease	normal control	liver	Treatment vs. Control	Tissue:Compound => liver -> tesaglitazar vs saline	87.71	62.45	65.64	39.89	63.92
5- normal control [liver] N	MouseDisease	normal control	liver	Treatment vs. Control	Tissue:Compound => liver -> fenofibrate vs saline	78.45	58.31	62.52	47.67	61.74
4- diet induced obesity [s	HumanDisease	diet induced obesity	subcutaneous adip...	Treatment vs. Control	Treatment => amorfrutin 4 vs DMSO	67.94	54.88	54.77	33.71	52.82
3- obesity [subcutaneous	HumanDisease	obesity	subcutaneous adip...	Treatment1 vs. Treatment2	Tissue:Treatment => subcutaneous adipose tissue -> differentiation medi...	73.38	50.00	46.90	38.14	52.11
2- normal control [white a	MouseDisease	normal control	white adipose tissue	Treatment vs. Control	Transfection:Treatment => PRDM16 shRNA -> rosiglitazone vs none	62.02	50.00	44.72	47.67	51.10
1- normal control [white a	MouseDisease	normal control	white adipose tissue	Treatment vs. Control	Transfection:Treatment => control shRNA -> rosiglitazone vs none	62.02	46.90	46.90	47.67	50.87
7- normal control [embryo	MouseDisease	normal control	embryo	Other Comparisons	Treatment:CultureCondition => DMSO -> N2B27 medium vs serum	67.94	53.85	50.99	30.15	50.73
1- normal control [liver] ar	MouseDisease	normal control	liver	Treatment vs. Control	Treatment => amiodarone vs DMSO	67.94	57.45	41.23	30.15	49.19
42- hypercholesterolemia	MouseDisease	hypercholesterolemia	visceral adipose tis...	Treatment1 vs. Treatment2	Tissue:ExperimentGroup => visceral adipose tissue -> high fat diet 9 wee...	73.38	57.45	61.64		48.12
8- lung adenocarcinoma (	HumanDisease	lung adenocarcino...	lung	Treatment vs. Control	Dosage => 10.56 ug/ml vs 0 ug/ml	67.94	52.92	41.23	30.15	48.06
1- obesity [mesenteric adi	HumanDisease	obesity	mesenteric adipos...	Treatment1 vs. Treatment2	Tissue:Treatment => mesenteric adipose tissue -> differentiation medium...	67.94	57.45	65.57		47.74
44- hypercholesterolemia	MouseDisease	hypercholesterolemia	gonadal adipose ti...	Treatment vs. Control	Tissue:SubjectTreatment => gonadal adipose tissue -> high fat diet;piogli...	62.02	37.71	53.85	36.93	47.63
8- normal control [embryo	MouseDisease	normal control	embryo	Other Comparisons	Treatment:CultureCondition => tazemetostat -> N2B27 medium vs serum	67.94	50.14	44.72	25.13	46.98
1- normal control [liver] N	MouseDisease	normal control	liver	Treatment vs. Control	SubjectTreatment => calorie restriction vs normal diet	62.02	45.36	40.17	39.89	46.86
7- diet induced obesity [in	MouseDisease	diet induced obesity	inguinal adipose tis...	Treatment1 vs. Treatment2	SubjectTreatment => high fat diet;rosiglitazone vs low fat diet	73.38	38.00	45.83	30.15	46.84
2- Alzheimer's disease (A	MouseDisease	Alzheimer's diseas...	hippocampus	Disease vs. Normal	DiseaseState => Alzheimer's disease (AD) vs normal control	67.94	43.59	44.72	30.15	46.60
1- diet induced obesity [li	MouseDisease	diet induced obesity	liver	Other Comparisons	AnimalStrain[maternal] => BFMI vs C57BL/6N	67.94	57.45	60.83		46.55
1- lung adenocarcinoma (	HumanDisease	lung adenocarcino...	lung	Treatment vs. Control	SamplingTime => 24 hpi vs 0 hpi	58.83	50.00	30.00	45.23	46.02
2- normal control [embryo	MouseDisease	normal control	embryo	Treatment vs. Control	Treatment:TreatTime[hours] => 12 -> miconazole vs DMSO	67.94	55.68	56.57		45.05
60- adrenocortical carcino	TCGA	adrenocortical carc...	adrenal gland	Other Comparisons	NOTCH2_Somatic_Mutation_[DNASeq]_Status => MUT vs WT	-55.47	-45.83	-34.64	-45.23	-45.29
94- atherosclerosis;hyperl	MouseDisease	atherosclerosis;hyp...	liver	Other Comparisons	AnimalStrain[maternal] => SM/J vs C57BL/6J	-73.38	-57.45	-51.96		-45.70
1- normal control [fetal ne	MouseDisease	normal control	fetal neostriatum	Treatment vs. Control	Treatment => 3-nitropropionic acid vs none	-67.94	-48.99	-40.00	-30.15	-46.77
6- liver carcinoma [liver] N	OncoGEO	liver carcinoma	liver	Treatment vs. Control	Treatment => N-nitrosodimethylamine (DMN) vs none	-67.94	-48.11	-37.42	-39.89	-48.34
3- normal control [embryo	MouseDisease	normal control	embryo	Treatment vs. Control	GeneticModification:Treatment => none -> knockdown IRF3 vs control	-62.02	-55.68	-33.17	-42.64	-48.38
7- liver carcinoma [liver] p	OncoGEO	liver carcinoma	liver	Treatment vs. Control	Treatment => phenol vs none	-73.38	-47.96	-40.00	-33.71	-48.76
2- atopic dermatitis [skin]	HumanDisease	atopic dermatitis	skin	Disease vs. Normal	DiseaseState => atopic dermatitis v					
3- normal control [white a	MouseDisease	normal control	white adipose tissue	Treatment vs. Control	Transfection:Treatment => none ->					

But what are the details behind the matching?

Matching and anti-matching analyses fall into three distinct biological clusters

Part of upstream regulator signature:



Clusters:

SCAP / SREBP / PPARA

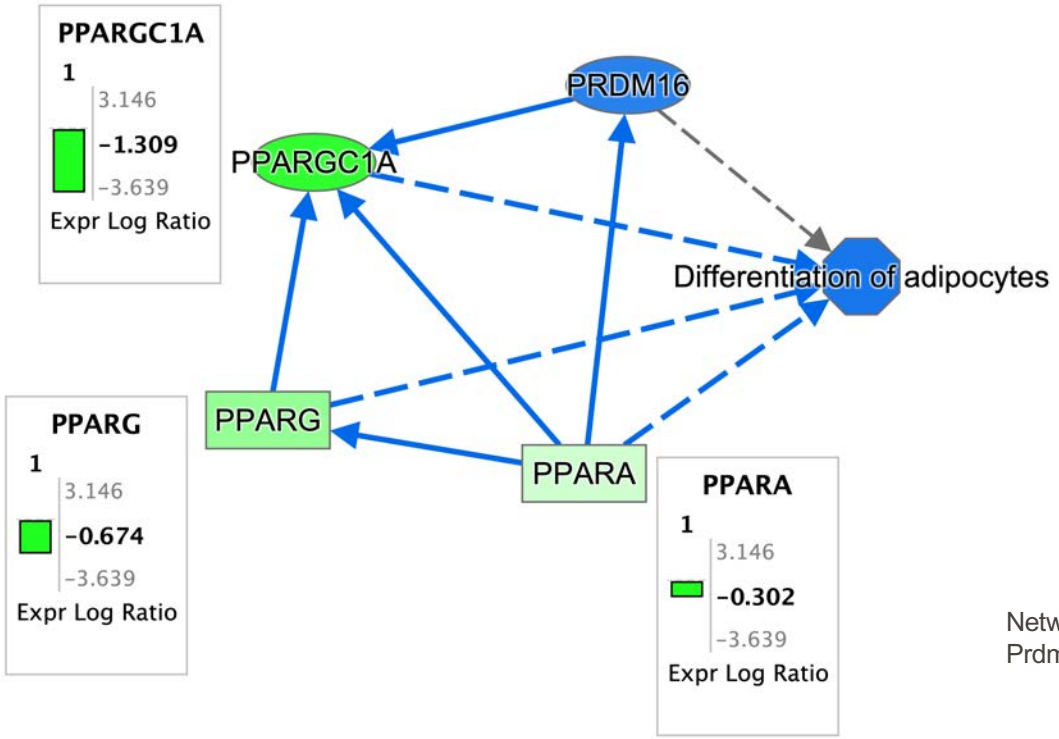
SCAP / SREBP / PPARA

SCAP / SREBP / PPARA

species	case.tissue	Notes:	comparisoncontrast
mouse	white adipose	KD of PPAR regulator	Transfection:Treatment => none -> PRDM16 shRNA vs control shRNA
human	skin	Disease state	DiseaseState => atopic dermatitis vs normal control
mouse	embryo		GeneticModification:Treatment => none -> knockdown IRF3 vs control
human	adrenal gland		NOTCH2_Somatic_Mutation_[DNASeq]_Status => MUT vs WT
mouse	liver		AnimalStrain[maternal] => SM/J vs C57BL/6J
human	liver		Treatment => N-nitrosodimethylamine (DMN) vs none
human	liver		Treatment => phenol vs none
mouse	fetal neostriatum		Treatment => 3-nitropropionic acid vs none
human	lung	Flu infection	SamplingTime => 24 hpi vs 0 hpi
human	lung	Adipocyte exosomes	Dosage => 10.56 ug/ml vs 0 ug/ml
mouse	liver	Caloric restriction	SubjectTreatment => calorie restriction vs normal diet
mouse	hippocampus		DiseaseState => Alzheimer's disease (AD) vs normal control
mouse	embryo		Treatment:TreatTime[hours] => 12 -> miconazole vs DMSO
mouse	embryo	Differentiation	Treatment:CultureCondition => tazemetostat -> N2B27 medium vs serum
mouse	embryo	Differentiation	Treatment:CultureCondition => DMSO -> N2B27 medium vs serum
rat	liver	PPAR alpha	Gemfibrozil vs corn oil (microarray)
rat	liver	PPAR alpha	Gemfibrozil vs corn oil (RNA-seq)
mouse	white adipose	PPAR gamma	Transfection:Treatment => control shRNA -> rosiglitazone vs none
mouse	white adipose	PPAR gamma	Transfection:Treatment => PRDM16 shRNA -> rosiglitazone vs none
mouse	liver	PPAR alpha	Tissue:Compound => liver -> fenofibrate vs saline
mouse	liver	PPAR gamma	Tissue:Compound => liver -> tesaglitazar vs saline
human	mesenteric adipose	Adipose differentiation	Tissue:Treatment => mesenteric adipose -> differentiation medium vs …
human	subcutaneous adipose	Adipose differentiation	Tissue:Treatment => subcutaneous adipose -> differentiation medium …
mouse	liver	PPAR gamma	Treatment => amiodarone vs DMSO
mouse	visceral adipose	High fat	Tissue:ExperimentGroup => visceral adipose -> high fat diet 9 weeks …
mouse	gonadal adipose	High fat	Tissue:SubjectTreatment => gonadal adipose -> high fat diet; pioglitazone
mouse	inguinal adipose	High fat, PPAR gamma	SubjectTreatment => high fat diet;rosiglitazone vs low fat diet
mouse	liver	High fat	AnimalStrain[maternal] => BFMI vs C57BL/6N
human	subcutaneous adipose	PPAR alpha	Treatment => amorfrutin 4 vs DMSO

PRDM16 knockdown leads to downregulation of several relevant genes

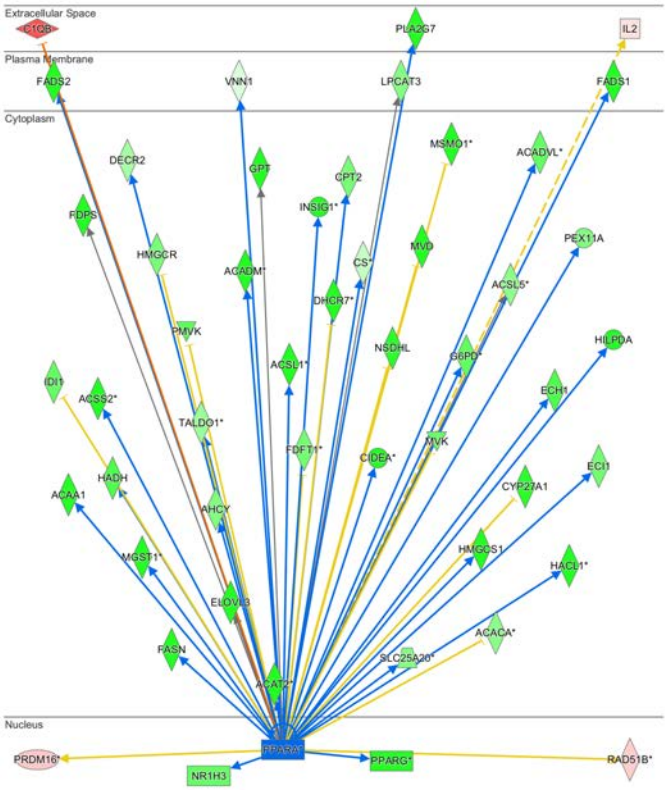
PRDM16 is a regulator of PPAR activity in adipose tissue and master transcriptional coregulator in brown adipocytes, promoting expression of brown fat-selective genes and repression of white-selective genes



Network overlaid with expression profile of Prdm16 shRNA vs. scrambled control

Atopic dermatitis “anti-matches” the gemfibrozil treatment

PPARα is predicted to be inhibited in this condition→ application of PPARα agonists may treat it



PPARA inhibited

Journal of Allergy and Clinical Immunology

Volume 121, Issue 4, April 2008, Pages 962-968.e6

Atopic dermatitis and skin disease

Peroxisome proliferator-activated receptor α regulates skin inflammation and humoral response in atopic dermatitis

Delphine Staumont-Sallé MD [a, b, c, d, *], Georges Abboud BSc [a, b, c, *], Céline Brénuchon MD [a, b, c], Akira Kanda MD, PhD [a, b, c], Thomas Roumier PhD [a, b, c], Céline Lavogiez MD [a, b, c, d], Sébastien Fleury [a, b, c], Patrick Rémy [a, b, c], Jean-Paul Papin [a, b, c], Justine Bertrand-Michel [e, f], François Tercé PhD [e, f, g], Bart Staels PhD [b, c, h], Emmanuel Delaporte MD [c, d], Monique Capron PhD [a, b, c], David Dombrowicz PhD [a, b, c]

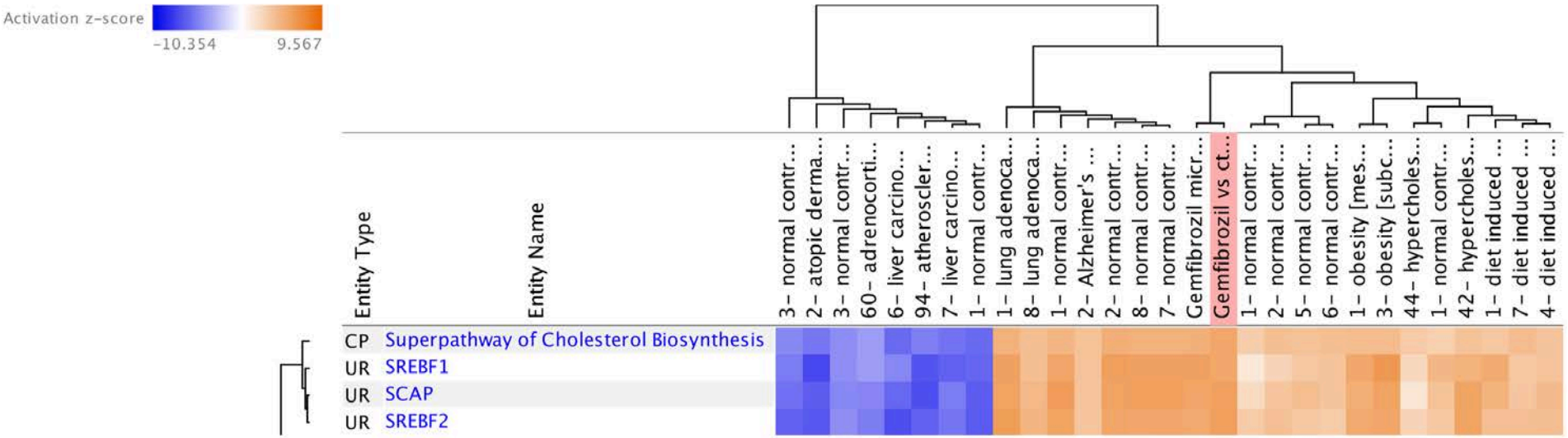
Allergy. 2012 Jul;67(7):936-42. doi: 10.1111/j.1398-9995.2012.02844.x. Epub 2012 May 15.

Topical application of PPARα (but not β/δ or γ) suppresses atopic dermatitis in NC/Nga mice.

Chiba T[1], Takeuchi S, Esaki H, Yamamura K, Kurihara Y, Moroi Y, Furue M.

Clustering provides insight into the signature entities as well

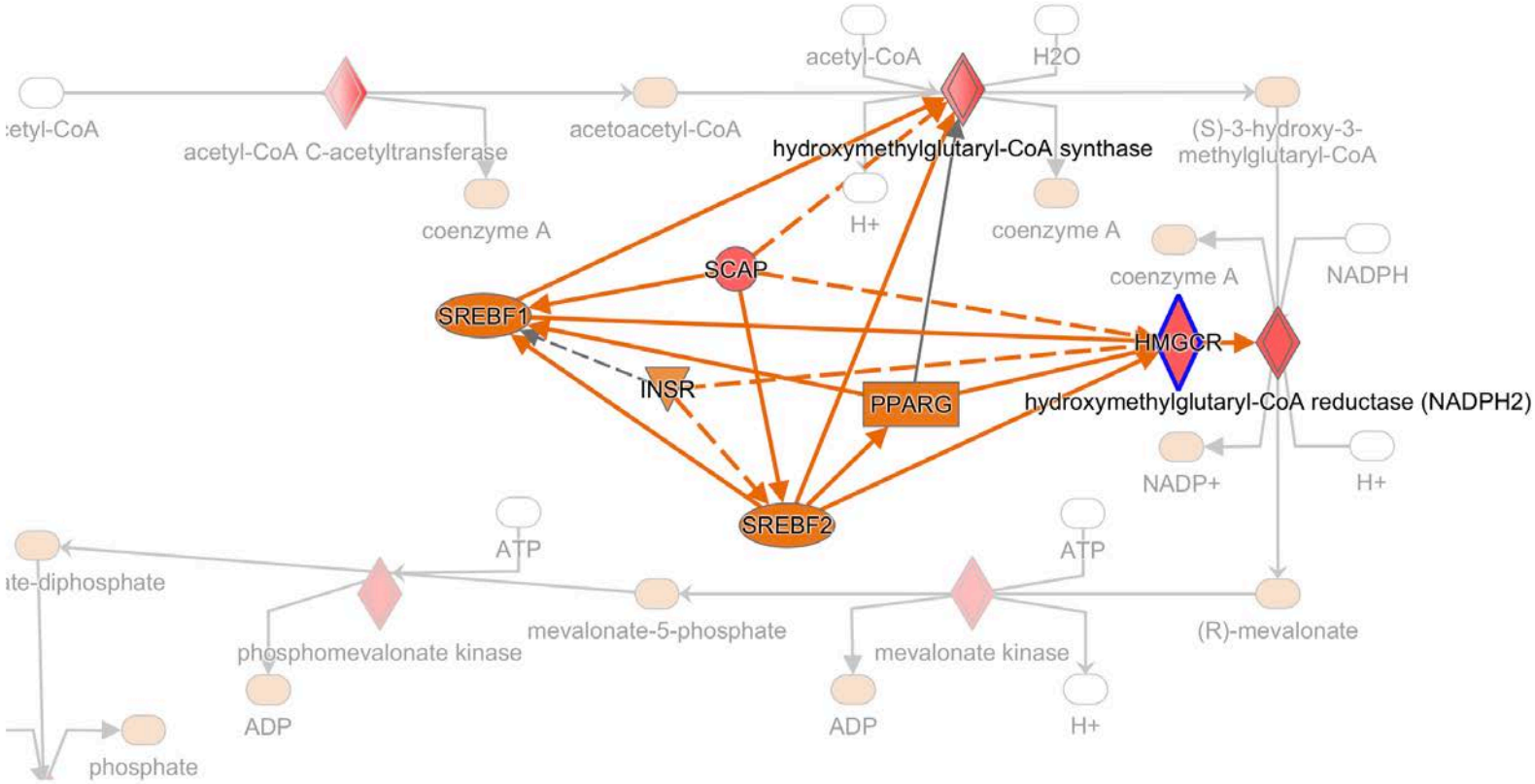
Key regulators of cholesterol biosynthesis cluster with the enzymatic pathway, though not *members* of the pathway



Heatmap rotated 90° from previous views

All three regulators activate the rate-limiting step in cholesterol synthesis

HMGCR is upregulated by gemfibrozil, consistent with the activation of the other regulators



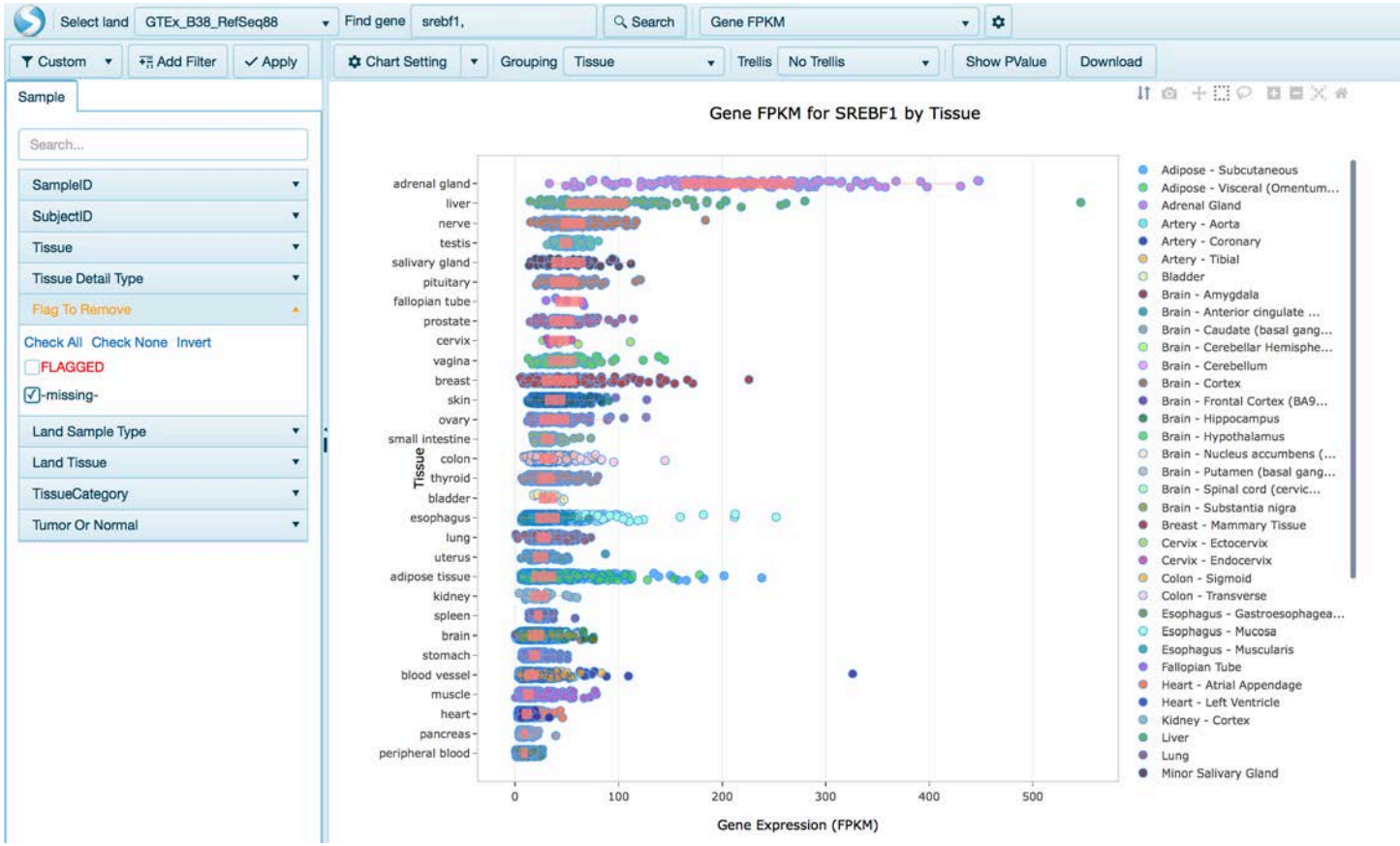
(Detail of Superpathway of Cholesterol Biosynthesis pathway)

What is the expression of a gene in normal human tissues?

Land Explorer for IPA integration

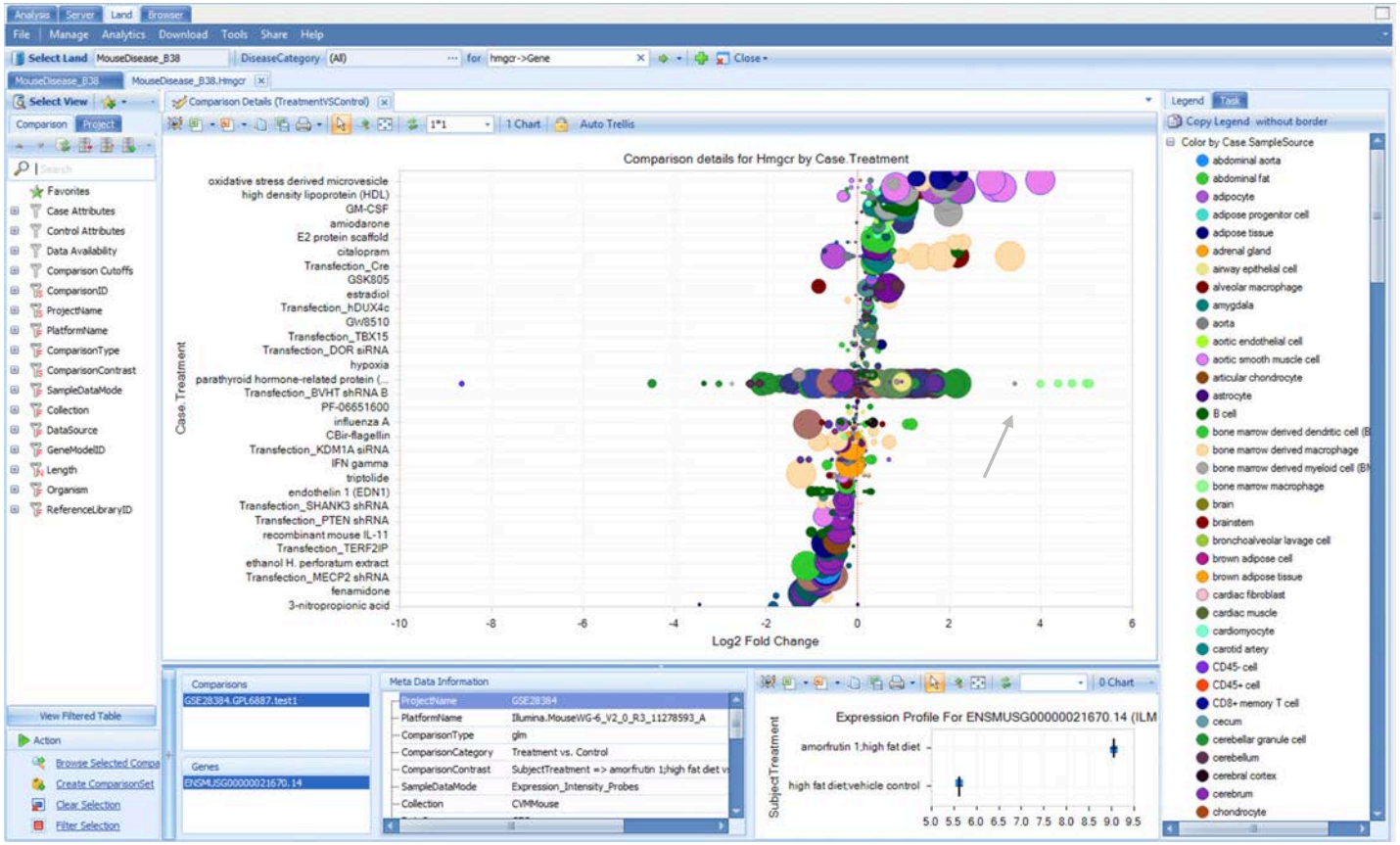
Land Explorer for IPA

Plot GTEx data for a whole gene or for individual splice variant in 51 human tissues



View detailed sample data in OmicSoft Array Studio Lands

Hmgcr is upregulated by amorfrutin and several other treatments in mouse (DiseaseLand)



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- https://go.qiagen.com/LP=1543

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