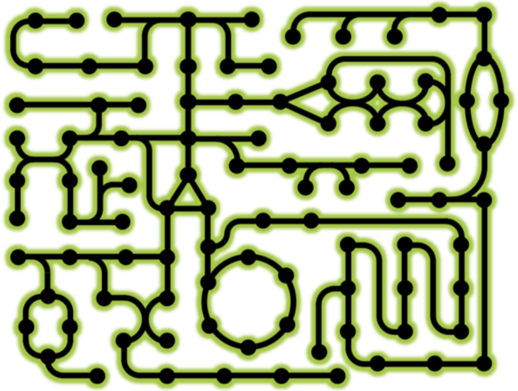

GEMs

Analyzing omics data in the context of metabolism

NBIS Omics Integration and Systems Biology workshop
Fall 2024, Lund University

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Science for Life Laboratory (SciLifeLab)
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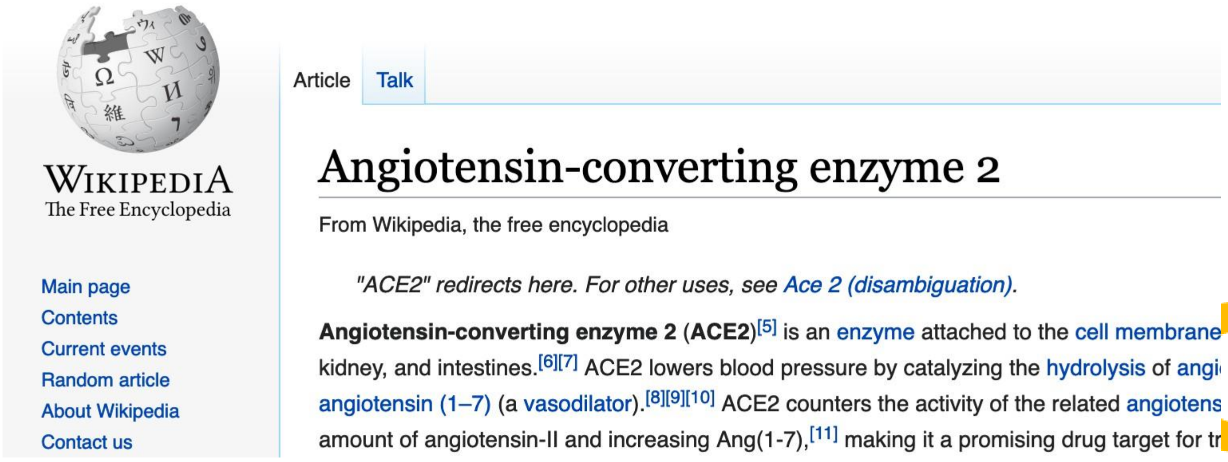
These slides are adapted from previous course materials created by **Jonathan Robinson**. Some updates have been made for this iteration.

Information paradox

ACE2

Information paradox



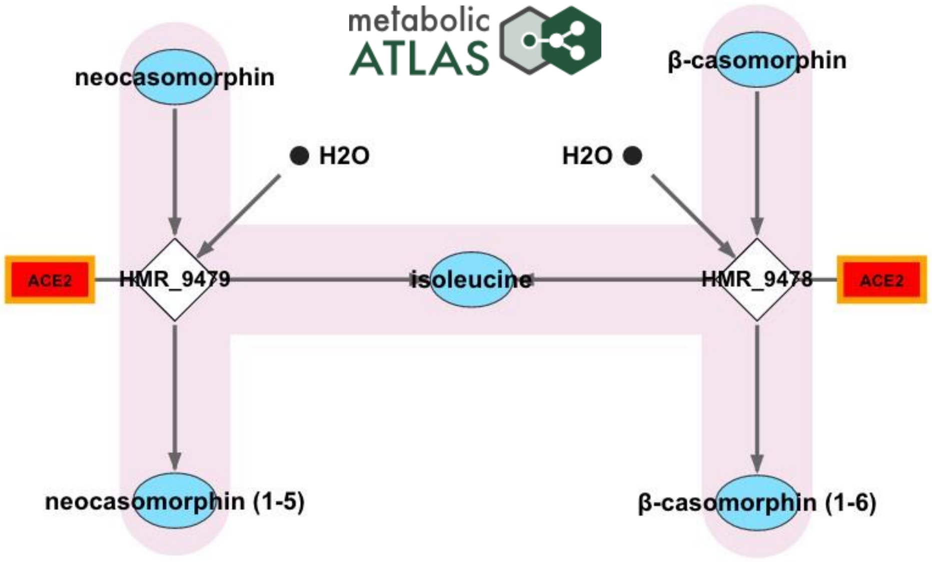
Article Talk

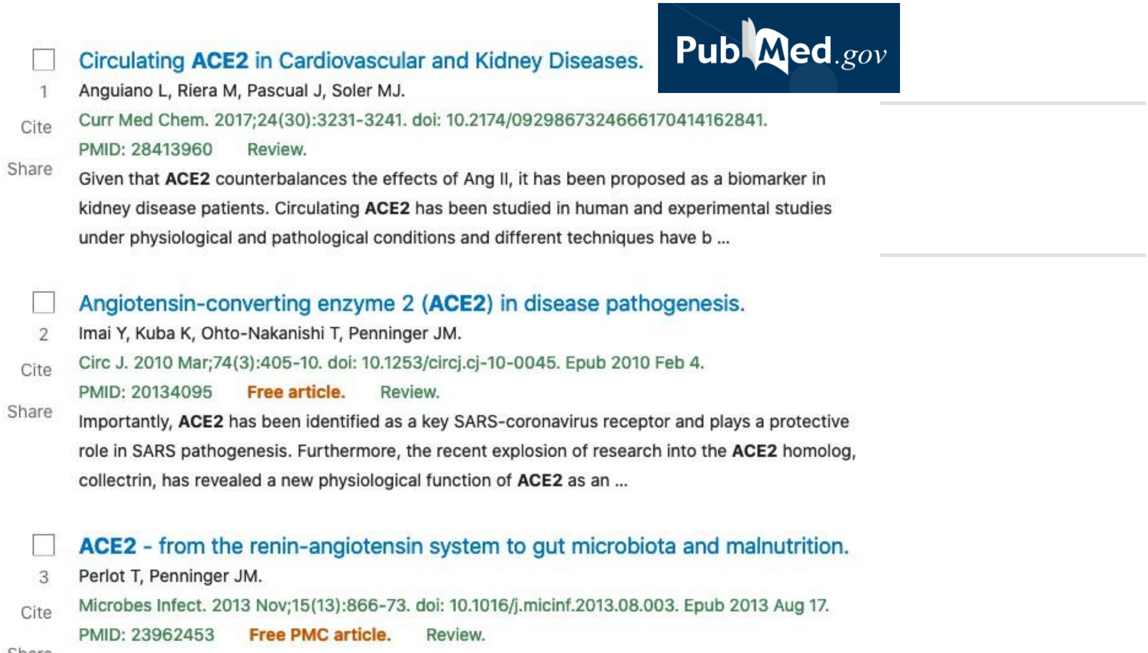
Angiotensin-converting enzyme 2

From Wikipedia, the free encyclopedia

"ACE2" redirects here. For other uses, see Ace 2 (disambiguation).

Angiotensin-converting enzyme 2 (ACE2)[5] is an enzyme attached to the cell membrane
kidney, and intestines.[6][7] ACE2 lowers blood pressure by catalyzing the hydrolysis of angi
angiotensin (1–7) (a vasodilator).[8][9][10] ACE2 counters the activity of the related angiotens
amount of angiotensin-II and increasing Ang(1-7),[11] making it a promising drug target for tr

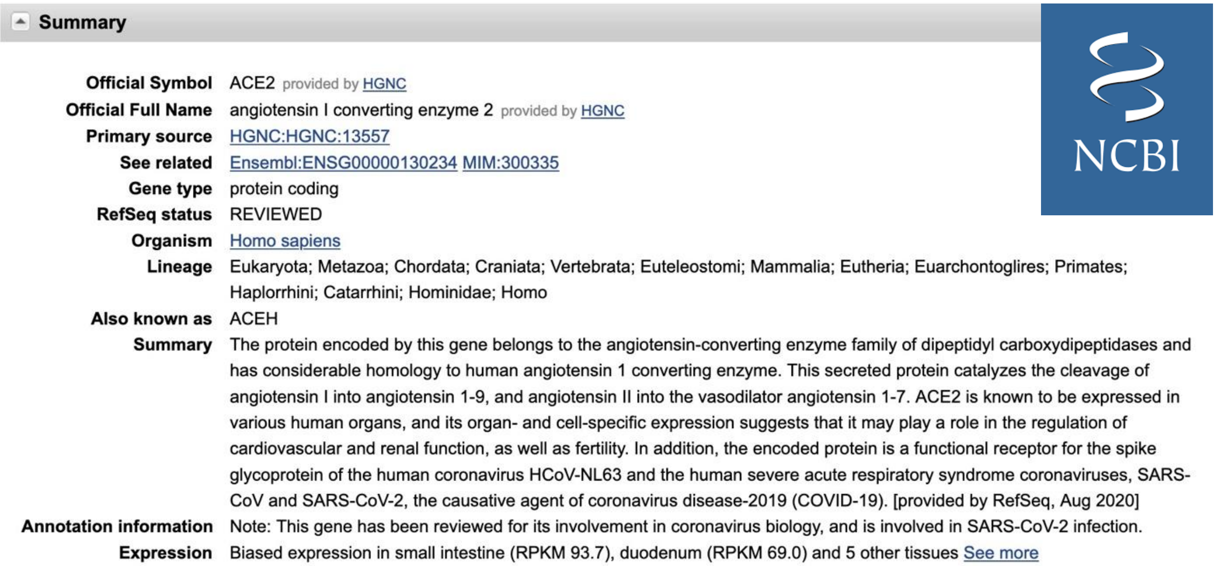




☐ 1 **Circulating ACE2 in Cardiovascular and Kidney Diseases.**
Anguiano L, Riera M, Pascual J, Soler MJ.
Curr Med Chem. 2017;24(30):3231-3241. doi: 10.2174/0929867324666170414162841.
PMID: 28413960 Review.
Given that **ACE2** counterbalances the effects of Ang II, it has been proposed as a biomarker in kidney disease patients. Circulating **ACE2** has been studied in human and experimental studies under physiological and pathological conditions and different techniques have b ...
Cite
Share

☐ 2 **Angiotensin-converting enzyme 2 (ACE2) in disease pathogenesis.**
Imai Y, Kuba K, Ohto-Nakanishi T, Penninger JM.
Circ J. 2010 Mar;74(3):405-10. doi: 10.1253/circj.cj-10-0045. Epub 2010 Feb 4.
PMID: 20134095 Free article. Review.
Importantly, **ACE2** has been identified as a key SARS-coronavirus receptor and plays a protective role in SARS pathogenesis. Furthermore, the recent explosion of research into the **ACE2** homolog, collectrin, has revealed a new physiological function of **ACE2** as an ...
Cite
Share

☐ 3 **ACE2 - from the renin-angiotensin system to gut microbiota and malnutrition.**
Perlot T, Penninger JM.
Microbes Infect. 2013 Nov;15(13):866-73. doi: 10.1016/j.micinf.2013.08.003. Epub 2013 Aug 17.
PMID: 23962453 Free PMC article. Review.
Cite



Summary

Official Symbol	ACE2 provided by HGNC
Official Full Name	angiotensin I converting enzyme 2 provided by HGNC
Primary source	HGNC:HGNC:13557
See related	Ensembl:ENSG00000130234 MIM:300335
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	ACEH
Summary	The protein encoded by this gene belongs to the angiotensin-converting enzyme family of dipeptidyl carboxydipeptidases and has considerable homology to human angiotensin 1 converting enzyme. This secreted protein catalyzes the cleavage of angiotensin I into angiotensin 1-9, and angiotensin II into the vasodilator angiotensin 1-7. ACE2 is known to be expressed in various human organs, and its organ- and cell-specific expression suggests that it may play a role in the regulation of cardiovascular and renal function, as well as fertility. In addition, the encoded protein is a functional receptor for the spike glycoprotein of the human coronavirus HCoV-NL63 and the human severe acute respiratory syndrome coronaviruses, SARS-CoV and SARS-CoV-2, the causative agent of coronavirus disease-2019 (COVID-19). [provided by RefSeq, Aug 2020]
Annotation information	Note: This gene has been reviewed for its involvement in coronavirus biology, and is involved in SARS-CoV-2 infection.
Expression	Biased expression in small intestine (RPKM 93.7), duodenum (RPKM 69.0) and 5 other tissues See more

Information paradox

ENOPH1, SLC25A2, GMPPB, SLC1A4, EGFL8, HDC, DNM1L, RHCG, SLC24A4, FABP4, PDSS1, ACSBG1, UGT3A1, TAOK1, CDY1B, PPIE, GCLM, GMPR2, USP9Y, DGKD, ATP2A2, FABP2, ZDHHC7, GLRX2, DPM3, NUP155, GPX1, SLC4A5, POLI, GCH1, APOE, PLPP7, RIPK3, HPSE, PLA2G1B, PYGL, CDK8, MGST1, DGAT2L6, PPP5C, TXNRD3, MACROD2, FABP4, DDR1, USP35, NARS, HERC1, WWP1, PIGF, MACROD1, SUOX, DGKG, PGS1, AURKB, CDY1, TKFC, PIM1, SLC1A4, GLDC, AFMID, FAR1, PHYKPL, ATP2B1, PTPDC1, LCT, ASPG, ACOT1, POLR1C, HEMK1, CDA, UPP2, PARP10, SLC15A1, ASNS, TGFBR2, POLR2F, CARS, CBL, SLC4A9, INPP4A, SUCLG1, MTAP, PKMYT1, CBLL1, MAP2K2, MARS, TECRL, SLC26A3, METTL7B, ME1, AK2, PLA2G12A, DHRS9, EPHA5, GGACT, GGT5, ACYP2, PI4K2A, SLC25A42, USP17L25, TRMT11, DUSP15, PTGR1, PPP3R1, CA1, FN3K, UBE2F, EFL1, TYMS, PPWD1, GCNT4, PFKP, RNF126, PRKCI, TAF9, FDPS, SLC19A3, AGK, BCKDHB, CALM2, HK1, UPRT, SRD5A1, SYVN1, GLA, CTDSPL, CYP2J2, ACOT9, PDE8B, AP000812.4, IDH3B, SULT1B1, MAP3K21, HMGCS1, JMJD7-PLA2G4B, CA3, SLC25A3, ACAT1, NEK9, NEK6, 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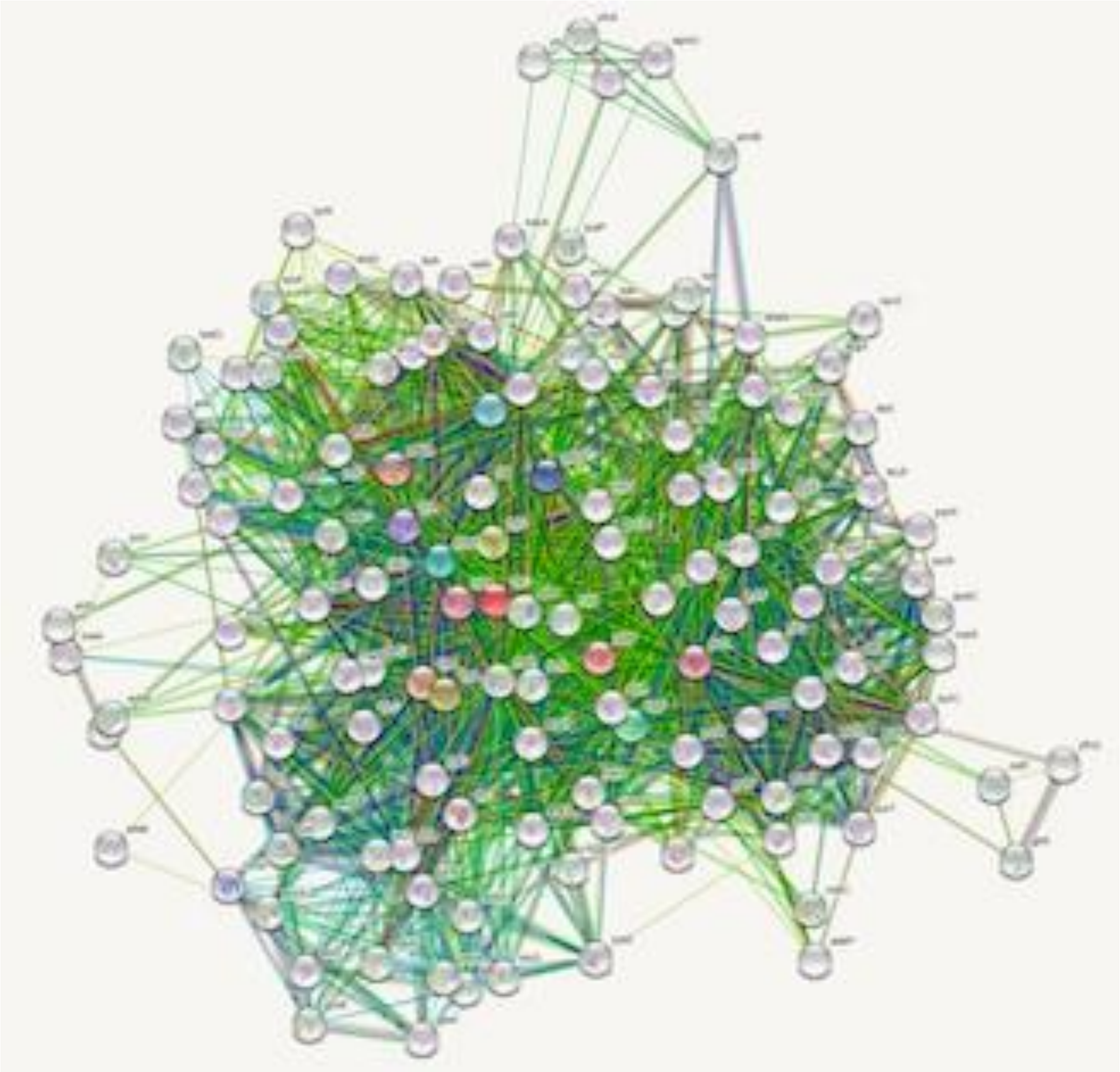
STAR, NDST3, SIRT6, NAAA, SLC5A7, RHBG, IREB2, HS3ST2, IDI1, RPEL1, PAFAH1B2, G6PC2, PRKCZ, UGT2B7, PDIA2, DOLPP1, TAF9, STARD8, SLC51A, TLK1, PIN1, MEPCE, PAPOLB, PCTP, ATP5ME, PRODH2, ME3, DUSP4, MIA3, AKR1B15, PIP4P1, AGMAT, PARP3, TRMT12, USP14, PTPRF, CTDSP2, WARS, GSTK1, CDC42BPG, F13B, ENPP2, METTL3, MAP4K4, UBE2Q2, POLR2C, GM2A, ABCC8, FXYD2, DHFR, PPM1G, CA5B, TYRP1, MARS2, CSNK1G1, PARP4, FLT3, SIN3B, HSD3B1, L1CAM, CYP27B1, SLC22A13, TST, CDY1B, NEDD4, MMAB, GK3P, CAMK1, FIG4, GMPS, ATP5MC2, IRAK4, PPP3R1, ZDHHC19, SLC22A7, FHL2, B3GAT3, SLC15A3, SIK3, DPM2, DPEP1, GK, POLD3, PCK2, ELOVL2, PRDX5, RAG1, FKBP14, PRKN, SLC22A3, CYP2C19, AGK, GPAT2, PRDX1, FNTA, GYG1, ATG9B, EGFL8, FMO5, MGAT2, PBK, SIK2, CLK2, NDUFA4, FADS1, STK39, GUK1, CTSZ, HS3ST6, SLC31A1, PLK4, PTPN5, STARD3, CYP2R1, MGST2, PIGA, LGALS13, OBSL1, TOPORS, LIPT2, PDPK1, PPT1, LGSN, PKN3, HS3ST5, MAP3K21, BDH2, SLC5A3, PANK3, ESCO2, PGLS, MARK3, TRMU, CDY1B, PCYT2, CHD9, SLC38A4, PTGIS, INPP5F, RING1, VRK3, AQP5, RNF144B, CYP7A1, SLC25A27, PDIA5, SLC7A11, CYP2A7, CES1, STT3A, SYNJ1, TRMT1, STK33, FKBP10, PNKP, MGAT4D, IL4I1, SLC16A8, HSD17B8, HELZ2, FOSL1, ALG10B, NDUFAF5, PLXNB3, MRPL58, ATP8A1, PDPK1, BCAP31, TGM5, PPP1R3C, PLA2G5, POLR3GL, TXNRD2, ALDH1A3, SPHK1, MRM1, PPP1R2, USP3, FHIT, IMPAD1, CPT1A, SIN3B, AP000812.4, MAPK4, MAP2K6, NME6, NDUFA4, PDE6A, ACAT2, COX10, PFKP, ALDH9A1, FXYD2, CTH, MTHFS, GSS, SEPHS1, METTL16, SLC38A1, POLE4, ATP5PD, PPP1R1A, SLC6A1, CYP27B1, MTRR, CAD, SERPINA3, NGLY1, PEAK1, ADCY1, RIPK3, GALNT18, CES2, SLC43A1, LPO, CA12, TNFRSF21, ANXA3, PPT1, UBLCP1, SLC35B4, ACADVL, SGMS2, SLC22A3, CDK7, PTPRD, ATP6V1E2, HKDC1, NDUFC2, USP6, SH3GLB1, SLCO1A2, UGGT1, TYMS, PHLPP1, SLC2A13, LYZL1, PHLPP2, RING1, SLC25A28, GLT6D1, MYLIP, LPCAT4, KMT2C, CTSC, SLC8A3, RFWD3, NDUFS2, GMPR, BCO1, STAMBP, PTPN22, SEPHS2, IRAK2, MPC1, FUT9, RNF103, AQP6, PPIAL4A, USP17L29, CPA1, NUP210L, SLC10A2, PPT2, NDUFS6, CHFR, MYBBP1A, PLPPR3, PRMT9, FADS3, RENBP, PAFAH1B1, PLCH1, MRM1, SLCO3A1, ALG5, GAD2, EYA2, EEF1A1, BRSK2, SLC27A5, DUSP19, MDH1, NEK9, GMDS, AL160269.1, G6PD, SLC12A3, SLC25A14, MRI1, CHST10, SHPRH, GBA, PLA2G12A, CDK14, TGFBR1, HSPG2, SMYD2, NAA15, CYP4V2, SGPP1, CARNS1, NSUN4, TMEM54, USP21, CLYBL, TPSD1, PLCD4, SLC15A2, NME5, AMY2A, HSD17B11, MYLK2, CNDP2, SPR, SLC7A8, CTDP1, UBE2D1, COASY, PPP2R3A, IMPA1, ETFB, ATP2A2, PRODH, STARD6, INPP5K, POLR1E, PDE1B, GUCY1A2, PYCR2, MAP3K7, SLC29A2, BMP2K, SULT1B1, DCT, TTLL10, DUSP14, ST6GALNAC3, GSTA3, TPMT, RNMT, MDH1, NUP85, SLC29A1, PDE6G, HERC1, ETFB, PTPRZ1, CYP11A1, MET, POR, NAA11, GPAA1, ACAT1, IRAK2, PTPN4, PTPN5, IDH3G, HELZ2, SLC7A9, QTRT2, CBLL2, USP13, FKBP6, USP38, PASK, PTPRB, ST8SIA1, WNK4, NDST3, CYP4F3, ENTPD1, MGAT5, APOC3, LCT, RPEL1, PADI4, PPM1B, NME2, TPSB2, PADI4, PFKM, ZNRD1, SLC2A3, CLOCK, HRASLS2, USP13, STK24, ACSM2A, IL18BP, SULT1E1, SLC1A6, CHST14, AKT2, POLD2, HDLBP, UGDH, NEK4, MDM2, SIRT2, SARDH, GMPPA, PRKG2, USP10

Information paradox



Information paradox

Often it seems that the more information we have, the less we can learn from it.

Using techniques such as clustering and enrichment analysis, we can package the information into bite-sized (human-friendly) pieces.

Gene set analysis (GSA)

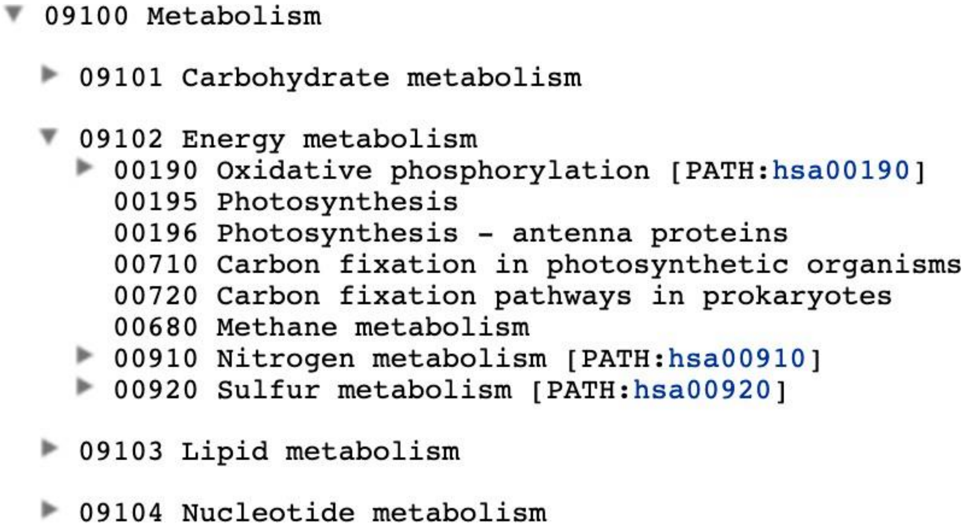
- Identifies patterns associated with the genes of interest
- Gene sets are defined based on shared properties, functions, interactions, etc. of the genes

MSigDB
Molecular Signatures Database

Gene Ontology

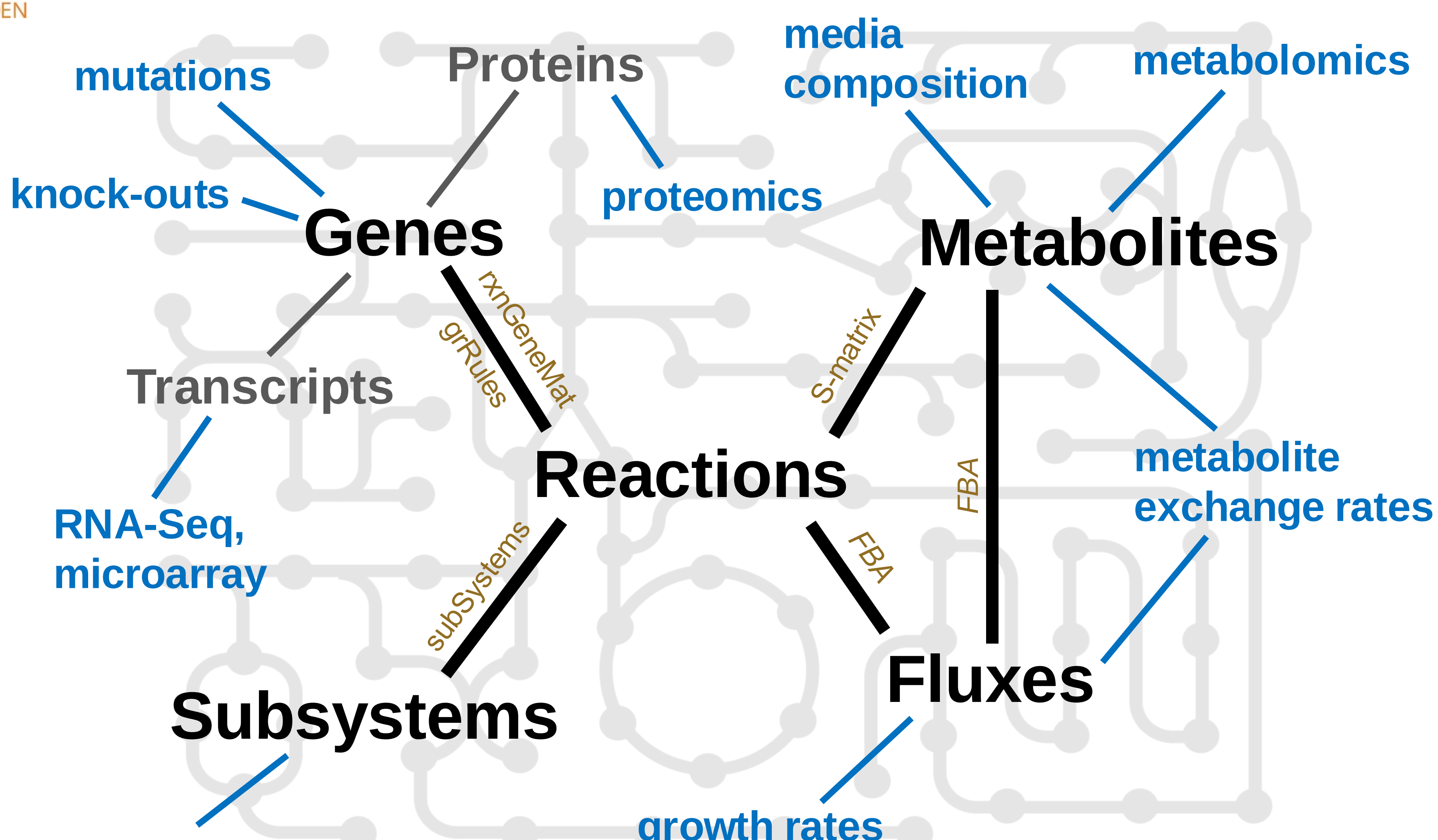
Biological Process	**Molecular Function**
Actin crosslink formation	Glucosidase activity
mRNA transport	Alpha actinin binding
Carbohydrate transport	Cytokine activity
Regulation of catabolic process	Oxidized DNA binding
Erythrocyte development	Iron ion binding
...	...

KEGG Pathways

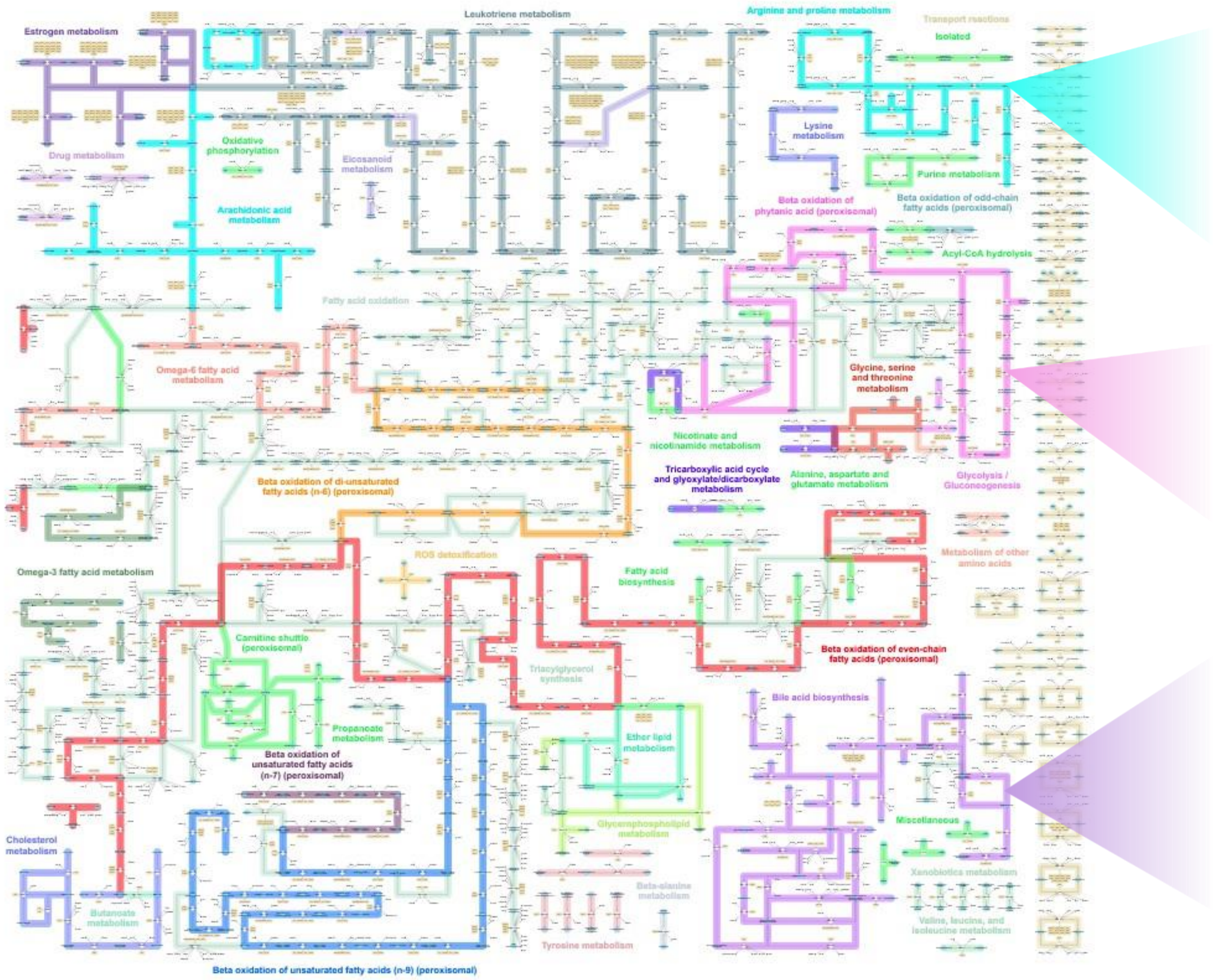


```
▼ 09100 Metabolism

  ▶ 09101 Carbohydrate metabolism

  ▼ 09102 Energy metabolism
    ▶ 00190 Oxidative phosphorylation [PATH:hsa00190]
      00195 Photosynthesis
      00196 Photosynthesis - antenna proteins
      00710 Carbon fixation in photosynthetic organisms
      00720 Carbon fixation pathways in prokaryotes
      00680 Methane metabolism
    ▶ 00910 Nitrogen metabolism [PATH:hsa00910]
    ▶ 00920 Sulfur metabolism [PATH:hsa00920]

  ▶ 09103 Lipid metabolism

  ▶ 09104 Nucleotide metabolism
```

GEM-derived gene sets



Subsystem gene sets



Arginine and proline metabolism

ABHD14A-ACY1 ACY1 AGMAT ALDH18A1 ALDH1B1 ALDH2 ALDH3A2 ALDH4A1 ALDH7A1 ALDH8A1 ALDH9A1 AMD1 AOC1 AOC2 AOC3 ARG1 ARG2 AZIN2 CA5A CA5B CARNS1 CKB CKM CKMT1A CKMT1B CKMT2 CNDP1 CNDP2 DAO DHPS FAR1 FAR2 GAMT GOT1 GOT2 HOGA1 LEFTY1 MAOA MAOB MTAP …

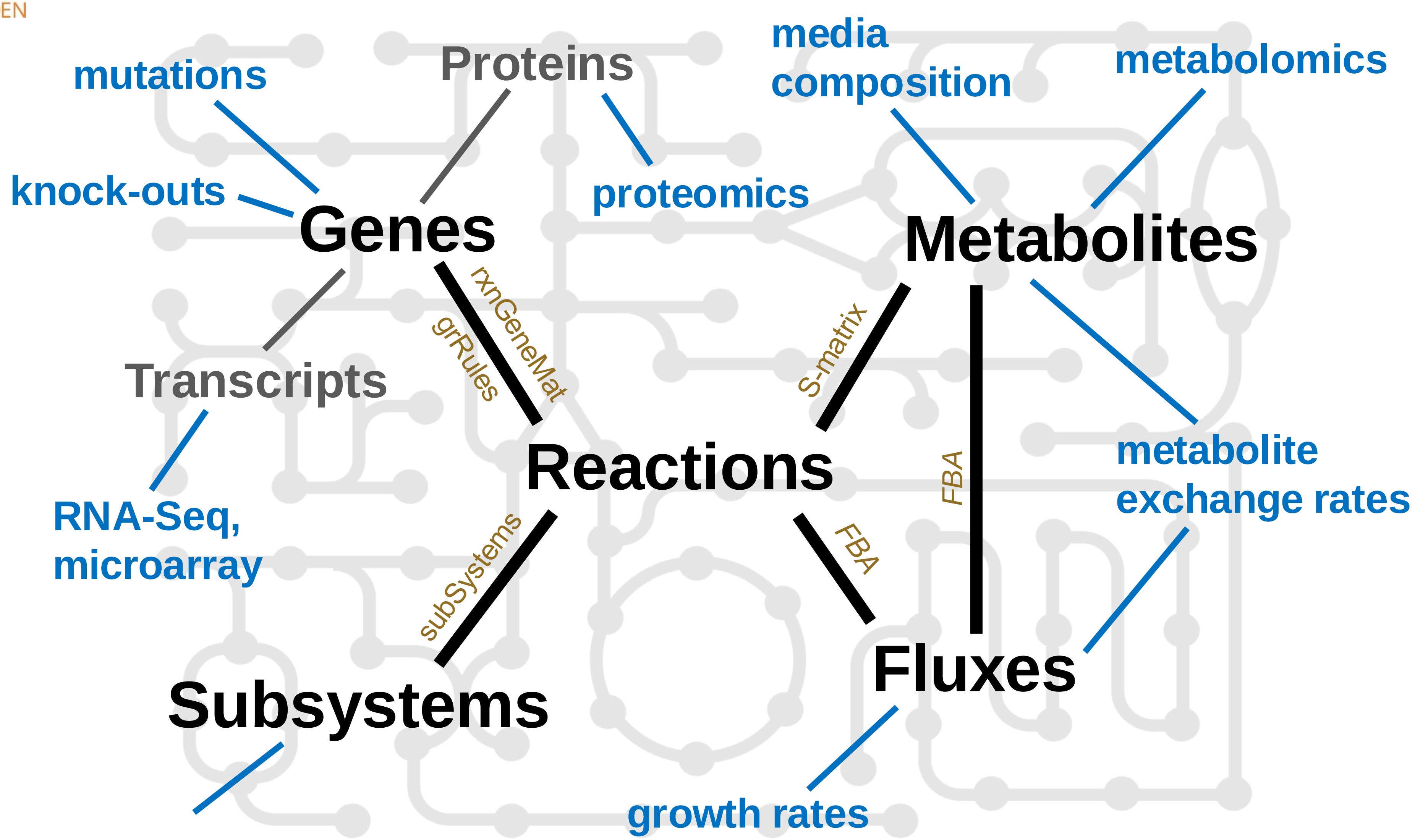
Beta oxidation of phytanic acid

ACAA1 ACOT2 ACOT4 ACOX1 ACOX3 ACSBG1 ACSBG2 ACSL1 ACSL3 ACSL4 ACSL5 ACSL6 AMACR ECI1 ECI2 EHHADH HACL1 HADHA HSD17B4 KRTAP11-1 MEIKIN MYO5B PHYH SLC27A2 …

Bile acid biosynthesis

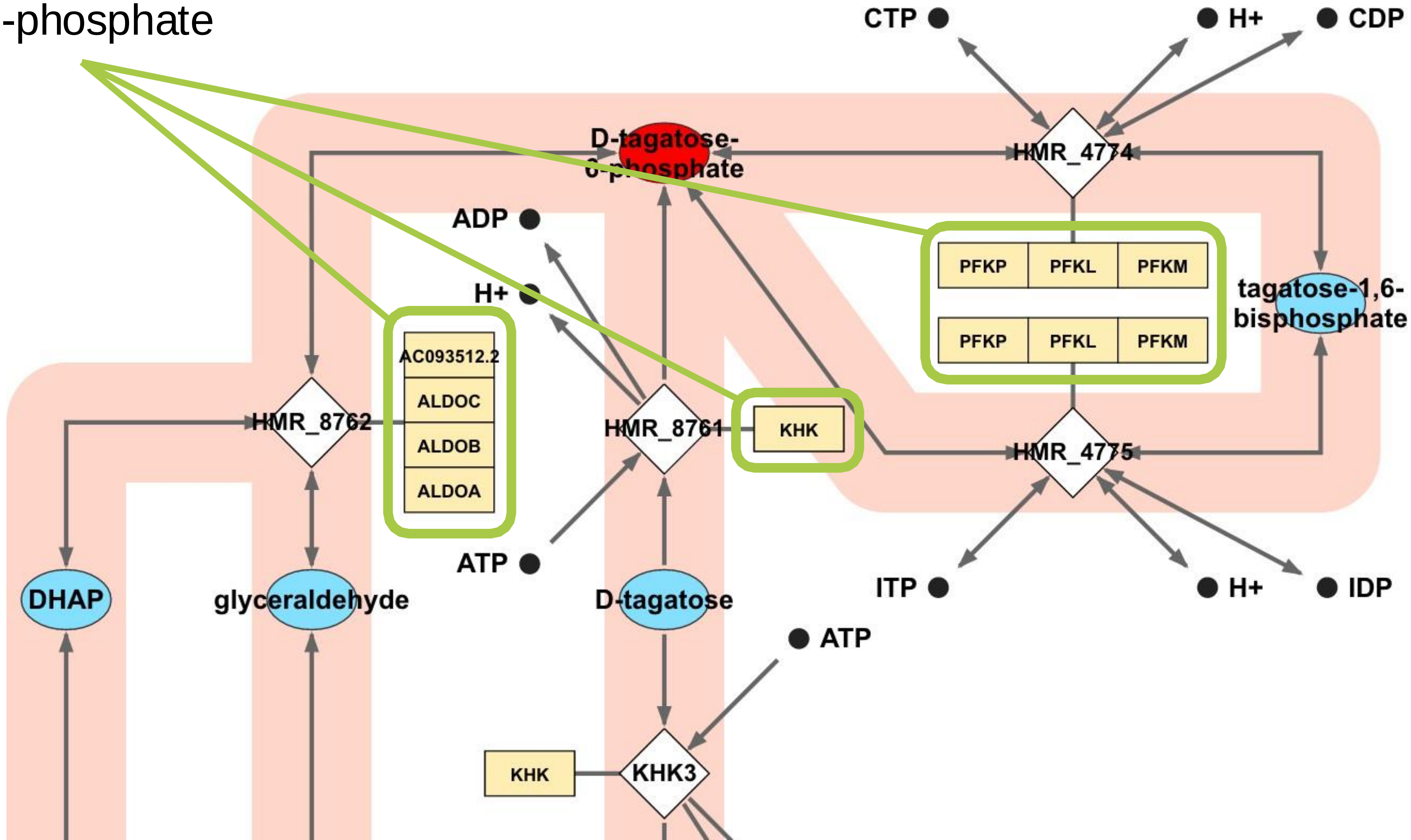
ABCB11 ABCC11 ABCC3 ABCD1 ACAA1 ACAA2 ACOT1 ACOT2 ACOT4 ACOT6 ACOT7 ACOT8 ACOX1 ACOX2 ACOX3 ADH1A ADH1B ADH1C ADH4 ADH5 ADH6 ADH7 ADHFE1 ADO AKR1B10 AKR1B15 AKR1C1 AKR1C2 AKR1C3 AKR1C4 AKR1D1 ALDH1B1 ALDH2 ALDH3A1 ALDH3A2 ALDH7A1 ALDH9A1 AMACR BAAT BCAP31 …

GEM-derived gene sets



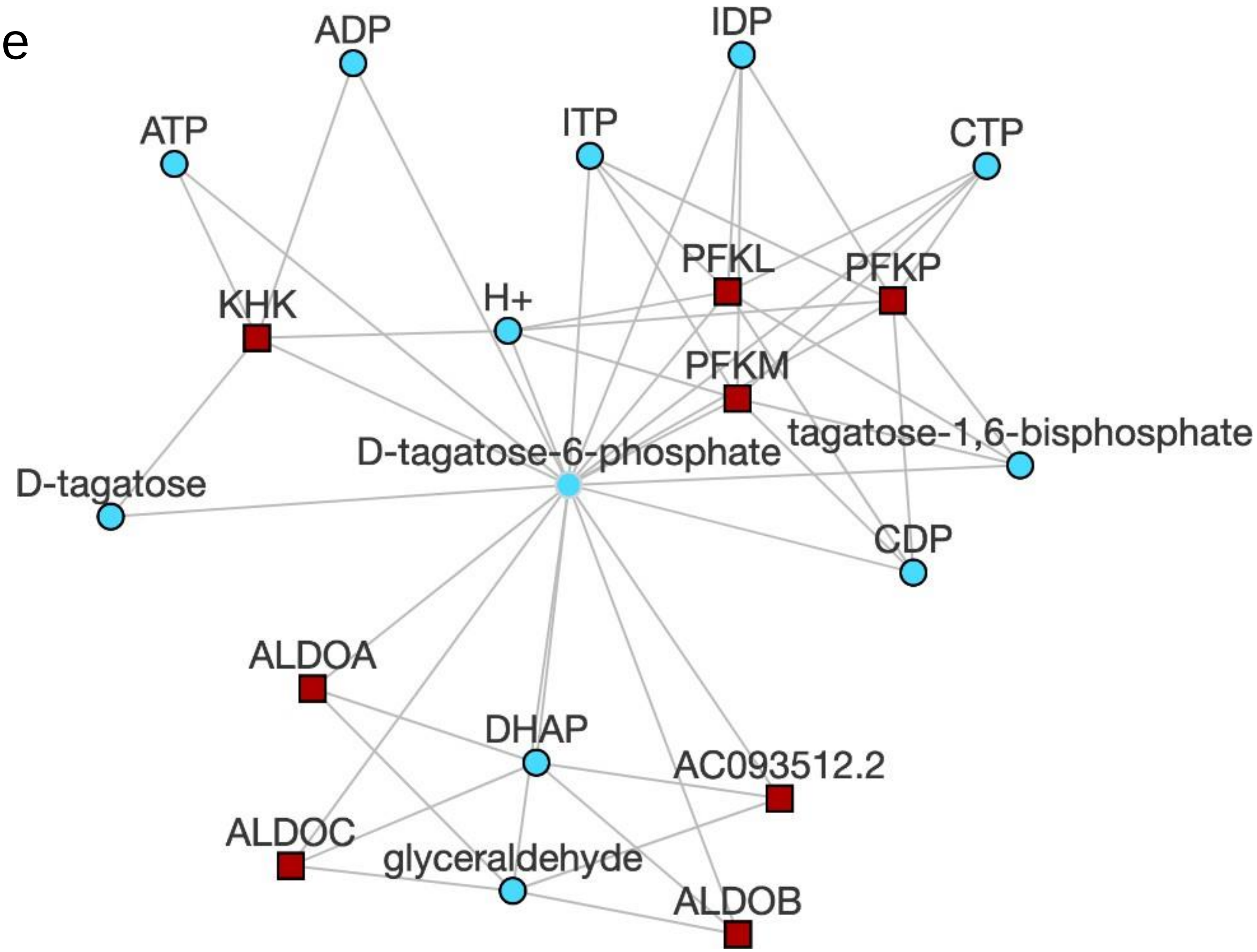
Reporter metabolites

Genes associated with
D-tagatose-6-phosphate



Reporter metabolites

D-tagatose-6-phosphate
interaction partners

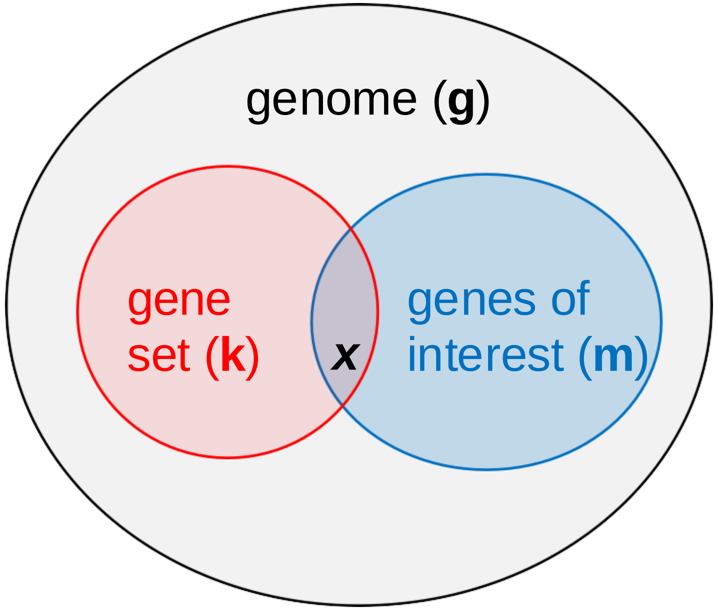


Gene list enrichment

Enrichment or over-representation analysis

Given a list of ***m*** genes of interest out of ***g*** in the genome and a gene-set of ***k*** genes, a statistical enrichment returns the probability that ***x*** out of the ***m*** genes of interest are in the gene-set.

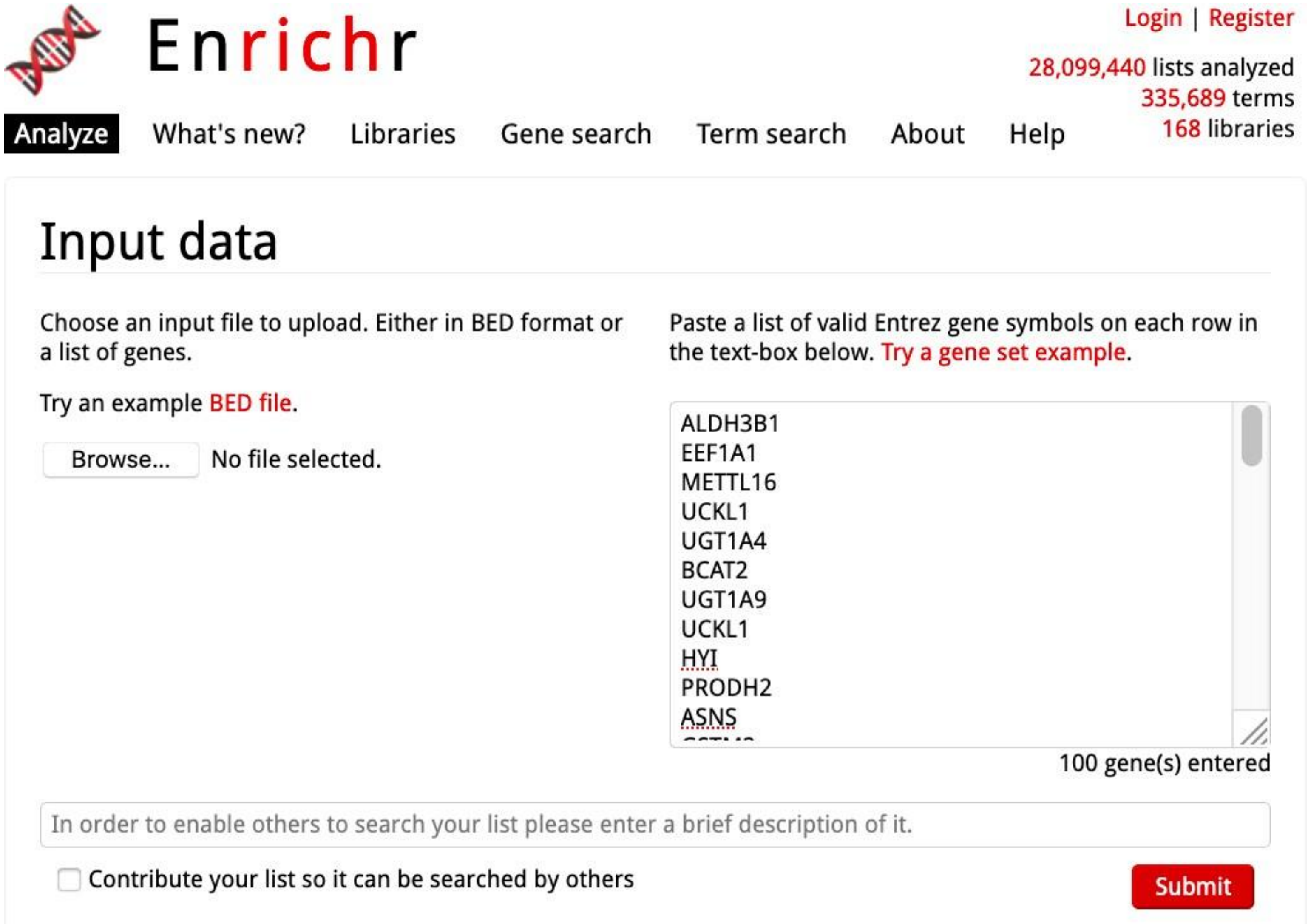
This is calculated using Fisher’s Exact Test (hypergeometric test):



$$p = \frac{\binom{k}{x}\binom{g-k}{m-x}}{\binom{g}{m}}$$

note: $\binom{n}{k} = \frac{n!}{k!(n-k)!}$

Gene list enrichment



28,099,440 lists analyzed
335,689 terms
168 libraries

Input data

Choose an input file to upload. Either in BED format or a list of genes.

Try an example BED file.

No file selected.

Paste a list of valid Entrez gene symbols on each row in the text-box below. Try a gene set example.

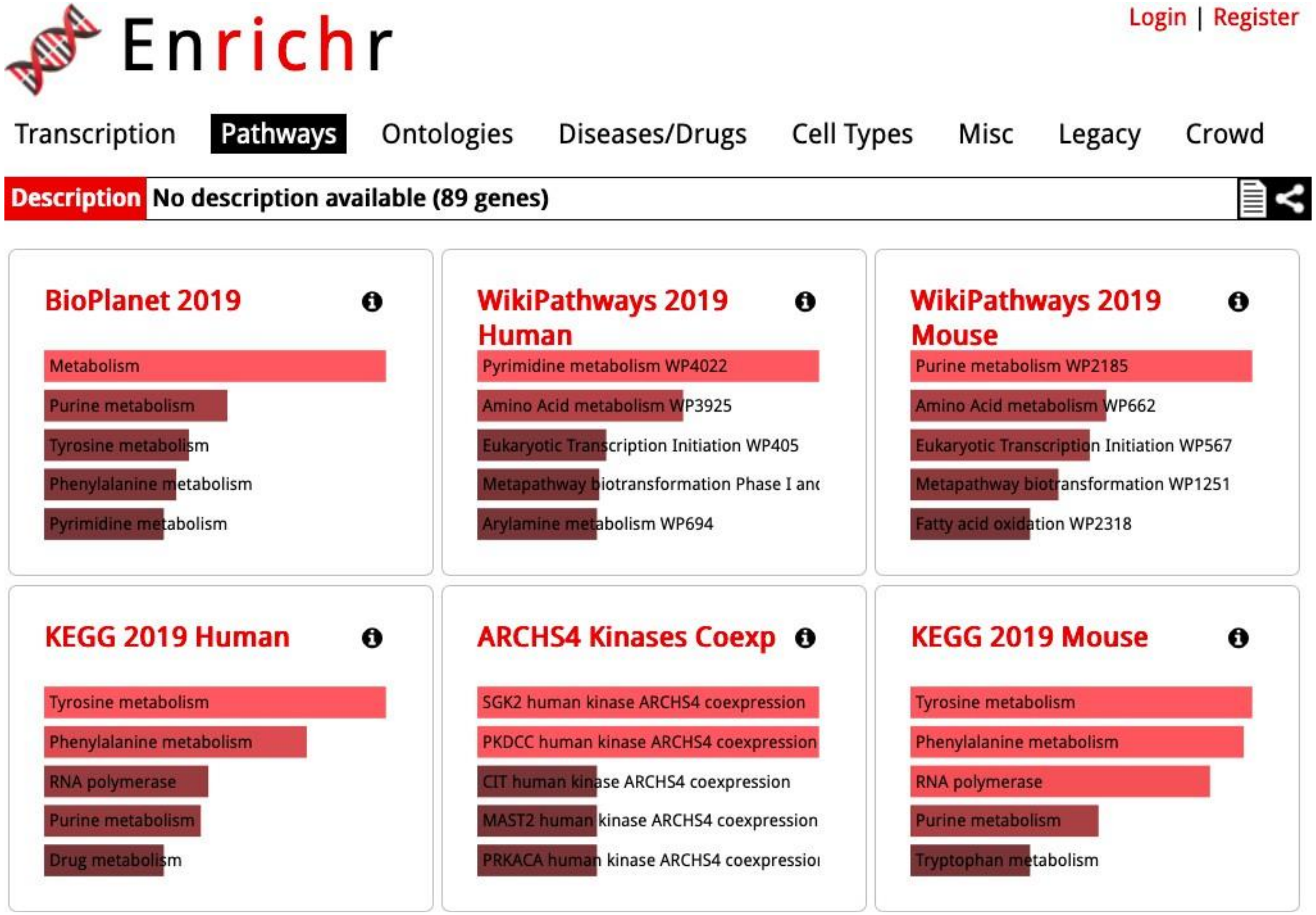
```
ALDH3B1
EEF1A1
METTL16
UCKL1
UGT1A4
BCAT2
UGT1A9
UCKL1
HYI
PRODH2
ASNS
```

100 gene(s) entered

In order to enable others to search your list please enter a brief description of it.

☐ Contribute your list so it can be searched by others

Gene list enrichment



Description No description available (89 genes)

BioPlanet 2019
- Metabolism
- Purine metabolism
- Tyrosine metabolism
- Phenylalanine metabolism
- Pyrimidine metabolism

WikiPathways 2019 Human
- Pyrimidine metabolism WP4022
- Amino Acid metabolism WP3925
- Eukaryotic Transcription Initiation WP405
- Metapathway biotransformation Phase I anc
- Arylamine metabolism WP694

WikiPathways 2019 Mouse
- Purine metabolism WP2185
- Amino Acid metabolism WP662
- Eukaryotic Transcription Initiation WP567
- Metapathway biotransformation WP1251
- Fatty acid oxidation WP2318

KEGG 2019 Human
- Tyrosine metabolism
- Phenylalanine metabolism
- RNA polymerase
- Purine metabolism
- Drug metabolism

ARCHS4 Kinases Coexp
- SGK2 human kinase ARCHS4 coexpression
- PKDCC human kinase ARCHS4 coexpression
- CIT human kinase ARCHS4 coexpression
- MAST2 human kinase ARCHS4 coexpression
- PRKACA human kinase ARCHS4 coexpressio

KEGG 2019 Mouse
- Tyrosine metabolism
- Phenylalanine metabolism
- RNA polymerase
- Purine metabolism
- Tryptophan metabolism

Gene list enrichment

Limitations

- Requires arbitrary cutoff to define gene list
- Does not correct for gene-gene correlations
  (false positives)
- No ranking or relative scoring of genes
  (gene at the top of the list is identical to bottom)

Gene set analysis

List of genes

ENOPH1
SLC25A2
GMPPB
SLC1A4
EGFL8
HDC

Includes **only** the genes of interest

Gene-level statistics

0.01	A4GALT
0.89	A4GNT
0.51	AAAS
0.02	AACS
0.33	AADAC
0.08	AADAT
…	…

Includes **ALL** measured/ detected genes

Types of statistics:

- Differential expression p-value
- Differential expression fold-change
- Coefficient or significance of correlation (with phenotype)
- Rank

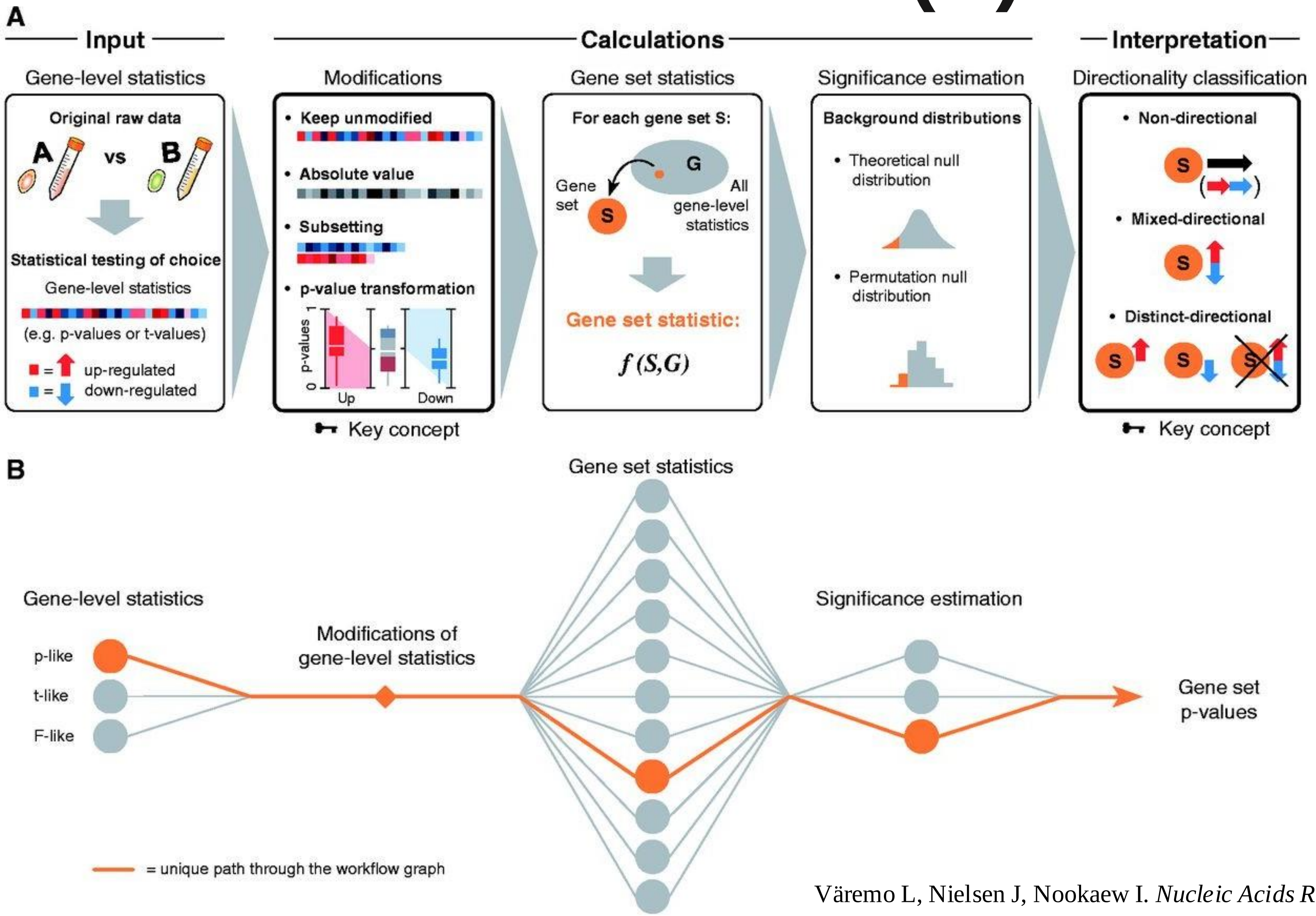
Gene set analysis

General GSA procedure

1. **Score each gene set** based on the statistics of the genes it contains
2. **Evaluate the significance** of each gene set score based on the score of the null or “background” score distribution

There are ***many*** methods for both steps 1 and 2

GSA Tools: Piano (R)



Väremo L, Nielsen J, Nookaew I. *Nucleic Acids Res.* 2013;41(8):4378-4391.

GSA Tools: Piano (R)

Gene-level statistics (DE results)

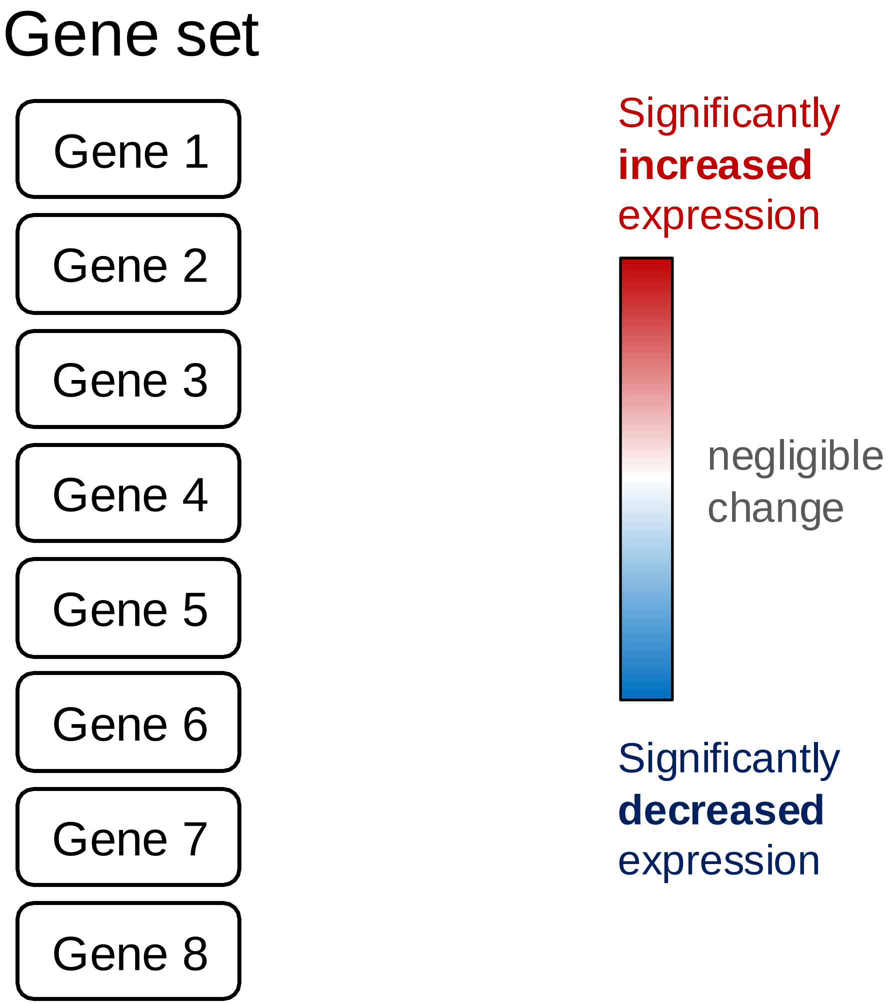
Gene	log2FC	p-value
ENOPH1	-2.4	0.0003
SLC25A2	1.1	0.09
GMPPB	0.3	0.8
SLC1A4	-0.9	0.2
EGFL8	-1.8	0.04
HDC	-6.2	0.0001
A4GALT	3.1	0.0002
...	...	...

GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

Non-directional:

Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.



Gene set

Gene 1

Gene 2

Gene 3

Gene 4

Gene 5

Gene 6

Gene 7

Gene 8

Significantly **increased** expression

negligible change

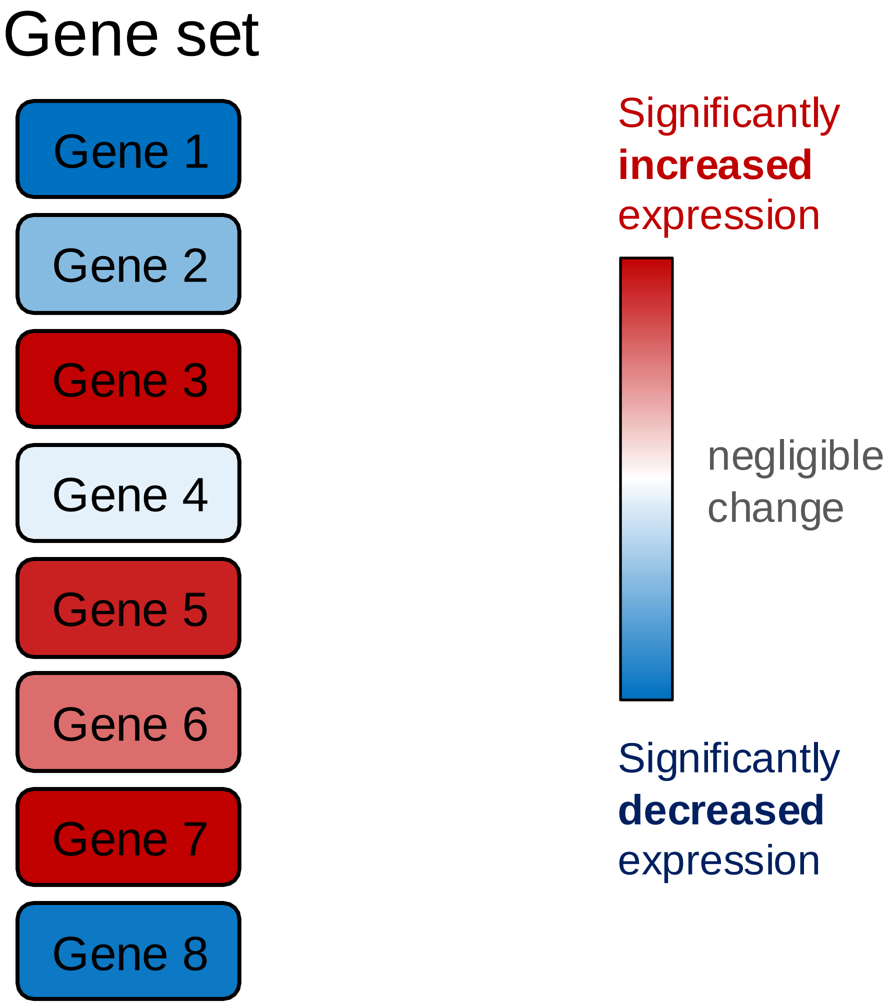
Significantly **decreased** expression

GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

✓ **Non-directional:**

Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.



GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

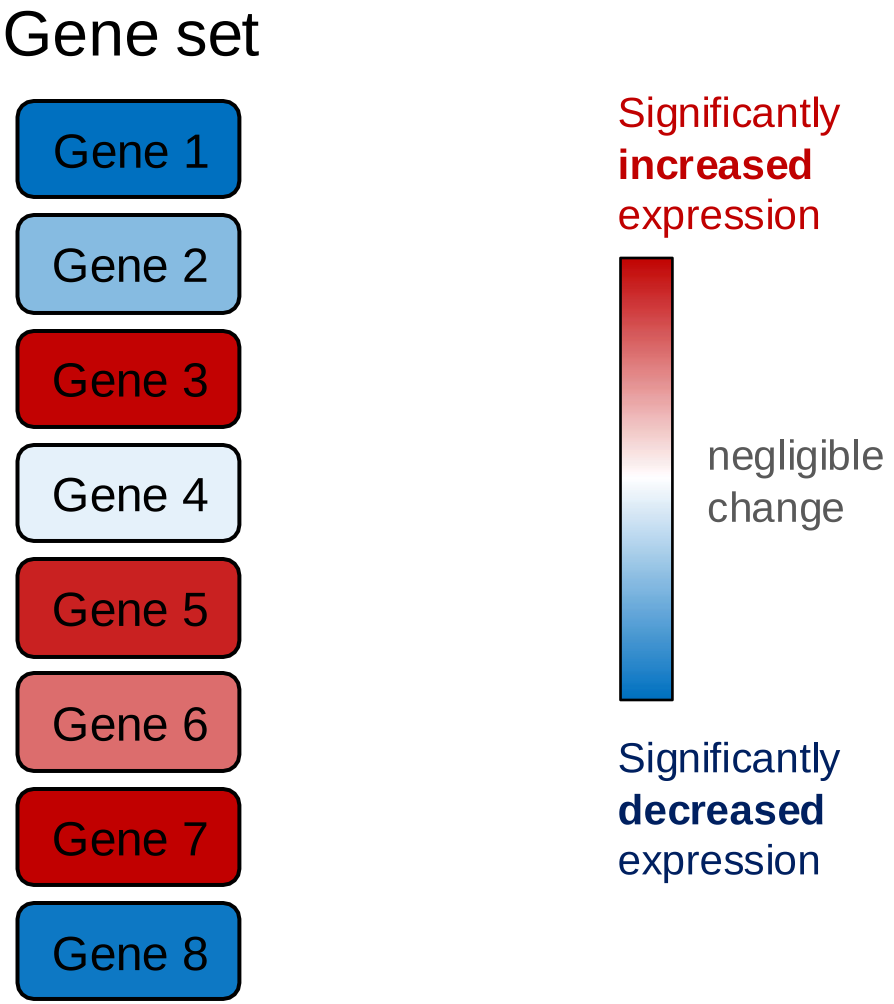
✓ **Non-directional:**

Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.

✓ ✓

Mixed-directional (down and up):

Test if a *subset* of the gene set is enriched in significantly increased or decreased genes



GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

✓ **Non-directional:**

Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.

✓ ✓

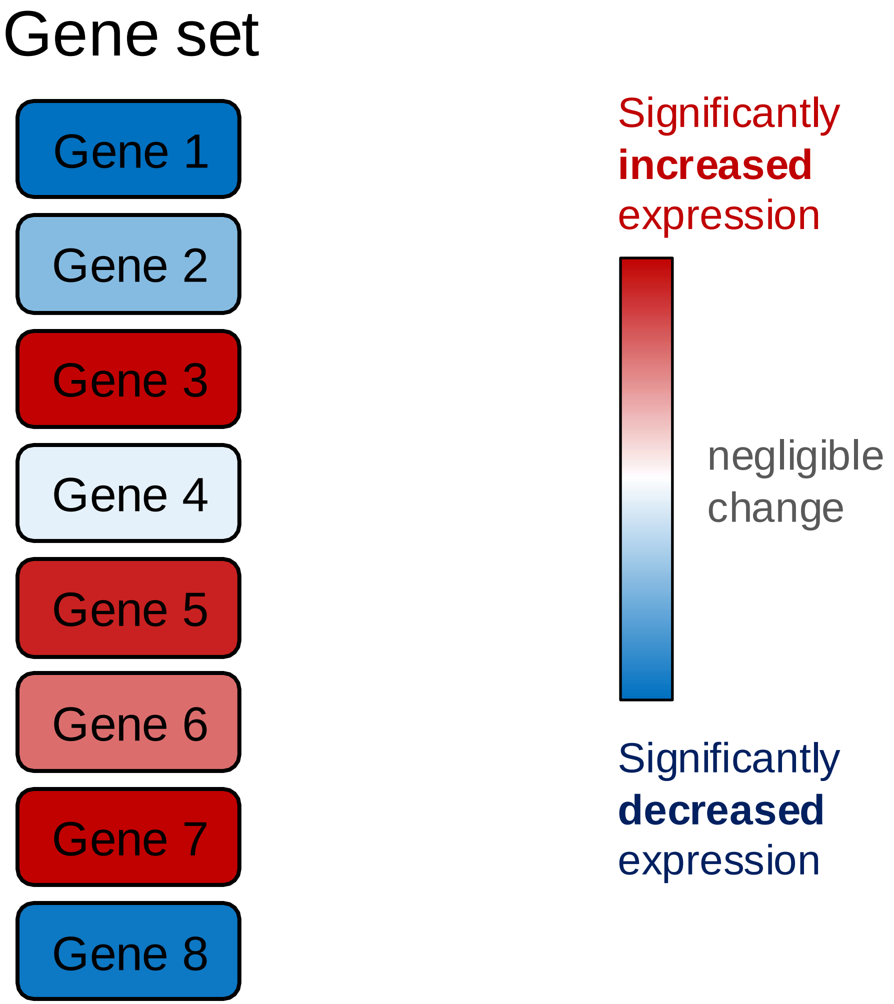
Mixed-directional (down and up):

Test if a *subset* of the gene set is enriched in significantly increased or decreased genes

✗ ✗

Distinct-directional (down and up):

Test if the gene set is enriched in significantly increased or decreased genes



GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

⊗ **Non-directional:**

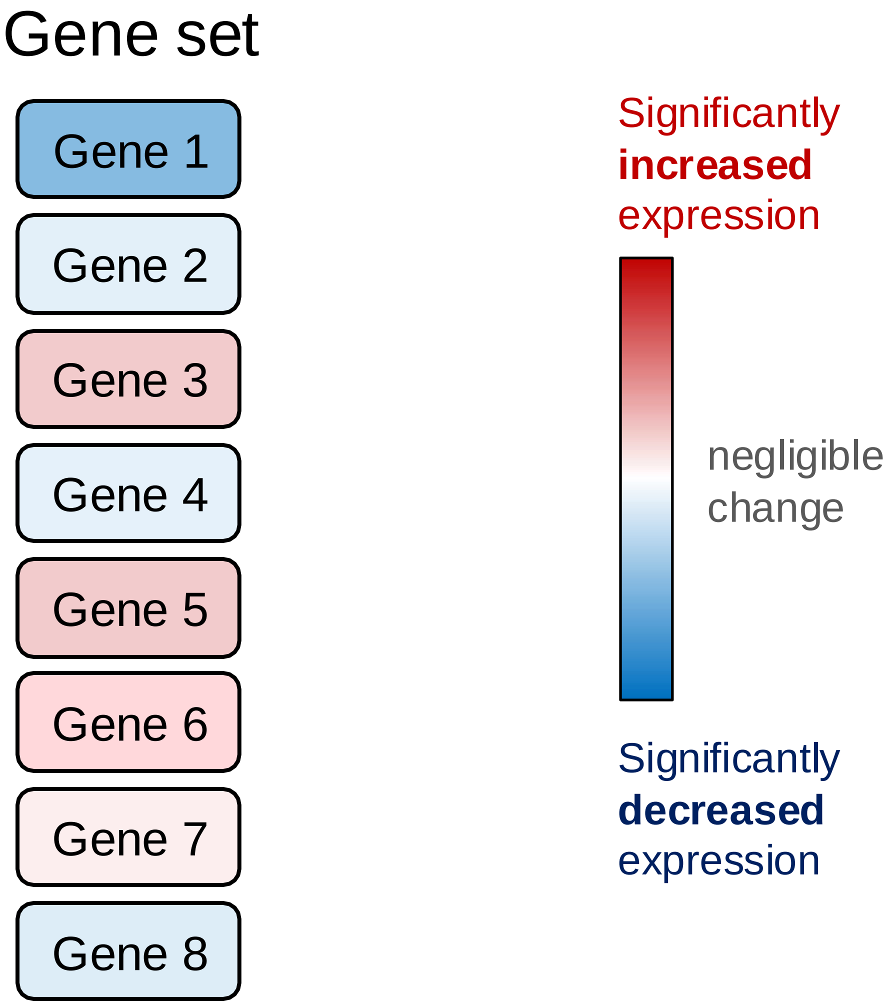
Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.

Mixed-directional (down and up):

Test if a *subset* of the gene set is enriched in significantly increased or decreased genes

Distinct-directional (down and up):

Test if the gene set is enriched in significantly increased or decreased genes



GSA Tools: Piano (R)

For each gene set, we can calculate 5 different p-values:

? **Non-directional:**

Test for enrichment of significant (low p-value) genes, ignoring fold-change direction.

✗ ?

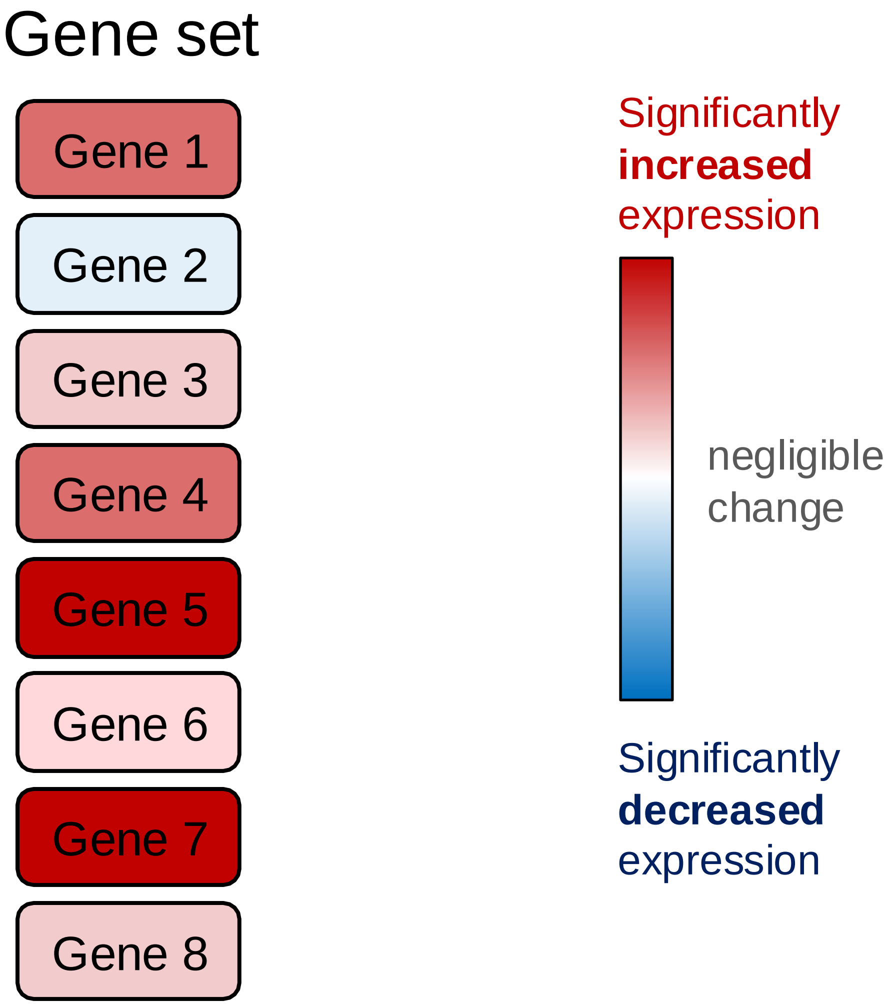
Mixed-directional (down and up):

Test if a *subset* of the gene set is enriched in significantly increased or decreased genes

✗ ✓

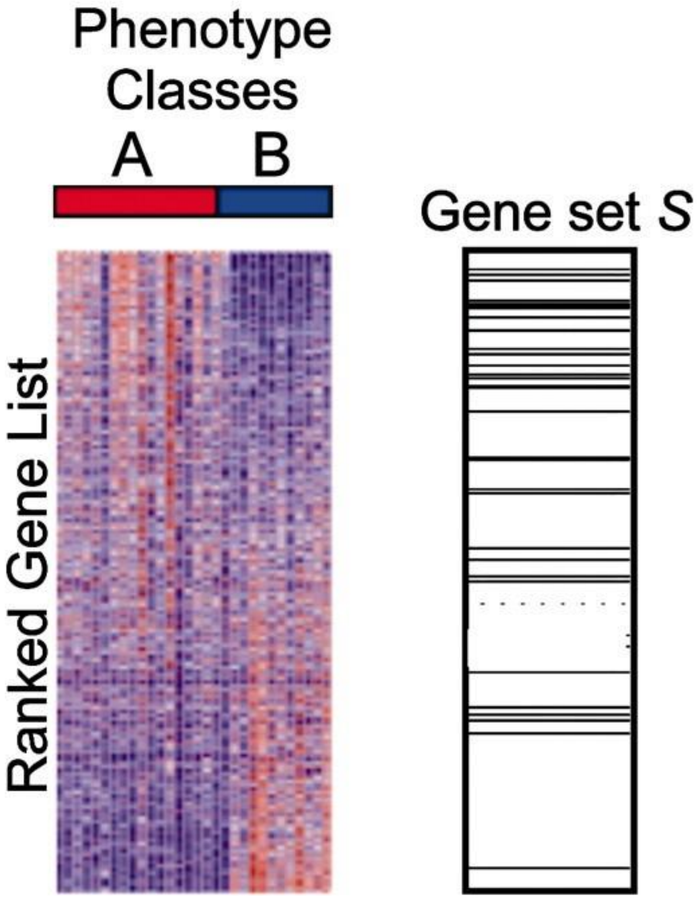
Distinct-directional (down and up):

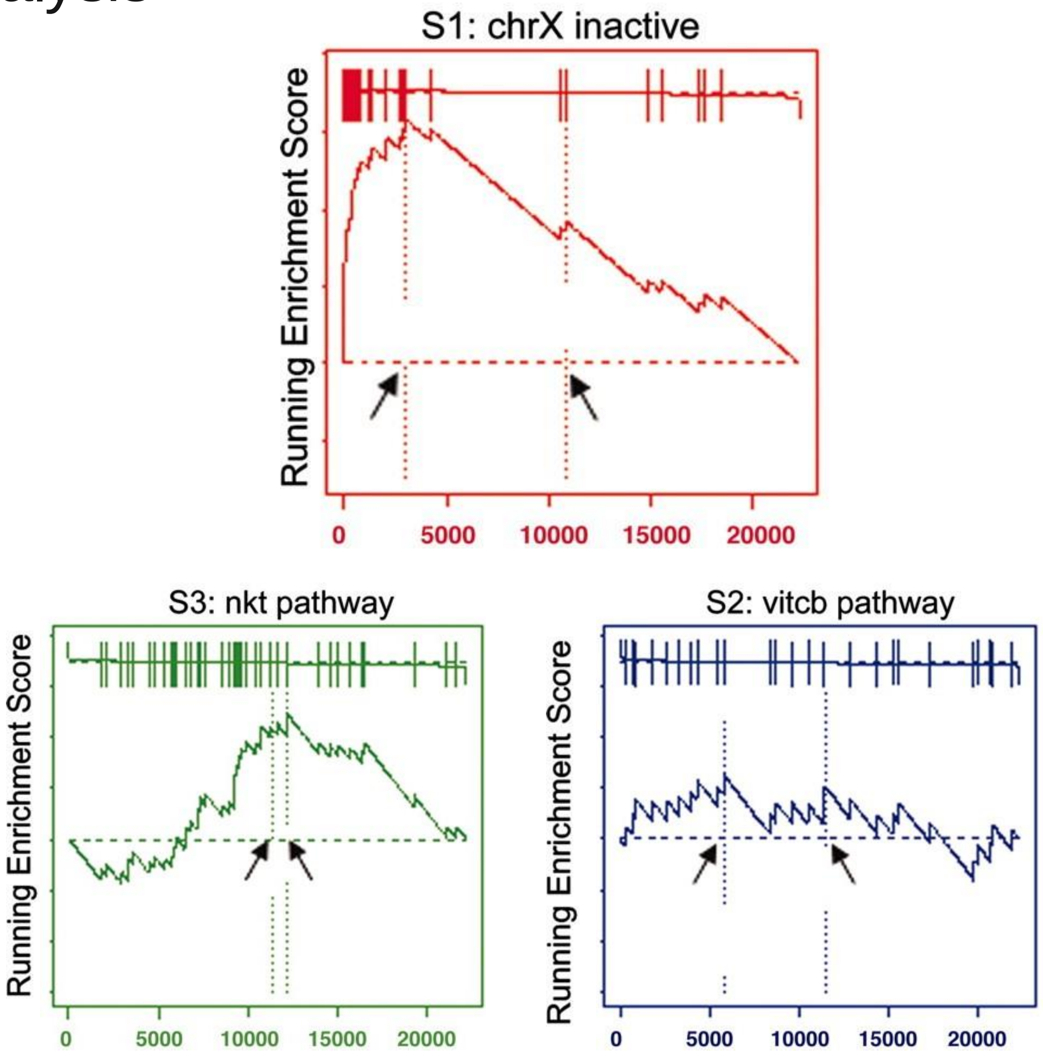
Test if the gene set is enriched in significantly increased or decreased genes



GSA Tools: GSEA (R, python)

Gene **S**et **E**nrichment **A**nalysis

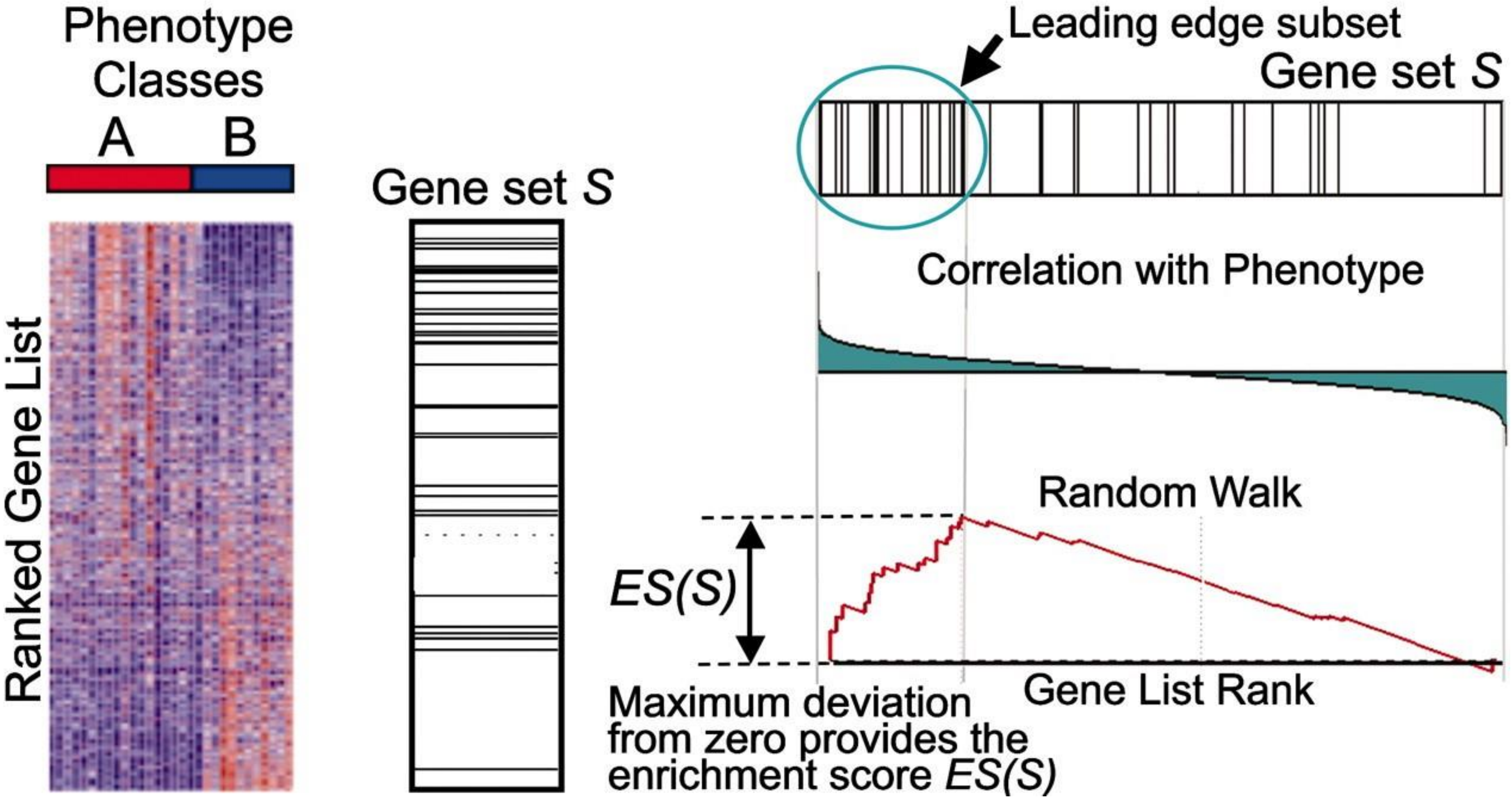




Subramanian, A, et al. *PNAS* 2005, 102 (43) 15545-15550

GSA Tools: GSEA (R, python)

Gene **S**et **E**nrichment **A**nalysis



Subramanian, A, et al. *PNAS* 2005, 102 (43) 15545-15550

Context-specific GEMs

A GEM contains all metabolic reactions that are known to occur within an organism

When working with multicellular organisms (e.g., humans), the **“generic” GEM containing all reactions** is not representative of any real cell or tissue type

We can use omics data to **extract a subset** of the generic GEM that is active in our system of interest

This GEM is called an “**extracted**” or **context-specific** GEM

Context-specific GEMs

There are many methods to generate context-specific GEMs.

For example:

- **iMAT** (Integrative Metabolic Analysis Tool)
- **MBA** (Model Building Algorithm)
- **mCADRE** (metabolic Context-specificity Assessed by Deterministic Reaction Evaluation)
- **tINIT** (Task-driven Integrative Network Inference for Tissues)
- **FASTCORE**

Unfortunately, they were all implemented in MATLAB.

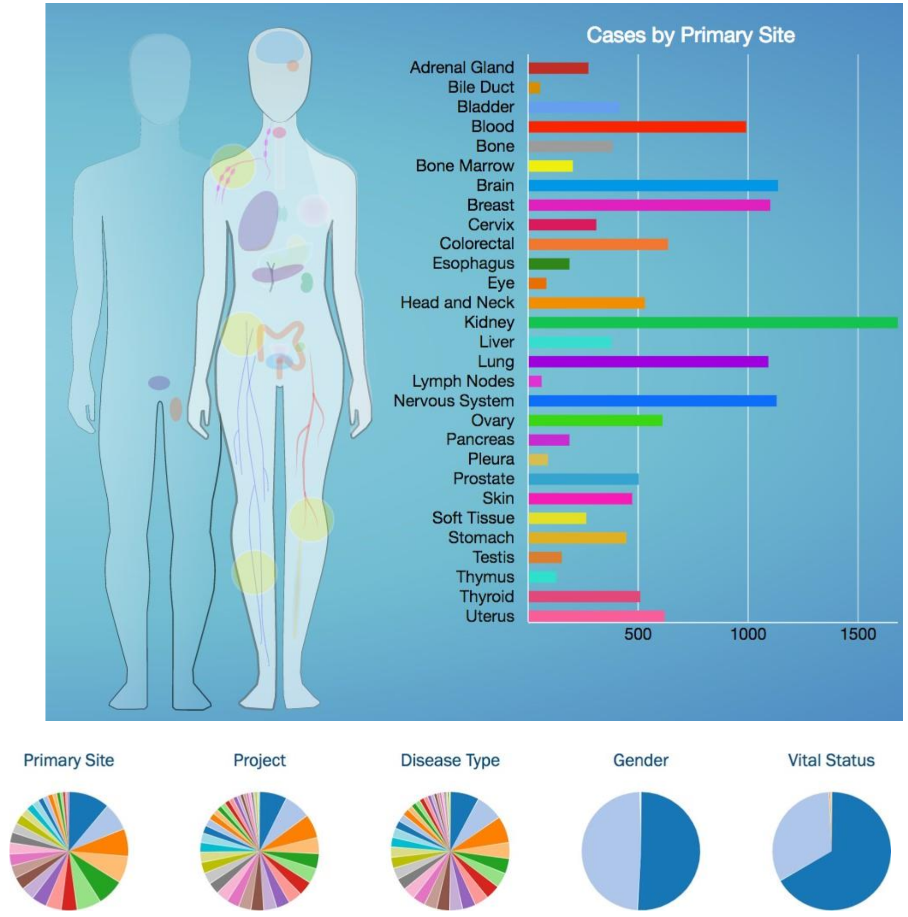
Here are some links to tutorials to using some of the methods:

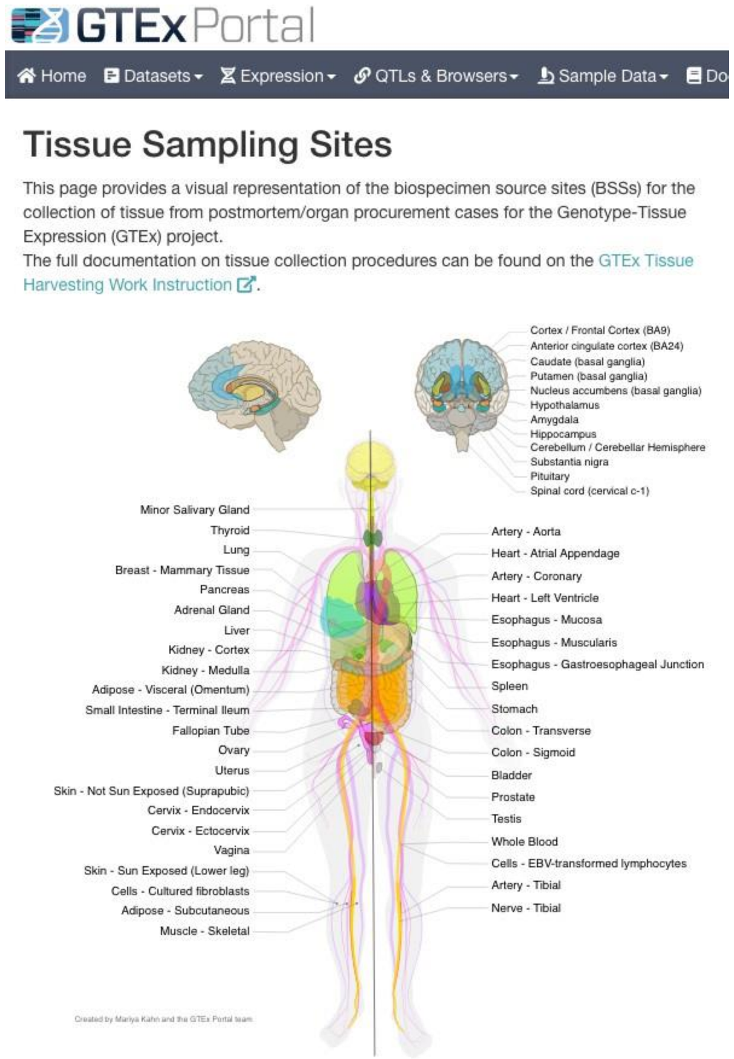
tINIT: https://sysbiochalmers.github.io/Human-GEM-guide/gem_extraction/
iMAT: https://opencobra.github.io/cobratoolbox/stable/tutorials/tutorialExtractionTranscriptomic.html

GEM-based comparison of transcriptomes

From the study Robinson, et al. An atlas of human metabolism. *Science Signaling* 2020

THE CANCER GENOME ATLAS
National Cancer Institute
National Human Genome Research Institute



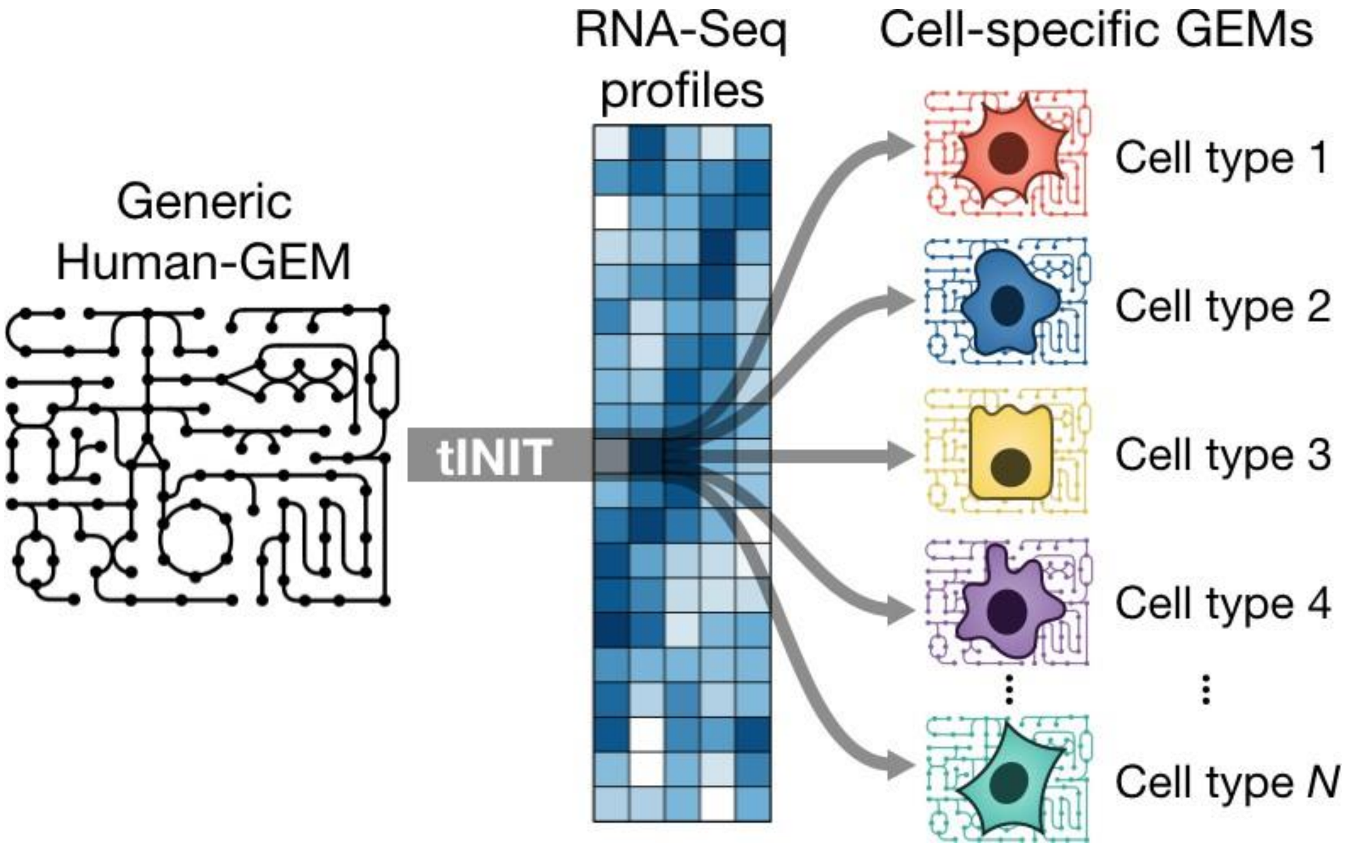


Tissue Sampling Sites

This page provides a visual representation of the biospecimen source sites (BSSs) for the collection of tissue from postmortem/organ procurement cases for the Genotype-Tissue Expression (GTEx) project.
The full documentation on tissue collection procedures can be found on the GTEx Tissue Harvesting Work Instruction.

GEM-based comparison of transcriptomes

Context-specific GEMs were extracted for each of the cancer types and healthy tissue types



GEM-based comparison of transcriptomes

GEM structure (reaction content) can be represented by a binary vector

Reaction	Lung Tumor	Lung Paired	Lung Healthy	Brain Tumor	Brain Paired
rxn1	1	0	1	1	1
rxn2	0	1	1	1	1
rxn3	0	0	0	0	0
rxn4	0	1	0	1	0
rxn5	1	1	0	1	1
rxn6	1	0	0	1	0
rxn7	0	0	1	1	0

…

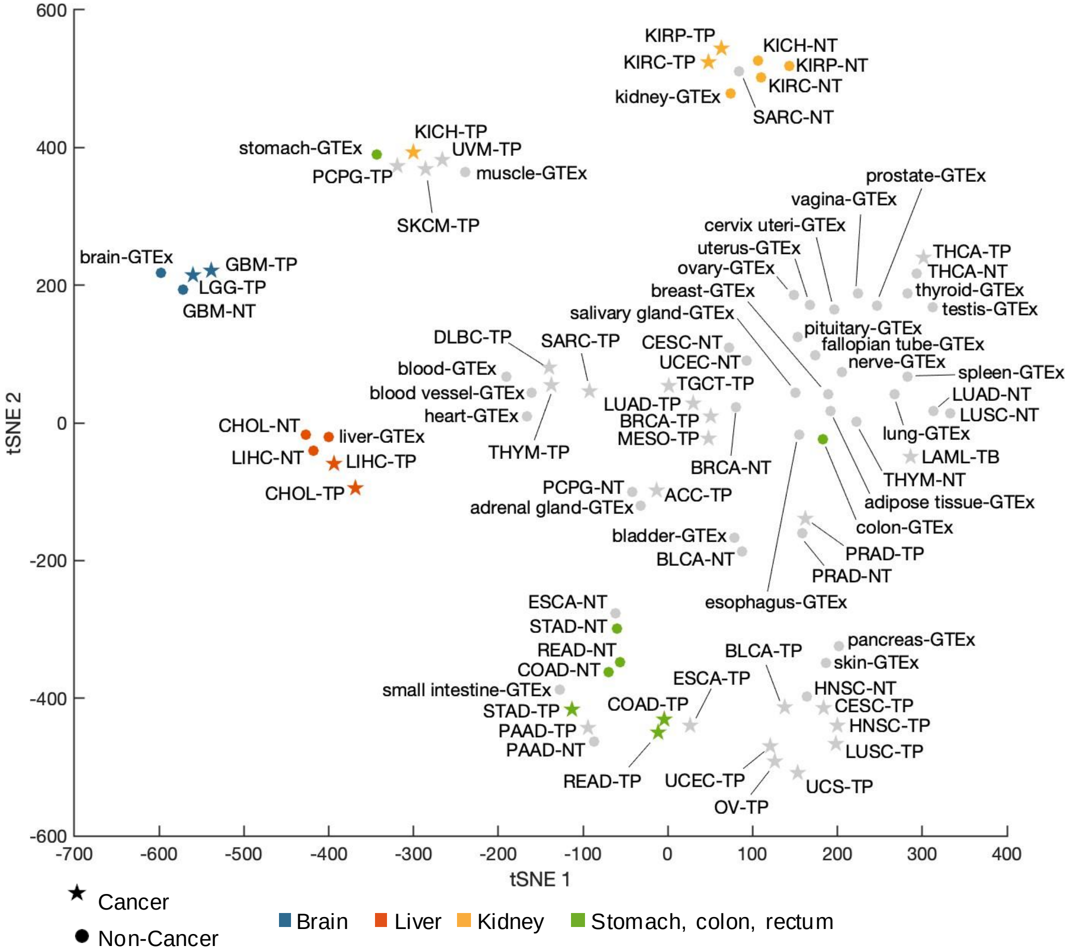
⋮ ⋱

Model **contains** reaction

Model **missing** reaction

GEM-based comparison of transcriptomes

Distance (Hamming) between each GEM reaction content vector can be calculated and projected in a tSNE embedding



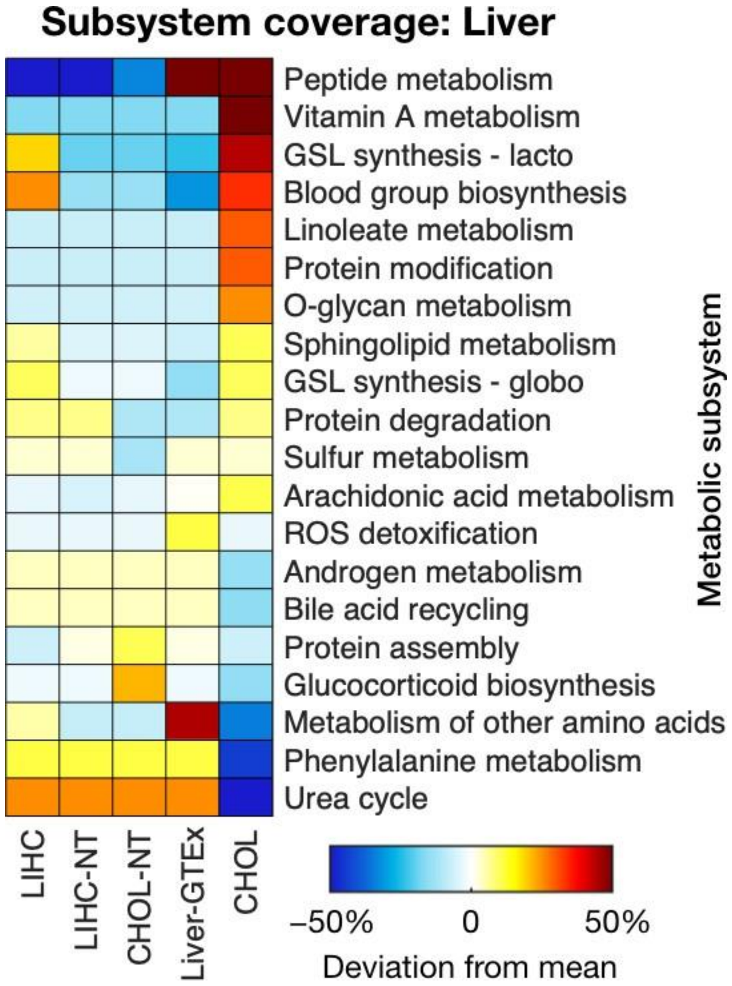
GEM-based comparison of transcriptomes

If reaction subsystem labels are included, we can look at subsystem-specific differences between GEMs

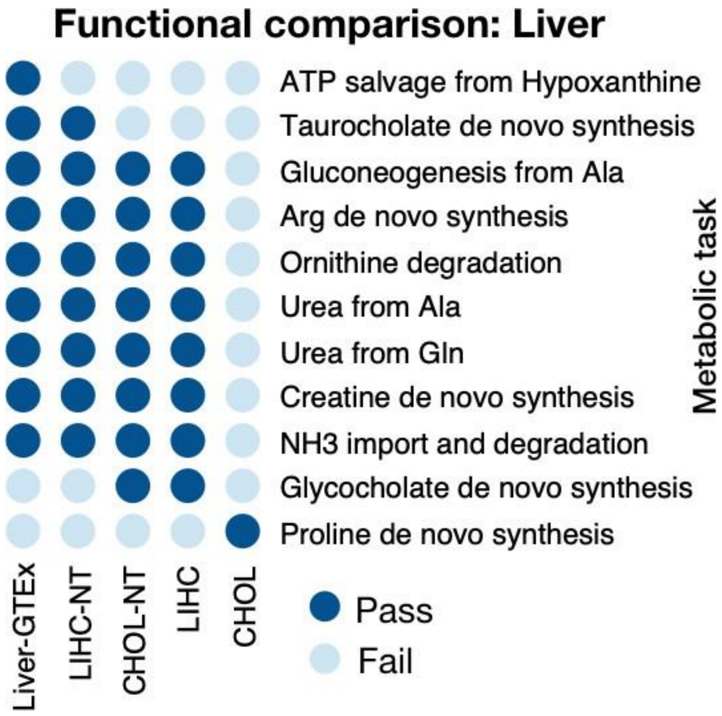
Subsystem	Reaction	Lung Tumor	Lung Paired	Lung Healthy	Brain Tumor	Brain Paired	…
TCA cycle	rxn1	1	0	1	1	1	
TCA cycle	rxn2	0	1	1	1	1	
Glycolysis	rxn3	0	0	0	0	0	
TCA cycle	rxn4	0	1	0	1	0	
Fatty acid oxidation	rxn5	1	1	0	1	1	
Carnitine shuttle	rxn6	1	0	0	1	0	
Glycolysis	rxn7	0	0	1	1	0	
	⋮						⋱

GEM-based comparison of transcriptomes

If reaction subsystem labels are included, we can look at subsystem-specific differences between GEMs



Furthermore, FBA can be used to determine what metabolic functions the GEMs can or cannot perform



Exercise: GEM-based GSA

Exercise: (Rstudio)

Use the GEM-derived gene set collections to evaluate enrichment of differentially expressed genes in different regions of the metabolic network.