

# Metabolizer: a web tool for analysis of modular architecture of metabolic pathways using transcriptomic data

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PhD in Biotechnology

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# High-Throughput Technologies

Next Generation Sequencing (NGS)



Microarrays

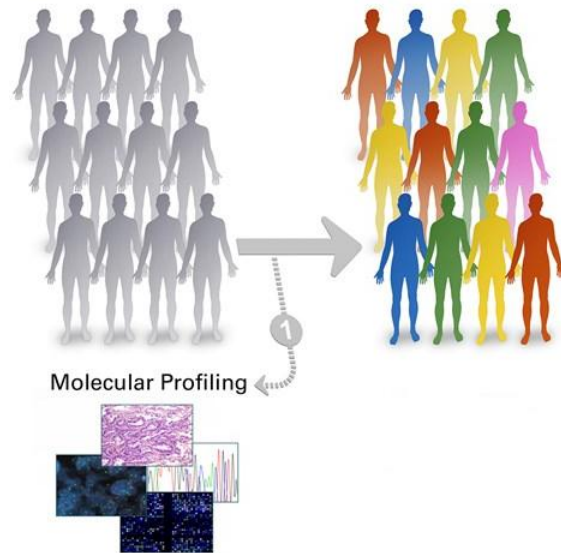


## Different Omics Data:



- Gene Expression (~ 30,000 genes)
- Mutation
- Copy Number Variation
- Methylation
- ...etc.

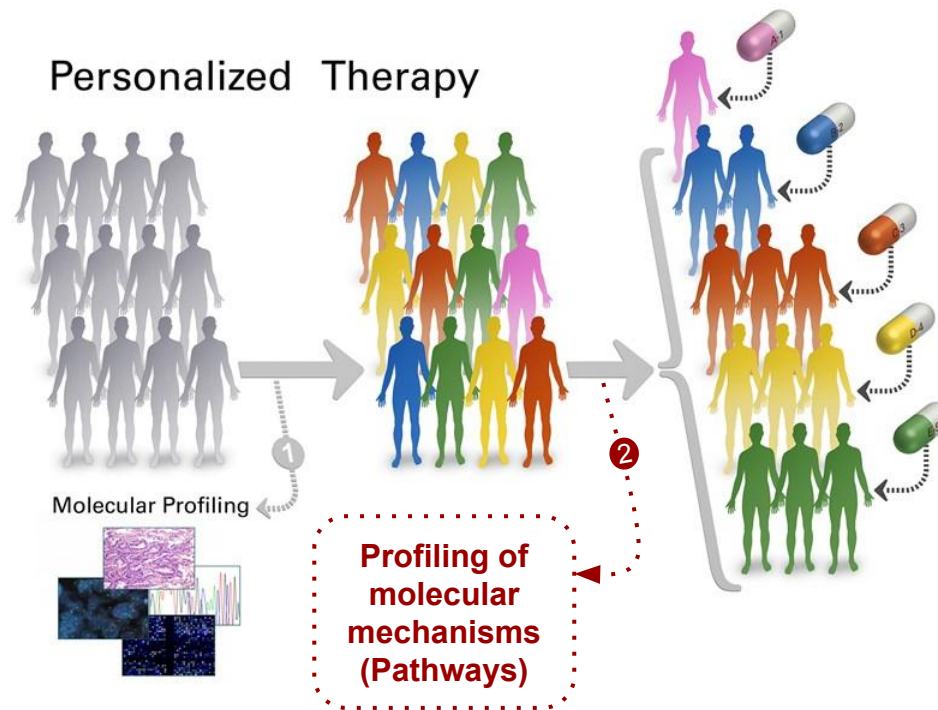
# OMICS: Biomedical Perspectives



pct.mdanderson.org

Genomic and transcriptomic data let us to identify subgroups of patients with the same disease.

# OMICS: Biomedical Perspectives

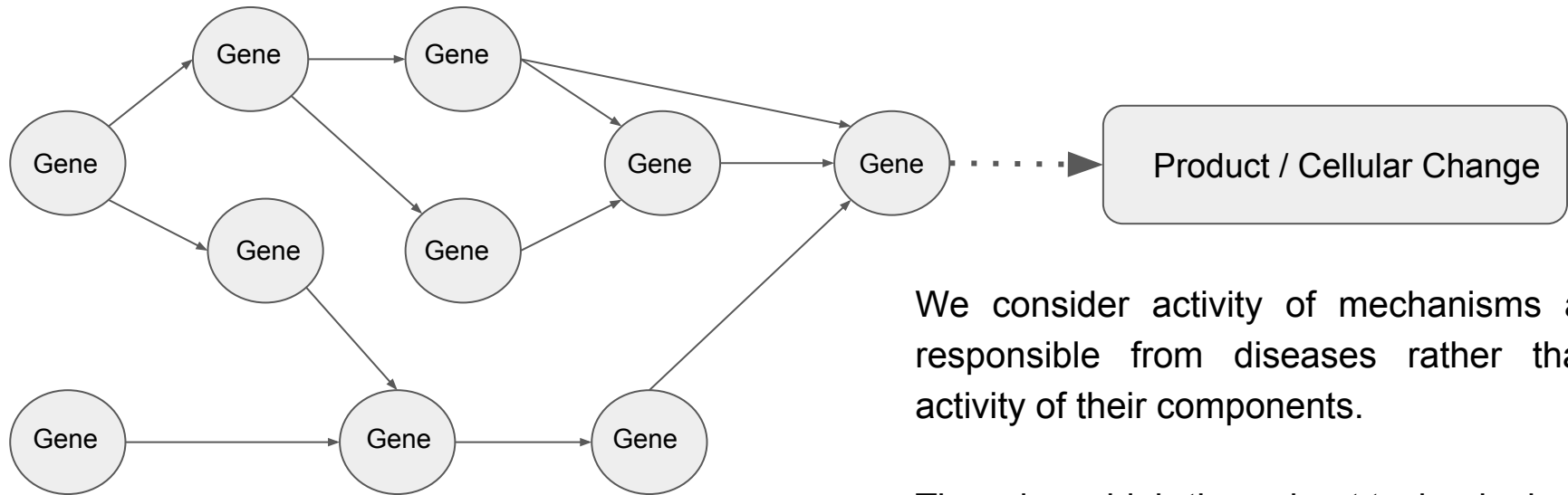


In spite of the increasing availability of genomic and transcriptomic data, there is still a *gap between* the detection of *perturbations in gene expression* and the understanding of its contribution to the *molecular mechanisms of the phenotype* studied.

# Molecular Mechanisms: Pathways

**A biological pathway** is a series of actions among molecules in a cell that leads to a certain product or a change in a cell.

- Metabolic
- Signaling



A pathway

We consider activity of mechanisms as responsible from diseases rather than activity of their components.

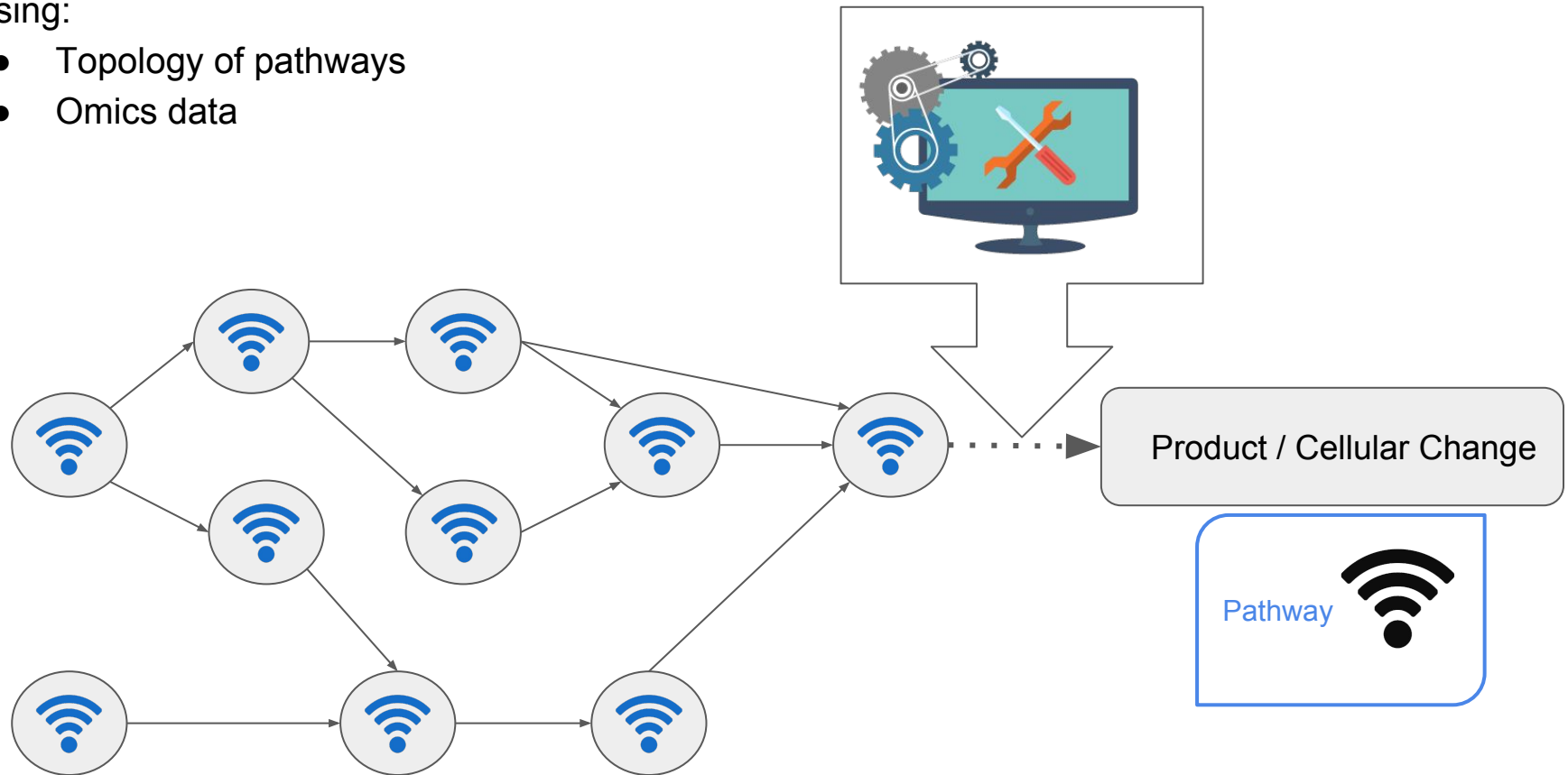
There is no high-throughput technologies available.



# Bioinformatics Tool: ?

Using:

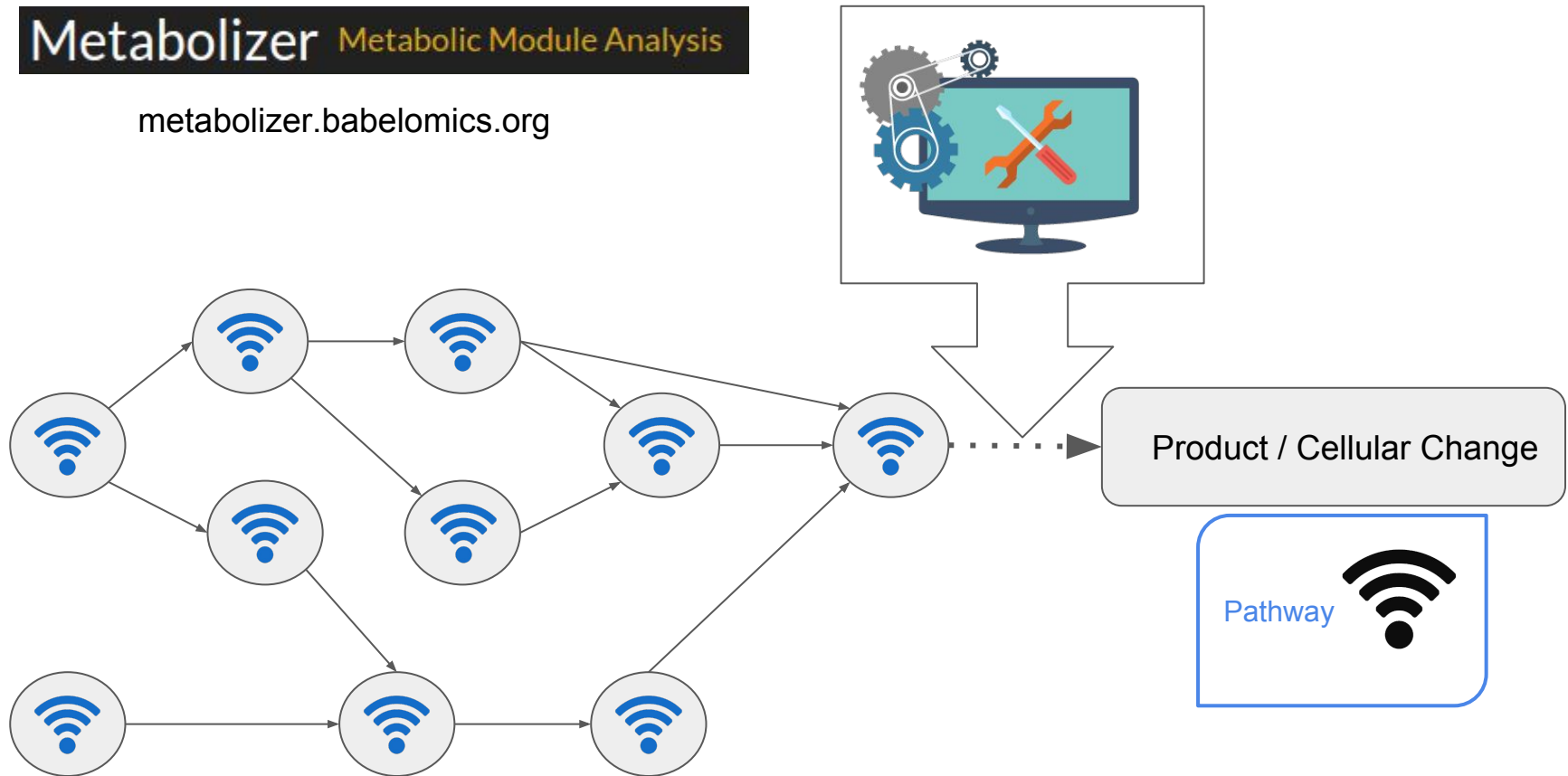
- Topology of pathways
- Omics data



# Bioinformatics Tool: *Metabolizer*


**Metabolizer** Metabolic Module Analysis




[metabolizer.babelomics.org](http://metabolizer.babelomics.org)



# What can Metabolizer do for you?

Metabolizer *Metabolic Module Analysis*

 [Home](#)

 Activity  Knockout  Prediction

Metabolizer integrates three different pathway tools:

- **Activity** allows you to see how module activity changes in different conditions.
- **Knockout** allows you to simulate knockouts or over-expressions of one or several genes or the effect of drugs in metabolic module genes.
- **Prediction** allows you to train a prediction model and test it with different/new data.

Metabolizer is able to integrate RNA-Seq and microarray data to produce accurate results.



# Results of *Metabolizer*

Continuous values of activity

Module Values

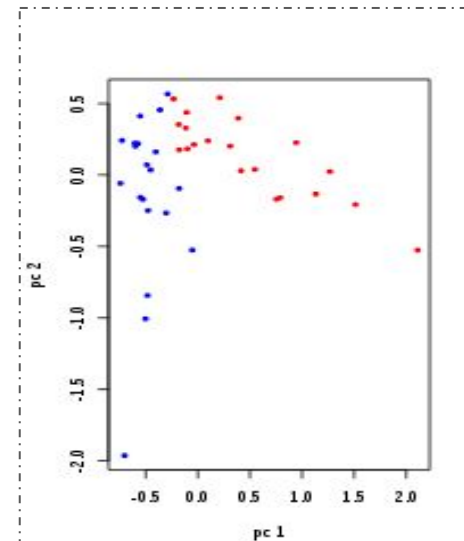
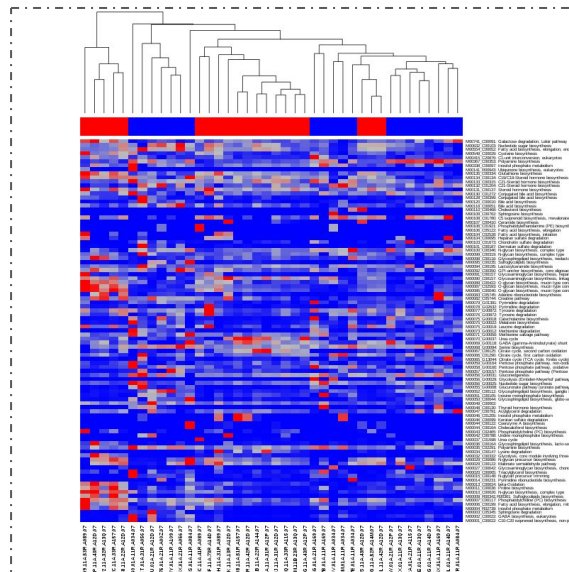
Module Values

Results of statistical analysis

Path significance

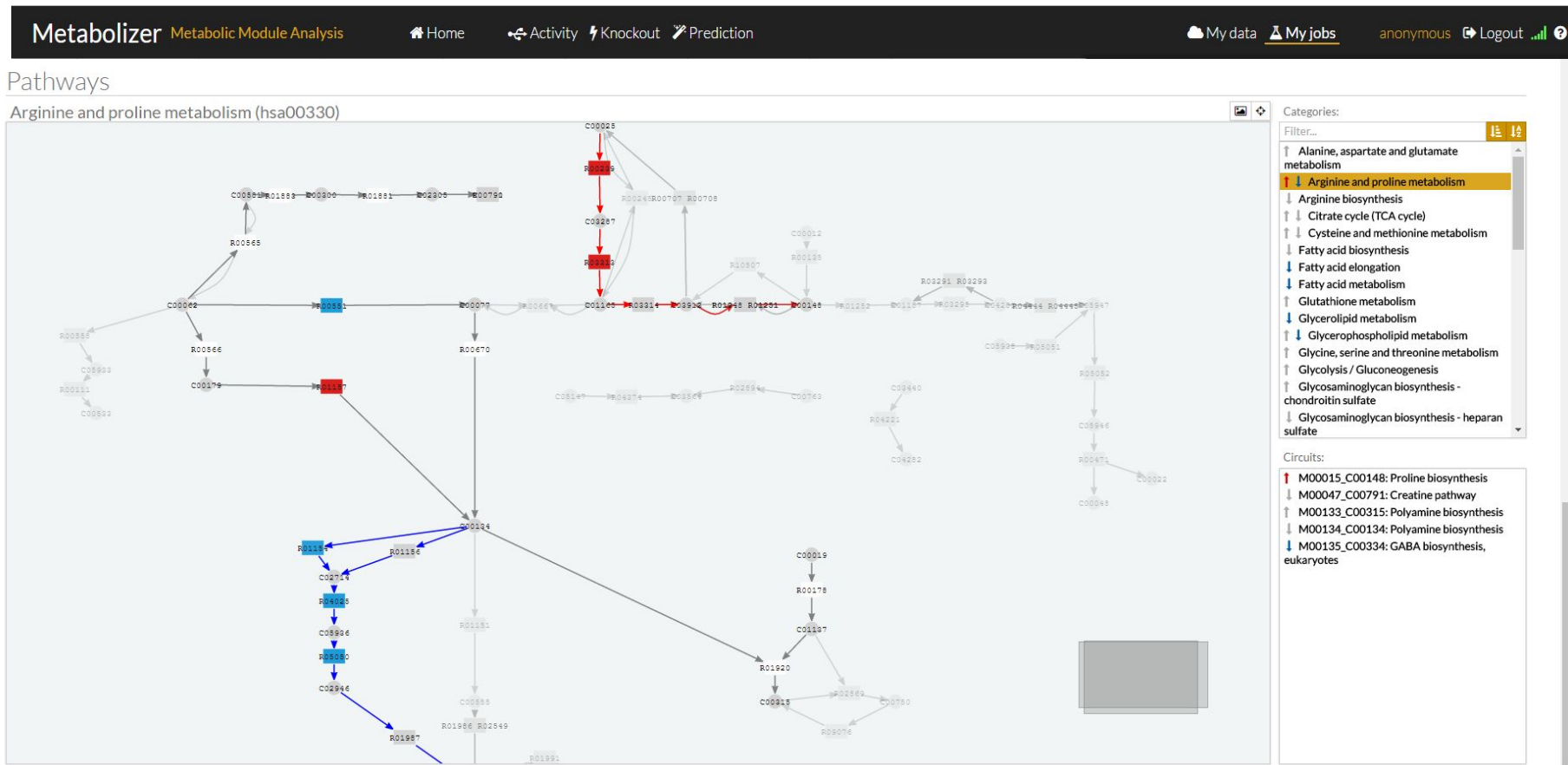
ModuleID	ModuleDescription	Pathway	statistic	p.value	adj.p.value	Status
M00035_C02291	Methionine degradation	Cysteine and methionin...	7.813	0.000	0.000	up
M00043_C02465	Thyroid hormone biosyn...	Tyrosine metabolism	-12.289	0.000	0.000	down
M00131_C00137	Inositol phosphate meta...	Inositol phosphate meta...	-7.086	0.000	0.000	down
M00098_C00116	Acylglycerol degradation	Glycerolipid metabolism	-5.901	0.000	0.001	down
M00047_C00791	Creatine pathway	Arginine and proline met...	-5.229	0.000	0.005	down

Plots



# Results of Metabolizer

Interactive  
graphic  
interface



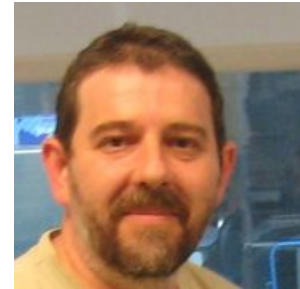
Metabolizer: CUBUK C, et al., Genome Medicine, 2017, under review.

Method used in Metabolizer: Hidalgo MR, CUBUK C, et al., Oncotarget. 2017; 8:5160-5178.

# Thank you for your attention



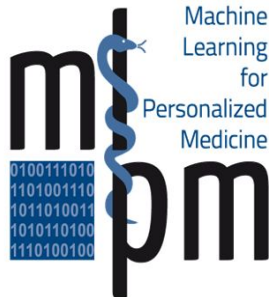
Dr. Joaquin Dopazo and his group members, CIPF.



Dr. Joaquin Canizares Sales, UPV.



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