

About OMICS Group

OMICS Group International is an amalgamation of [Open Access publications](#) and worldwide international science conferences and events. Established in the year 2007 with the sole aim of making the information on Sciences and technology 'Open Access', OMICS Group publishes 400 online open access [scholarly journals](#) in all aspects of Science, Engineering, Management and Technology journals. OMICS Group has been instrumental in taking the knowledge on Science & technology to the doorsteps of ordinary men and women. Research Scholars, Students, Libraries, Educational Institutions, Research centers and the industry are main stakeholders that benefitted greatly from this knowledge dissemination. OMICS Group also organizes 300 [International conferences](#) annually across the globe, where knowledge transfer takes place through debates, round table discussions, poster presentations, workshops, symposia and exhibitions.

About OMICS Group Conferences

OMICS Group International is a pioneer and leading science event organizer, which publishes around 400 open access journals and conducts over 300 Medical, Clinical, Engineering, Life Sciences, Pharma scientific conferences all over the globe annually with the support of more than 1000 scientific associations and 30,000 editorial board members and 3.5 million followers to its credit.

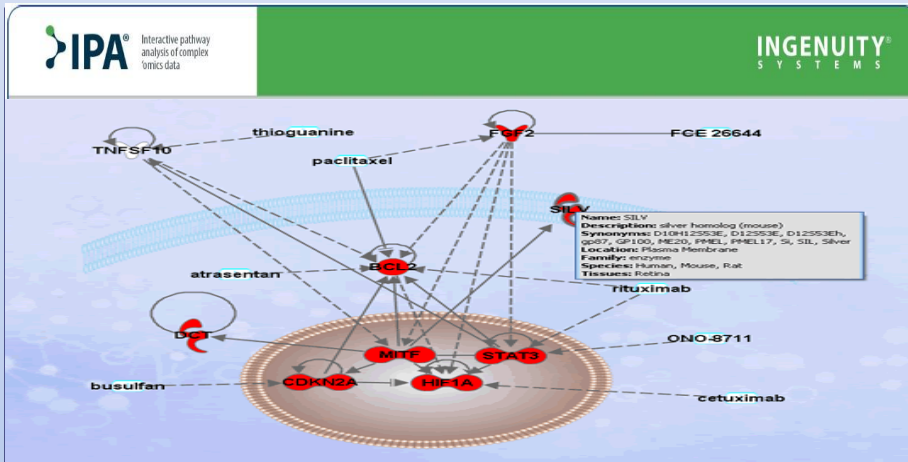
OMICS Group has organized 500 conferences, workshops and national symposiums across the major cities including San Francisco, Las Vegas, San Antonio, Omaha, Orlando, Raleigh, Santa Clara, Chicago, Philadelphia, Baltimore, United Kingdom, Valencia, Dubai, Beijing, Hyderabad, Bengaluru and Mumbai.

Clinical Metabolomics: Case study CKD. Cross-platform omics data integration in Ingenuity Systems.

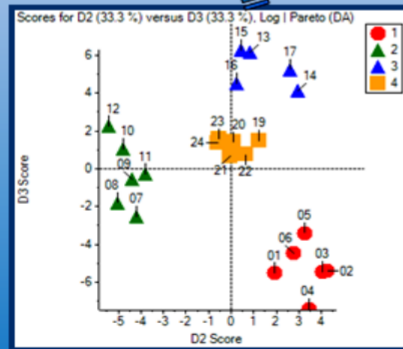
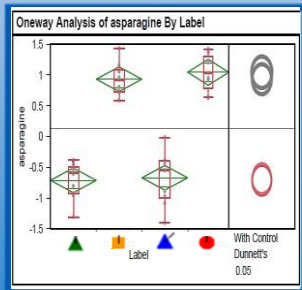
Vladimir Tolstikov, Ph.D.

*3rd International Conference and Exhibition on
Metabolomics & Systems Biology
(March 24-26, 2014)
San Antonio, TX, USA*

Metabolomics workflow

[illegible]

Pathway Analysis



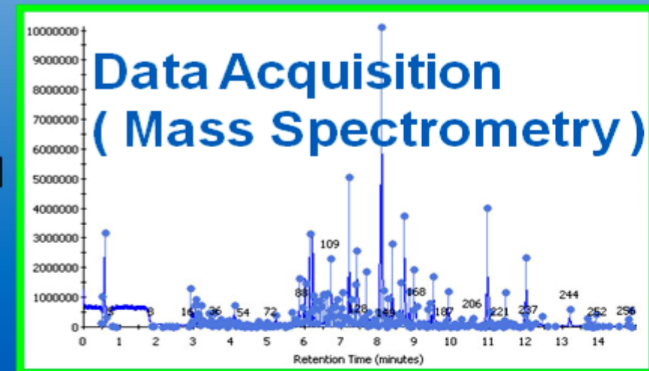
Data Analysis (Univariate and Multivariate Statistics)

[illegible]

Data Annotation Data pre- processing

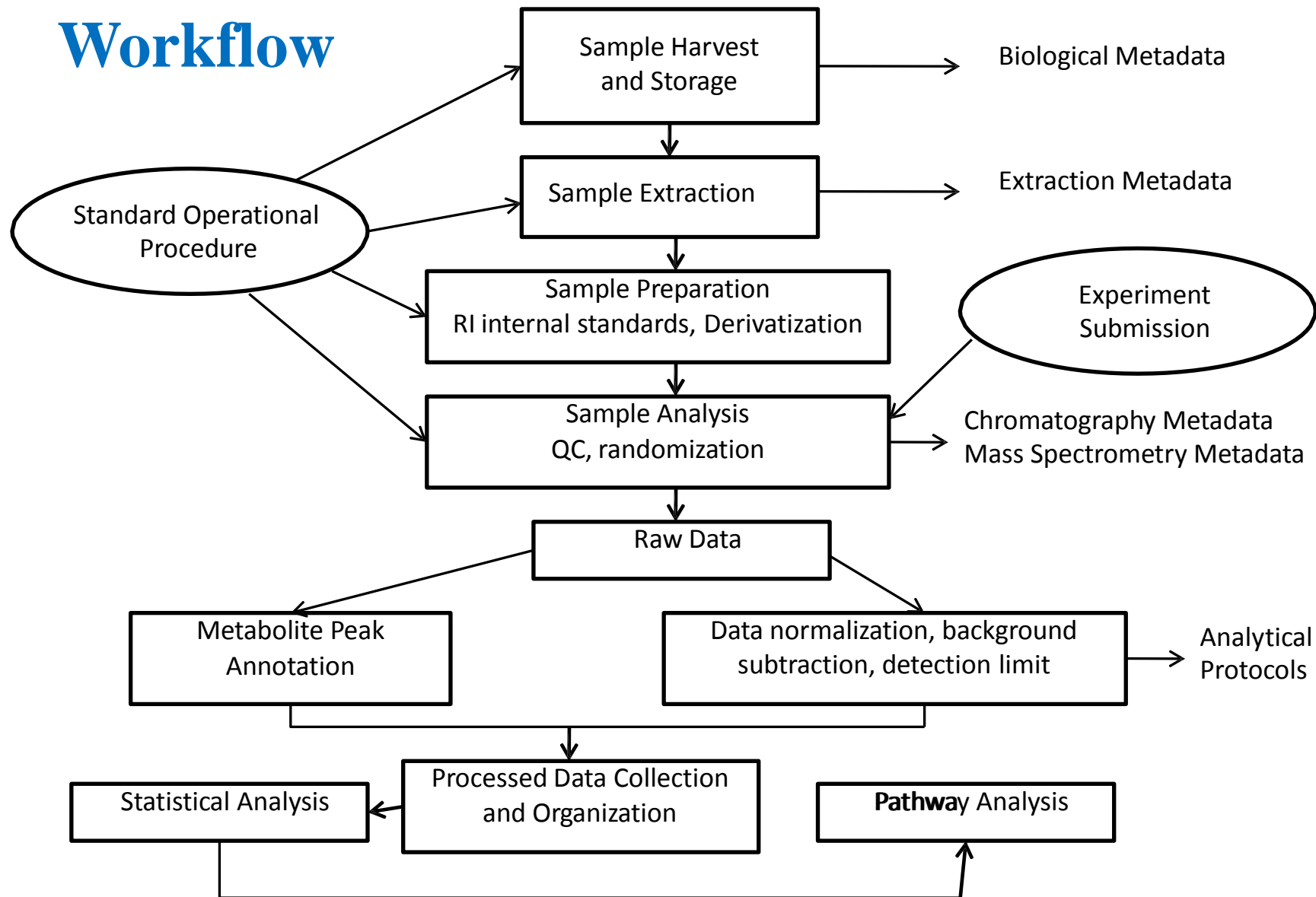


Sample Preparation (wet chemistry)



Lilly

Workflow



Lilly Metabolomics Platform

Ultimate combination of targeted and non-targeted approaches.

GC/M
S
Volatiles
Essential oils
Esters
Perfumes
Terpenes
Carotenoids
Flavanoids
Perfumes

Alcohols
Amino acids
Catecholamines
Fatty acids
Phenolics
Prostaglandins
Steroids
Sugar phosphates

Organic acids
Organic amines
Nucleosides
Nucleotides
Oligosaccharides
LC/M
S
Peptides
Co-factors
Polar Lipids



PEGASUS GC-HRT accurate mass TOF
Gerstel ALEX/CIS MultiPurpose
Autosampler

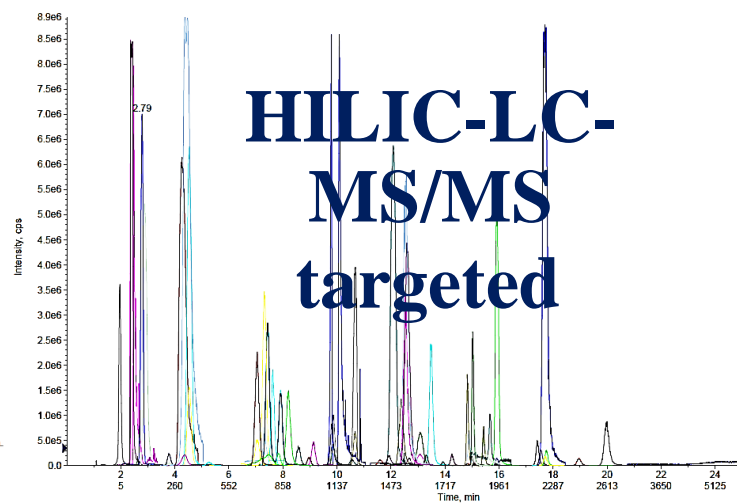
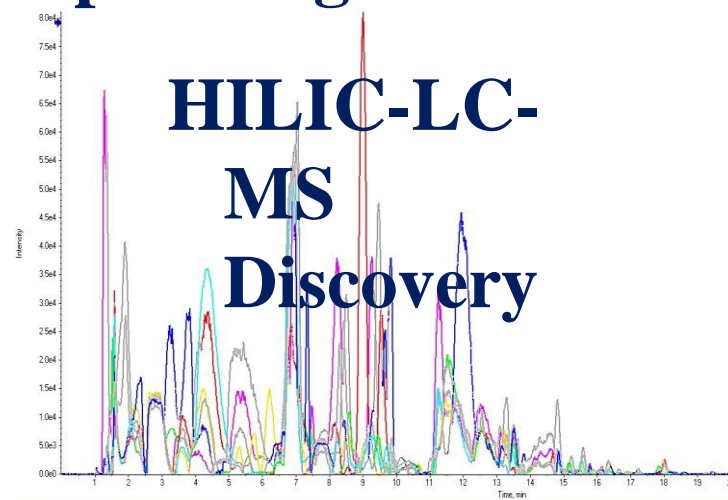
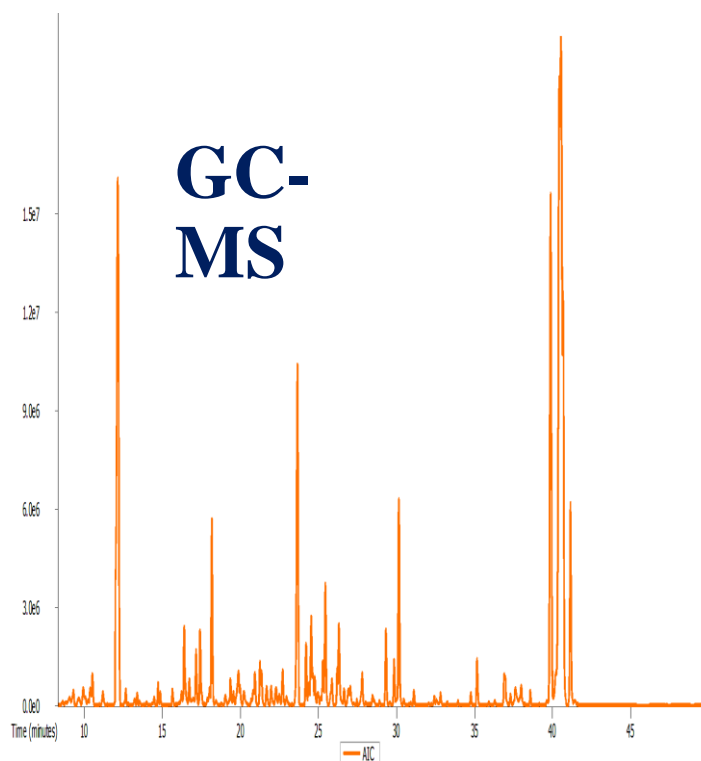
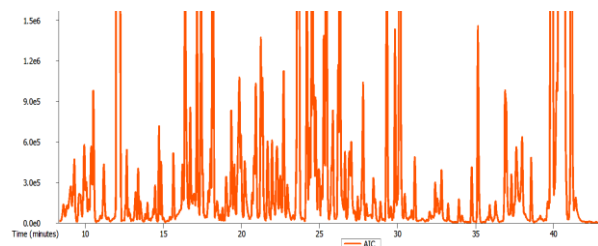


Triple quad 5500



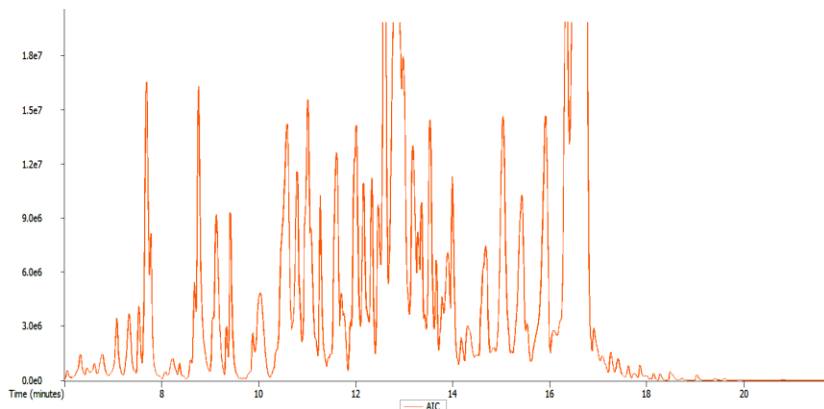
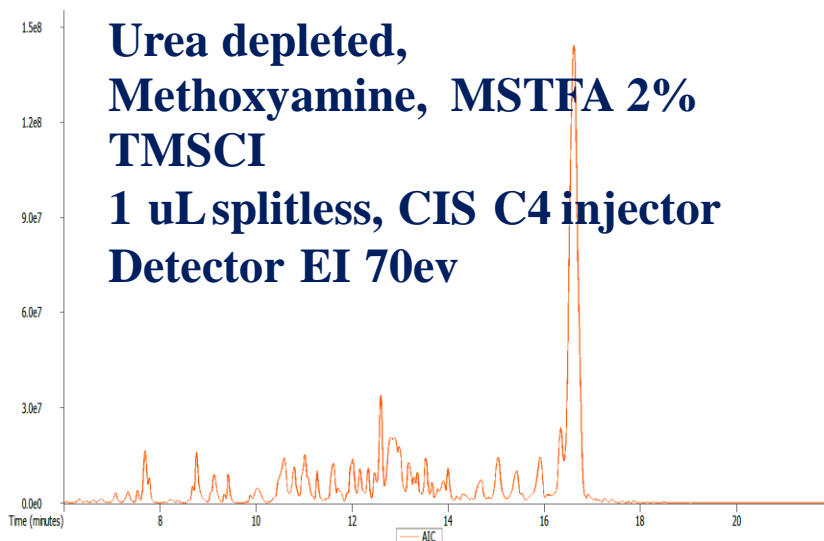
Triple TOF 5600 accurate mass

Human urine profiling

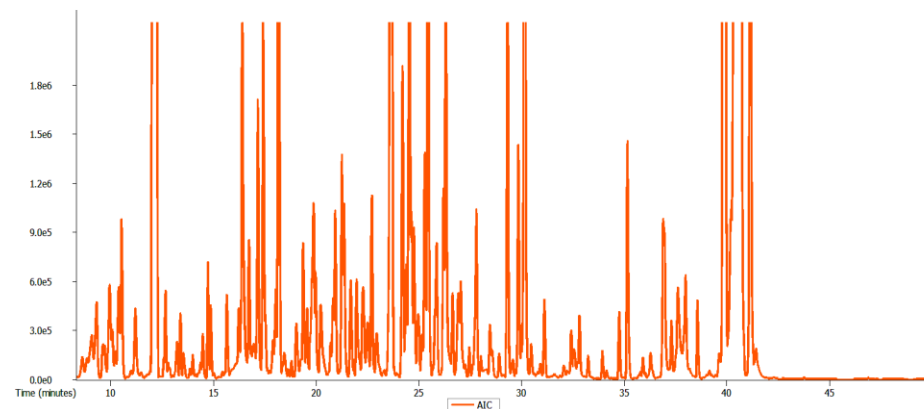
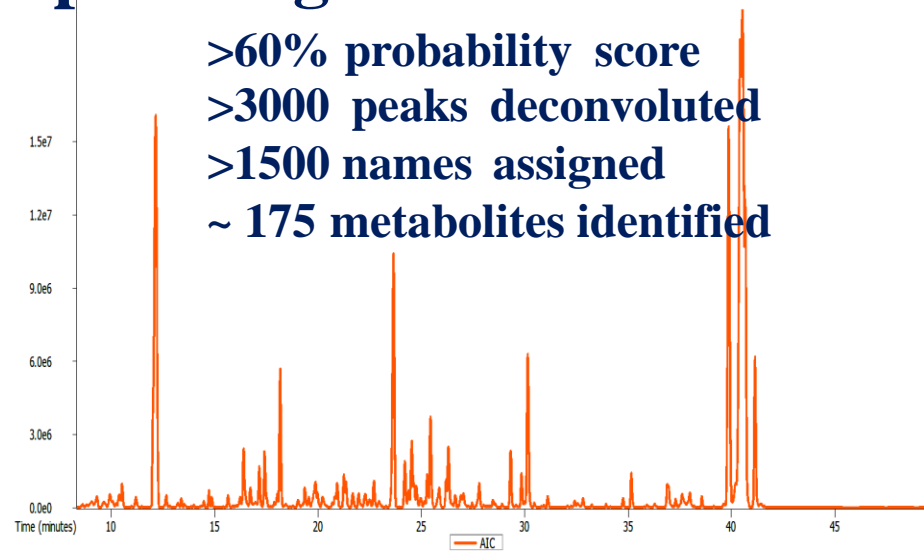


Human urine GC/MS profiling

**Urea depleted,
Methoxyamine, MSTFA 2%
TMSCI
1 uL splitless, CIS C4 injector
Detector EI 70ev**



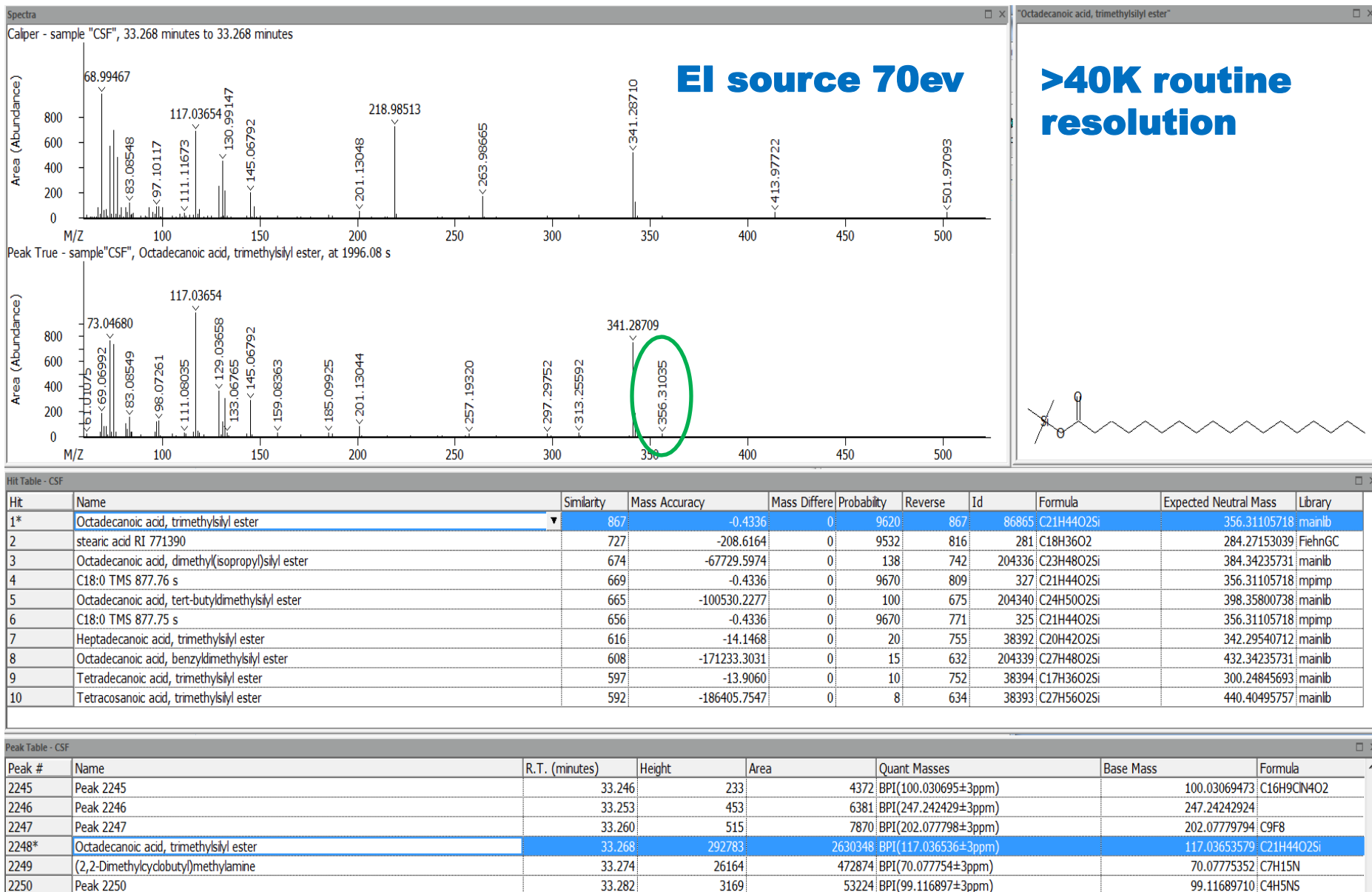
**>60% probability score
>3000 peaks deconvoluted
>1500 names assigned
~ 175 metabolites identified**



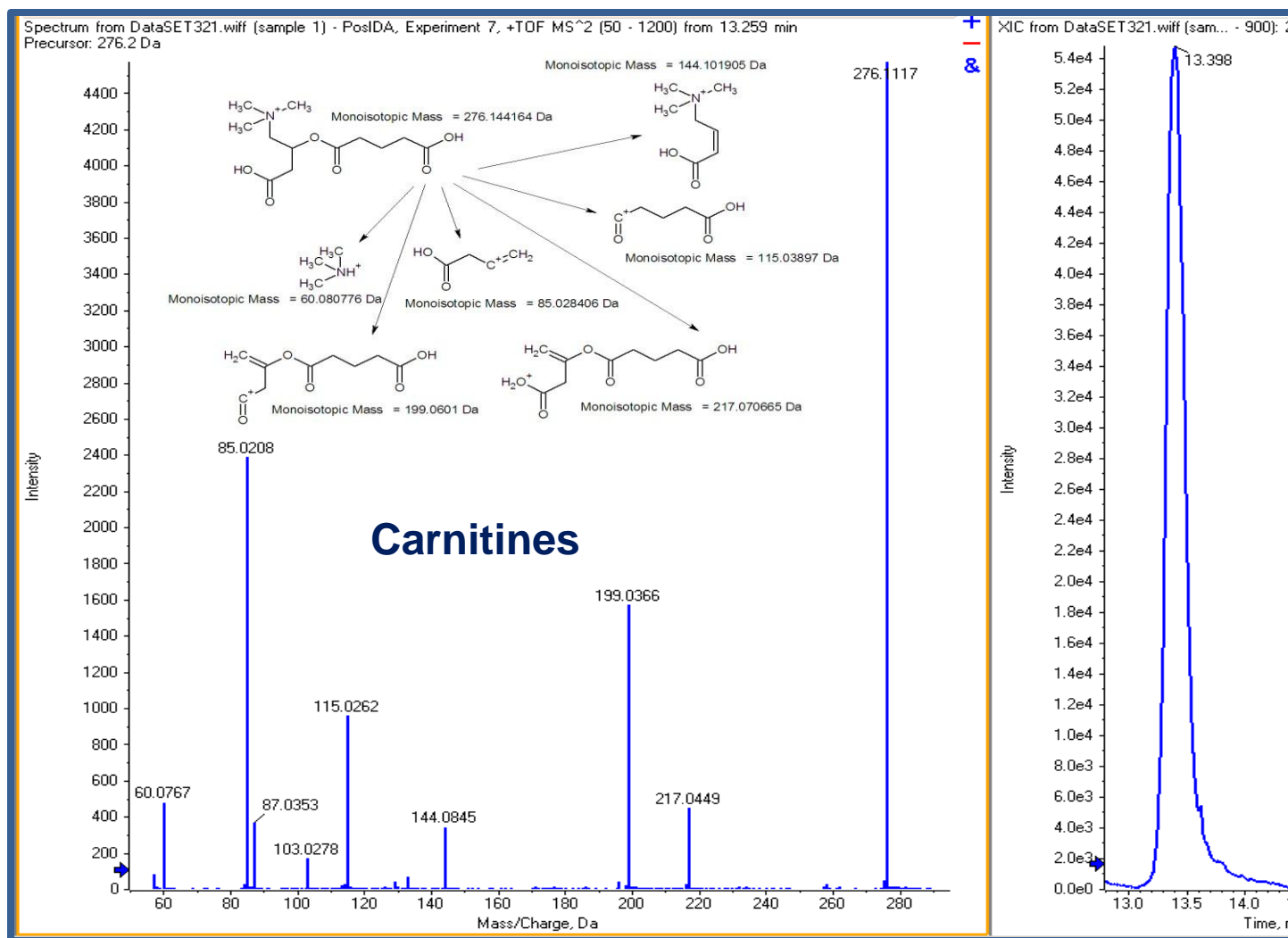
Throughput

Quality

High Resolution, High Mass Accuracy: YES or NO ID



LC-HRMS - Online Identification



Case study:

Chronic Kidney Disease

- Chronic kidney disease (CKD) is a progressive loss in renal function over a period of months or years. The symptoms of worsening kidney function are non-specific. Often, chronic kidney disease is diagnosed as a result of screening of people known to be at risk of kidney problems, such as those with high blood pressure or diabetes and those with a blood relative with chronic kidney disease. It is differentiated from acute kidney disease in that the reduction in kidney function must be present for over 3 months.
- The two main causes of chronic kidney disease are diabetes and high blood pressure, which are responsible for up to two-thirds of the cases
- Chronic kidney disease is identified by a blood test for creatinine. Higher levels of creatinine indicate a lower glomerular filtration rate and as a result a decreased capability of the kidneys to excrete waste products. Creatinine levels may be normal in the early stages of CKD, Recent professional guidelines classify the severity of chronic kidney disease in five stages, with stage 1 being the mildest and usually causing few symptoms and stage 5 being a severe illness with poor life expectancy if untreated. Stage 5 CKD is often called end stage renal disease (ESRD). There is no specific treatment unequivocally shown to slow the worsening of chronic kidney disease.

Chronic Kidney Disease

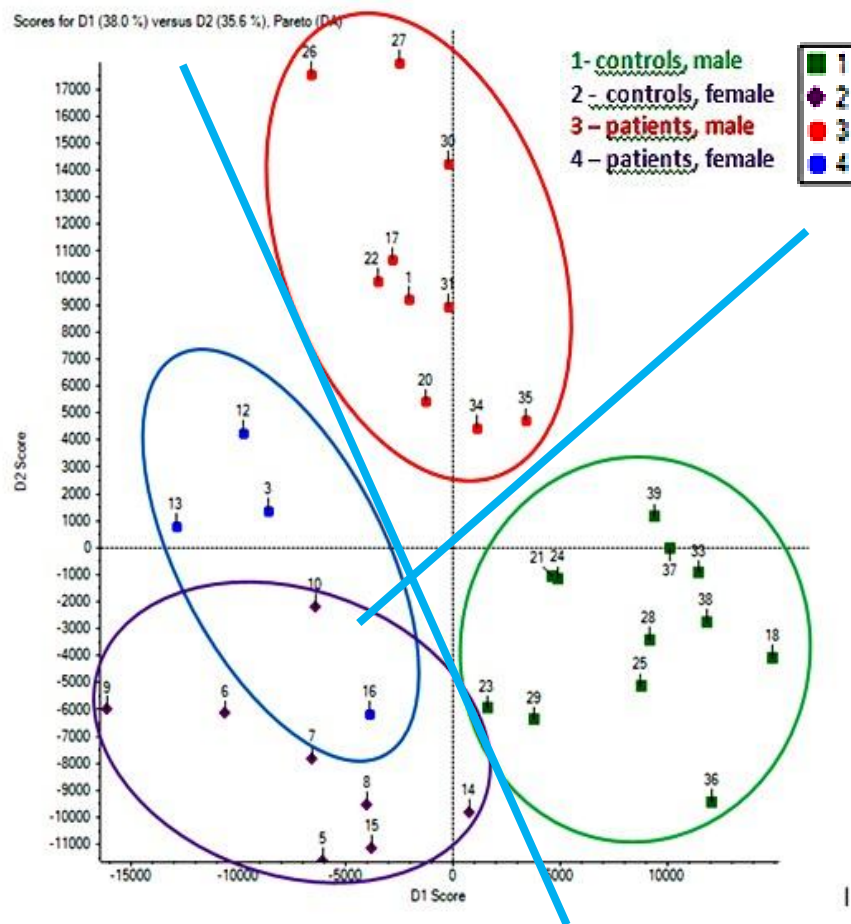
In the present exploratory cross-sectional studies, donor matched urine and serum clinical samples were obtained, extracted and analyzed. The first study was powered with 39 healthy, type II diabetic CKD (stages 3-5), and non-diabetic CKD (stages 3-5) patients. The second study was powered with 71 healthy, diabetic, diabetic CKD, and non-diabetic CKD patients.

We applied non-targeted and targeted Metabolomics Mass Spectrometry based approaches. Our in-house Lilly Metabolomics platform allowed routine detection of > 5000 features.

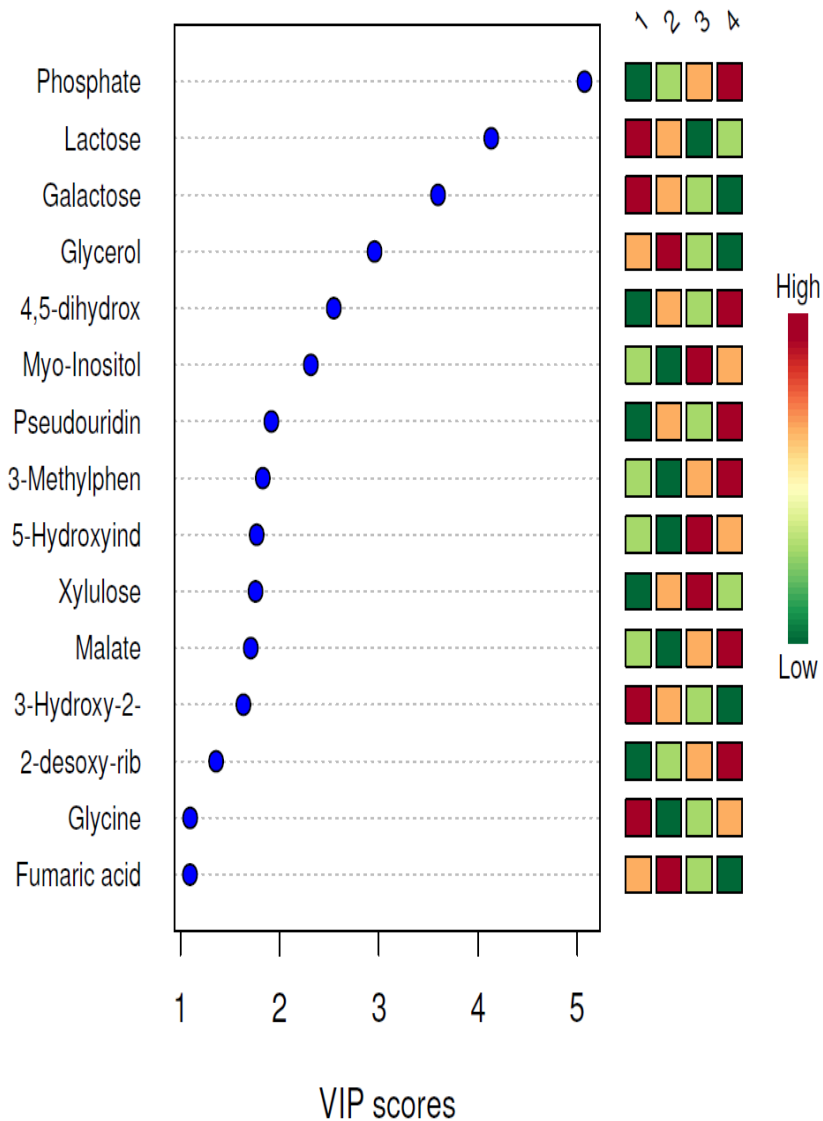
The dataset yielded several statistically significant biochemical alterations represented with >290 polar metabolites, excluding peptides, intact lipids and metabolites which levels were not changed.

We were able to glean a variety of subtle yet distinct metabolic signatures and perform Metabolic Pathway analysis. Pathway analysis allowed pinpointing the most disturbed metabolic pathways in CKD patients and offered new hypotheses.

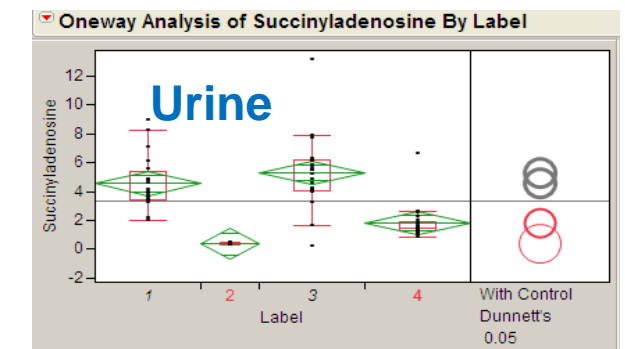
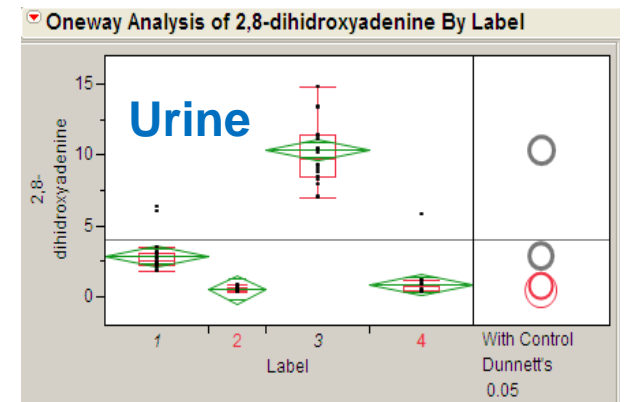
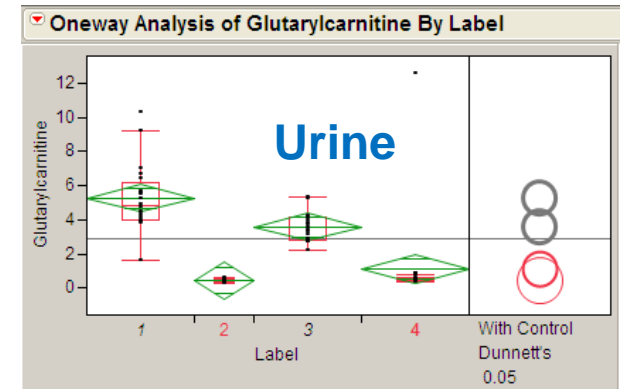
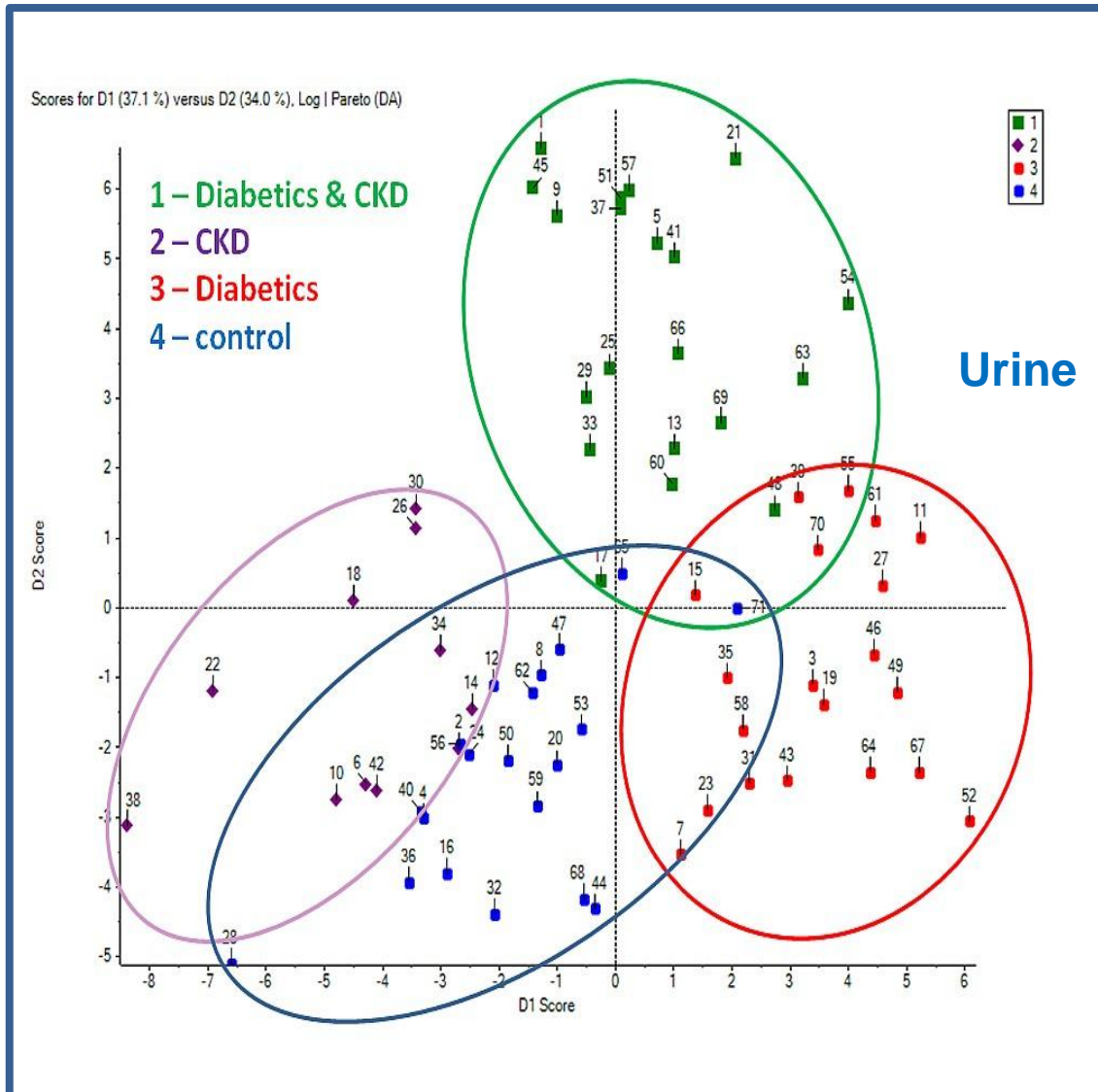
Male vs female; CKD vs control



Urines

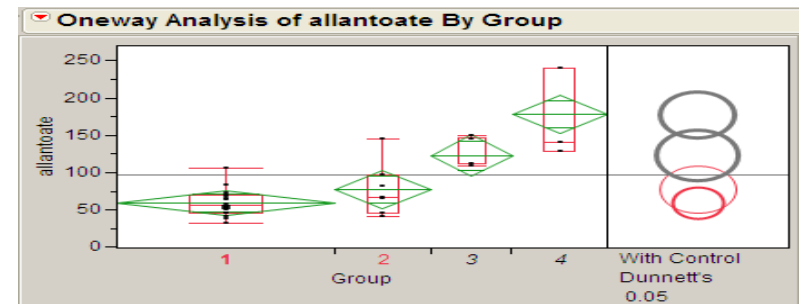
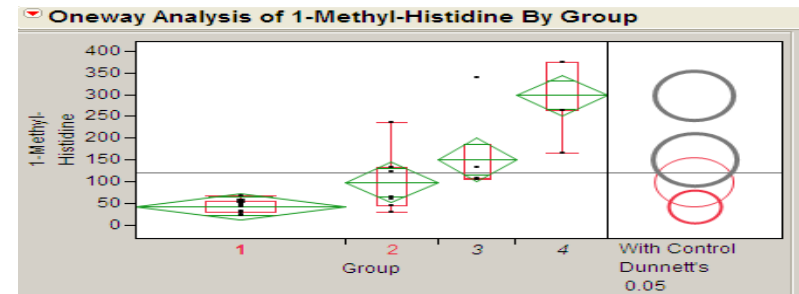
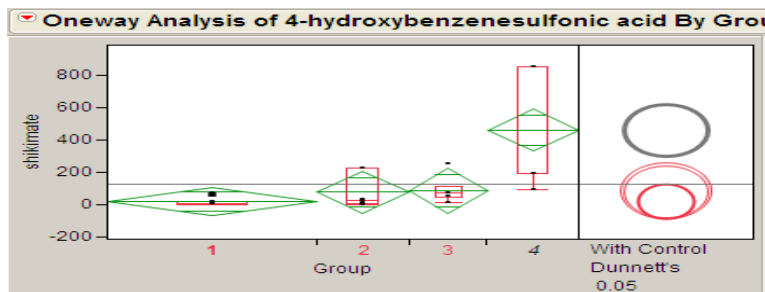
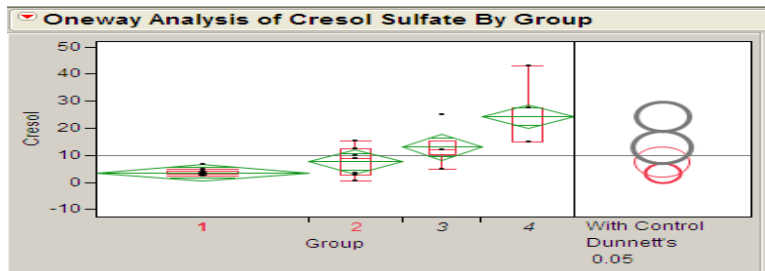
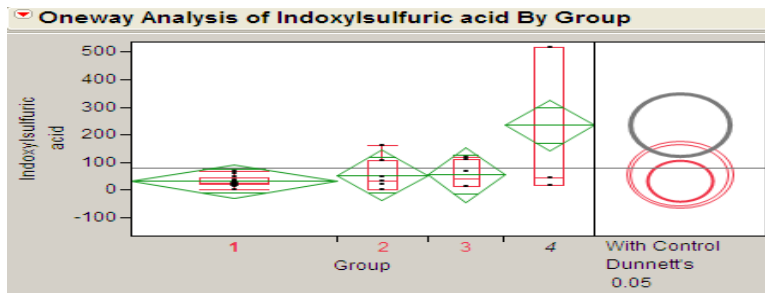
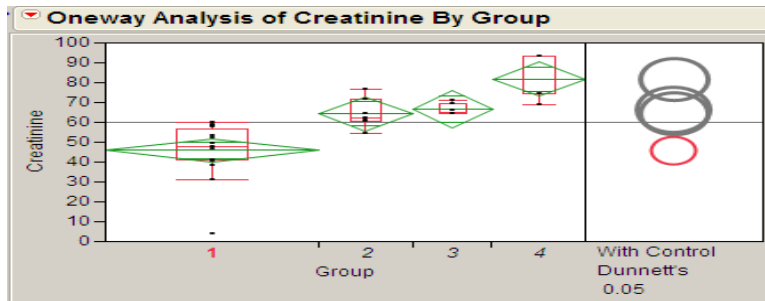


Diabetics versus non-diabetics



1 – Diabetics & CKD 2 – CKD
3 – Diabetics 4 – control

Uremic toxins accumulation in blood plasma



CKD stages: **controls**, **III**, **IV**, **ESRD**

Accumulation of known uremic toxins in plasma, in particular indoxylsulfate, cresol sulfate, 4-hydroxybenzenesulfonic acid, and others were observed. Uremic toxins are produced by liver and/or gastrointestinal flora metabolism and eliminated from plasma via active kidney tubular secretion.

Omics data integration characterizing CKD

Experimental Data:

**Genes – 1500 (gene expression) kidney
tissue, cDNA Bank**

proteins - 22 (ELISA) serum/urine, in house

**metabolites – 290 (GC/LC/MS) serum/urine, in
house (from the same samples)**

Groups:

CKD stages: controls, III, IV, ESRD

Experimental data form literature

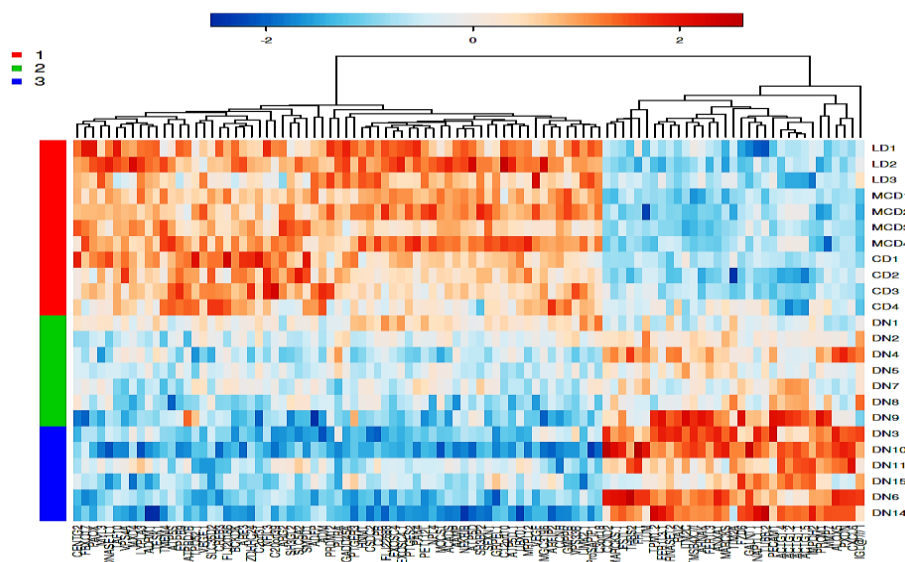
TABLE 1

Clinical and histological characteristics of reference biopsies analyzed by oligonucleotide array-based gene expression profiling and real-time RT-PCR

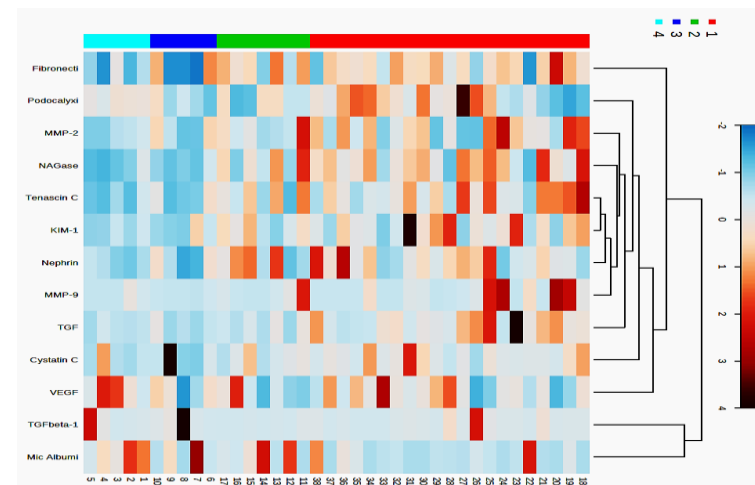
Sample name	Sex	Age (years)	Histology major diagnosis	Histology score	Creatinine (mg/dl)	Urine proteinuria (g/day)
Living donor						
Array						
LD1	F	66	LDx	NA	<1.1	<0.2
LD2	M	26	LDx w/o prev. damage	NA	0.9	<0.2
LD3	M	49	LDx w/o prev. damage	NA	<1.1	<0.2
Mean \pm SEM		47 \pm 9.6				<0.2
RT-PCR						
LD4	F	35	LDx	NA	<1.1	<0.2
LD5	M	39	LDx	NA	<1.1	<0.2
LD6	F	55	LDx	NA	<1.1	<0.2
LD7	M	41	LDx	NA	<1.1	<0.2
LD8	M	61	LDx	NA	<1.1	<0.2
LD9	F	58	LDx	NA	<1.1	<0.2
LD10	M	27	LDx	NA	<1.1	<0.2
LD11	F	54	LDx	NA	<1.1	<0.2
LD12	F	61	LDx	NA	<1.1	<0.2
Mean \pm SEM		48 \pm 14			<1.1	<0.2
Cadaveric donor						
Array						
CD1	M	50	CDx, minor int. fibrosis	NA	0.9	<0.2
CD2	M	54	CDx w/o prev. damage	NA	0.9	<0.2
CD3	M	61	CDx w/o prev. damage	NA	1.2	<0.2
CD4	F	51	CDx, minor int. fibrosis	NA	0.7	<0.2
Mean \pm SEM		54 \pm 2.1			0.9 \pm 0.1	<0.2
RT-PCR						
CD5	NA	NA	CDx	NA	<1.1	<0.2
MCD/ no histological changes						
Array						
MCD1	M	32	Minimal-change GN	1	1.3	11.0
MCD2	F	32	Minimal-change GN	1	0.7	3.0
MCD3	M	16	Minimal-change GN	0	1.2	5.4
MCD4	M	20	Minimal-change GN in remission	0	0.9	0.2
Mean \pm SEM		25 \pm 3.6			1.0 \pm 0.2	4.9 \pm 2.3
RT-PCR						
MCD5	F	57	Minimal-change GN	0	1.1	10
MCD6	M	33	Minimal-change GN	1	1.4	9.1
MCD7	M	24	No histological changes	0	0.6	0.4
Mean \pm SEM		38 \pm 8			1.0 \pm 0.2	6.5 \pm 2.5

European Renal cDNA Bank (ERCB) Consortium

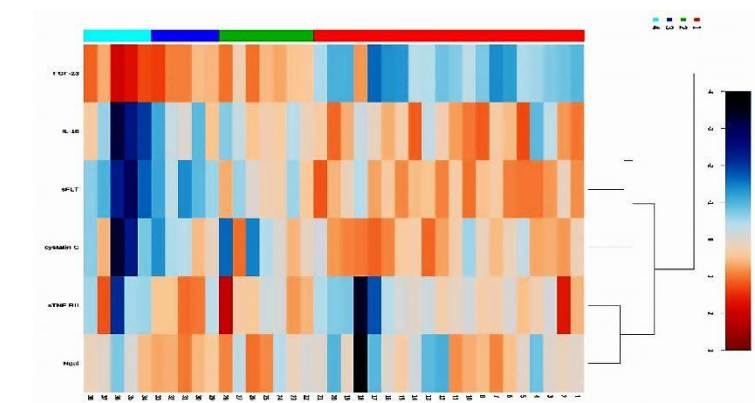
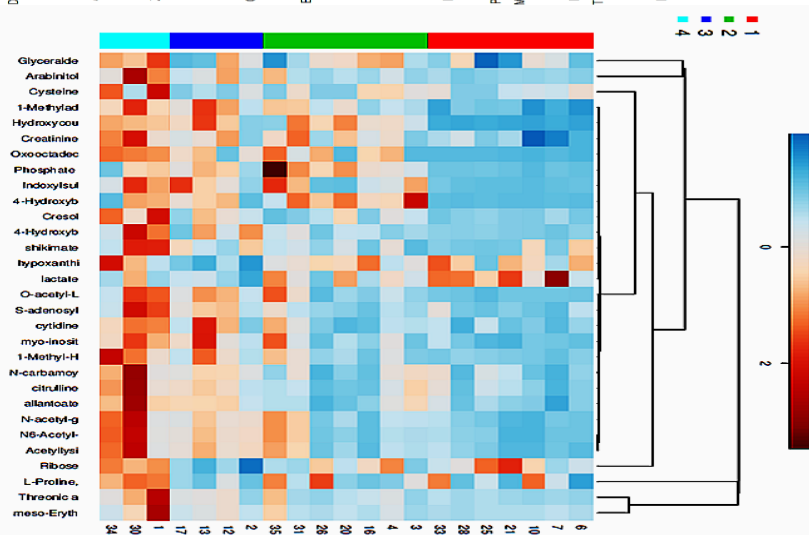
Kidney biopsies CKD levels: Control, III-IV, ESRD



Urine



Plasma



Proteomics data: controls, III, IV, ESRD

Plasma

Metabolomics data: controls, III, IV, ESRD

Red cells show increases vs. control, blue cells show decreases vs. control

Lilly

Analysis: Observation 3

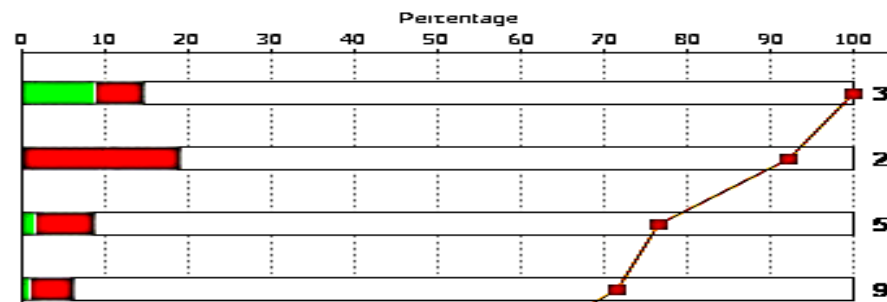
☒ Downregulated
 ☒ No change
 ☒ Upregulated
 ☐ No overlap with dataset
 ☒ -log(p-value)

Increases Glomerular Injury

Genes associated with Chronic Allograft Nephropathy (Human)

Acute Renal Failure Panel (Rat)

Hepatic Fibrosis



Observation 3

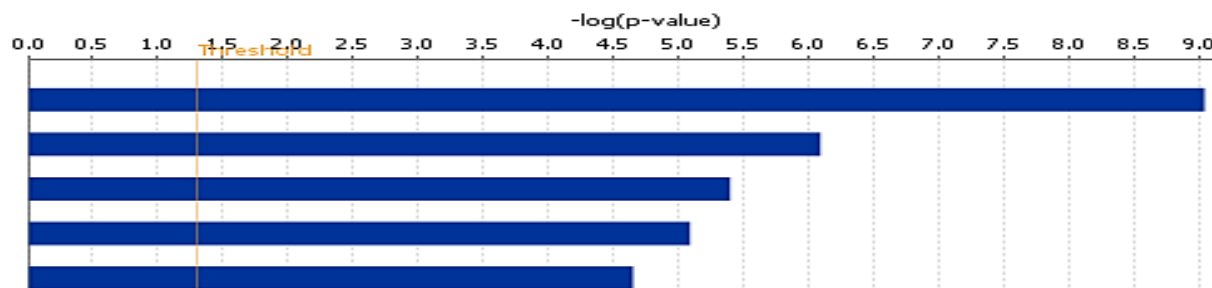
Kidney Failure

Increased Levels of LDH

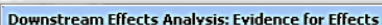
Cardiac Necrosis/Cell Death

Liver Necrosis/Cell Death

Liver Steatosis



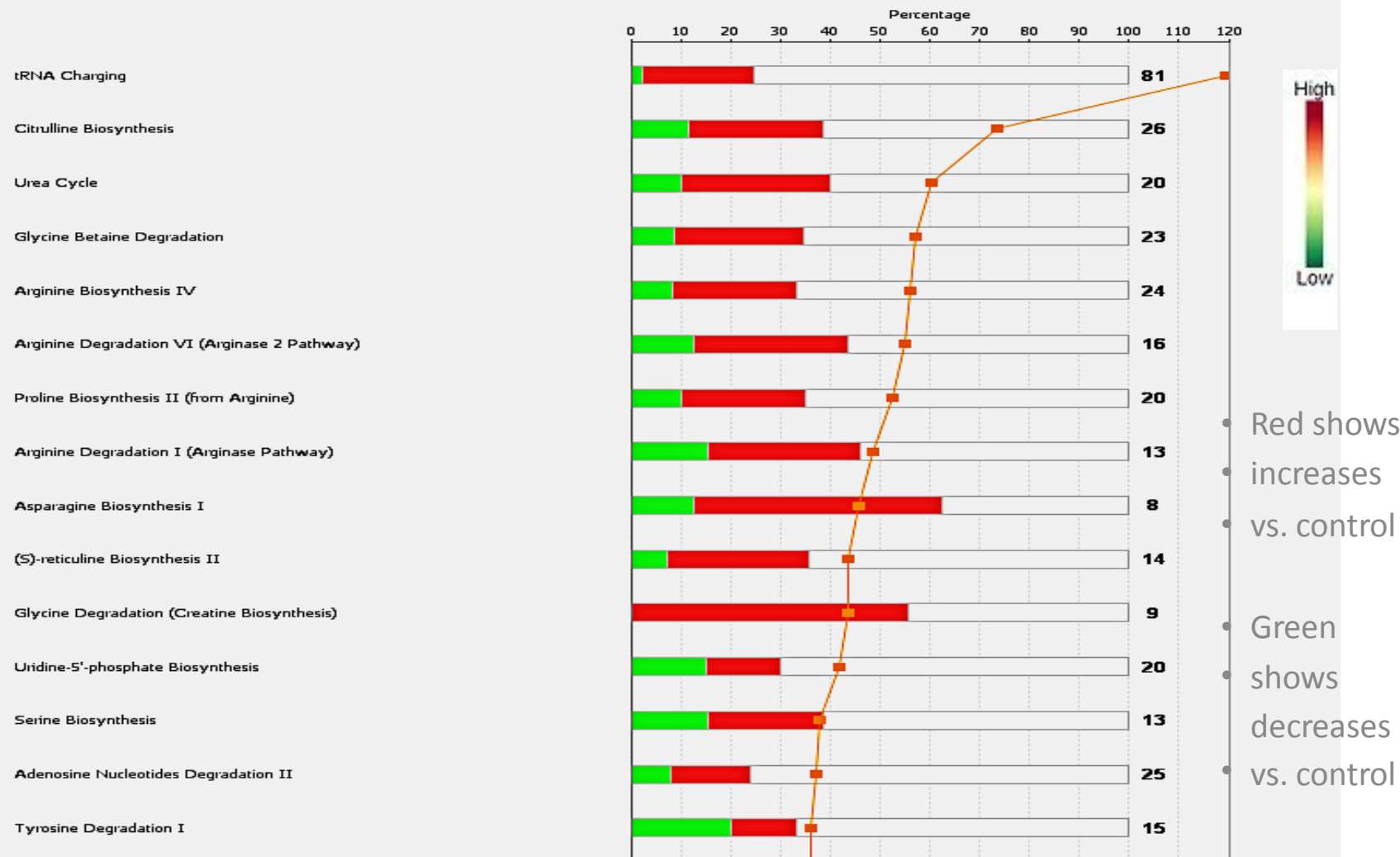
Diseases or Functions Annotation	p-Value	Molecules
failure of kidney	9.01E-10	↓ADM, ↑cholesterol, ↑citric acid, ↑creatinine, ↓D-glucose, ↓DPP4*, ↓GHR, ↑indican, ↑LCN2, ↓mannitol, ↓phosphate, ↑urea, ↓... all 14
chronic renal failure	7.97E-05	↓ADM, ↑citric acid, ↓DPP4*, ↓GHR, ↑indican, ↓phosphate, ↑WFDC2 all 7
acute renal failure	1.24E-04	↑creatinine, ↑LCN2, ↓mannitol, ↓phosphate, ↑urea all 5
interstitial fibrosis of kidney	4.04E-03	↑indican, ↑WFDC2 all 2
end stage renal disease	6.44E-03	↑citric acid, ↓GHR, ↑indican, ↑WFDC2 all 4
septic acute kidney injury	1.09E-02	↑LCN2 all 1
ischemic acute renal failure	4.28E-02	↑LCN2 all 1
acute tubular necrosis	5.33E-02	↑LCN2 all 1



[ADD TO MY PATHWAY](#)
[ADD TO MY LIST](#)
[CUSTOMIZE TABLE](#)
[CREATE DATASET](#)

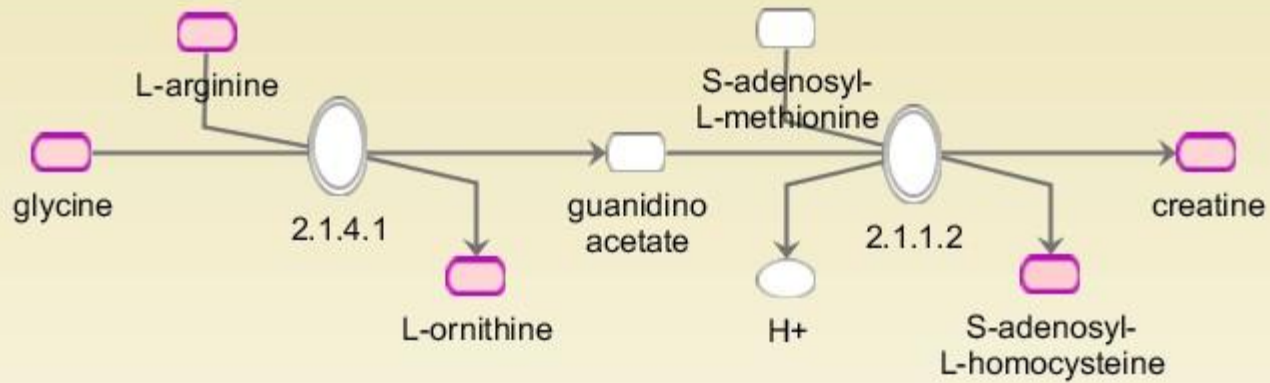
Lilly

■ Downregulated
 ■ No change
 ■ Upregulated
 No overlap with dataset
 —■— -log(p-value)

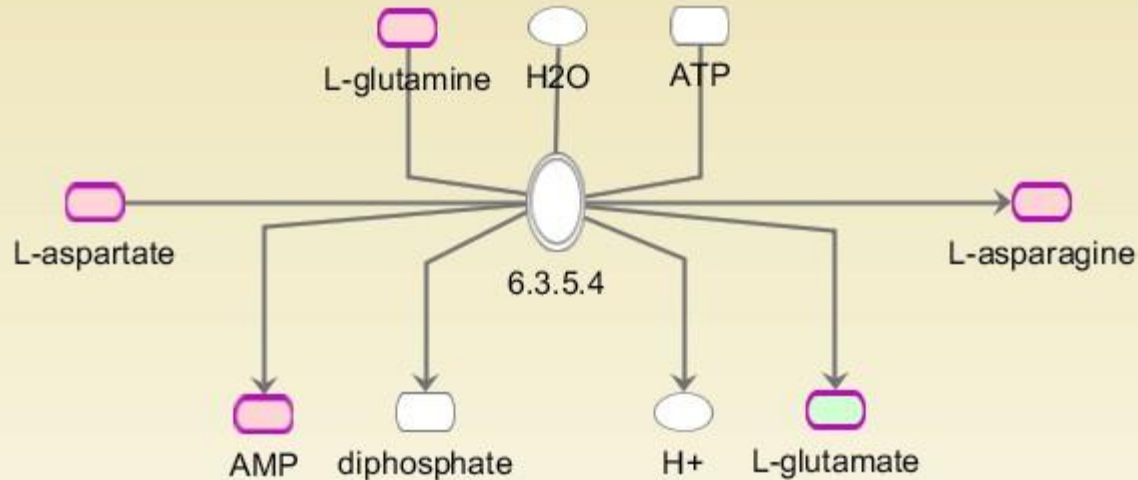


370 pathways retrieved with uploaded data

Glycine degradation

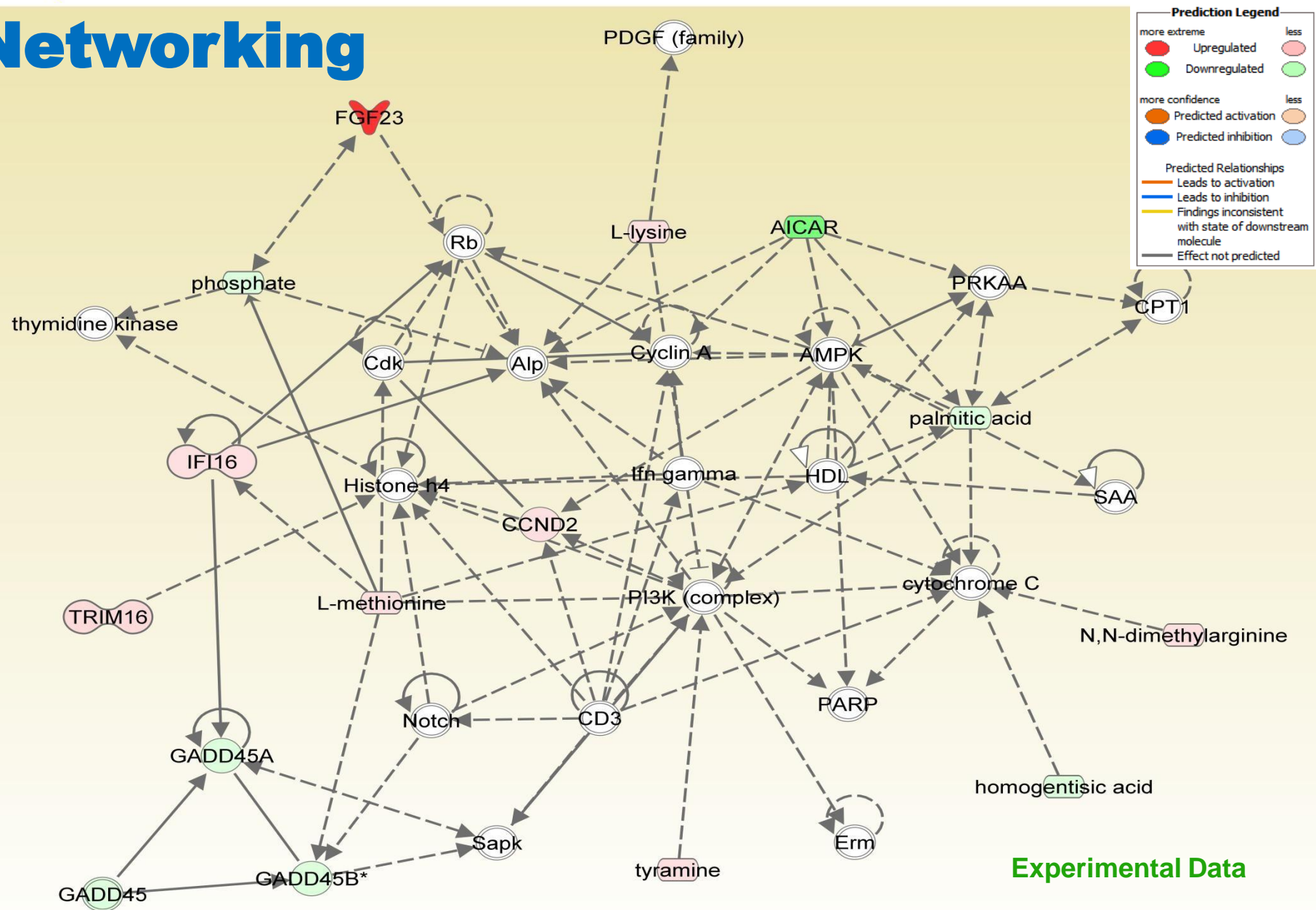


Asparagine biosynthesis



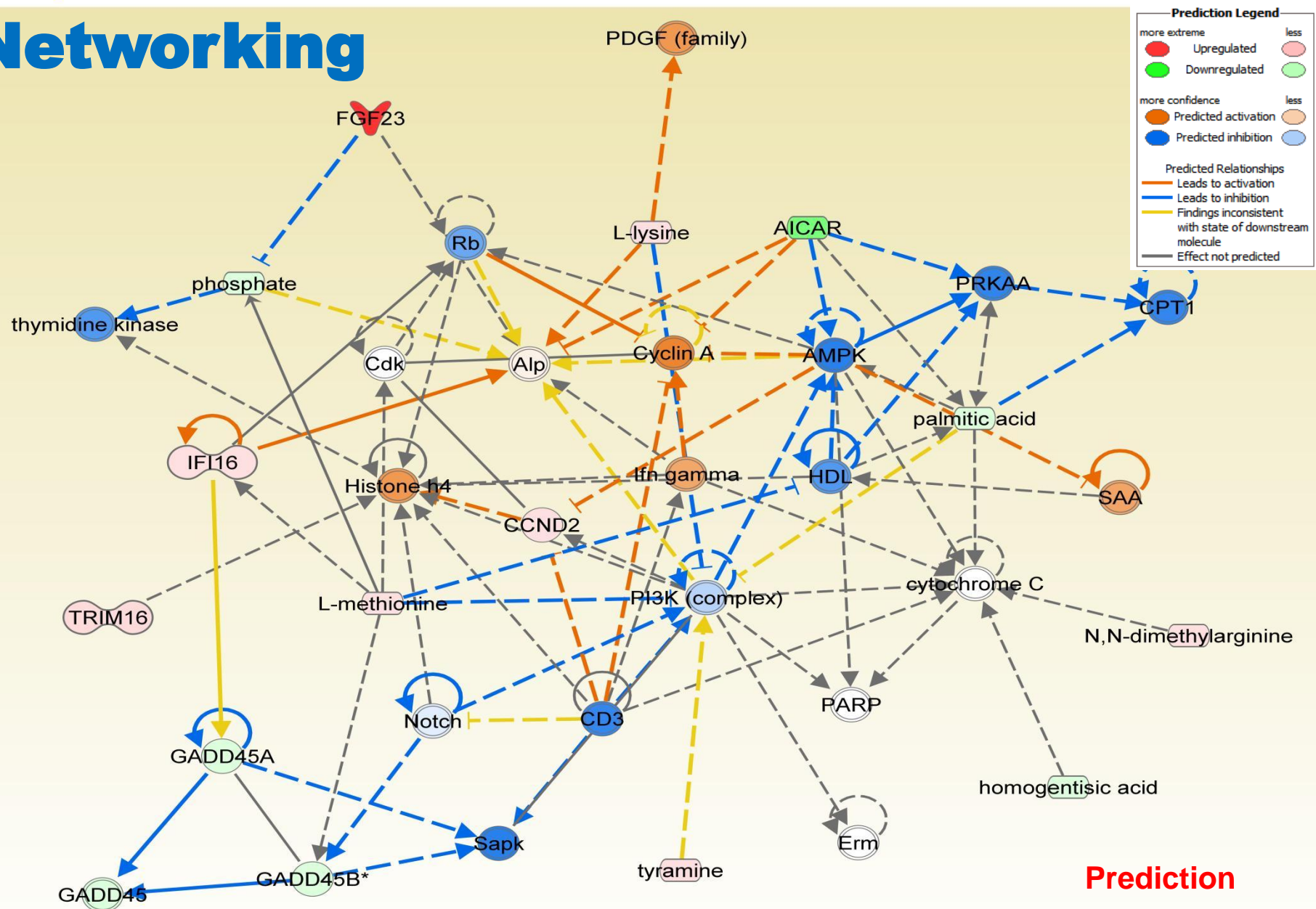
Red shows increases vs. control, green shows decreases vs. control

Networking



Red shows increases vs. control, green shows decreases vs. control

Networking

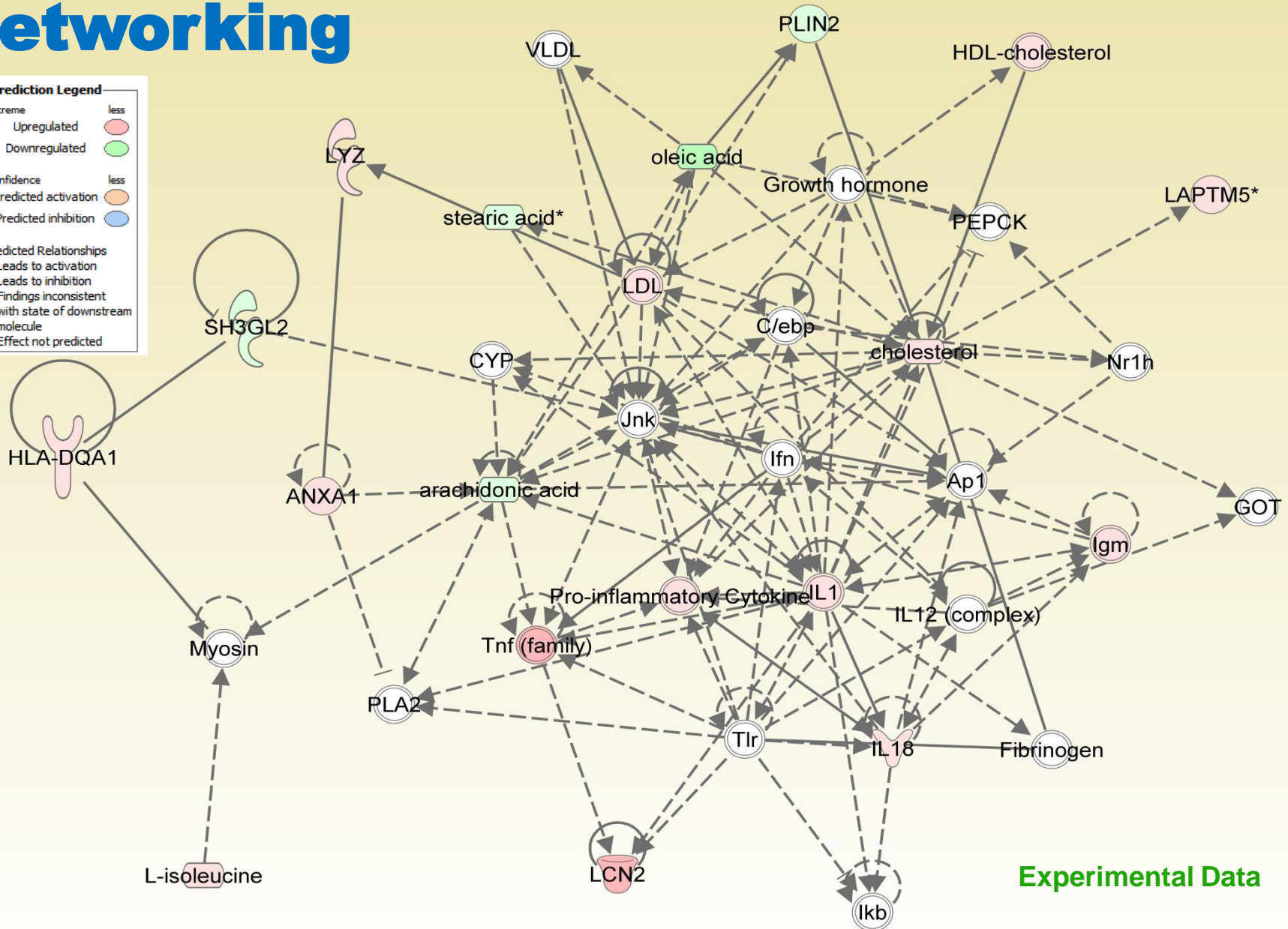
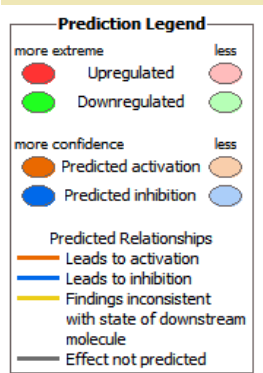


Prediction

MAP (Molecular Activity Predictor)



Networking



Experimental Data

Red shows increases vs. control, green shows decreases vs. control



Conclusions

- Comprehensive metabolomics platform allowed to collect information on metabolic alterations for more than 290 polar metabolites excluding peptides, intact lipids and metabolites which levels were not changed.
- Statistical analysis demonstrated small molecules capable of discriminating CKD patients at different stages of disease. Diabetics were discriminated from non-diabetics based on small molecules found in patient urine and plasma.
- Omics data integration, upstream and downstream analysis offered a number of targets and hypotheses to be explored.

Acknowledgments

**Dr. Kevin L. Duffin, PhD,
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Research Fellow**

**Dr. Alexander Nikolayev, MS
Consultant Scientist**

**Dr. Dennis A. Laska, BS,
Consultant Biologist**

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