

Plasma Metabolomic Profiles in Different Stages of CKD

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Summary

Background and objectives CKD is a common public health problem. Identifying biomarkers adds prognostic/diagnostic value by contributing to an understanding of CKD at the molecular level and possibly defining new drug targets. Metabolomics provides a snapshot of biochemical events at a particular time in the progression of CKD. This cross-sectional metabolomics study ascertained whether plasma metabolite profiles are significantly different in CKD stages 2, 3, and 4.

Design, setting, participants, & measurements An analysis of plasma metabolites, using gas and liquid chromatography coupled to mass spectrometry, was conducted on 30 nondiabetic men ages 40–52 years, with 10 participants each in CKD stages 2, 3, and 4 based on their estimated GFR (calculated by the Modified Diet in Renal Disease formula). Participants were recruited in late 2008, and plasma samples were tested at Metabolon Inc and analyzed in 2012.

Results Comparison of stage 3/stage 2 identified 62 metabolites that differed ($P \leq 0.05$), with 39 higher and 23 lower in stage 3 compared with stage 2; comparisons of stage 4/stage 2 identified 111 metabolites, with 66 higher and 45 lower; and comparisons of stage 4/stage 3 identified 11 metabolites, with 7 higher and 4 lower. Major differences in metabolite profiles with increasing stage of CKD were observed, including altered arginine metabolism, elevated coagulation/inflammation, impaired carboxylate anion transport, and decreased adrenal steroid hormone production.

Conclusions Global metabolite profiling of plasma uncovered potential biomarkers of stages of CKD. Moreover, these biomarkers provide insight into possible pathophysiologic processes that may contribute to progression of CKD.

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Introduction

CKD encompasses a spectrum of kidney diseases, ranging from kidney damage with normal kidney function to ESRD. The National Kidney Foundation has devised a five-stage classification system for CKD based on the level of GFR (1). Cardiovascular disease (CVD) is a major cause of morbidity and mortality in patients with all forms of CKD and contributes to the complexity of CKD (2–6). This complexity introduces new challenges in predicting and treating patients sufficiently early in the course of CKD to positively alter patient outcome. Until recently, most risk factor analysis of kidney diseases has focused on ESRD. Little is known about the effect of various risk factors at each stage of disease and how these contribute to the rate of progression to ESRD. In addition, there has been little study of the potential differences in risk factors for transition from one stage to the next and whether the risk factors for onset and transition from stage 1 to stage 2 may differ from those for transition to stage 3 and stage 4 CKD or for final development of ESRD. Currently, both the incidence and prevalence of CKD leading to ESRD continue to increase at an alarming rate in the United States. There are at

least 19 million people in the United States with some degree of CKD (7), with enormous costs to society (8), prompting the Surgeon General to include CKD as a focus area for improving the nation's health in Healthy People 2010. An understanding of the characteristics of early stage CKD, as well as the factors that differentially affect the progression of CKD from one stage to the next, is essential for determining appropriate therapy and predicting long-term outcomes.

Metabolomics, which is the most recent systems-biology approach to complement the genomic, transcriptomic, and proteomic efforts to characterize an entire biologic system, is increasingly being used to study kidney function (9–11). Because metabolites represent the end products of the genome and proteome, metabolomics holds the promise of providing an integrated physiologic phenotype of a system. Such metabolic profiling involves a comprehensive measurement of the types and concentrations of metabolites in a system at a specified time, such as each stage of CKD. Metabolomics also provides insight into metabolic pathways and networks downstream of gene expression. Complex metabolite profiles may

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provide the data required to enable the diagnosis, risk stratification, treatment, and evaluation of treatment response of patients. This may be through the identification of single biomarkers as in the more traditional methods or more likely by identification of patterns across many metabolites.

In this cross-sectional study, we determined plasma metabolite profiles of 30 participants; these were non-diabetic men aged 40–52 years, with 10 each in CKD stages 2, 3, and 4 based on their estimated GFR. Our goal was to determine whether there are significant differences in specific metabolites by stage of CKD and whether these may be useful stage-specific biomarkers. A related goal was to consider whether these differences might offer insight into potential pathophysiologic mechanisms that contribute to progression of CKD.

Materials and Methods

Study Participants

Plasma samples, which were obtained from the University of Pennsylvania from patients recruited in late 2008, were stored at -80°C for this study. Samples from 30 participants with CKD, 10 each in stages 2, 3 and 4, were selected for metabolite analysis at Metabolon Inc in 2012. Informed consent was obtained from all participants. Descriptions of the participants are summarized in Table 1.

Sample Accessioning/Preparation

All mass spectrometry data were collected at Metabolon Inc. Each plasma sample was accessioned into the Metabolon LIMS system and was assigned by the LIMS unique identifier, which was associated with the original source identifier only. The nontargeted metabolic profiling platform utilized for this analysis combined three independent platforms: ultrahigh performance liquid chromatography–tandem mass spectrometry (UHPLC–MS/MS²) optimized for basic species, UHPLC–MS/MS² optimized for acidic species, and gas chromatography/mass spectrometry (GC/MS). Samples were processed essentially as described previously (12,13). For each sample, 100 μl was used for analyses. Using an automated liquid handler (Hamilton LabStar, Salt Lake City, UT), protein was precipitated from the plasma with methanol that contained four standards to report on extraction efficiency. The resulting supernatant was

split into equal aliquots for analysis on the three platforms. Aliquots, dried under nitrogen and vacuum-desiccated, were subsequently either reconstituted in 50 μl 0.1% formic acid in water (acidic conditions) or in 50 μl 6.5 mM ammonium bicarbonate in water, pH 8 (basic conditions) for the two UHPLC–MS/MS² analyses, or were derivatized to a final volume of 50 μl for GC/MS analysis using equal parts bistrimethyl-silyl-trifluoroacetamide and solvent mixture acetonitrile:dichloromethane:cyclohexane (5:4:1) with 5% triethylamine at 60°C for 1 hour. In addition, three types of controls were analyzed in concert with the experimental samples: aliquots of a well characterized human plasma pool served as technical replicates throughout the data set, extracted water samples served as process blanks, and a cocktail of standards spiked into every analyzed sample allowed instrument performance monitoring. Experimental samples and controls were randomized across platform run days.

LC/MS, LC/MS²

For UHPLC–MS/MS² analysis, aliquots were separated using a Waters Acquity UPLC (Waters, Millford, MA) and were analyzed using an LTQ mass spectrometer (Thermo Fisher Scientific Inc, Waltham, MA) that consisted of an electrospray ionization source and linear ion-trap mass analyzer. The MS instrument scanned 99–1000 m/z and alternated between MS and MS² scans using dynamic exclusion with approximately six scans per second.

GC/MS

Derivatized samples for GC/MS were separated on a 5% phenyldimethyl silicone column with helium as the carrier gas and a temperature ramp from 60°C to 340°C and then analyzed on a Thermo-Finnigan Trace DSQ MS (Thermo Fisher Scientific Inc.) operated at unit mass resolving power with electron impact ionization and a 50–750 atomic mass unit scan range.

Compound Identification

Compounds were identified by automated comparison of the ion features in the experimental samples with a reference library of chemical standard entries that included retention time, molecular weight (m/z), preferred adducts,

Table 1. Study participant baseline characteristics

	Kidney Disease Progression		
	CKD Stage 2	CKD Stage 3	CKD Stage 4
Number of patients	10	10	10
Sex	Male	Male	Male
Ethnicity	NHW	NHW	NHW
Age (yr)	51.4 \pm 3.3	58.2 \pm 2.6	61.5 \pm 4.7
Height (cm)	168.1 \pm 6.9	174.5 \pm 5.3	175.5 \pm 6.1
Weight (kg)	92.9 \pm 9.6	97.3 \pm 7.9	100.5 \pm 10.0
Body mass index	32.8 \pm 2.6	31.9 \pm 2.2	32.5 \pm 1.8
Estimated GFR (ml/min per 1.73 m ²)	63.6 \pm 13.2	37.9 \pm 9.9	27.4 \pm 4.4

Data are presented as mean \pm SD. NHW, non-Hispanic white.

and in-source fragments as well as associated MS spectra, and were curated by visual inspection for quality control using software developed at Metabolon (14). At present, >2500 commercially available purified standards are registered into LIMS for distribution to both the LC and GC platforms for determination of their analytical characteristics. Compound abundance was quantified by calculating the area under the curve for the quantification ion of the compound.

Statistical Analyses

To aid data visualization, the raw area counts for each biochemical were rescaled by dividing each sample value by the median value for that specific biochemical. For statistical analyses, any missing values were assumed to be below the limits of detection and these values were imputed with the compound minimum (minimum value imputation). Statistical analyses of log-transformed data were performed using “R” (<http://cran.r-project.org/>), which is a freely available, open-source software package. Welch’s *t* tests were performed to compare data between experimental groups. Multiple comparisons were accounted for by estimating the false discovery rate (FDR) using *q* values (15). CKD groups were classified using Random Forest analyses. Random Forests give an estimate of how well we can classify *individuals* in a *new* data set into each group, in contrast to a *t* test, which tests whether the unknown means for two populations are different or not. Random Forests create a set of classification trees based on continual sampling of the experimental units and compounds. Each observation is then classified based on the majority votes from all of the classification trees (16,17).

Results

Global Metabolite Determination

Initially, metabolites were measured in all plasma samples and were then evaluated by comparing values from CKD stage 3 with stage 2, CKD stage 4 with stage 2, and CKD stage 4 with stage 3. In total, 258 metabolites were identified. A subset of these metabolites was identified, with significant differences in one or more of these CKD stage comparisons ($P \leq 0.05$); an additional set of metabolites was identified that approached significance ($0.05 < P < 0.10$). Supplemental Table 1 lists the fold of the differences and statistical test results, including the *q*-value statistic, which is an estimate of the FDR in multiparametric datasets, for every metabolite detected in this study. Supplemental Table 2 shows the median re-scaled raw area counts with missing values imputed with the observed minimum detection value and represents the individual sample values that contributed to the statistical results in Supplemental Table 1. A total of 62 metabolites were identified that were significantly higher or lower in comparisons of CKD stage 3 with stage 2, with 39 higher and 23 lower; in comparisons of CKD stage 4 with stage 2, a total of 111 metabolites differed significantly, with 66 higher and 45 lower; and in comparisons of CKD stage 4 with stage 3, 11 metabolites were identified, with 7 higher and 4 lower. The number of different metabolites that differed significantly was 117. The raw data for all 258 metabolites are presented in the Supplemental Material.

Identification of Thematic Changes

Differences in level of a specific metabolite among a large number may be significant by chance. Therefore, it was of interest to search for thematic differences in which multiple metabolites are significantly higher or lower, which would unlikely be due to chance. Random Forest classification of CKD stage 2 compared with stage 3 and of CKD stage 4 compared with stage 2 identified metabolites based upon their abilities to identify groups. The 30 top-ranking metabolites for the Random Forest classification that compared CKD stages 2 and 4 are listed in Figure 1, denoted as the biochemical importance plot. These metabolites were evaluated, along with related metabolites beyond the top 30, to identify thematic differences. These differences may reveal CKD stage-specific biomarkers. They may also reflect significant alterations of pathophysiology that promote progression from CKD stage 2 to higher stages. Several themes were identified.

Altered Arginine Metabolism

A large difference in relative metabolite concentration was observed for dimethylarginine, as shown in Table 2, as a combination of asymmetric and symmetric dimethylarginine. Dimethylarginine in CKD stage 3 is higher compared with stage 2 (8.1-fold) and in CKD stage 4 compared with stage 2 (4.8-fold). This represents one of the larger metabolite fold increases that were observed in this cross-sectional comparison of CKD stage 2 with higher stages. Other metabolites related to arginine metabolism that were also significantly different in CKD stages 3 and 4 compared with stage 2 include ornithine and citrulline. Ornithine was markedly lower in CKD stages 3 and 4 compared with CKD stage 2.

Elevated Coagulation/Inflammation

The largest fold difference that was observed in comparisons of CKD stage 2 with stage 3, which remained elevated in stage 4, was the increase in coagulation/inflammation factor fibrinopeptide-A and phosphorylated fibrinopeptide-A (Table 2). The higher level of fibrinopeptide-A in CKD stage 3 compared with stage 2 (689-fold) is maintained in CKD stage 4 compared with stage 2 (827-fold). The higher level of phosphorylated fibrinopeptide-A (phosphorylated at serine-3) in CKD stage 3 compared with stage 2 (18-fold) remained elevated in stage 4 compared with stage 2 (45-fold) and was significantly higher in CKD stage 4 compared with stage 3 (2.5-fold). Proline-hydroxyproline dipeptide was significantly higher in CKD stage 3 compared with stage 2 (2.5-fold) and in stage 4 compared with stage 2 (4.5-fold), which may reflect matrix degradation in response to increased coagulation/inflammation.

Impaired Carboxylate Anion Transport

Numerous mono- and di-carboxylate anions are higher in CKD stages 3 and 4 compared with CKD stage 2 (Table 2). A number of these are γ -glutamyl amino acid dipeptides. γ -glutamylglutamine, for example, is higher in CKD stage 3 compared with stage 2 (3.8-fold) and in stage 4 compared with stage 2 (4.8-fold). The γ -glutamyl amino acid dipeptides in Table 2 are involved in the γ -glutamyl cycle,

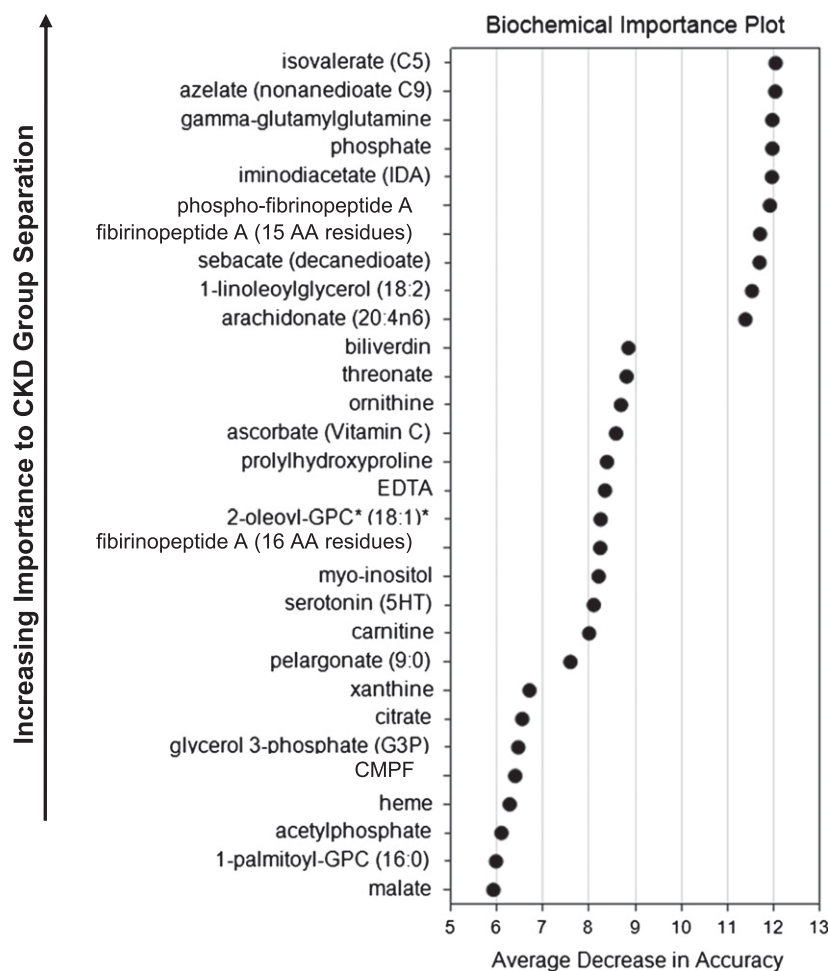


Figure 1. | Top 30 metabolites important to CKD stage 2 versus stage 4 separation by Random Forest classification. Random Forest multi-variate classification was conducted by randomly choosing CDK stage 2 and CDK stage 4 samples (“in-bag”), randomly choosing variables (metabolites) to build classification and regression trees (CART) based on the in-bag samples, and then using several CART trees (50,000) to classify the remaining “out-of-bag” samples between CDK stage 2 and CDK stage 4 (17). The final prediction is based on an aggregation of the predictions across all trees for which the observation was part of the out-of-bag samples. Average decrease in accuracy was obtained by computing the classification error, based on out-of-bag samples, for each CART tree, permuting each variable, and re-computing the error for each permuted tree. The average difference between the two errors was computed and scaled by dividing the SD of these differences yielding a relationship of the more important the variable to the classification, the higher its average decrease in accuracy.

which is involved in glutathione homeostasis. These increases may reflect increased oxidative stress related to depletion of glutathione. Other carboxylate anions also are increased. 3-Carboxy-4-methyl-5-propyl-2-furanpropanoate (CMPF), a known uremic toxin that accumulates in ESRD, is higher in CKD stage 3 compared with stage 2 (18.3-fold) and in stage 4 compared with stage 2 (23.6-fold).

Decreased Adrenal Steroid Hormone Production

A number of adrenal steroid hormones, especially sulfated metabolites, were significantly lower in CKD stage 4 compared with stage 2 (Table 2). These are also anions. However, unlike the situation with carboxylate anions, in which higher levels were observed in higher stages of CKD, the sulfated metabolites were lower in the higher stages of CKD. Cortisol was also significantly lower in CKD stage 4 compared with stage 2 (0.62-fold). This suggests that a decrease in production of adrenal steroid hormones may explain these data.

Discussion

Major differences in metabolite profiles in the various stages of CKD were observed, consistent with altered arginine metabolism, elevated coagulation/inflammation, impaired carboxylate anion transport, and decreased adrenal steroid hormone production. These differences may reveal stage-specific biomarkers of CKD. Of particular interest are the major differences in metabolite profiles related to arginine metabolism and the significance of these changes with respect to impaired production of NO and the effect that this may have on endothelial function. Also of particular interest are the large fold increases in the levels of fibrinopeptide-A in comparisons of CKD stages 3 and 4 with CKD stage 2 and the significance of these increases with respect to development of a procoagulation/proinflammation state.

Arginine Metabolism

There are extensive data on the possible role of asymmetric dimethylarginine in kidney disease owing to its

Table 2. Ratios of significant changes of specific metabolites by stage of CKD ($P \leq 0.05$), mean values, and P values

	Fold of Change				Mean \pm SD				P Value			
	Stages 3/2	Stages 4/2	Stages 4/3		CKD Stage 2	CKD Stage 3	CKD Stage 4		Stages 3/2	Stages 4/2	Stages 4/3	
Altered arginine metabolism												
Dimethylarginine (SDMA + ADMA)	8.1	4.8			0.497 \pm 0.133	4.01 \pm 2.27	2.40 \pm 1.77		7.9E-05	0.01	0.17	
Citrulline	1.6	1.3 ^a			0.825 \pm 0.194	1.30 \pm 0.586	1.08 \pm 0.362		0.03	0.08		
Ornithine	0.28	0.16			4.33 \pm 1.39	1.19 \pm 1.32	0.683 \pm 0.334		2.0E-4	1.4E-06		
Arginine	1.5 ^a	1.5 ^a			0.675 \pm 0.238	1.02 \pm 0.480	1.03 \pm 0.559		0.06	0.10		
Elevated coagulation/inflammation												
Fibrinopeptide A	689	827			0.002 \pm 0.001	1.03 \pm 0.765	1.24 \pm 0.795		3.0E-4	1.1E-14		
Phosphorylated fibrinopeptide A	18	45	2.5		0.045 \pm 0.017	0.818 \pm 0.683	2.06 \pm 2.62		0.002	4.4E-08	0.04	
Proline-hydroxyproline	2.5	4.5			0.466 \pm 0.251	1.16 \pm 1.26	2.08 \pm 1.68		0.03	8.3E-05		
Impaired carboxylate anion transport												
γ -Glutamylleucine		1.3			0.821 \pm 0.283		1.07 \pm 0.161			0.03		
γ -Glutamylisoleucine	1.6	1.7			0.670 \pm 0.196	1.12 \pm 0.440	1.18 \pm 0.510		0.01	0.01		
γ -Glutamylglutamine	3.8	4.8			0.275 \pm 0.166	1.05 \pm 0.417	1.31 \pm 0.349		5.5E-05	8.9E-06		
γ -Glutamylphenylalanine	1.5	1.3			0.903 \pm 0.240	1.31 \pm 0.480	1.17 \pm 0.181		0.03	0.01		
CMPF	18.3 ^a	23.6			0.307 \pm 0.279	5.61 \pm 11.9	7.23 \pm 7.20		0.06	5.0E-4		
Decreased adrenal steroid hormone production												
Dehydroisoandrosterone sulfate		0.55			1.48 \pm 0.878		0.819 \pm 0.685			0.04		
4-androsten-3- β ,17- β -diol disulfate		0.26			3.91 \pm 3.76		1.02 \pm 0.958			0.01		

ADMA, asymmetric dimethylarginine; SDMA, symmetric dimethylarginine; CMPF, 3-Carboxy-4-methyl-5-propyl-2-furanpropanoate.

^a0.1 > P > 0.05.

ability to inhibit nitric oxide synthase (NOS) and limit production of NO, thereby contributing to vascular complications associated with CKD (18,19). The presence of asymmetric dimethylarginine (ADMA) and symmetric dimethylarginine (SDMA) in human urine was first reported in 1970 (20). Inhibition of NOS by ADMA but not by SDMA was reported in 1992, with the observation that plasma levels of SDMA and ADMA were markedly elevated in CKD and ESRD and the suggestion that inhibition of NOS by ADMA may contribute to CVD, hypertension, and immune dysfunction associated with kidney disease (21). ADMA and SDMA are produced as post-translational modifications of selected arginine residues in specific proteins by methyl transfer from *S*-adenosylmethionine, which is catalyzed by protein arginine methyltransferases (PRMTs) (22,23). In turnover of proteins with methylated arginine residues, ADMA and SDMA, as well as mono-methylated arginine residues, are released. Most of the SDMA is released into plasma for clearance by the kidney. ADMA, however, is primarily converted into dimethylamine and citrulline, catalyzed by dimethylarginine dimethylaminohydrolases (DDAH-1 and DDAH-2) with distinct tissue distribution and regulation (24). Hydrolysis catalyzed by DDAH accounts for about 80% of the fate of ADMA. The remaining ADMA is excreted into the urine. It has been suggested that the plasma concentrations of ADMA are determined primarily by DDAH-1, which is highly expressed in kidney (25) and is colocalized with NOS (26). Thus, impaired kidney function may directly dictate the plasma concentrations of ADMA, which can inhibit endothelial NOS (eNOS) at low micromolar concentrations. In addition, methylarginines and dimethylarginines reduce uptake of arginine and other cationic amino acids by inhibition of amino acid transporters CAT-1 and CAT-2, which may also contribute to diminished production of NO (27).

Coagulation/Inflammation

Damage to the endothelium normally exposes collagen and other subendothelial proteins that are recognized by platelet receptors to initiate platelet activation. In addition, tissue factor is exposed on the damaged endothelium and can form a complex with factor VII to initiate the proteolysis cascades that produce thrombin. The activated platelets bind thrombin, which results in release of additional factors to recruit platelets to the site of clot formation. Platelet-bound thrombin also catalyzes the degradation of fibrinogen to form fibrin at the surface of the aggregated platelets, which is then cross-linked to form the clot. Patients with CKD can exhibit defects with any of these aspects of hemostasis, suggesting that CKD is a procoagulation state (28). Impaired platelet activation has been reported in CKD patients with mild-to-moderate CKD (29).

Fibrinopeptide-A is a 16 amino acid peptide derived from the thrombin-catalyzed proteolysis of the N-terminal end of the A α -chain in fibrinogen. Accumulation of fibrinopeptide-A may reflect diminished capacity to clear this metabolite concomitant with a decrease in estimated GFR or may indicate development of a procoagulation state in the progression of CKD stage 2 to stages 3 and 4. Fibrinopeptide-A is a proinflammatory peptide (30), which suggests that this potential development of a procoagulation state is accompanied by the development of inflammation.

Fibrinopeptide-A may be a useful stage-specific biomarker. However, the marked differences in levels of fibrinopeptide-A with stage of CKD may also reflect the development of a procoagulation/proinflammation state and may define the critical point of progression of CKD to states that eventually lead to ESRD. In support of this suggestion, recent studies of several animal models of CKD demonstrated the involvement of coagulation factor Xa and the ability of inhibitors of factor Xa to suppress development of some of the pathologic factors associated with CKD (31).

A critical component of endothelial control of hemostasis is the generation of NO at the appropriate time and levels. In experimental animal studies, eNOS production of NO regulates expression of tissue factor, suggesting that impairment of NO production will result in elevated tissue factor and promotion of coagulation (32). In addition, NO produced by the endothelium acts locally to inhibit platelet aggregation and therefore is essential for dampening the procoagulation response (33). The differences in levels of dimethylarginines (Table 2) observed in comparisons of CKD stage 2 with stage 3 suggests impaired NO production, which therefore may exacerbate the development of a procoagulation/proinflammation state in early stage CKD and enhance its progression (34).

Carboxylate Anions

CMPF is one of a number of uremic toxins that accumulate in ESRD, due to tight binding to albumin, and present problems in removal during hemodialysis (35). CMPF is toxic both to endothelial cells and to proximal tubular cells (36,37). CMPF was higher in CKD stage 3 compared with stage 2 and higher in stage 4 compared with stage 3.

In summary, in this cross-sectional metabolomics study, we determined metabolite patterns in different stages of CKD. The results demonstrated that, for the specific population that was studied, significant differences in metabolite patterns occur. Specifically, markedly higher levels of dimethylarginine and fibrinopeptide-A in comparisons of CKD stage 3 with CKD stage 2 suggest that these may be stage-specific biomarkers. These differences also point to endothelial dysfunction and suggest that a convergence of impaired NO production and enhanced production of coagulation/inflammation factor fibrinopeptide-A may collectively act to enhance progression of CKD beyond stage 2. These are testable hypotheses.

Study Limitations

This was an initial proof-of-concept study in which to address the question whether metabolomics might provide meaningful data for comparison of differences in CKD by stage. As such, it was a cross-sectional study with a limited study population. The results, although interesting and potentially meaningful for identification of stage-specific biomarkers and for insight into CKD progression, are preliminary to a longitudinal study of metabolite changes in CKD progression. The approved future longitudinal study will utilize the Chronic Renal Insufficiency Cohort population in order to compare CKD progression in diabetic and nondiabetic CKD populations that are further divided by age, sex, and ethnicity.

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Disclosures

E.K. and K.L.P. are employees of Metabolon Inc and, as such, have affiliations with or financial involvement with Metabolon Inc.

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Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
glycine	GC/MS	1.3	1.36	1.04	0.08	0.08	0.04	0.03	0.73	0.98	0.845	1.100	1.147	0.341	0.344	0.333
N-acetylglycine	GC/MS	1.45	1.21	0.84	0.02	0.04	0.30	0.14	0.24	0.88	0.641	0.929	0.777	0.125	0.320	0.336
serine	GC/MS	1.31	1.31	1	0.02	0.04	0.01	0.01	0.96	0.99	0.812	1.063	1.063	0.239	0.180	0.154
threonine	GC/MS	1.15	1.21	1.06	0.41	0.20	0.10	0.06	0.58	0.92	0.898	1.028	1.088	0.194	0.327	0.264
betaine	LC/MS pos	0.82	0.54	0.66	0.15	0.12	0.00	0.00	0.13	0.88	1.478	1.209	0.793	0.410	0.802	0.402
aspartate	GC/MS	1.15	1.22	1.06	0.33	0.18	0.28	0.13	0.83	0.98	0.869	0.998	1.057	0.387	0.331	0.434
asparagine	GC/MS	1.36	1.58	1.16	0.09	0.09	0.01	0.01	0.29	0.88	0.798	1.087	1.261	0.302	0.435	0.475
alanine	GC/MS	1.31	1.42	1.09	0.02	0.04	0.01	0.01	0.32	0.88	0.803	1.051	1.144	0.253	0.175	0.216
N-acetylalanine	LC/MS neg	1.38	1.54	1.12	0.13	0.11	0.06	0.05	0.68	0.98	0.815	1.127	1.258	0.314	0.594	0.833
glutamate	GC/MS	0.8	1.07	1.34	0.43	0.21	0.79	0.29	0.32	0.88	1.188	0.950	1.276	0.746	0.245	0.676
glutamine	LC/MS pos	0.98	0.92	0.94	0.69	0.26	0.22	0.11	0.53	0.92	1.043	1.024	0.963	0.127	0.212	0.178
pyroglutamine*	LC/MS pos	2.03	1.33	0.65	0.11	0.10	0.58	0.22	0.30	0.88	0.825	1.677	1.095	0.462	1.325	0.813
histidine	LC/MS neg	1.09	1.09	1	0.16	0.12	0.16	0.09	0.98	0.99	0.918	1.004	1.003	0.132	0.128	0.134
3-methylhistidine	LC/MS neg	1.65	2.66	1.61	0.46	0.21	0.44	0.18	0.88	0.98	1.013	1.674	2.693	0.886	1.952	4.134
lysine	LC/MS pos	0.66	0.59	0.9	0.02	0.04	0.00	0.00	0.79	0.98	1.270	0.834	0.751	0.286	0.454	0.342
pipecolate	LC/MS pos	1.1	0.96	0.87	0.96	0.31	0.84	0.29	0.82	0.98	1.395	1.538	1.337	1.149	1.344	1.133
N6-acetyllysine	LC/MS pos	1.47	1.56	1.06	0.03	0.04	0.13	0.07	0.86	0.98	0.902	1.328	1.406	0.266	0.541	0.967
glutaroyl carnitine	LC/MS pos	1.57	1.63	1.04	0.04	0.06	0.30	0.14	0.59	0.92	0.813	1.275	1.329	0.429	0.585	1.199
phenylalanine	LC/MS pos	1.3	1.21	0.92	0.02	0.04	0.01	0.01	0.55	0.92	0.853	1.112	1.029	0.124	0.320	0.140
phenylacetate	LC/MS neg	1.39	1	0.72	0.07	0.07			0.07	0.88	0.507	0.707	0.507	0.000	0.311	0.000
p-cresol sulfate	LC/MS neg	1.91	1.61	0.84	0.22	0.15	0.31	0.14	0.82	0.98	0.945	1.802	1.521	0.860	1.939	1.288
tyrosine	LC/MS pos	1.26	0.91	0.72	0.52	0.23	0.34	0.15	0.27	0.88	1.049	1.327	0.956	0.212	0.776	0.175
3-(4-hydroxyphenyl)lactate	GC/MS	1.5	0.99	0.66	0.51	0.22	0.79	0.29	0.41	0.90	0.901	1.353	0.892	0.373	1.261	0.574
3-methoxytyrosine	LC/MS pos	1.42	1.43	1.01	0.00	0.01	0.01	0.01	0.97	0.99	0.697	0.987	0.995	0.144	0.212	0.279
phenylacetylglutamine	LC/MS pos	2.31	1.62	0.7	0.28	0.17	0.39	0.16	0.69	0.98	0.817	1.885	1.322	0.608	2.027	1.724
phenol sulfate	LC/MS neg	1.32	1.78	1.35	0.83	0.28	0.12	0.07	0.24	0.88	1.040	1.370	1.847	0.709	1.566	1.393
kynurenine	LC/MS pos	1.16	1.24	1.07	0.37	0.19	0.10	0.06	0.55	0.92	0.944	1.093	1.171	0.234	0.391	0.337
tryptophan	LC/MS pos	1	0.88	0.88	0.70	0.26	0.29	0.14	0.78	0.98	1.064	1.060	0.933	0.254	0.426	0.186
indolelactate	LC/MS pos	0.98	1.28	1.3	0.69	0.26	0.46	0.19	0.33	0.88	1.017	0.998	1.300	0.357	0.538	0.800
indoleacetate	LC/MS pos	0.65	0.55	0.85	0.03	0.04	0.01	0.01	0.25	0.88	1.572	1.015	0.859	0.731	0.384	0.428
tryptophan betaine	LC/MS pos	1.36	1.34	0.98	0.63	0.25	0.59	0.22	0.95	0.99	1.215	1.656	1.631	1.434	1.751	1.439
serotonin (5HT)	LC/MS pos	1.48	1.8	1.21	0.01	0.04	0.00	0.01	0.35	0.88	0.592	0.877	1.065	0.001	0.318	0.482
C-glycosyltryptophan*	LC/MS pos	1.78	2.31	1.3	0.04	0.06	0.01	0.01	0.44	0.91	0.734	1.306	1.694	0.314	1.076	1.771

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
3-indoxyl sulfate	LC/MS neg	1.35	1.35	1	0.56	0.23	0.29	0.14	0.67	0.98	1.186	1.595	1.600	0.914	1.499	1.414
indolepropionate	LC/MS pos	1.44	0.78	0.54	0.57	0.23	0.40	0.17	0.18	0.88	1.179	1.703	0.920	0.620	1.802	0.603
3-methyl-2-oxobutyrate	LC/MS neg	1.07	1.08	1.02	0.91	0.29	0.65	0.24	0.81	0.98	0.954	1.018	1.033	0.207	0.349	0.296
3-methyl-2-oxovalerate	LC/MS neg	0.97	1.1	1.13	0.87	0.28	0.42	0.17	0.33	0.88	0.961	0.933	1.058	0.305	0.302	0.284
beta-hydroxyisovalerate	LC/MS neg	0.97	0.96	1	0.82	0.28	0.81	0.29	0.99	0.99	0.779	0.752	0.751	0.283	0.281	0.280
alpha-hydroxyisocaproate	LC/MS neg	1.1	1.24	1.13	0.72	0.26	0.60	0.23	0.83	0.98	0.580	0.635	0.718	0.148	0.321	0.585
isoleucine	LC/MS pos	0.95	1.08	1.15	0.79	0.27	0.32	0.14	0.07	0.88	1.004	0.950	1.088	0.279	0.185	0.161
leucine	LC/MS pos	0.96	0.98	1.02	0.64	0.25	0.92	0.31	0.66	0.98	1.029	0.989	1.009	0.212	0.280	0.150
valine	LC/MS pos	0.98	1.02	1.04	0.84	0.28	0.68	0.25	0.51	0.92	0.991	0.970	1.011	0.222	0.210	0.128
3-hydroxyisobutyrate	GC/MS	1.37	1.16	0.85	0.21	0.14	0.56	0.22	0.51	0.92	0.792	1.087	0.920	0.251	0.569	0.418
4-methyl-2-oxopentanoate	LC/MS neg	0.99	1.07	1.09	0.71	0.26	0.58	0.22	0.44	0.91	0.974	0.961	1.045	0.269	0.395	0.277
alpha-hydroxyisovalerate	LC/MS neg	1.05	0.85	0.81	0.27	0.17	0.12	0.07	0.77	0.98	2.256	2.360	1.920	1.314	3.850	3.316
isobutyrylcarnitine	LC/MS pos	1.44	1.59	1.1	0.32	0.18	0.14	0.08	0.66	0.98	1.066	1.534	1.693	1.030	1.283	1.554
2-methylbutyrylcarnitine	LC/MS pos	1.31	1.12	0.86	0.52	0.23	0.85	0.29	0.46	0.91	0.843	1.103	0.946	0.438	0.733	0.950
isovalerylcarnitine	LC/MS pos	1.07	1.16	1.09	0.77	0.27	0.60	0.23	0.80	0.98	1.039	1.109	1.206	0.438	0.479	0.570
cysteine	GC/MS	1.03	0.85	0.82	0.99	0.31	0.27	0.13	0.31	0.88	1.052	1.078	0.890	0.297	0.408	0.322
methionine	LC/MS neg	1.36	1.09	0.8	0.15	0.12	0.13	0.07	0.35	0.88	0.943	1.285	1.025	0.128	0.660	0.101
2-hydroxybutyrate (AHB)	GC/MS	1.4	1.37	0.98	0.25	0.17	0.28	0.13	0.94	0.99	0.832	1.164	1.136	0.454	0.732	0.689
dimethylarginine (SDMA + ADMA)	LC/MS pos	8.06	4.84	0.6	0.00	0.00	0.01	0.01	0.17	0.88	0.497	4.006	2.403	0.133	2.273	1.774
arginine	LC/MS neg	1.51	1.53	1.01	0.06	0.07	0.10	0.06	0.93	0.99	0.675	1.020	1.032	0.238	0.480	0.559
ornithine	LC/MS pos	0.28	0.16	0.57	0.00	0.00	0.00	0.00	0.34	0.88	4.327	1.195	0.683	1.387	1.316	0.334
urea	GC/MS	1.32	1.51	1.14	0.17	0.13	0.09	0.06	0.67	0.98	0.803	1.062	1.210	0.351	0.474	0.772
proline	LC/MS pos	1.28	0.97	0.76	0.21	0.14	0.84	0.29	0.15	0.88	0.966	1.239	0.936	0.260	0.518	0.246
citrulline	LC/MS pos	1.58	1.31	0.83	0.03	0.05	0.08	0.05	0.42	0.90	0.825	1.304	1.082	0.194	0.586	0.362
N-acetylorithine	LC/MS pos	1.66	1.39	0.84	0.09	0.09	0.07	0.05	0.87	0.98	0.905	1.501	1.257	0.762	0.999	0.400
trans-4-hydroxyproline	GC/MS	1.23	1.4	1.14	0.44	0.21	0.25	0.12	0.71	0.98	0.973	1.199	1.361	0.362	0.581	0.937
creatine	LC/MS pos	0.97	1.22	1.25	0.64	0.25	0.85	0.29	0.58	0.92	0.978	0.952	1.192	0.460	0.752	0.694
creatinine	LC/MS pos	1.16	1.23	1.06	0.75	0.26	0.98	0.33	0.82	0.98	1.085	1.264	1.337	0.296	0.655	1.344
2-aminobutyrate	LC/MS pos	1.14	1.28	1.13	0.59	0.24	0.05	0.04	0.28	0.88	0.889	1.010	1.140	0.262	0.401	0.237
4-acetamidobutanoate	LC/MS pos	2.17	1.71	0.79	0.17	0.13	0.15	0.08	0.85	0.98	0.866	1.876	1.483	0.232	2.613	1.542
5-oxoproline	LC/MS pos	1.46	1.42	0.97	0.03	0.04	0.09	0.06	0.74	0.98	0.806	1.180	1.140	0.309	0.388	0.391
aspartylphenylalanine	LC/MS pos	2	3.56	1.78	0.02	0.04	0.00	0.00	0.07	0.88	0.354	0.710	1.261	0.000	0.496	0.798
pro-hydroxy-pro	LC/MS pos	2.49	4.46	1.79	0.03	0.05	0.00	0.00	0.05	0.88	0.466	1.162	2.079	0.251	1.268	1.677

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
cyclo(leu-pro)	LC/MS pos	0.55	0.36	0.65	0.42	0.21	0.11	0.07	0.33	0.88	1.971	1.093	0.716	2.732	1.073	0.516
phenylalanyltryptophan	LC/MS pos	1.11	2.39	2.16	0.74	0.26	0.02	0.02	0.04	0.88	0.736	0.817	1.762	0.543	0.570	1.150
gamma-glutamylvaline	LC/MS pos	1.17	1.22	1.04	0.27	0.17	0.07	0.05	0.62	0.95	0.912	1.065	1.108	0.236	0.311	0.250
gamma-glutamylleucine	LC/MS pos	1.12	1.3	1.16	0.51	0.22	0.03	0.02	0.15	0.88	0.821	0.921	1.070	0.283	0.310	0.161
gamma-glutamylisoleucine*	LC/MS pos	1.61	1.7	1.06	0.01	0.03	0.01	0.01	0.78	0.98	0.695	1.117	1.184	0.196	0.440	0.510
gamma-glutamylmethionine	LC/MS pos	1.09	0.85	0.78	0.70	0.26	0.37	0.16	0.21	0.88	1.044	1.138	0.887	0.387	0.474	0.291
gamma-glutamylglutamine	LC/MS pos	3.83	4.78	1.25	0.00	0.00	0.00	0.00	0.13	0.88	0.275	1.053	1.313	0.166	0.417	0.349
gamma-glutamylphenylalanine	LC/MS pos	1.45	1.29	0.89	0.03	0.04	0.01	0.01	0.59	0.92	0.903	1.311	1.165	0.240	0.480	0.181
gamma-glutamyltyrosine	LC/MS pos	1.19	0.97	0.82	0.55	0.23	0.95	0.32	0.53	0.92	0.993	1.179	0.966	0.366	0.631	0.193
bradykinin, des-arg(9)	LC/MS pos	4.95	1.42	0.29	0.26	0.17	0.17	0.09	0.60	0.92	0.764	3.779	1.083	0.306	7.550	0.651
ADSGEGDFXAEGGGVR*	LC/MS pos	2.06	2.82	1.37	0.01	0.03	0.00	0.00	0.24	0.88	0.465	0.957	1.311	0.000	0.516	0.761
DSGEGDFXAEGGGVR*	LC/MS pos	689.13	826.73	1.2	0.00	0.00	0.00	0.00	0.21	0.88	0.002	1.034	1.240	0.001	0.765	0.795
ADpSGEGDFXAEGGGVR*	LC/MS pos	18.01	45.27	2.51	0.00	0.01	0.00	0.00	0.04	0.88	0.045	0.818	2.055	0.017	0.683	2.624
erythronate*	GC/MS	1.61	1.45	0.9	0.31	0.18	0.28	0.13	0.95	0.99	0.992	1.597	1.438	0.393	1.737	1.299
fructose	GC/MS	2.83	1.76	0.62	0.03	0.04	0.00	0.01	0.50	0.92	0.763	2.157	1.343	0.346	1.695	0.534
mannitol	GC/MS	6.94	3.8	0.55	0.08	0.09	0.02	0.02	0.98	0.99	0.216	1.495	0.819	0.059	2.326	0.745
mannose	GC/MS	0.67	0.68	1.02	0.19	0.14	0.24	0.12	0.78	0.98	1.572	1.046	1.070	1.004	0.444	0.365
1,5-anhydroglucitol (1,5-AG)	LC/MS neg	0.76	0.62	0.82	0.54	0.23	0.26	0.13	0.53	0.92	1.291	0.978	0.801	0.711	0.487	0.295
glycerate	GC/MS	0.69	0.51	0.74	0.04	0.05	0.00	0.00	0.02	0.88	1.185	0.823	0.608	0.378	0.225	0.163
glucose	GC/MS	0.69	0.71	1.02	0.09	0.09	0.11	0.06	0.83	0.98	1.422	0.984	1.003	0.697	0.307	0.293
1,6-anhydroglucose	GC/MS	0.55	0.49	0.89	0.33	0.18	0.29	0.14	0.96	0.99	1.391	0.759	0.675	1.891	0.751	0.510
pyruvate	GC/MS	0.48	0.39	0.8	0.01	0.03	0.00	0.00	0.33	0.88	1.921	0.925	0.744	1.014	0.526	0.453
lactate	GC/MS	0.91	0.93	1.02	0.63	0.25	0.58	0.22	0.86	0.98	1.210	1.100	1.127	0.434	0.310	0.558
arabitol	GC/MS	1.3	1.75	1.35	0.24	0.16	0.01	0.01	0.19	0.88	0.826	1.073	1.450	0.206	0.557	0.904
gluconate	GC/MS	1.43	1.01	0.7	0.99	0.31	0.69	0.25	0.73	0.98	0.859	1.232	0.866	0.663	2.085	0.462
arabinose	GC/MS	0.8	0.68	0.84	0.61	0.24	0.32	0.14	0.56	0.92	0.787	0.631	0.531	0.656	0.421	0.165
xylonate	GC/MS	1.8	2.35	1.3	0.13	0.11	0.05	0.04	0.56	0.92	0.636	1.145	1.493	0.025	1.131	1.648
citrate	GC/MS	0.76	0.51	0.67	0.08	0.08	0.00	0.00	0.04	0.88	1.506	1.147	0.773	0.499	0.501	0.218
alpha-ketoglutarate	GC/MS	1.34	0.95	0.71	0.51	0.22	0.84	0.29	0.41	0.90	0.625	0.839	0.593	0.253	0.755	0.172
succinate	GC/MS	1.15	1.23	1.07	0.31	0.18	0.04	0.03	0.45	0.91	0.824	0.951	1.015	0.170	0.314	0.209
malate	GC/MS	0.68	0.51	0.75	0.06	0.07	0.00	0.00	0.23	0.88	1.344	0.918	0.690	0.471	0.486	0.162
acetylphosphate	GC/MS	1.7	1.92	1.13	0.00	0.00	0.00	0.00	0.40	0.90	0.630	1.073	1.213	0.169	0.280	0.332
phosphate	GC/MS	0.44	0.3	0.69	0.00	0.00	0.00	0.00	0.41	0.90	2.679	1.167	0.804	0.452	0.910	0.190

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
linoleate (18:2n6)	LC/MS neg	1.42	1.63	1.15	0.38	0.19	0.00	0.00	0.30	0.88	0.740	1.050	1.210	0.195	0.485	0.364
linolenate [alpha or gamma; (18:3n3 or 6)]	LC/MS neg	1.64	2.11	1.29	0.33	0.18	0.00	0.00	0.22	0.88	0.661	1.085	1.398	0.238	0.525	0.559
dihomo-linolenate (20:3n3 or n6)	LC/MS neg	1.3	1.48	1.14	0.42	0.21	0.01	0.01	0.29	0.88	0.870	1.128	1.290	0.284	0.545	0.359
eicosapentaenoate (EPA; 20:5n3)	LC/MS neg	2.37	3.73	1.57	0.16	0.13	0.00	0.00	0.12	0.88	0.607	1.438	2.262	0.365	1.432	1.490
docosapentaenoate (n3 DPA; 22:5n3)	LC/MS neg	1.84	2.55	1.39	0.13	0.11	0.00	0.00	0.11	0.88	0.623	1.143	1.590	0.288	0.641	0.552
docosahexaenoate (DHA; 22:6n3)	LC/MS neg	2.08	2.3	1.1	0.10	0.09	0.00	0.00	0.46	0.91	0.671	1.399	1.542	0.229	0.847	0.705
caproate (6:0)	LC/MS neg	1.67	2.11	1.26	0.06	0.07	0.00	0.00	0.17	0.88	0.562	0.940	1.186	0.374	0.435	0.383
heptanoate (7:0)	LC/MS neg	1.39	1.72	1.23	0.07	0.08	0.00	0.00	0.10	0.88	0.598	0.834	1.027	0.258	0.313	0.201
caprylate (8:0)	LC/MS neg	1.41	1.31	0.93	0.11	0.10	0.05	0.04	0.95	0.99	0.751	1.058	0.980	0.372	0.381	0.178
pelargonate (9:0)	LC/MS neg	1.3	1.5	1.15	0.04	0.05	0.00	0.00	0.10	0.88	0.744	0.970	1.112	0.172	0.217	0.114
caprate (10:0)	LC/MS neg	1.14	1.04	0.91	0.45	0.21	0.52	0.21	0.73	0.98	1.002	1.147	1.046	0.256	0.463	0.150
undecanoate (11:0)	LC/MS neg	1.44	1.57	1.09	0.01	0.03	0.00	0.00	0.48	0.92	0.818	1.178	1.283	0.194	0.356	0.371
laurate (12:0)	LC/MS neg	1.03	1.01	0.98	0.82	0.28	0.82	0.29	0.98	0.99	1.049	1.079	1.055	0.353	0.343	0.214
5-dodecenoate (12:1n7)	LC/MS neg	2.46	0.71	0.29	0.09	0.09	0.16	0.09	0.01	0.88	1.084	2.663	0.767	0.629	2.585	0.309
myristate (14:0)	LC/MS neg	1.09	1.13	1.04	0.94	0.30	0.32	0.14	0.48	0.92	1.038	1.127	1.174	0.425	0.670	0.343
myristoleate (14:1n5)	LC/MS neg	1.2	0.91	0.76	0.62	0.25	0.63	0.23	0.89	0.98	1.463	1.756	1.331	1.409	1.773	0.544
palmitate (16:0)	LC/MS neg	1.2	1.25	1.04	0.64	0.25	0.08	0.05	0.50	0.92	0.920	1.104	1.150	0.315	0.528	0.313
palmitoleate (16:1n7)	LC/MS neg	1.14	1.07	0.94	0.87	0.28	0.36	0.16	0.40	0.90	1.263	1.440	1.357	1.006	1.394	0.555
margarate (17:0)	LC/MS neg	1.54	1.49	0.97	0.25	0.17	0.03	0.03	0.70	0.98	0.804	1.237	1.194	0.375	0.633	0.414
10-heptadecenoate (17:1n7)	LC/MS neg	1.21	1.28	1.05	0.83	0.28	0.10	0.06	0.36	0.89	0.898	1.090	1.145	0.509	0.738	0.342
stearate (18:0)	LC/MS neg	1.2	1.25	1.04	0.53	0.23	0.11	0.06	0.59	0.92	0.938	1.123	1.171	0.294	0.441	0.367
oleate (18:1n9)	LC/MS neg	1.34	1.39	1.04	0.48	0.22	0.03	0.03	0.45	0.91	0.871	1.164	1.212	0.399	0.685	0.355
cis-vaccenate (18:1n7)	GC/MS	0.23	0.64	2.73	0.09	0.09	0.62	0.23	0.19	0.88	1.181	0.277	0.757	1.524	0.187	0.839
stearidonate (18:4n3)	LC/MS neg	2.42	2.38	0.98	0.07	0.07	0.01	0.01	0.57	0.92	0.511	1.237	1.215	0.511	1.221	0.599
nonadecanoate (19:0)	LC/MS neg	1.58	1.59	1.01	0.11	0.10	0.01	0.01	0.59	0.92	0.705	1.115	1.124	0.263	0.668	0.345
10-nonadecenoate (19:1n9)	LC/MS neg	1.61	1.37	0.85	0.50	0.22	0.05	0.04	0.57	0.92	0.909	1.461	1.248	0.712	1.338	0.419
eicosenoate (20:1n9 or 11)	LC/MS neg	1.72	1.39	0.81	0.45	0.21	0.08	0.05	0.70	0.98	0.980	1.686	1.365	0.655	1.755	0.575
dihomo-linoleate (20:2n6)	LC/MS neg	1.66	1.39	0.83	0.32	0.18	0.07	0.05	0.88	0.98	0.783	1.303	1.086	0.444	0.965	0.422
dihomo-alpha-linolenate (20:3n3)	LC/MS neg	1.3	1.48	1.14	0.42	0.21	0.01	0.01	0.29	0.88	0.870	1.128	1.290	0.284	0.545	0.359
arachidonate (20:4n6)	LC/MS neg	1.86	2.2	1.18	0.01	0.03	0.00	0.00	0.19	0.88	0.631	1.176	1.386	0.180	0.501	0.304
adrenate (22:4n6)	LC/MS neg	1.39	1.41	1.01	0.34	0.18	0.02	0.02	0.52	0.92	0.869	1.210	1.221	0.403	0.625	0.291
3-hydroxydecanoate	LC/MS neg	1.18	0.72	0.61	0.83	0.28	0.39	0.16	0.34	0.88	1.193	1.407	0.857	0.931	1.349	0.261
16-hydroxypalmitate	LC/MS neg	0.95	0.63	0.67	0.73	0.26	0.07	0.05	0.20	0.88	1.491	1.422	0.946	0.859	0.935	0.229

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
2-hydroxystearate	LC/MS neg	1.57	1.29	0.82	0.28	0.18	0.01	0.01	0.96	0.99	0.791	1.245	1.020	0.226	0.661	0.130
2-hydroxypalmitate	LC/MS neg	1.35	1.18	0.87	0.75	0.26	0.08	0.05	0.69	0.98	0.920	1.240	1.082	0.253	1.000	0.160
sebacate (decanedioate)	LC/MS pos	4.87	8.13	1.67	0.00	0.02	0.00	0.00	0.03	0.88	0.155	0.756	1.263	0.019	0.570	0.445
azelate (nonanedioate)	LC/MS neg	8.58	17.95	2.09	0.01	0.03	0.00	0.00	0.02	0.88	0.127	1.087	2.272	0.021	0.972	1.286
octadecanedioate	LC/MS neg	0.98	0.67	0.69	0.14	0.12	0.05	0.04	0.87	0.98	1.215	1.195	0.819	0.532	1.897	0.703
3-carboxy-4-methyl-5-propyl-2-furanpropanoate (CMPE)	LC/MS neg	18.28	23.58	1.29	0.06	0.07	0.00	0.00	0.17	0.88	0.307	5.608	7.234	0.279	11.864	7.195
oleamide	LC/MS pos	1.03	1.28	1.24	0.73	0.26	0.87	0.30	0.64	0.96	1.029	1.061	1.313	0.727	1.201	1.174
propionylcarnitine	LC/MS pos	0.86	0.81	0.95	0.36	0.19	0.21	0.11	0.72	0.98	1.126	0.968	0.917	0.418	0.336	0.376
butyrylcarnitine	LC/MS pos	0.49	0.38	0.76	0.02	0.04	0.00	0.00	0.86	0.98	2.492	1.229	0.936	1.803	1.319	0.774
isovalerate	LC/MS neg	2.03	2.43	1.2	0.01	0.03	0.00	0.00	0.16	0.88	0.481	0.975	1.168	0.148	0.421	0.211
carnitine	LC/MS pos	0.62	0.61	0.97	0.00	0.01	0.00	0.00	0.87	0.98	1.390	0.867	0.844	0.185	0.372	0.207
3-dehydrocarnitine*	LC/MS pos	1.08	1.53	1.41	0.52	0.23	0.13	0.07	0.26	0.88	1.023	1.105	1.563	0.469	0.409	1.167
acetylcarnitine	LC/MS pos	0.95	0.88	0.92	0.61	0.24	0.37	0.16	0.73	0.98	1.219	1.156	1.069	0.428	0.581	0.487
hexanoylcarnitine	LC/MS pos	0.88	0.97	1.1	0.58	0.24	0.95	0.32	0.52	0.92	1.234	1.085	1.194	0.791	0.549	0.507
octanoylcarnitine	LC/MS pos	0.88	0.84	0.96	0.91	0.29	0.97	0.32	0.85	0.98	1.369	1.201	1.151	1.279	0.769	0.663
decanoylcarnitine	LC/MS pos	0.71	0.62	0.87	0.54	0.23	0.30	0.14	0.63	0.96	1.712	1.216	1.056	1.794	0.696	0.583
laurylcarnitine	LC/MS pos	0.82	0.56	0.68	0.75	0.26	0.35	0.15	0.58	0.92	2.043	1.683	1.143	2.256	1.323	0.675
palmitoylcarnitine	LC/MS pos	0.93	0.55	0.59	0.50	0.22	0.02	0.02	0.19	0.88	1.511	1.412	0.837	0.746	1.112	0.386
oleoylcarnitine	LC/MS pos	0.87	0.66	0.76	0.33	0.18	0.11	0.07	0.76	0.98	1.749	1.514	1.147	1.334	1.525	0.959
cholate	LC/MS neg	0.55	1.4	2.54	0.62	0.25	0.89	0.30	0.55	0.92	2.633	1.454	3.696	4.482	2.108	6.210
glycocholate	LC/MS pos	1.96	0.13	0.07	0.45	0.21	0.01	0.01	0.14	0.88	4.207	8.244	0.549	4.058	20.881	0.310
taurocholate	LC/MS neg	14.75	0.36	0.02	0.58	0.24	0.05	0.04	0.15	0.88	1.346	19.863	0.491	1.163	44.588	0.189
taurochenodeoxycholate	LC/MS neg	12.48	0.19	0.01	0.83	0.28	0.04	0.03	0.29	0.88	2.078	25.940	0.386	2.057	62.115	0.351
ursodeoxycholate	LC/MS neg	1.23	1.12	0.91	0.68	0.26	0.83	0.29	0.85	0.98	1.016	1.250	1.138	0.452	1.606	1.089
hyodeoxycholate	LC/MS neg	0.24	0.36	1.51	0.00	0.00	0.00	0.00	0.07	0.88	2.681	0.641	0.967	1.772	0.549	0.596
glycochenodeoxycholate	LC/MS neg	2.92	0.11	0.04	0.20	0.14	0.00	0.00	0.21	0.88	12.067	35.263	1.339	12.006	99.211	1.991
glycolithocholate sulfate*	LC/MS neg	0.64	0.7	1.1	0.48	0.22	0.41	0.17	0.80	0.98	1.459	0.933	1.022	1.220	0.533	0.803
tauroolithocholate 3-sulfate	LC/MS neg	1.68	0.89	0.53	0.53	0.23	0.88	0.30	0.44	0.91	1.002	1.684	0.896	0.741	1.675	0.604
glycochenolate sulfate*	LC/MS neg	0.76	1.05	1.38	0.28	0.17	0.77	0.28	0.16	0.88	1.091	0.832	1.147	0.524	0.436	0.538
taurochenolate sulfate*	LC/MS neg	2.68	1.76	0.66	0.02	0.04	0.03	0.03	0.42	0.90	0.678	1.816	1.193	0.376	1.586	0.755
glycerol	GC/MS	0.74	0.79	1.06	0.03	0.05	0.08	0.05	0.83	0.98	1.153	0.856	0.906	0.290	0.331	0.375
choline	LC/MS pos	1.38	1.32	0.95	0.05	0.06	0.08	0.05	0.73	0.98	0.836	1.157	1.100	0.334	0.344	0.376

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
glycerol 3-phosphate (G3P)	GC/MS	1.36	1.76	1.29	0.06	0.07	0.00	0.00	0.04	0.88	0.791	1.080	1.395	0.221	0.385	0.297
glycerophosphorylcholine (GPC)	LC/MS pos	1.72	2.54	1.48	0.32	0.18	0.00	0.00	0.08	0.88	0.557	0.959	1.416	0.254	0.974	0.835
myo-inositol	GC/MS	2.27	2.01	0.89	0.03	0.05	0.01	0.01	0.98	0.99	0.810	1.841	1.631	0.340	1.671	1.157
scyllo-inositol	GC/MS	1.97	1.27	0.64	0.15	0.12	0.34	0.15	0.45	0.91	0.586	1.156	0.742	0.335	1.214	0.467
3-hydroxybutyrate (BHBA)	GC/MS	1.56	1.3	0.84	0.36	0.19	0.34	0.15	0.96	0.99	1.258	1.958	1.641	1.174	2.082	1.290
1-oleoylglycerophosphoethanolamine	LC/MS neg	0.69	0.46	0.66	0.09	0.09	0.01	0.01	0.40	0.90	1.702	1.172	0.779	0.943	1.106	0.422
1-linoleoylglycerophosphoethanolamine*	LC/MS neg	0.66	0.61	0.93	0.04	0.05	0.02	0.02	0.82	0.98	1.534	1.012	0.940	0.742	0.560	0.397
1-arachidonoylglycerophosphoethanolamine*	LC/MS neg	0.83	0.93	1.12	0.15	0.12	0.49	0.20	0.40	0.90	1.104	0.912	1.025	0.288	0.294	0.302
2-arachidonoylglycerophosphoethanolamine*	LC/MS neg	0.74	0.95	1.29	0.06	0.07	0.55	0.21	0.36	0.89	1.061	0.783	1.008	0.367	0.277	0.528
1-myristoylglycerophosphocholine	LC/MS pos	0.53	0.46	0.86	0.03	0.05	0.01	0.01	0.89	0.98	1.741	0.931	0.805	0.785	0.651	0.492
1-palmitoylglycerophosphocholine	LC/MS pos	0.73	0.69	0.94	0.01	0.03	0.00	0.00	0.78	0.98	1.266	0.923	0.870	0.241	0.287	0.194
2-palmitoylglycerophosphocholine*	LC/MS pos	0.56	0.53	0.95	0.00	0.01	0.00	0.00	0.82	0.98	1.519	0.843	0.802	0.378	0.431	0.428
1-palmitoleoylglycerophosphocholine*	LC/MS pos	0.33	0.36	1.11	0.01	0.03	0.04	0.03	0.51	0.92	2.690	0.882	0.976	1.815	1.057	0.668
1-heptadecanoylglycerophosphocholine	LC/MS pos	0.87	0.55	0.63	0.52	0.23	0.01	0.01	0.02	0.88	1.349	1.173	0.741	0.536	0.545	0.255
1-stearoylglycerophosphocholine	LC/MS pos	0.88	0.75	0.85	0.29	0.18	0.05	0.04	0.58	0.92	1.243	1.096	0.928	0.328	0.544	0.359
2-stearoylglycerophosphocholine*	LC/MS pos	0.67	0.61	0.91	0.11	0.10	0.05	0.04	0.71	0.98	1.426	0.956	0.869	0.703	0.609	0.591
1-oleoylglycerophosphocholine	LC/MS pos	0.6	0.57	0.95	0.03	0.04	0.02	0.02	0.84	0.98	1.591	0.962	0.911	0.635	0.440	0.351
2-oleoylglycerophosphocholine*	LC/MS pos	0.58	0.43	0.73	0.01	0.03	0.00	0.00	0.33	0.88	1.764	1.030	0.756	0.714	0.628	0.269
1-linoleoylglycerophosphocholine	LC/MS pos	0.75	0.68	0.91	0.03	0.04	0.00	0.01	0.52	0.92	1.270	0.948	0.866	0.323	0.259	0.232
1-eicosatrienoylglycerophosphocholine*	LC/MS pos	0.69	0.75	1.1	0.18	0.13	0.35	0.15	0.50	0.92	1.457	1.004	1.100	0.768	0.474	0.422
1-arachidonoylglycerophosphocholine*	LC/MS pos	1.26	1.47	1.17	0.68	0.26	0.01	0.01	0.23	0.88	0.905	1.139	1.333	0.227	0.613	0.394
1-docosahexaenoylglycerophosphocholine*	LC/MS pos	1.18	1.46	1.23	0.21	0.14	0.00	0.01	0.11	0.88	0.863	1.019	1.256	0.163	0.284	0.341
1-palmitoylglycerol (1-monopalmitin)	GC/MS	0.67	0.43	0.64	0.21	0.15	0.01	0.01	0.09	0.88	1.287	0.866	0.556	0.793	0.532	0.188
1-linoleoylglycerol (1-monolinolein)	LC/MS neg	4.79	6.73	1.41	0.00	0.00	0.00	0.00	0.09	0.88	0.310	1.481	2.084	0.193	0.923	0.762
stearoyl sphingomyelin	GC/MS	2.14	2.07	0.96	0.34	0.18	0.29	0.14	0.97	0.99	0.574	1.232	1.187	0.416	1.097	1.034
lathosterol	GC/MS	1.14	0.82	0.72	0.65	0.25	0.53	0.21	0.28	0.88	0.524	0.596	0.428	0.386	0.409	0.201
cholesterol	GC/MS	1.03	1.01	0.97	1.00	0.31	0.98	0.32	0.99	0.99	1.017	1.051	1.022	0.160	0.328	0.210
dehydroisoandrosterone sulfate (DHEA-S)	LC/MS neg	0.87	0.55	0.64	0.32	0.18	0.04	0.03	0.52	0.92	1.478	1.280	0.819	0.878	0.933	0.685
epiandrosterone sulfate	LC/MS neg	0.51	0.77	1.5	0.06	0.07	0.15	0.08	0.94	0.99	1.594	0.819	1.232	1.022	0.481	1.267
androsterone sulfate	LC/MS neg	0.45	0.53	1.18	0.05	0.07	0.06	0.05	0.95	0.99	2.135	0.956	1.124	1.846	0.709	1.180
cortisol	LC/MS pos	0.68	0.62	0.9	0.10	0.09	0.03	0.03	0.79	0.98	1.449	0.992	0.894	0.718	0.469	0.379
cortisone	LC/MS pos	0.86	0.59	0.69	0.20	0.14	0.00	0.01	0.08	0.88	1.059	0.907	0.628	0.203	0.320	0.276
7-alpha-hydroxy-3-oxo-4-cholestenoate (7-Hoca)	LC/MS neg	0.78	0.86	1.09	0.30	0.18	0.43	0.18	0.86	0.98	1.550	1.214	1.326	1.084	1.102	1.122

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
4-androsten-3beta,17beta-diol disulfate 1*	LC/MS neg	0.55	0.26	0.47	0.09	0.09	0.01	0.01	0.54	0.92	3.909	2.164	1.020	3.756	3.462	0.958
4-androsten-3beta,17beta-diol disulfate 2*	LC/MS neg	0.97	0.54	0.55	0.52	0.23	0.01	0.01	0.11	0.88	1.254	1.219	0.675	0.535	0.802	0.452
5alpha-androstan-3beta,17beta-diol disulfate	LC/MS neg	0.39	0.27	0.7	0.02	0.04	0.00	0.00	0.42	0.90	2.602	1.008	0.710	1.989	1.040	0.848
pregnen-diol disulfate*	LC/MS neg	0.67	0.34	0.5	0.17	0.13	0.00	0.00	0.13	0.88	2.035	1.360	0.682	1.725	1.112	0.483
xanthine	LC/MS pos	2.37	4.27	1.8	0.04	0.06	0.00	0.01	0.18	0.88	0.502	1.189	2.146	0.118	1.196	2.334
hypoxanthine	LC/MS neg	1.01	1.03	1.02	0.34	0.18	0.26	0.13	0.48	0.92	0.938	0.947	0.964	0.000	0.026	0.068
inosine	LC/MS neg	2.91	4.72	1.62	0.02	0.04	0.00	0.00	0.14	0.88	0.300	0.873	1.416	0.000	0.817	0.931
N1-methyladenosine	LC/MS pos	0.93	0.78	0.84	0.38	0.19	0.02	0.02	0.39	0.90	1.087	1.013	0.851	0.202	0.422	0.216
adenosine 5'-monophosphate (AMP)	LC/MS pos	0.55	0.54	0.98	0.02	0.04	0.02	0.02	0.34	0.88	1.350	0.742	0.729	0.964	0.039	0.000
guanosine	LC/MS neg	1.52	2	1.32	0.06	0.07	0.01	0.01	0.22	0.88	0.505	0.765	1.007	0.000	0.436	0.492
urate	LC/MS neg	1.11	1.06	0.95	0.28	0.17	0.44	0.18	0.64	0.96	0.978	1.085	1.034	0.191	0.221	0.161
uridine	LC/MS neg	1.05	1.31	1.25	0.75	0.26	0.04	0.03	0.07	0.88	0.906	0.948	1.184	0.289	0.258	0.238
pseudouridine	LC/MS neg	1.48	1.64	1.11	0.11	0.10	0.07	0.05	0.76	0.98	0.946	1.403	1.554	0.256	0.993	1.274
ascorbate (Vitamin C)	GC/MS	7.15	11.46	1.6	0.00	0.01	0.00	0.00	0.19	0.88	0.114	0.811	1.301	0.000	0.668	0.999
threonate	GC/MS	2.65	3.27	1.23	0.03	0.04	0.00	0.00	0.18	0.88	0.453	1.203	1.483	0.296	0.711	0.439
heme	LC/MS pos	0.34	0.1	0.3	0.01	0.03	0.00	0.00	0.23	0.88	5.139	1.747	0.529	4.173	2.381	0.492
bilirubin (Z,Z)	LC/MS neg	2.01	1.43	0.71	0.33	0.18	0.08	0.05	0.97	0.99	0.901	1.814	1.291	0.312	1.979	0.521
bilirubin (E,E)*	LC/MS neg	1.29	1.07	0.83	0.72	0.26	0.57	0.22	0.97	0.99	1.058	1.368	1.129	0.428	0.848	0.353
bilirubin (E,Z or Z,E)*	LC/MS pos	1.02	0.74	0.73	0.44	0.21	0.25	0.12	0.87	0.98	1.288	1.319	0.958	0.862	1.312	0.458
biliverdin	LC/MS pos	0.92	0.33	0.36	0.14	0.12	0.00	0.00	0.62	0.95	1.729	1.595	0.568	1.245	1.879	0.295
nicotinamide	LC/MS pos	0.86	0.65	0.76	0.37	0.19	0.04	0.03	0.35	0.88	1.240	1.064	0.810	0.539	0.594	0.408
pantothenate	LC/MS pos	0.95	1.44	1.52	0.73	0.26	0.47	0.19	0.34	0.88	0.847	0.804	1.220	0.407	0.472	1.031
alpha-tocopherol	GC/MS	1.31	1.79	1.36	0.16	0.12	0.03	0.03	0.03	0.88	0.782	1.026	1.397	0.428	0.331	0.472
gamma-tocopherol	GC/MS	1.02	1.81	1.77	0.82	0.28	0.04	0.03	0.05	0.88	0.502	0.512	0.908	0.059	0.089	0.552
pyridoxate	LC/MS neg	1.55	1.81	1.17	0.59	0.24	0.01	0.01	0.14	0.88	0.818	1.270	1.485	0.525	1.797	0.753
hippurate	LC/MS neg	2.88	1.62	0.56	0.34	0.18	0.92	0.31	0.42	0.90	1.092	3.145	1.765	0.936	5.985	3.096
2-hydroxyhippurate (salicylurate)	LC/MS neg	1.11	4.34	3.92	0.84	0.28	0.34	0.15	0.42	0.90	0.524	0.581	2.275	0.437	0.508	5.448
catechol sulfate	LC/MS neg	1.44	1.24	0.86	0.78	0.27	0.29	0.14	0.48	0.92	1.089	1.573	1.352	1.007	2.604	0.806
4-vinylphenol sulfate	LC/MS neg	1.32	2.18	1.65	0.92	0.29	0.25	0.12	0.34	0.88	1.059	1.403	2.310	0.788	1.524	2.576
glycolate (hydroxyacetate)	GC/MS	0.85	0.83	0.98	0.18	0.13	0.12	0.07	0.81	0.98	0.850	0.721	0.706	0.247	0.139	0.096
iminodiacetate (IDA)	GC/MS	0.32	0.15	0.45	0.00	0.00	0.00	0.00	0.20	0.88	4.452	1.439	0.655	2.340	1.630	0.266
salicylate	LC/MS neg	0.46	0.63	1.38	0.70	0.26	0.61	0.23	0.28	0.88	1.509	0.692	0.958	3.378	0.873	0.736
salicyluric glucuronide*	LC/MS neg	1.72	4.67	2.71	0.33	0.18	0.18	0.09	0.49	0.92	0.397	0.684	1.855	0.248	0.890	3.931

Supplemental Data Table 1 UNNM-01-12VW		Fold of Change			Statistical Values						Mean Values			Standard Deviation		
		CKD3 CKD2	CKD4 CKD2	CKD4 CKD3	CKD3 CKD2		CKD4 CKD2		CKD4 CKD3		CKD2	CKD3	CKD4	CKD2	CKD3	CKD4
					p-value	q-value	p-value	q-value	p-value	q-value						
Biochemical Name	Platform															
4-acetamidophenol	LC/MS pos	1.37	1.24	0.91	0.69	0.26	0.85	0.29	0.84	0.98	0.414	0.568	0.514	0.281	0.607	0.605
p-acetamidophenylglucuronide	LC/MS neg	1.61	1.32	0.82	0.40	0.20	0.37	0.16	0.91	0.99	0.387	0.624	0.510	0.192	0.733	0.363
2-propylpentanoate (valproate)	LC/MS neg	2.32	2.29	0.98	0.00	0.00	0.00	0.00	0.91	0.99	0.541	1.257	1.238	0.251	0.561	0.394
pioglitazone*	LC/MS pos	1	1	1							1.000	1.000	1.000	0.000	0.000	0.000
hydroxypioglitazone*	LC/MS pos	1	1	1							1.000	1.000	1.000	0.000	0.000	0.000
naproxen	GC/MS	1	1	1							1.000	1.000	1.000	0.000	0.000	0.000
metformin	LC/MS pos	1	1	1							1.000	1.000	1.000	0.000	0.000	0.000
metoprolol	LC/MS pos	1	2.04	2.04			0.17	0.09	0.17	0.88	0.190	0.190	0.388	0.000	0.000	0.427
metoprolol acid metabolite*	LC/MS pos	9.28	64.82	6.98	0.29	0.18	0.16	0.09	0.48	0.92	0.454	4.216	29.440	0.046	11.746	75.934
hydrochlorothiazide	LC/MS neg	1	1	1							1.000	1.000	1.000	0.000	0.000	0.000
EDTA	LC/MS neg	0.67	0.55	0.83	0.00	0.02	0.00	0.00	0.17	0.88	0.933	0.621	0.514	0.232	0.227	0.000
quininate	GC/MS	1.25	3.03	2.42	0.74	0.26	0.12	0.07	0.21	0.88	0.451	0.564	1.368	0.267	0.517	2.202
piperine	LC/MS pos	2.65	3.61	1.36	0.04	0.06	0.01	0.01	0.43	0.91	0.460	1.217	1.658	0.459	0.830	1.495
thymol sulfate	LC/MS neg	1.03	2.46	2.38	0.75	0.26	0.51	0.20	0.37	0.90	0.925	0.957	2.278	0.981	1.295	3.941
N-(2-furoyl)glycine	LC/MS neg	0.76	0.75	0.98	0.59	0.24	0.55	0.21	0.92	0.99	0.770	0.585	0.576	0.746	0.163	0.132
stachydrine	LC/MS pos	2.07	0.58	0.28	0.36	0.19	0.95	0.32	0.26	0.88	2.383	4.932	1.384	3.495	8.117	1.796
homostachydrine*	LC/MS pos	0.86	0.72	0.83	0.45	0.21	0.08	0.05	0.27	0.88	1.206	1.043	0.867	0.463	0.380	0.299
caffeine	LC/MS pos	0.92	0.17	0.19	0.17	0.13	0.00	0.00	0.29	0.88	3.474	3.202	0.606	2.179	4.686	0.319
paraxanthine	LC/MS pos	0.78	0.37	0.48	0.29	0.18	0.03	0.03	0.38	0.90	1.693	1.318	0.626	1.165	1.723	0.341
theobromine	LC/MS pos	0.45	0.36	0.81	0.21	0.14	0.14	0.08	0.82	0.98	2.499	1.125	0.908	2.701	0.962	0.473
theophylline	LC/MS pos	0.85	0.54	0.63	0.56	0.23	0.07	0.05	0.24	0.88	1.348	1.150	0.727	0.816	0.859	0.255
1-methylurate	LC/MS pos	2.05	0.94	0.46	0.50	0.22	0.74	0.27	0.38	0.90	0.652	1.336	0.613	0.321	2.258	0.342
1,7-dimethylurate	LC/MS pos	1.51	0.79	0.52	0.70	0.26	0.10	0.06	0.24	0.88	0.701	1.059	0.553	0.264	1.442	0.000
1-methylxanthine	LC/MS pos	1.03	1	0.97	0.86	0.28	0.89	0.30	0.95	0.99	0.749	0.774	0.749	0.163	0.418	0.237
3-methylxanthine	LC/MS pos	0.87	0.7	0.8	0.40	0.20	0.38	0.16	0.87	0.98	0.836	0.729	0.586	0.652	0.931	0.218
5-acetylamino-6-amino-3-methyluracil	LC/MS neg	1.8	1	0.55	0.34	0.18			0.34	0.88	0.199	0.360	0.199	0.000	0.506	0.000
cotinine	LC/MS pos	1	1.05	1.05			0.34	0.15	0.34	0.88	0.785	0.785	0.828	0.000	0.000	0.136
erythritol	GC/MS	1.53	1.55	1.02	0.29	0.18	0.15	0.08	0.80	0.98	0.986	1.508	1.533	0.376	1.390	1.228

