

Supporting Information

Machine Learning-enabled Renal Cell Carcinoma Status Prediction Using Multi-Platform Urine-based Metabolomics

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Table of Contents

Supporting information section S1. NMR quality assurance and quality control and Spectra Binning

Supporting information scheme S1. NMR peak picking methods.

Supporting information section S2. Model evaluation metrics.

Figure S1: Relative quantification of all discriminating metabolomic features identified in the study, for RCC samples collected in the clinic vs. operating room.

Figure S2: Relative quantification of the 10-metabolite panel.

Figure S3: Selection of metabolomic features with q -values and classification with logistic regression using the Metaboanalyst 5.0 biomarker analysis platform.

Figure S4: Machine learning pipeline focused on upregulated features in RCC vs. controls.

Figure S5: Relative abundances for the panel of upregulated metabolites.

Figure S6: Machine learning pipeline focused only on NMR features.

Figure S7: Relative quantification of features in the NMR RCC metabolic panel.

Figure S8: MS/MS annotation of 2-mercaptobenzothiazole and dibutylamine/ *n*-butylisobutylamine/disobutylamine.

Table S1: Propensity score matching and study cohort characteristics.

Table S2: Model cohort RCC characteristics.

Table S3: Test cohort characteristics.

Table S4: Quantified NMR features. ppm values, confidence score, fold changes, and q -values.

Table S5: Chemical information of the 10-metabolite panel.

Table S6: Machine learning hyperparameters used for binary classification using the MS-based 10-metabolite panel.

Table S7: Machine learning performance using the MS RCC 10 panel biomarker.

Table S8: Compound annotation and identification for the 5-metabolite panel upregulated in RCC.

Table S9: Hyperparameters tuned for machine learning methods used for binary classification for the upregulated RCC biomarkers.

Table S10: Machine learning performance using the upregulated MS RCC biomarkers.

Table S11: Detailed MS/MS information for the panel of 7 metabolites that distinguish RCC from control samples.

Table S12: Machine learning hyperparameters tuned for binary classification using only the 7-identified metabolite panel.

Table S13: Machine learning hyperparameters tuned for binary classification using only NMR RCC biomarkers.

Table S14: Machine learning performance using NMR RCC biomarkers.

Table S15: Review of some notable urine metabolomics studies comparing RCC to controls.

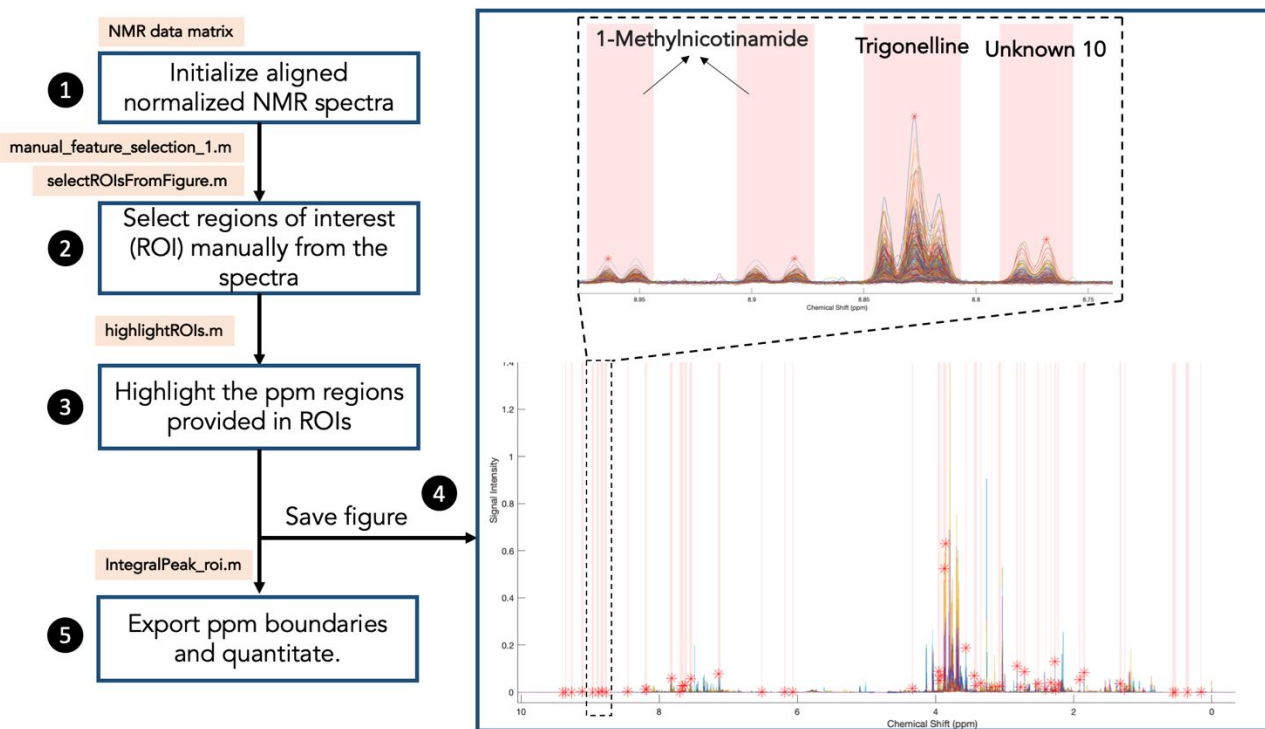
Table S16: Metabolomic features with q values < 0.05 and > 1 -fold change.

Supporting information section S1. NMR quality assurance and quality control and Spectral Binning

All study cohort urine samples were randomized prior to running NMR experiments. Twelve NMR buffer blanks, 3 per run, were added to ensure there is no carry-over of samples between urine samples. One buffer blank was added at the beginning, middle, and end of each run. Thirty-two external controls (Nicotine, Ethanol & Drug Free Human Urine, Female; Golden West Diagnostics, LLC), 8 in each of the four NMR racks (run) used, were added to the study to ascertain the reliability of the sample acquisition process particularly for comparing across runs. One external control was added after the first blank at the beginning the run, and one before the last blank at the end of the run, while the remaining six external controls were randomized with the study's urine samples. The external pooled controls served its purpose as the controls were clustered tightly together on a PCA plot (data not shown). Also, 27 μL were taken out of each study urine sample for two internal pooled controls. 1D ^1H NMR experiment was conducted on all samples, while HSQC was carried out on one internal pooled control sample, and HSQC-TOCSY was carried out on the other. The NMR data for the internal pooled samples were used for metabolite annotation using AssureNMR and COLMARm¹ as described in the manuscript. Fifty metabolomic features in the aligned and normalized 1D ^1H NMR spectra were manually binned and quantified by taking spectral areas for integration in regions without overlap, and combined with MS features for downstream analysis. A manual binning workflow in the Edison laboratory in-house metabolomics toolbox MATLAB scripts was used for binning (https://github.com/artedison/Edison_Lab_Shared_Metabolomics_UGA). **Scheme S1**

shows the steps involved in this process: aligned normalized NMR spectra were initialized, the functions `manual_feature_selection1.m` and `selectROIsFromFigure.m` allowed us to manually select multiple regions in the displayed spectra, where a rectangle is drawn around the region of interest (ROI) for binning in an interactive fashion. The `highlightROIs.m` function highlights the ppm regions provided in ROI, and the binned, highlighted NMR spectra figure is saved. Finally, ppm boundaries are exported, and `IntegralPeak_roi.m` function was used to integrate metabolomic features in the binned spectra.

Supporting information scheme S1. NMR Peak Picking Methods



Supporting information section S2. Model evaluation metrics

The following metrics were used for model evaluation, where TP is true positive, TN is true negative, FP is false positive, and FN is false negative:

Accuracy measures the percentage of all correctly predicted samples.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

Sensitivity (or recall) measures the percentage of correctly predicted RCC patients out of the total RCC samples.

$$Sensitivity = \frac{TP}{TP + FN}$$

Specificity measures the percentage of correctly predicted controls out of the total control samples.

$$Specificity = \frac{TN}{TN + FP}$$

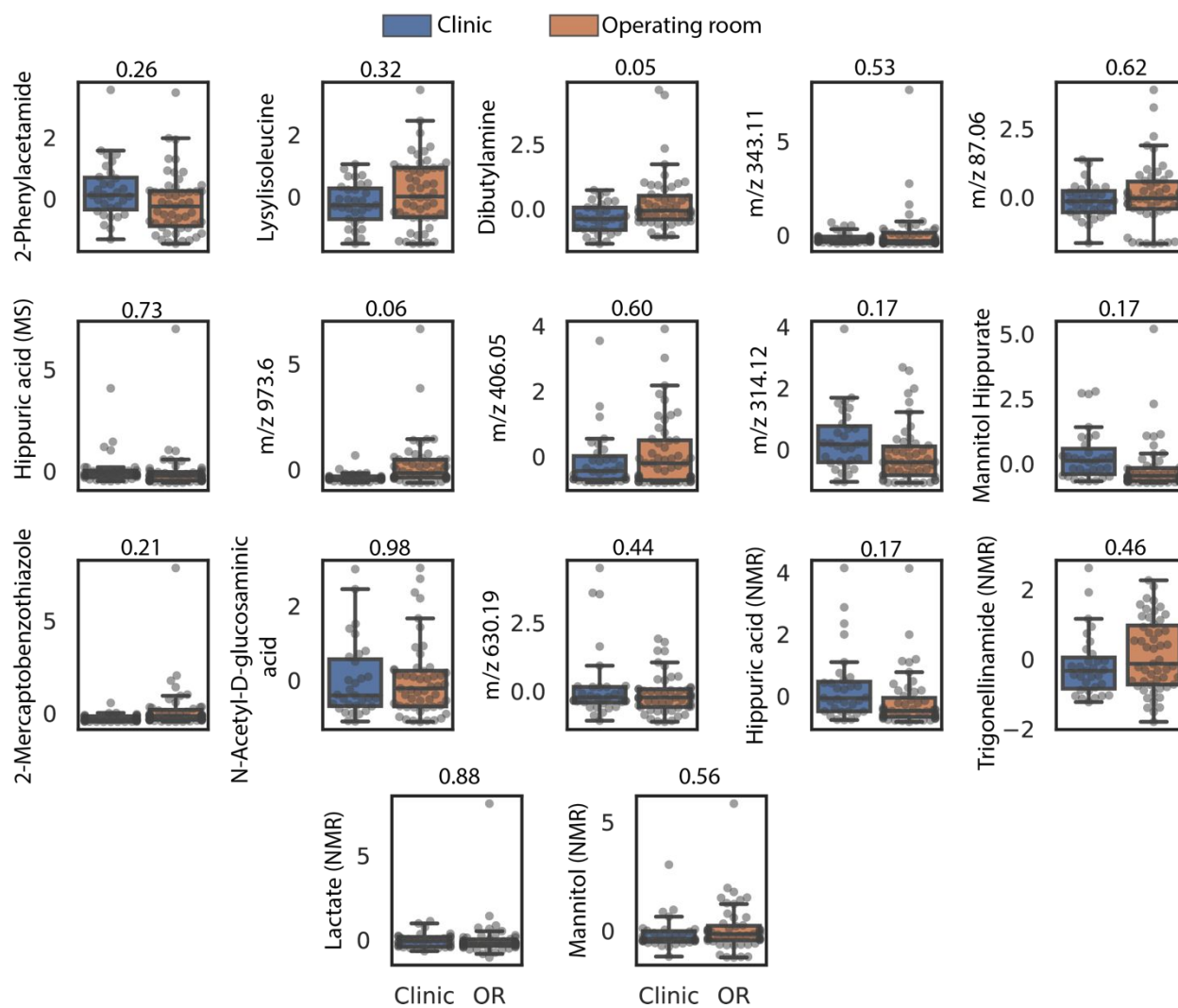


Figure S1: Relative quantification of all discriminating metabolomic features identified in the study, for RCC samples collected in the clinic vs. operating room. q -values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent t -test. All features were statistically insignificant. Raw data were transformed *via* autoscaling for visualization.

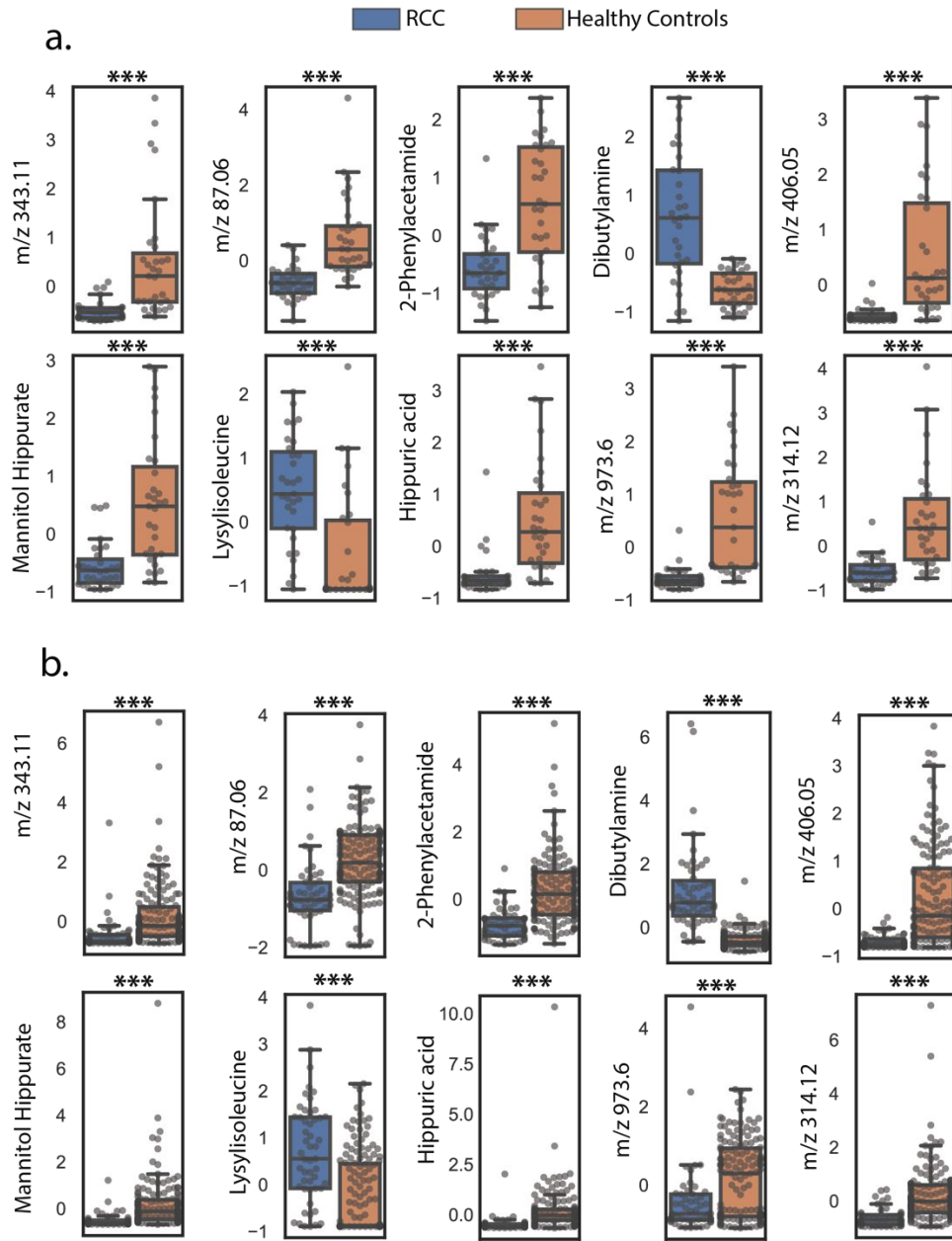


Figure S2: Relative quantification of the 10-metabolite panel in (a) the model cohort.

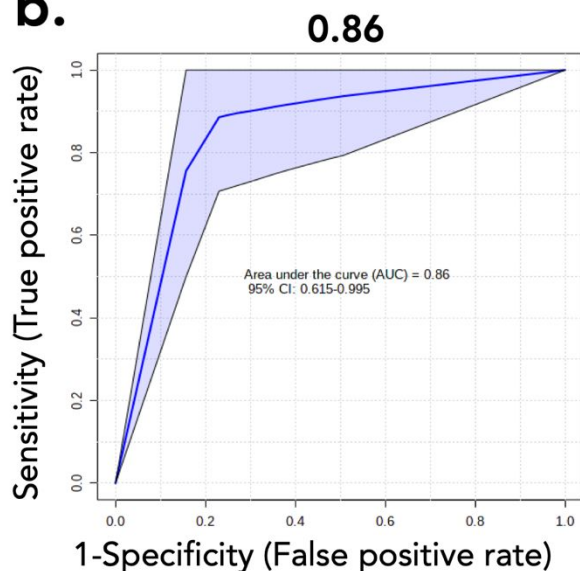
After selecting features with greater than a one-fold change between control and RCC groups, q -values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent t -test. ($* q \leq 0.05$, $** q \leq 0.01$, $*** q \leq 0.001$). (b) Test cohort, p -values from the Welch t -test were reported (unequal sample size). (

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$). Raw data were transformed *via* autoscaling for visualization

a.

ID	Metabolite ID	Mode	RT [min]	FC	q-value
2102	dibutylamine, N-butylisobutylamine, diisobutylamine (isomer)	positive	3.449	1.57	7.87E-05
3872	3872	positive	4.049	-2.58	1.90E-04
3675	3675	positive	1.184	-1.08	2.62E-04
3757	3757	positive	4.003	-2.39	3.26E-04
6261	6261	negative	2.591	-1.88	3.68E-04
5383	5383	negative	4.067	-2.62	3.85E-04
720	2-phenylacetamide	positive	2.562	-1.07	3.86E-04
4401	4401	positive	4.039	-2.69	4.81E-04
6276	6276	negative	2.636	-1.65	4.81E-04

b.



c.

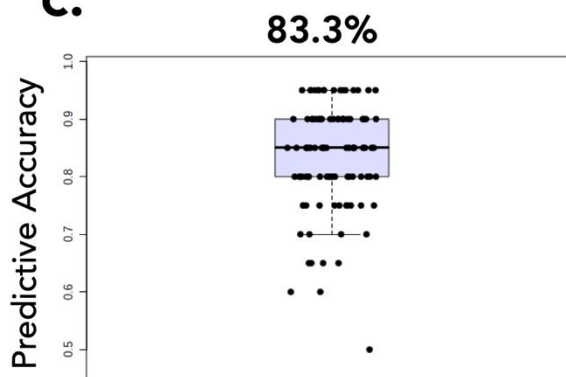


Figure S3: Selection of metabolomic features with q -values and classifying with logistic regression using the Metaboanalyst 5.0 biomarker analysis platform. (a) Metabolomic features with the top ten highest q -values from univariate analysis. (b) ROC-AUC (c) Predictive accuracy. Analysis was carried out using the model cohort.

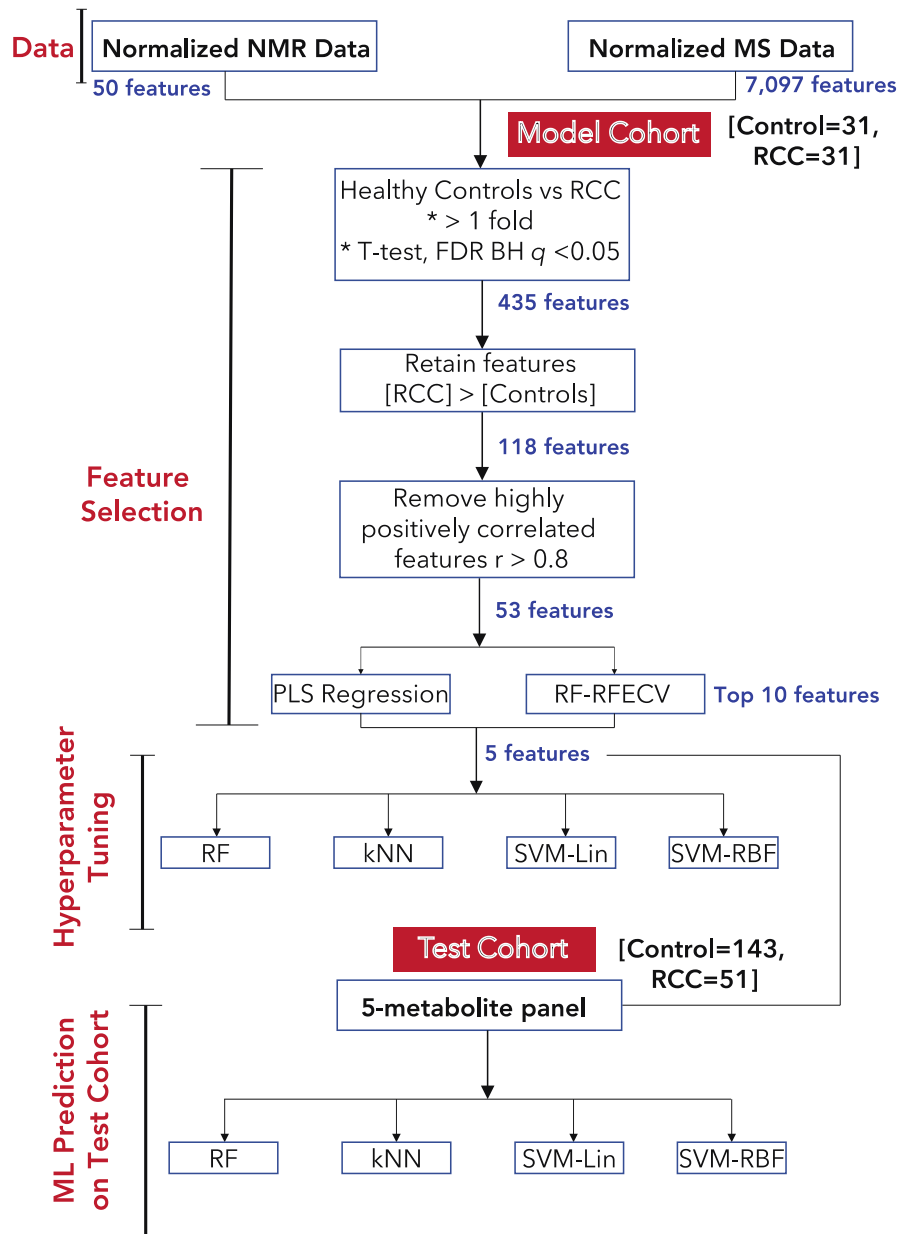


Figure S4: Machine learning pipeline focused on upregulated features in RCC vs. controls. **PLS:** partial least squares, **RF- RFECV:** random forest recursive feature elimination – cross validation, **FDR-BH:** false discovery rate Benjamini-Hochberg procedure, **k-NN:** *k*-nearest neighbors.

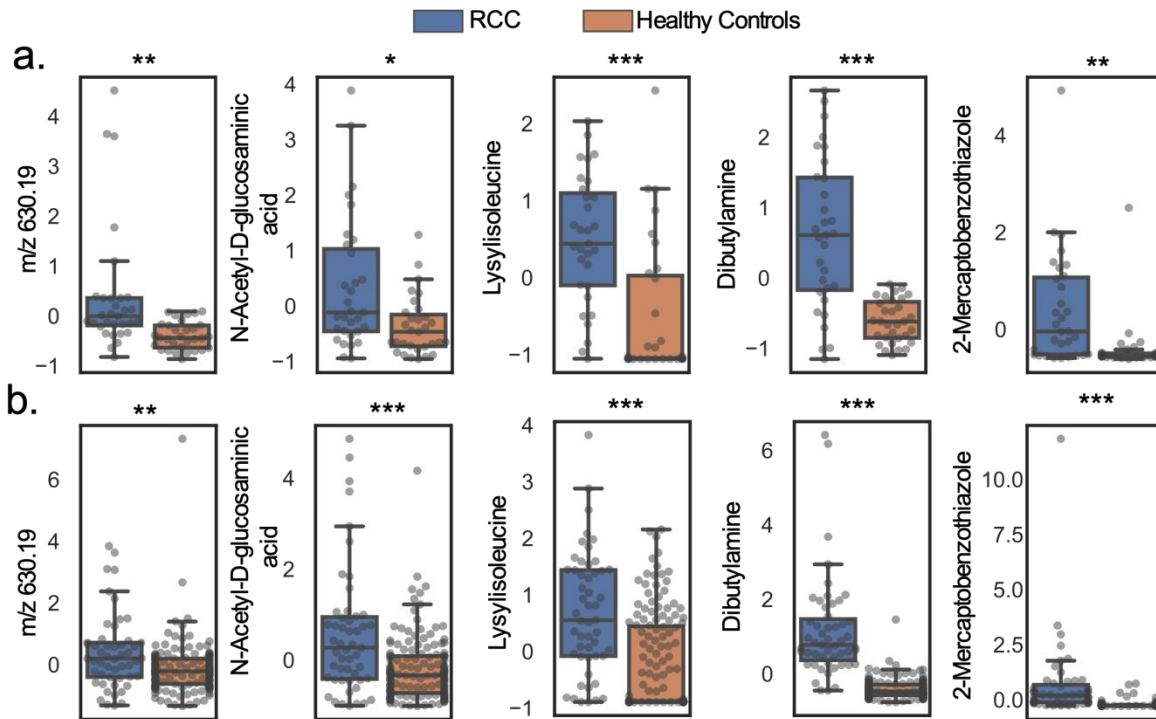


Figure S5: Relative abundances for the panel of upregulated metabolites. (a) Model cohort. q -values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent t -test. (* $q \leq 0.05$, ** $q \leq 0.01$, *** $q \leq 0.001$). (b) In the test cohort, p -values from the Welch t -test were reported (unequal sample size). (* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$). Raw data were transformed *via* autoscaling for visualization

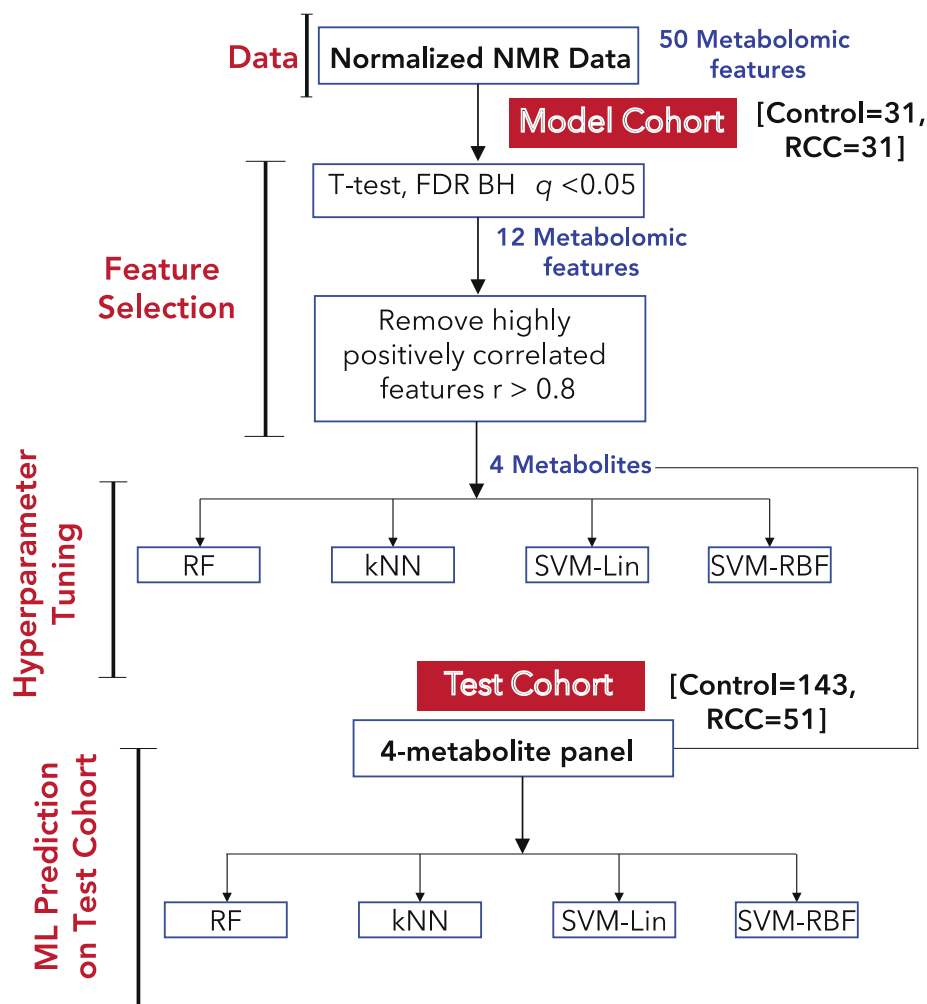


Figure S6: Machine learning pipeline focused only on NMR features. Using the model cohort, all NMR features were subjected to feature selection strategies culminating in four selected metabolites (hippurate, trigonellinamide, lactate, and mannitol). Hyperparameters for four different machine learning models were tuned using the model cohort and the 4-metabolite panel. Final predictions were made using the test cohort under cross-validated conditions. **PLS:** partial least squares, **RF- RFECV:** random forest recursive feature elimination – cross validation, **FDR-BH:** false discovery rate Benjamini-Hochberg procedure, **k-NN:** *k*-nearest neighbors, **SVM:** support vector machines (Lin: linear, RBF: radial basis function).

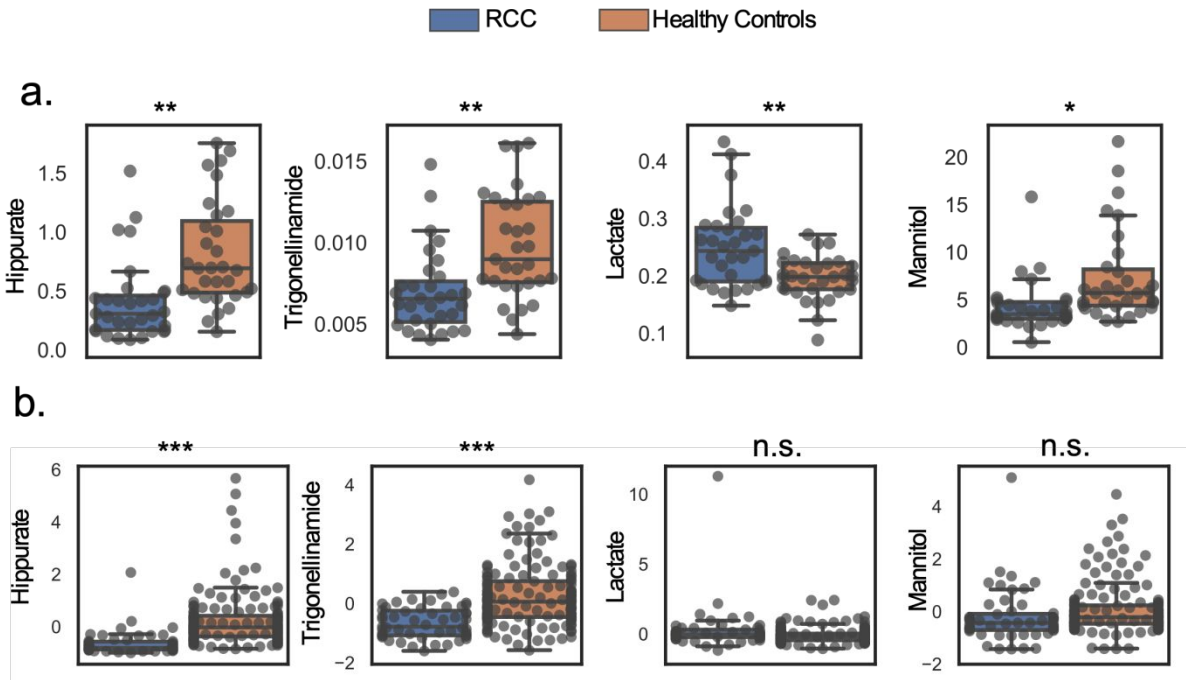


Figure S7: Relative quantification of features in the NMR RCC metabolic panel. (a) Model cohort. q -values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent t -test. ($* q \leq 0.05$, $** q \leq 0.01$, $*** q \leq 0.001$). (b) In the test cohort, p -values from the Welch t -test were reported (unequal sample size). (n.s. not significant $* p \leq 0.05$, $** p \leq 0.01$, $*** p \leq 0.001$). Raw data were transformed *via* autoscaling for visualization

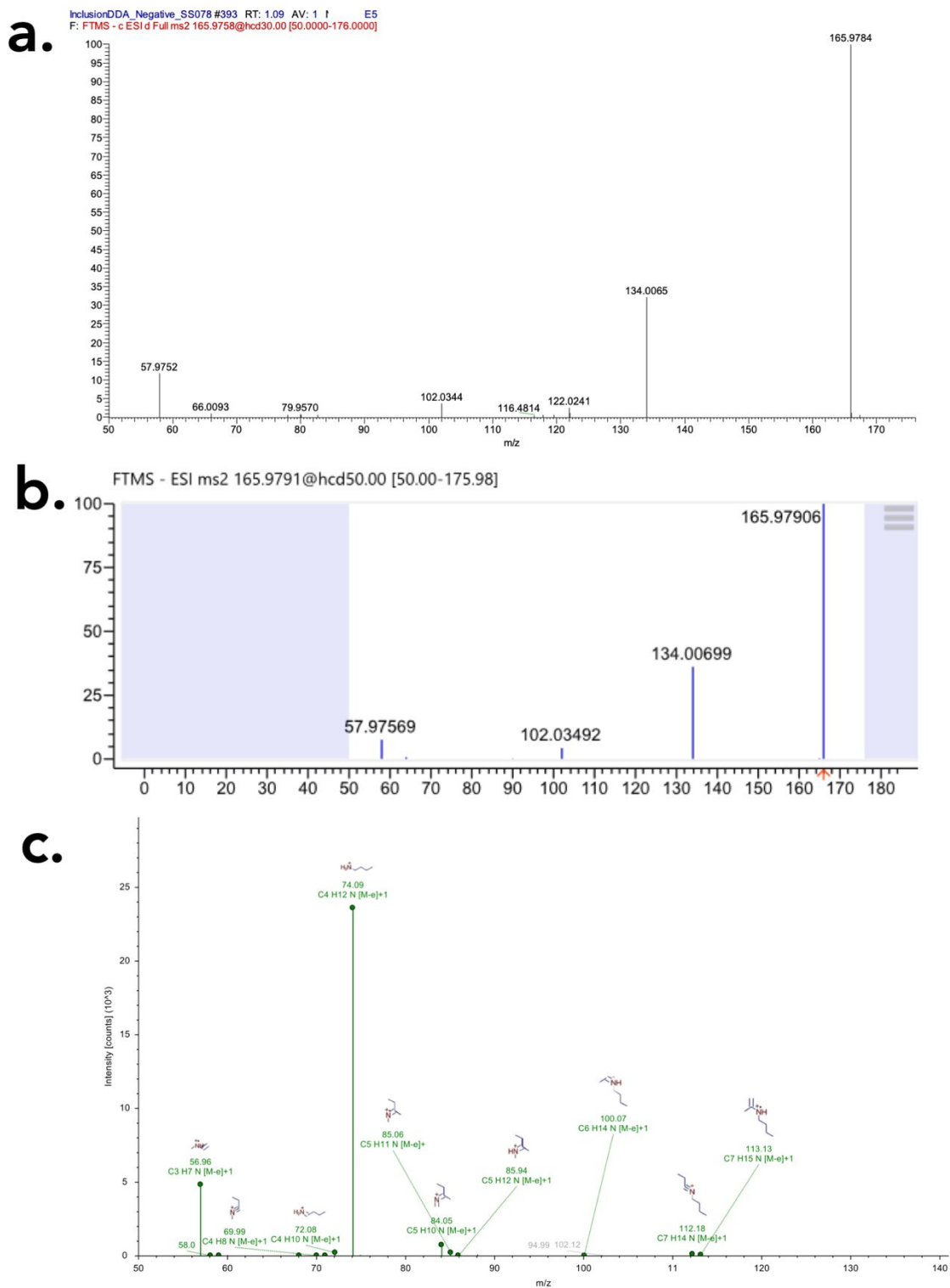


Figure S8: MS/MS annotation of 2-mercaptobenzothiazole and dibutylamine/ n-butylisobutylamine/disobutylamine. a) Experimental spectra of 2-mercaptobenzothiazole

b) MS/MS of spectrum of 2-mercaptobenzothiazole from mzCloud database. c)

Annotated MS/MS spectrum of feature identified as dibutylamine/n-butylisobutylamine/disobutylamine. Annotations are obtained from in silico fragmentation in Compound Discoverer (Thermo Fisher).

Table S1: Propensity score matching and model cohort characteristics. *p*-Values were calculated using Welch and Student *t*-test, for unequal and equal sample sizes, respectively. Race: unknown/missing (6), mixed (1), and Asian (1) were all classified as others (8); Smoker: former (46) and current (9) were all classified as former/current (55).

RCC: Renal Cell Carcinoma.

Characteristic	Pre-match Groups			Post-match Groups		
	Controls	RCC	<i>p</i> -Value	Controls	RCC	<i>p</i> -Value
No of Urine Samples	174	31		31	31	
Mean Age \pm SD	54.4 \pm 10.3	59.5 \pm 12.4	0.03	58.0 \pm 13.0	59.5 \pm 12.1	0.64
BMI	27.3 \pm 4.5	29.1 \pm 5.8	0.11	26.5 \pm 4.9	29.1 \pm 5.8	0.06
Race						
Caucasian	162 (93.1%)	21 (67.7%)		25 (80.6%)	21 (67.7%)	
Black/African American	5 (4.0%)	9 (29.0%)		3 (9.7%)	9 (29.0%)	
Others	7 (2.8%)	1 (3.2%)		3 (9.7%)	1 (3.2%)	
Smoker						
Never	131 (75.3%)	19 (61.3%)		17 (54.8%)	19 (61.3%)	
Former/Current	43 (24.7%)	12 (38.7%)		14 (45.2%)	12 (38.7%)	
Gender						
Male	145 (83.3%)	14 (45.2%)		14 (45.2%)	14 (45.2%)	
Female	29 (16.6%)	17 (54.8%)		17 (54.8%)	17 (54.8%)	

Table S2: Model Cohort RCC Characteristics.

Characteristic	Frequency	Percentage
<i>Metastasis</i>		
Yes	7	22.6%
No	24	77.4%
<i>Histological Subtypes</i>		
Pure Clear Cell	23	71%
Papillary	3	9.7%
Chromophobe	2	6.5%
Clear Cell Papillary	2	6.5%
Unclassified	2	6.5%
^a <i>Nuclear Grade</i>		
1	0	0%
2	10	33.3%
3	8	26.7%
4	12	40%
<i>T-Stage</i>		
T1a	11	35.4%
T1b	5	16.1%
T2a	2	6.4%
T2b	1	3.2%
T3a	11	35.4%
T4	1	3.2%
<i>M-Stage</i>		
M0	24	77.4%
M1	7	22.6%
<i>N-Stage</i>		
N0	25	80.6%
N1	4	12.9%
NX	2	6.5%
^b <i>RCC Stage</i>		
I	13	44.8%
II	3	10.3%
III	6	20.7%
IV	7	24.1%

^a One nuclear grade missing. ^b Two individuals cancer stages are not reported due to inconclusive TNM staging.

Table S3: Test Cohort Characteristics. *p*-Values were calculated using the Welch *t*-test.

Characteristic	Controls	RCC	<i>p</i> -Value
No. of Urine Samples	143	51	
<i>Mean Age ± SD</i>	53.6 ± 9.5	61.7 ± 13.7	0.0002
<i>BMI</i>	27.5 ± 4.4	29.1 ± 5.6	0.03
<i>Race</i>			
Caucasian	136(95.1%)	35(70.0%)	
Black/African American	5(3.4%)	11(22.0%)	
Others	2(1.4%)	4(8.0%)	
<i>Smoker</i>			
Never	113 (79%)	32 (62.7%)	
Former/Current	30 (21%)	19 (37.3%)	
<i>Gender</i>			
Male	131 (91.6%)	31 (62.0%)	
Female	12 (8.4%)	19 (38.0%)	
<i>Histological Subtypes</i>			
Pure Clear Cell		35 (68.6%)	
Papillary		7 (13.7%)	
Clear Cell Papillary		4 (7.8%)	
Chromophobe		3 (5.9%)	
Unclassified		2 (3.9%)	
<i>Metastasis</i>			
No		41 (80.4%)	
Yes		10 (19.6%)	
^a <i>Nuclear Grade</i>			
1		0 (0%)	
2		20 (41.7%)	
3		21 (43.8%)	
4		7 (14.6%)	
^b <i>RCC Stage</i>			
I		20 (48.8%)	
II		5 (12.2%)	
III		9 (22.0%)	
IV		7 (17.1%)	

^a For nuclear grades, three samples were missing. ^b Ten samples have missing RCC staging because of inconclusive TNM staging.

Table S4: Quantified NMR features. ppm values, confidence score, fold changes, and q-values.

Metabolite/ Features	¹H (ppm)	¹³C(ppm)	Peak patterns	Confidence Score	Fold Change	q-value
<i>unknown 1</i>	0.15	-	(s)	-	0.01	0.957
<i>unknown 2</i>	0.36	-	(m)	-	0.42	0.050
<i>***bile acid 1</i>	0.53	-	(s)	1	0.32	0.119
<i>***bile acid 2</i>	0.56	-	(s)	1	0.12	0.560
<i>3- hydroxyisov aleric acid</i>	1.26	30.84	(s)	3	0.07	0.704
<i>lactate</i>	1.31	22.97	(d)	4	0.34	0.003
<i>unknown 3</i>	1.85	-	(s)	-	0.59	0.560
<i>acetate</i>	1.90	26.04	(s)	3	0.57	0.196
<i>acetone</i>	2.23	32.40	(s)	3	-0.12	0.196
<i>unknown 4</i>	2.26	-	(s)	-	-0.06	0.704
<i>acetoacetate</i>	2.27	32.19	(s)	3	-0.07	0.634
<i>unknown 5</i>	2.33	-	(s)	-	-0.03	0.860
<i>**pyruvate</i>	2.41	-	(s)	2	0.05	0.560
<i>citrate</i>	2.53	48.52	(d)	3	-0.05	0.811
<i>dimethylami ne (DMA)</i>	2.71	37.5	(s)	3	0.22	0.119
<i>unknown 6</i>	2.77	-	(s)	-	0.05	0.827
<i>methylguali dine</i>	2.82	30.21	(s)	3	0.16	0.256
<i>unknown 7</i>	3.08	-	(t)	-	-0.34	0.126
<i>choline</i>	3.19	56.69	(s)	3	-0.06	0.686
<i>^ascyllo- inositol</i>	3.35	76.4	(s)	3	-1.14	0.002
<i>taurine</i>	3.42	38.07	(t)	4	-0.03	0.811
<i>acetoacetate</i>	3.44	56.22	(s)	3	0.23	0.368
<i>4- hydroxyphen ylacetate (4- HPA)</i>	3.44	46.34	(s)	4	0.23	0.368
<i>glycine</i>	3.56	44.18	(s)	3	0.48	0.368
<i>mannitol</i>	3.86	65.94	(d)	4	-0.78	0.012
<i>mannitol</i>	3.88	65.94	(d)	4	-0.68	0.022
<i>creatine</i>	3.92	-	(s)	3	0.07	0.811
<i>^aglycolate</i>	3.94	64.32	(s)	3	0.07	0.663

<i>hippurate</i>	3.96	46.46	(d)	4	-0.68	0.004
4- <i>hydroxyhippuric acid</i>	3.96	46.58	(d)	3	-0.68	0.004
<i>tartrate</i>	4.34	76.55	(s)	3	0.13	0.728
<i>unknown 8</i>	6.07	-	(s)	-	0.09	0.415
<i>unknown 9</i>	6.18	-	(s)	-	0.59	0.267
<i>fumarate</i>	6.52	-	(s)	2	0.17	0.560
4- <i>hydroxyphenylacetate (4-HPA)</i>	7.13	133.15	(d)	4	0.83	0.168
<i>hippurate</i>	7.55	131.50	(t)	4	-0.98	0.002
<i>hippurate</i>	7.65	134.92	(m)	4	-0.96	0.002
^a 4- <i>aminohippuric acid</i>	7.67	133.02	(d)	3	-1.64	0.002
<i>indoxyl sulfate (IS)</i>	7.70	127.07	(d)	3	0.18	0.492
<i>hippurate</i>	7.83	129.85	(dd)	4	-0.91	0.003
<i>hypoxanthine</i>	8.18	148.27	(s)	3	0.21	0.811
<i>hypoxanthine</i>	8.20	144.75	(s)	3	0.86	0.368
<i>formate</i>	8.45	173.71	(s)	3	0.22	0.488
<i>unknown 10</i>	8.77	-	(d)	-	0.19	0.791
<i>trigonelline</i>	8.83	147.46	(t)	3	-0.2	0.686
<i>trigonellinamide</i>	8.89	-	(d)	2	-0.49	0.002
<i>trigonellinamide</i>	8.97	-	(d)	2	-0.49	0.002
<i>trigonelline</i>	9.11	148.50	(s)	3	-0.33	0.524
<i>trigonellinamide</i>	9.27	-	(s)	2	-0.51	0.009
<i>unknown 11</i>	9.36	-	(s)	-	-0.14	0.686

^a Quantification may be unreliable because of spectral overlaps. Tentative assignment (Monteiro *et al*

2016¹) s=singlet, d=doublet, dd=doublet of doublet, m=multiplet. Fold change (FC) was calculated as the base 2 logarithm of the average integral ratios between RCC and controls samples. Positive FC values indicate increased abundance in RCC, while negative values indicate higher abundance in control samples. *q*-values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent *t*-test.

Table S5: Chemical information for the 10-metabolite panel.

ID no.	Retention Time (min)	m/z		Adduct Type	Mass error (ppm)	Elemental Formula	Metabolite Identity
		Theoretical	Experimental				
720	5.68	136.0757	136.0755	[M+H] ⁺	-1.47	C ₈ H ₉ NO	2-phenylacetamide
1481	8.83	260.1969	260.1969	[M+H] ⁺	0.00	C ₁₂ H ₂₅ N ₃ O ₃	Lys-Ile
2102	4.39	130.1590	130.1591	[M+H] ⁺	0.77	C ₈ H ₁₉ N	dibutylamine, N-butylisobutylamine, diisobutylamine (isomer)
3141	2.27	343.1135	343.1134	[M+H] ⁺	-0.20	C ₁₄ H ₁₈ N ₂ O ₈	--
3675	1.18	--	87.0641	[M+H] ⁺	--	--	--
3804	2.59	202.0474	202.0478	[M+H] ⁺	1.70	C ₄ H ₁₂ NO ₆ P	hippuric acid
3872	4.05	973.6038	973.6027	[M+2H] ²⁺	-1.13	C ₁₀₀ H ₁₅₈ N ₁₉ O ₂₀	--
4080	0.82	406.0597	406.0594	[M+H] ⁺	-0.78	C ₁₀ H ₂₁ N ₃ O ₈ P ₂ S	
6261	2.59	314.1248	314.1244	[M-H] ⁻	-1.27	C ₉ H ₁₈ N ₉ O ₂ P	--
6262	2.67	376.1249, 358.1143	376.1246, 358.1147	[M+H ₂ O-H] ⁻ [M-H]	-0.68	C ₁₅ H ₂₁ NO ₉	hippurate-mannitol derivative

Table S6: Machine learning hyperparameters used for binary classification using the MS-based 10-metabolite panel.

Parameters	Initial distribution	Optimized
Random Forest		
<i>Max_depth</i>	10, 20, 30	10
<i>Max_features</i>	'auto', 'sqrt', 'log2'	'auto'
<i>Min_samples_leaf</i>	1, 2, 3, 4, 5	1
<i>Min_samples_split</i>	2, 4, 6, 8	2
<i>N_estimators</i>	50, 100, 150, 200	100
SVM-RBF		
<i>C</i>	0.1, 1, 10, 100	10
<i>gamma</i>	0.01, 0.03, 0.1, 0.3, 1.0	0.1
Lin-SVM		
<i>C</i>	0.001, 0.01, 0.1, 1, 5, 10	0.1
k-NN		
<i>Number of neighbors</i>	2 - 30	4
<i>Distance Measure</i>	Manhattan, Euclidean	Manhattan

Table S7: Machine learning performance using the MS RCC 10 panel biomarker.

<i>Algorithm</i>	<i>RF</i>	<i>K-NN</i>	<i>SVM-RBF</i>	<i>Linear SVM</i>
<i>AUC</i>	1.0 +/- 0.0 (0.95)	0.96 +/- 0.04 (0.96)	0.99 +/- 0.01 (0.94)	1.0 +/- 0.0 (0.97)
<i>Accuracy</i>	0.95 +/- 0.04 (80%)	0.95 +/- 0.07 (87%)	0.93 +/- 0.06 (82%)	0.95 +/- 0.07 (81%)
<i>Sensitivity</i>	0.94 +/- 0.08 (100%)	0.93 +/- 0.13 (96%)	0.93 +/- 0.08 (84%)	0.97 +/- 0.07 (100%)
<i>Specificity</i>	0.97 +/- 0.07 (73%)	0.97 +/- 0.07 (83%)	0.93 +/- 0.08 (81%)	0.93 +/- 0.13 (75%)

Table S8: Compound annotation and identification for the panel of 5-metabolites

upregulated in RCC.

ID no.	Retention Time (min)	m/z		Adduct Type	Mass error (ppm)	Elemental Formula	Metabolite Identity
		Theoretical	Experimental				
1481	8.83	260.1969	260.1969	[M+H] ⁺	0.00	C ₁₂ H ₂₅ N ₃ O ₃	Lys-Ile
2102	4.39	130.1590	130.1591	[M+H] ⁺	0.77	C ₈ H ₁₉ N	dibutylamine, N-butylisobutylamine, diisobutylamine (isomer)
6578	1.09	165.9790	165.9784	[M-H] ⁻	-3.61	C ₇ H ₅ NS ₂	2-mercaptobenzothiazole
6594	6.89	236.0776	236.0777	[M+H] ⁺	0.42	C ₈ H ₁₅ NO ₇	N-acetylglucosaminic acid
5698	3.38	630.1909	630.1895	[M-H] ⁻	-2.64	C ₂₄ H ₄₃ NO ₁₂ P ₂ S	--

Table S9: Hyperparameters tuned for machine learning methods used for binary classification for the upregulated RCC biomarkers.

Parameters	Initial distribution	Optimized
Random Forest		
<i>Max_depth</i>	10, 20, 30	10
<i>Max_features</i>	'auto', 'sqrt', 'log2'	'auto'
<i>Min_samples_leaf</i>	1, 2, 3, 4, 5	1
<i>Min_samples_split</i>	2, 4, 6, 8	2
<i>N_estimators</i>	50, 100, 150, 200	150
SVM-RBF		
<i>C</i>	0.1, 1, 10, 100	10
<i>gamma</i>	0.01, 0.03, 0.1, 0.3, 1.0	0.3
Lin-SVM		
<i>C</i>	0.001, 0.01, 0.1, 1, 5, 10	10
k-NN		
<i>Number of neighbors</i>	2 - 30	11
<i>Distance Measure</i>	Manhattan, Euclidean	Euclidean

Table S10: Machine learning performance using the upregulated MS RCC biomarkers.

	MS Upregulated Biomarkers			
Algorithm	RF	K-NN	SVM-RBF	Linear SVM
AUC	0.95 +/- 0.06 (0.97)	0.92 +/- 0.1 (0.92)	0.9 +/- 0.08 (0.80)	0.9 +/- 0.08 (0.91)
Accuracy	0.87 +/- 0.04 (70%)	0.77 +/- 0.14 (81%)	0.89 +/- 0.1 (61%)	0.82 +/- 0.07 (71%)
Sensitivity	0.87 +/- 0.12 (98%)	0.7 +/- 0.27 (86%)	0.87 +/- 0.16 (96%)	0.8 +/- 0.12 (94%)
Specificity	0.87 +/- 0.12 (59%)	0.83 +/- 0.18 (79%)	0.9 +/- 0.13 (49%)	0.83 +/- 0.11 (62%)

Table S11: Detailed MS/MS information for the 7-metabolite panel that distinguishes RCC from control samples. The m/z of fragment ions were obtained from DDA experiments. The corresponding collision energy (CE) is also listed in the table. Selected precursor ions are underlined. Fragment ions that matched to literature spectra or were consistent with potential structures are in bold. Metabolite identification level was assigned based on the following criteria: 1) exact mass, isotopic pattern, retention time, and MS/MS spectrum of standard matched to the feature. 2) exact mass, isotopic pattern, and MS/MS spectrum matched with literature spectra or fragmentation ions observed are consistent with the proposed structure. 3) tentative ID assignment based on elemental formula matches with literature. 4) unknowns.

Feature ID no.	CE (eV), Mode	Fragment ion m/z	Metabolite identification level	Match details	Metabolite Name
720	10,30,45 (+)	<u>136.0755</u> , 119.0489 , 118.0648 , 107.0490, 91.0541 , 95.0602, 101.2184, 87.466, 70.9133, 65.0383	2	Fragmentation consistent with spectrum (HMDB)	2-phenylacetamide
1481	10,30,45 (+)	<u>260.1977</u> , 171.1495, 144.1021, 100.0757, 84.0808, 72.0444, 65.8753, 54.7500	2	Fragmentation consistent with structure	lys-ile or lys-leu
2102	10,30,45 (+)	<u>130.1592</u> , 84.0445, 74.0965, 57.0700	2	Fragmentation consistent with structure	dibutylamine (alkyl chain branching not determined)
3804	---	180.0880 , 105.0339 , 162.0771 , 95.0497, 53.0395, 110.0345, 120.0812, 138.0556	2	Fragmentation consistent with spectrum (m/z cloud)	hippuric acid
6262	10,30,45 (-)	342.2521, 310.2751, 280.0701, 194.0449 , 181.0375, 150.0594 , 148.0392 , 138.0297, 121.0285 , 124.0061 , 113.0230 , 93.0332 , 85.0281 , 89.0240 , 71.0134 , 73.0290	2	Fragmentation consistent with spectrum (m/z cloud)	hippurate-mannitol derivative
6578	10,30,45 (-)	165.9784 , 134.0065 , 122.01241, 117.9193, 102.0344 , 79.9570, 66.0093, 57.9752	2	Fragmentation consistent with spectrum (m/z cloud)	2-mercaptobenzothiazole

6594	10,30,45 (+)	236.0773, 230.1947, 208.9668, 149.0452, 131.0346, 119.0349, 113.0241, 104.0350, 98.9556, 89.0240, 86.0244, 85.0291, 71.0134, 59.0134,	2	Fragmentation consistent with structure	N-acetyl- glucosaminic acid
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Table S12: Machine learning hyperparameters tuned for binary classification using only the 7-identified metabolite panel.

Parameters	Initial distribution	Optimized
Random Forest		
<i>Max_depth</i>	10, 20, 30	10
<i>Max_features</i>	'auto', 'sqrt', 'log2'	'auto'
<i>Min_samples_leaf</i>	1, 2, 3, 4, 5	5
<i>Min_samples_split</i>	2, 4, 6, 8	2
<i>N_estimators</i>	50, 100, 150, 200	50
SVM-RBF		
<i>C</i>	0.1, 1, 10, 100	1
<i>gamma</i>	0.01, 0.03, 0.1, 0.3, 1.0	0.03
Lin-SVM		
<i>C</i>	0.001, 0.01, 0.1, 1, 5, 10	0.1
k-NN		
<i>Number of neighbors</i>	2 - 30	7
<i>Distance Measure</i>	Manhattan, Euclidean	Manhattan

Table S13: Machine learning hyperparameters tuned for binary classification using only NMR RCC biomarkers.

Parameters	Initial distribution	Optimized
Random Forest		
<i>Max_depth</i>	10, 20, 30	10
<i>Max_features</i>	'auto', 'sqrt', 'log2'	'auto'
<i>Min_samples_leaf</i>	1, 2, 3, 4, 5	3
<i>Min_samples_split</i>	2, 4, 6, 8	2
<i>N_estimators</i>	50, 100, 150, 200	50
SVM-RBF		
<i>C</i>	0.1, 1, 10, 100	10
<i>gamma</i>	0.01, 0.03, 0.1, 0.3, 1.0	0.3
Lin-SVM		
<i>C</i>	0.001, 0.01, 0.1, 1, 5, 10	1
k-NN		
<i>Number of neighbors</i>	2 - 30	5
<i>Distance Measure</i>	Manhattan, Euclidean	Manhattan

Table S14: Machine learning performance using only NMR RCC biomarkers.

	NMR Biomarkers			
Algorithm	<i>RF</i>	<i>K-NN</i>	<i>SVM-RBF</i>	<i>Linear SVM</i>
AUC	0.95 +/- 0.03 (0.89)	0.94 +/- 0.05 (0.88)	0.94 +/- 0.06 (0.89)	0.89 +/- 0.08 (0.87)
Accuracy	0.84 +/- 0.05 (0.76)	0.87 +/- 0.1 (0.77)	0.86 +/- 0.06 (0.78)	0.81 +/- 0.08 (0.74)
Sensitivity	0.81 +/- 0.12 (0.86)	0.87 +/- 0.06 (0.84)	0.9 +/- 0.08 (0.86)	0.83 +/- 0.11 (0.84)
Specificity	0.87 +/- 0.19 (0.72)	0.87 +/- 0.19 (0.75)	0.81 +/- 0.12 (0.76)	0.77 +/- 0.23 (0.71)

Table S15: Review of some notable urine metabolomics studies comparing RCC to controls.

Study	Sample Size	Race/Locaton of Sample Collection	Platform	Biomarker (Increase in RCC)	Biomarker (Decrease in RCC)
<i>Kind et al 2007</i> ²	6C, 6N	Tennessee, US	HILIC-LC-MS, GC-TOF-MS, RP-UHPLC-MS	No compound identification	No compound identification
<i>Kim et al 2009</i> ³	11C*, 15N	Texas, US California, US	HILIC LC-MS	No compound identification	
<i>Kim et al 2011</i> ⁴	29C, 33N	California, US	UHPLC-MS, GC-MS	Quinolate, alpha-ketoglutarate	Gentisate
<i>Monteiro, M. et al 2016</i> ⁵	42C, 49N	Portugal	NMR	2-ketoglutarate, N-methyl-2-pyridone-5-carboxamide, bile acids, galactose, pyruvate, succinate and valine	4-hydroxyhippurate, 4-hydroxyphenylacetate, acetone, GAA, glycine, hippurate, malonate, phenylacetylglutamine, tartrate, trigonelline
<i>Ragone et al 2016</i> ⁶	40C*, 29N	Italy	NMR	Creatine, alanine, lactate and pyruvate	Hippurate, citrate, and betaine
<i>Monteiro, M. et al 2017</i> ⁷	30C, 37N	Portugal	GC-MS	2-oxopropanal	2,5,8-trimethyl-1,2,3,4-tetrahydronaphthalene-1-ol
<i>Niziol et al 2018</i> ⁸	7C*, 15N	Poland	LC-HRMS	Hydroxybutyrylcarnitine, decanoylcarnitine, propanoylcarnitine, carnitine, dodecanoylcarnitine, and norepinephrine sulfate.	riboflavin, acetylaspartylglutamate
<i>Liu et al 2019</i> ⁹	100C, 129N	China (all Chinese subjects)	LC-MS	N-Jasmonoyltyrosine, Androstenedione, Dopamine 4-sulfate, 3-Methylazelaic acid, 7alpha-hydroxy-3-oxochol-4-en-24-oic acid, Lithocholytaurine, 11-Dodecenoic acid	Tetrahydroaldosterone-3-glucuronide, Cortolone-3-glucuronide
<i>Wang et al 2019</i> ¹⁰	117 C**, 98N	China	UPLC-MS	α -CEHC, flunisolid, glycerol tripropanoate	β -cortolone, deoxyinosine, 11b,17a,21-trihydroxypregnenolone
<i>Zhang et al 2020</i> ¹¹	39C, 68N	China	LC-MS	–	Amino adipic acid, 2-(formamido)-N1-(5-phosphod-riboseyl) acetamide and alpha-N-phenylacetyl-l-glutamine

Studies comparing benign renal tumor and RCC were not included in this review. In Monteiro, M. *et al* 2016⁵, hypoxanthine and isoleucine are potentially confounded. In Monteiro, M. *et al* 2017⁷, the biomarkers were selected from the 21 initial VOCs, using two independent small samples sets. In Niziol *et al* 2018⁸, the biomarkers in urine were also present in tissue. In Wang *et al* 2019¹⁰, bladder cancer patients are confounders; the biomarkers identified were validated in an external cohort consisting of 30 RCC and 44 controls; and in addition, only early stage RCC patients (T1 and T2 stages) were considered. C* = clear cell renal cell carcinoma. C = renal cell carcinoma, N=healthy controls, C** = 53 bladder cancer patients and 64 RCC. HILIC-LC-MS: Hydrophilic Interaction Chromatography Liquid Chromatography Mass Spectrometry, GC-TOF-MS: Gas Chromatography Time-Of-Flight Mass Spectrometry, RP-UHPLC-MS: Reverse Phase Ultra High-Performance Liquid Chromatography Mass Spectrometry, LC-HRMS: Liquid Chromatography-High Resolution Mass Spectrometry, VOC: Volatile organic compounds.

Table S16: Metabolomic features with q -values < 0.05 and > 1 -fold change in the model cohort. (Fold change (FC) was calculated as the base 2 logarithm of the average intensity ratios between RCC and controls samples). Positive FC values indicate increased abundance in RCC, while negative values indicate higher abundance in control samples. q -values were computed by taking the FDR correction (Benjamini-Hochberg) after an independent t -test. 433 features from LC-MS are included in the table, and 2 features from NMR (*scyllo*-Inositol and aminohippurate) are in Table S4.

ID	Metabolite ID	Mode	RT [min]	FC	FDR p-value
1	1	positive	2.317	-1.4885	0.045959
9	5-acetylamino-6-amino-3-methyluracil	positive	1.901	-1.22771	0.008743
95	3-(1H-1,2,4-Triazol-3-yl)alanine	positive	1.898	-1.23304	0.005531
147	147	positive	2.58	-1.20166	0.007443
163	venlafaxine	positive	2.654	-1.27957	0.018961
170	170	positive	2.313	-1.56798	0.017014
173	173	positive	2.605	-1.23927	0.004285
245	245	positive	4	-2.33614	0.00089
250	250	positive	2.581	-2.11065	0.009913
260	leupeptin	positive	3.989	-2.30823	0.000917
278	278	positive	3.057	-1.65576	0.002262
293	293	positive	2.617	-1.64467	0.020423
312	312	positive	4.523	1.113604	0.022578
314	314	positive	2.592	-2.15533	0.012163
332	N-(3-amino-4-methyl-5-nitrophenyl)acetamide	positive	1.591	-2.21385	0.035889
347	6-methylquinoline	positive	2.322	-1.64636	0.008933
363	363	positive	1.903	-1.38184	0.003166
429	429	positive	4.525	1.279205	0.018937
435	paraxanthine	positive	1.12	-1.17746	0.006372
474	474	positive	1.917	-1.29632	0.009562
479	phenylacetaldehyde	positive	2.404	-1.95368	0.011539
523	523	positive	2.183	-1.06828	0.017172
562	6-methylquinoline	positive	2.594	-1.95682	0.010866
595	595	positive	2.67	-2.75395	0.0418
610	610	positive	2.952	-1.95838	0.005316
640	1_5-anhydro-mannitol	positive	1.895	-1.22667	0.00129
643	643	positive	2.869	-2.0903	0.03379

666		666	positive	2.961	-1.67651	0.009093
672	moxaverine		positive	2.66	-1.15696	0.039852
688		688	positive	4.009	1.099602	0.023352
712	3-dehydrocarnitine		positive	1.449	-1.19664	0.02724
720	2-phenylacetamide		positive	2.562	-1.06888	0.000386
726		726	positive	6.009	1.043296	0.04006
790	2-acetolactate		positive	1.914	-1.03801	0.001699
798	indole;1-benzazole		positive	2.653	-1.46462	0.000526
800		800	positive	4.125	3.41514	0.033921
819	4-dehydropantoate		positive	1.896	-1.19163	0.00116
825	3-methyldioxyindole		positive	1.942	-1.20393	0.002882
880		880	positive	4.528	1.182288	0.032715
900		900	positive	4.532	1.172157	0.02614
926		926	positive	2.25	-1.29961	0.015545
954		954	positive	4.019	-2.6166	0.000917
958		958	positive	0.579	-2.49872	0.032106
960		960	positive	0.58	-2.4511	0.034206
995		995	positive	0.882	-1.5801	0.035476
1035	zeatin		positive	3.628	1.022119	0.039696
1047		1047	positive	2.631	-2.17057	0.012641
1066		1066	positive	2.591	-2.28759	0.005362
1098	4-imidazolone-5-propanoate		positive	3.729	-1.0197	0.027361
1153		1153	positive	4.533	1.222509	0.017014
1163		1163	positive	2.45	-1.39804	0.00089
1214		1214	positive	1.242	-1.57143	0.020423
1261		1261	positive	1.855	1.046534	0.04275
1262		1262	positive	1.9	-1.49775	0.003903
1307		1307	positive	1.147	-5.46823	0.001452
1356	delta-guanidinovalericacid		positive	3.929	-1.93217	0.043481
1365		1365	positive	4.524	1.098536	0.009093
1391	N- glucosylarylamine		positive	3.97	1.803794	0.04275
1481	lys-Ile		positive	6.29	1.447371	0.001342
1550		1550	positive	2.611	-2.04338	0.012124
1566		1566	positive	3.909	-1.29952	0.035716
1579		1579	positive	5.937	1.358104	0.041545
1587		1587	positive	4.509	1.376935	0.024
1662		1662	positive	2.502	2.944322	0.047485
1673		1673	positive	0.804	-3.74992	0.001296
1676		1676	positive	2.648	-1.80767	0.01703
1689		1689	positive	4.715	4.292918	0.017731
1691		1691	positive	3.418	-1.91163	0.040973

1701	4-(2-aminoethyl)benzenesulfonyl fluoride	positive	1.807	-1.93725	0.000526
1723	1723	positive	2.574	-1.7161	0.00597
1741	PEG monolaurate n5	positive	3.738	-2.74589	0.001453
1760	4-(2-aminoethyl)benzenesulfonyl fluoride	positive	1.704	-2.14754	0.000826
1771	1771	positive	3.001	1.262088	0.030398
1776	N-acetylleucylleucine	positive	2.587	-1.89519	0.021927
1820	1820	positive	1.953	-2.10726	0.004044
1839	2_3-diaminopropionic acid	positive	2.6	-2.15507	0.008703
1858	1858	positive	3.883	-3.72213	0.006498
1861	1861	positive	4.81	-2.79138	0.019817
1870	1870	positive	3.824	-3.63177	0.010482
1880	1880	positive	4.528	1.332245	0.017731
1931	anisole	positive	2.618	-1.12591	0.009093
1942	1942	positive	3.603	-1.29462	0.049502
1961	1961	positive	2.434	-1.87936	0.000515
1969	1969	positive	2.583	-1.36431	0.009913
1991	1991	positive	3.247	-3.24599	0.015568
2005	2005	positive	4.876	-2.9057	0.016077
2056	2056	positive	2.649	-1.55177	0.008562
2082	2082	positive	2.594	-1.30732	0.008588
2102	dibutylamine, N-butylisobutylamine, diisobutylamine (isomer)	positive	3.449	1.567367	7.87E-05
2138	2138	positive	1.12	-1.15134	0.014564
2158	2158	positive	4.528	1.256293	0.021194
2196	2196	positive	0.814	-2.89012	0.00089
2207	2207	positive	1.097	-3.82236	0.003166
2218	2218	positive	2.432	-1.70991	0.000586
2230	2230	positive	2.59	-2.19533	0.006379
2239	2239	positive	1.101	-3.85416	0.002882
2240	2240	positive	2.886	1.631405	0.00451
2241	2241	positive	4.838	-1.06192	0.015545
2242	2242	positive	2.587	-2.31188	0.006372
2259	2259	positive	3.706	-2.85038	0.032369
2267	beta-Ionone	positive	2.371	-2.11197	0.011891
2306	2306	positive	2.623	-1.92523	0.009819
2320	2320	positive	0.866	-2.38259	0.000912
2321	2321	positive	1.138	-3.78215	0.001432
2348	2348	positive	3.89	-1.05941	0.02614
2353	leucinamide	positive	1.118	-3.10452	0.003468
2359	2359	positive	6.637	1.794645	0.023123
2385	2385	positive	4.513	1.09136	0.01182

2403		2403	positive	4.53	1.352297	0.012999
2418		2418	positive	4.477	-3.95489	0.027524
2426		2426	positive	2.851	1.572021	0.035289
2448		2448	positive	4.712	6.772872	0.024075
2455		2455	positive	1.14	-1.32081	0.00129
2462		2462	positive	4.536	1.262401	0.005734
2476		2476	positive	4.534	1.481945	0.027785
2496		2496	positive	2.581	-2.27665	0.004492
2499		2499	positive	4.508	1.286938	0.027563
2524		2524	positive	1.299	1.044756	0.048626
2540		2540	positive	4.732	7.106785	0.020956
2568		2568	positive	3.711	-1.24199	0.013193
2571		2571	positive	3.122	-1.9284	0.035889
2577	pipecolicacid		positive	1.457	-1.52805	0.013548
2601		2601	positive	2.658	-2.07536	0.009562
2621		2621	positive	3.989	-2.63727	0.001453
2625		2625	positive	1.869	-1.023	0.022102
2652		2652	positive	4.544	1.009831	0.04275
2653		2653	positive	2.602	-1.53429	0.016708
2668	cyclo(leucylprolyl)		positive	1.067	-1.04975	0.048489
2702		2702	positive	4.518	1.167157	0.018248
2709	N-acetyl- glucosaminat		positive	3.857	1.090917	0.037911
2731		2731	positive	4.714	4.920091	0.007029
2732		2732	positive	4.653	4.191832	0.017527
2749	2_3-dimethylmalate		positive	2.894	1.338155	0.043239
2803		2803	positive	4.539	1.220539	0.005355
2804		2804	positive	1	-3.42199	0.009073
2809		2809	positive	3.775	-1.14183	0.016836
2815		2815	positive	4.557	1.935817	0.047151
2821		2821	positive	4.504	1.247197	0.033979
2829		2829	positive	0.823	-1.68661	0.001711
2840		2840	positive	3.317	-2.53883	0.005362
2850		2850	positive	3.157	-2.40116	0.001896
2852		2852	positive	4.529	1.310407	0.021409
2853		2853	positive	0.923	-3.21639	0.003894
2860		2860	positive	4.531	1.181536	0.030398
2905		2905	positive	2.579	-1.84755	0.013293
2914		2914	positive	5.316	-3.13431	0.00451
2924		2924	positive	4.727	5.847712	0.023309
2926		2926	positive	4.809	-2.25885	0.018961
2932		2932	positive	2.649	-1.82929	0.018961

2971		2971	positive	4.531	1.228874	0.013964
2973		2973	positive	2.385	-1.31894	0.004285
2986		2986	positive	0.904	-2.80027	0.023728
2992		2992	positive	3.323	-4.44632	0.014442
3025		3025	positive	4.7	3.344933	0.032349
3033		3033	positive	4.52	1.085292	0.013193
3035		3035	positive	4.53	1.226327	0.022578
3043		3043	positive	4.532	1.480025	0.016585
3074		3074	positive	4.539	1.62393	0.017014
3082		3082	positive	1.951	-1.10581	0.004436
3116	3-hydroxyaminophenol		positive	1.107	1.515954	0.040104
3127		3127	positive	1.232	-1.43787	0.02724
3141		3141	positive	1.133	-2.42642	0.001216
3148		3148	positive	0.812	-3.09632	0.000826
3154		3154	positive	3.884	-2.69949	0.000828
3159		3159	positive	1.095	-1.68751	0.011539
3160		3160	positive	0.927	-1.16062	0.008933
3169	2-hydroxyphenethylamine		positive	4.094	2.210126	0.042089
3171		3171	positive	1.131	-3.39246	0.011164
3175		3175	positive	2.581	-1.89816	0.003896
3200		3200	positive	3.487	1.035815	0.038541
3208		3208	positive	1.098	-5.19983	0.00451
3234		3234	positive	1.147	-2.41971	0.016388
3260		3260	positive	3.056	1.146707	0.012962
3262		3262	positive	4.751	3.143639	0.048424
3283		3283	positive	2.138	-1.42525	0.006117
3297		3297	positive	4.706	6.646371	0.016585
3301		3301	positive	4.531	1.001697	0.016003
3309		3309	positive	0.934	-2.04523	0.003896
3353		3353	positive	4.509	1.111479	0.043452
3362		3362	positive	4.073	-5.08514	0.001646
3370		3370	positive	4.703	6.087944	0.014648
3371		3371	positive	0.922	-3.51338	0.003894
3385		3385	positive	3.329	-2.60407	0.008088
3390		3390	positive	2.633	-1.751	0.006372
3409		3409	positive	1.857	-1.26767	0.014577
3415		3415	positive	4.534	1.165491	0.009093
3427		3427	positive	2.631	-2.44854	0.013293
3441	2-hydroxyphenethylamine		positive	3.894	2.55209	0.033619
3446	deoxycytidine		positive	3.531	1.085392	0.0313
3449		3449	positive	1.861	-1.22268	0.008986

3492	cathinone		positive	4.181	1.918288	0.022548
3514		3514	positive	4.533	1.39721	0.016455
3517	pyridafenthion		positive	0.812	-3.76591	0.00132
3526		3526	positive	1.914	-1.09411	0.002947
3528		3528	positive	2.258	-1.87687	0.015545
3545		3545	positive	0.826	-1.63608	0.00144
3546		3546	positive	0.827	-1.63797	0.00144
3552		3552	positive	4.531	1.223489	0.013193
3558		3558	positive	4.54	1.239042	0.022102
3564		3564	positive	0.848	2.507408	0.019028
3582		3582	positive	1.214	-1.5372	0.011539
3586		3586	positive	4.159	-2.72666	0.014442
3596	beta-ionone		positive	2.632	-1.75123	0.003896
3613		3613	positive	3.957	-2.40024	0.000586
3624		3624	positive	1.069	-1.34416	0.021839
3626		3626	positive	4.523	1.198337	0.01772
3632		3632	positive	4.555	1.298889	0.013193
3657		3657	positive	1.293	-1.85846	0.009093
3675		3675	positive	1.184	-1.08046	0.000262
3701		3701	positive	0.819	-1.69784	0.00105
3757		3757	positive	4.003	-2.38649	0.000326
3763		3763	positive	4.009	-2.27464	0.001528
3764		3764	positive	3.954	-2.33779	0.00089
3777		3777	positive	3.639	-2.09303	0.00144
3791		3791	positive	3.69	-2.04221	0.002947
3797		3797	positive	3.938	-2.28156	0.001221
3799		3799	positive	3.621	-2.11755	0.001216
3804	hippuric acid		positive	2.595	-2.02465	0.000526
3820		3820	positive	3.979	-2.26378	0.000579
3823		3823	positive	3.924	-2.42884	0.000734
3829		3829	positive	3.894	-2.35241	0.001496
3842		3842	positive	3.673	-2.06698	0.001737
3856		3856	positive	4.016	-2.4126	0.000734
3863		3863	positive	3.373	-2.05737	0.043366
3871		3871	positive	1.021	-2.67385	0.002122
3872		3872	positive	4.049	-2.5791	0.00019
3873		3873	positive	3.698	-2.19666	0.004044
3876		3876	positive	3.998	-2.39598	0.000515
3893		3893	positive	3.727	-2.47178	0.004492
3905		3905	positive	3.87	-2.37325	0.000826
3906		3906	positive	3.848	-2.54952	0.003254
3907		3907	positive	3.779	-2.70752	0.004285

3909		3909	positive	3.579	-2.32192	0.00089
3923		3923	positive	4.016	-3.24391	0.00089
3925		3925	positive	3.751	-2.62574	0.004245
3939		3939	positive	3.304	-2.57864	0.028679
3944		3944	positive	3.035	1.066588	0.048739
3960		3960	positive	3.996	-2.13732	0.001054
3963		3963	positive	2.184	1.099552	0.008986
3968		3968	positive	4.566	-2.64268	0.01657
3976		3976	positive	4.73	6.193516	0.022548
3987		3987	positive	3.971	-2.30352	0.000679
3991	leucinamide		positive	1.074	-3.08451	0.002279
3992		3992	positive	3.954	-2.7693	0.001256
4001		4001	positive	1.099	-4.10801	0.025007
4025		4025	positive	3.439	1.279099	0.008317
4042		4042	positive	3.883	-2.52495	0.000734
4075		4075	positive	3.416	-2.03456	0.008933
4080		4080	positive	0.821	-3.4898	0.000515
4133		4133	positive	4.036	-2.72562	0.004666
4162		4162	positive	3.455	-2.11785	0.005543
4179		4179	positive	3.602	-1.00487	0.021297
4180		4180	positive	3.622	-1.00845	0.018248
4189		4189	positive	1.281	-1.58871	0.0418
4195		4195	positive	1.114	-1.26086	0.008469
4210		4210	positive	3.555	-2.31772	0.001701
4218		4218	positive	3.48	-2.25802	0.00129
4250		4250	positive	4.057	-2.558	0.00132
4258	5-hydroxy-tryptophan		positive	3.033	1.202781	0.04448
4265		4265	positive	4.102	-2.60288	0.00129
4267		4267	positive	3.758	-1.26957	0.04047
4278		4278	positive	3.072	1.28831	0.011416
4279		4279	positive	6.949	2.098916	0.046946
4281		4281	positive	4.05	-2.76374	0.00089
4283		4283	positive	4.687	2.857637	0.017731
4288		4288	positive	4.612	1.304232	0.030454
4303		4303	positive	2.623	-1.02546	0.00597
4318		4318	positive	4.037	-2.72294	0.00073
4323		4323	positive	4.122	-2.34523	0.001873
4328		4328	positive	3.96	-2.35681	0.002367
4340		4340	positive	5.076	-1.9714	0.02593
4352	leucinamide		positive	0.919	-2.16241	0.00132
4355		4355	positive	4.057	-2.73285	0.00129

4367	pregabalin	positive	1.06	-2.97568	0.001496
4370	4370	positive	4.113	-2.29843	0.002367
4381	4381	positive	4.646	1.122786	0.030398
4382	4382	positive	4.541	-3.18497	0.004544
4384	4384	positive	4.073	-2.25311	0.001565
4392	4392	positive	3.941	-2.10559	0.000734
4401	4401	positive	4.039	-2.69474	0.000481
4408	1-aAmino-1-deoxy-scylo-inositol	positive	3.867	-1.12923	0.011113
4413	4413	positive	4.052	-2.37203	0.001699
4428	4428	positive	4.057	-2.22436	0.002596
4444	4444	positive	3.998	-2.43206	0.000912
4447	4447	positive	4.061	-2.50909	0.000579
4490	4490	positive	3.94	-2.3298	0.001721
4553	4553	positive	3.85	-2.1915	0.002694
4587	4587	positive	4.035	-2.55891	0.002251
4616	4616	positive	0.847	1.303658	0.008088
4632	1,7-dimethyluric acid	negative	2.337	-1.11272	0.013263
4659	hippuric acid	negative	2.622	-1.12485	0.003896
4670	cinnamoylglycine	negative	2.651	-1.55137	0.012441
4672	cinnamoylglycine	negative	2.616	-1.814	0.017993
4673	7-methylxanthine	negative	1.221	-1.13939	0.009031
4685	hippuric acid	negative	4.039	1.414079	0.032791
4704	2-furoylglycine	negative	2.58	1.951921	0.04693
4706	2-furoylglycine	negative	2.512	2.68069	0.030454
4719	1-methyluric acid	negative	2.545	-1.157	0.011539
4739	5-hydroxyindole	negative	2.626	-1.0839	0.004436
4740	5-hydroxyindole	negative	2.581	-1.15681	0.005204
4766	theophylline	negative	1.432	-2.1935	0.001975
4775	4775	negative	0.869	-2.28845	0.027288
4791	4791	negative	4.511	1.244399	0.016348
4801	4801	negative	4.554	1.085615	0.016222
4844	4844	negative	3.257	2.311035	0.036851
4870	3-[-5-oxo-7-oxabicyclo[4.1.0]hept-2-yl]-alanine	negative	3.24	-1.41362	0.015568
4953	7,8-dihydro-8-oxoguanine	negative	1.198	-1.23311	0.008986
4958	4958	negative	3.679	-1.25361	0.048489
5010	5010	negative	4.637	2.953354	0.003254
5029	5029	negative	4.152	-2.73447	0.008511
5038	5038	negative	2.632	2.080506	0.037266
5065	5065	negative	0.855	-1.47704	0.003254
5077	5077	negative	1.965	1.045916	0.012965
5083	5083	negative	2.564	1.75927	0.04448

5106		5106	negative	3.534	1.315406	0.025624
5110	1-O-[5-(3,4-dihydroxyphenyl)-4-hydroxypentanoyl]-beta-glucopyranuronic acid		negative	3.5	-1.96301	0.0151
5129		5129	negative	2.64	-1.94809	0.00129
5133		5133	negative	3.707	-2.21718	0.032369
5137		5137	negative	2.517	-1.15218	0.023309
5153		5153	negative	1.421	-1.48097	0.007752
5216		5216	negative	0.863	-1.85939	0.005858
5239		5239	negative	3.529	-1.09635	0.043366
5241	butopyronoxyl		negative	0.908	1.206619	0.038863
5248		5248	negative	4.531	1.057774	0.012999
5285		5285	negative	4.644	3.023183	0.009913
5310		5310	negative	0.87	2.988694	0.017548
5341		5341	negative	0.706	-1.09358	0.03992
5352		5352	negative	2.355	-1.00687	0.04099
5358		5358	negative	3.897	1.636177	0.021839
5379		5379	negative	0.863	-1.86478	0.009093
5381		5381	negative	3.395	1.698478	0.004044
5383		5383	negative	4.067	-2.62497	0.000385
5393		5393	negative	0.862	-1.87627	0.006038
5423		5423	negative	3.745	-1.83453	0.030529
5463	N-acetyl-methionine		negative	3.758	-1.85466	0.033538
5470	sulfuroil acetate		negative	3.902	-2.52855	0.034206
5482		5482	negative	0.858	-1.17721	0.034734
5507		5507	negative	3.132	-1.06713	0.01418
5514	5514		negative	2.517	-1.48437	0.004245
5553		5553	negative	2.562	-1.25185	0.03108
5576		5576	negative	0.728	-1.56108	0.008088
5604		5604	negative	3.891	-3.78571	0.003896
5612		5612	negative	3.805	-1.02889	0.043481
5647		5647	negative	3.993	-2.70499	0.000679
5648		5648	negative	3.966	-2.75565	0.006117
5683		5683	negative	4.089	-3.72301	0.001247
5698		5698	negative	3.381	1.402511	0.011539
5712		5712	negative	4.376	-1.96165	0.029132
5724		5724	negative	4.531	1.170521	0.015527
5728		5728	negative	2.931	-1.11438	0.039852
5737	gly-Lys		negative	3.995	1.486072	0.017371
5770		5770	negative	0.855	-1.45399	0.00451
5796	pidotimod		negative	2.951	1.72657	0.040795
5799		5799	negative	4	-2.4648	0.038921

5818		5818	negative	0.948	1.355602	0.048525
5820		5820	negative	4.663	1.182431	0.020072
5849		5849	negative	0.708	-1.10963	0.039503
5868		5868	negative	4.66	1.321084	0.010661
5887		5887	negative	4.532	-1.65544	0.001001
5899		5899	negative	3.5	1.151716	0.032924
5911		5911	negative	3.966	-2.51989	0.001092
5925		5925	negative	2.671	-1.32396	0.006117
5931		5931	negative	2.571	-1.02026	0.010661
5941		5941	negative	1.148	1.901496	0.032924
5942		5942	negative	2.631	-1.18178	0.002324
5994		5994	negative	2.625	-1.08762	0.00451
6001		6001	negative	2.782	-1.94029	0.006743
6007		6007	negative	0.678	-1.21015	0.041623
6014	N-acetyl-tyrosine		negative	2.632	-1.5866	0.009093
6021		6021	negative	0.708	-1.36188	0.003896
6057	6057		negative	0.947	1.642112	0.031478
6094	5-acetylamino-6-formylamino-3-methyluracil		negative	0.727	-1.59148	0.004603
6095	chiro-inositol		negative	1.118	-1.37163	0.00129
6101		6101	negative	4.052	-1.52997	0.045816
6111		6111	negative	2.577	2.205537	0.04782
6148		6148	negative	2.587	1.33016	0.028806
6161		6161	negative	0.711	-1.44766	0.005882
6190		6190	negative	2.594	-1.31465	0.027361
6212	glauucarubin		negative	3.361	-2.88626	0.025629
6233		6233	negative	1.515	-1.15693	0.015545
6236		6236	negative	0.625	1.384644	0.025156
6261		6261	negative	2.591	-1.8809	0.000368
6262	hippurate-mannitol derivative		negative	2.667	-1.80394	0.000515
6267		6267	negative	2.581	2.159467	0.032369
6276		6276	negative	2.636	-1.65054	0.000481
6286	2_5_6-trihydroxy-5_6-dihydroquinoline		negative	2.622	-1.30303	0.005058
6314		6314	negative	2.625	-1.08453	0.004492
6322		6322	negative	2.623	-1.04139	0.00451
6325		6325	negative	2.64	-1.97981	0.001564
6327		6327	negative	2.637	-1.5487	0.028679
6337		6337	negative	0.862	-1.69061	0.002457
6348		6348	negative	2.993	-2.21045	0.017548
6349		6349	negative	0.93	-1.14826	0.021927
6361		6361	negative	2.619	-1.1059	0.001844
6375		6375	negative	2.775	-1.81499	0.009031

6385		6385	negative	2.655	-1.00016	0.008703
6389		6389	negative	2.516	-1.13448	0.011046
6390		6390	negative	2.627	-1.00038	0.004603
6392		6392	negative	0.75	-1.01094	0.012242
6396		6396	negative	0.884	-1.32351	0.027563
6406		6406	negative	0.903	-2.03474	0.04006
6425	leupeptin		negative	4.004	-2.47724	0.00119
6447		6447	negative	2.421	3.406793	0.024455
6496		6496	negative	1.25	-1.16132	0.008933
6504		6504	negative	2.582	2.311681	0.032369
6508		6508	negative	2.569	-1.00789	0.004285
6534		6534	negative	3.989	-2.43582	0.001737
6544		6544	negative	0.719	-1.5791	0.004603
6545		6545	negative	4.005	-2.41651	0.001342
6565		6565	negative	2.935	-1.08416	0.041344
6569	4-[-(2-amino-1-hydroxyethyl)-2-hydroxyphenyl hydrogen sulfate		negative	1.181	1.368161	0.047987
6578	2-mercaptobenzothiazole		negative	0.832	2.229249	0.009064
6594	N-acetyl-glucosaminat		negative	3.871	1.156155	0.021542
6628		6628	negative	2.908	-1.35524	0.022578
6637		6637	negative	4.866	1.31038	0.01503
6662		6662	negative	3.528	-2.06367	0.011539
6668		6668	negative	2.612	-1.00887	0.004285
6676		6676	negative	3.184	-2.34598	0.002651
6683		6683	negative	3.025	-2.14478	0.012441
6687		6687	negative	0.866	-1.68528	0.003166
6731		6731	negative	0.859	-1.79499	0.002105
6762		6762	negative	3.751	-2.80798	0.003896
6802		6802	negative	1.504	-1.71402	0.030398
6819		6819	negative	1.109	-3.47044	0.008588
6882		6882	negative	3.692	-3.0581	0.011543
6885		6885	negative	2.615	-1.03401	0.002324
6939		6939	negative	2.586	-1.33936	0.043481
6956		6956	negative	2.715	1.925851	0.017014
6972		6972	negative	1.112	-3.3917	0.008088
6990		6990	negative	2.647	-1.67258	0.011539
6996		6996	negative	2.535	-1.04791	0.021194
7001		7001	negative	0.869	-1.71768	0.003166
7087		7087	negative	2.399	-1.19546	0.007612

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