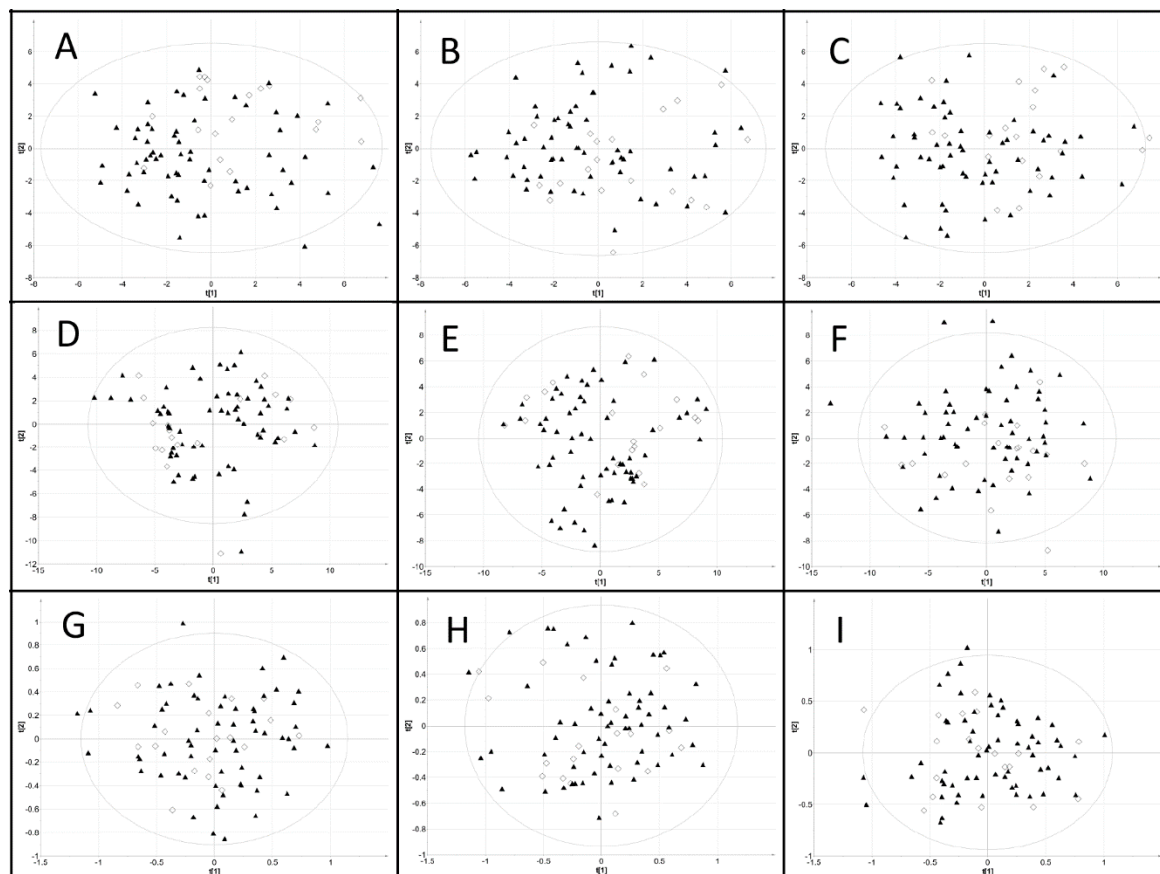
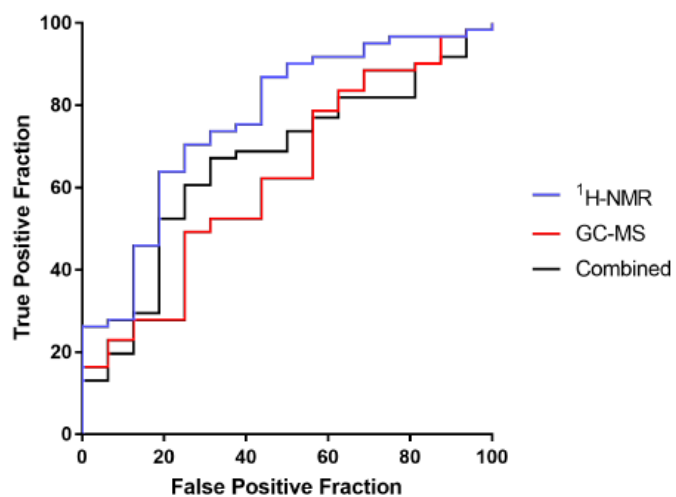


# Supplementary Materials: Distinguishing Benign from Malignant Pancreatic and Periampullary Lesions Using Combined Use of $^1\text{H-NMR}$ Spectroscopy and Gas Chromatography–Mass Spectrometry

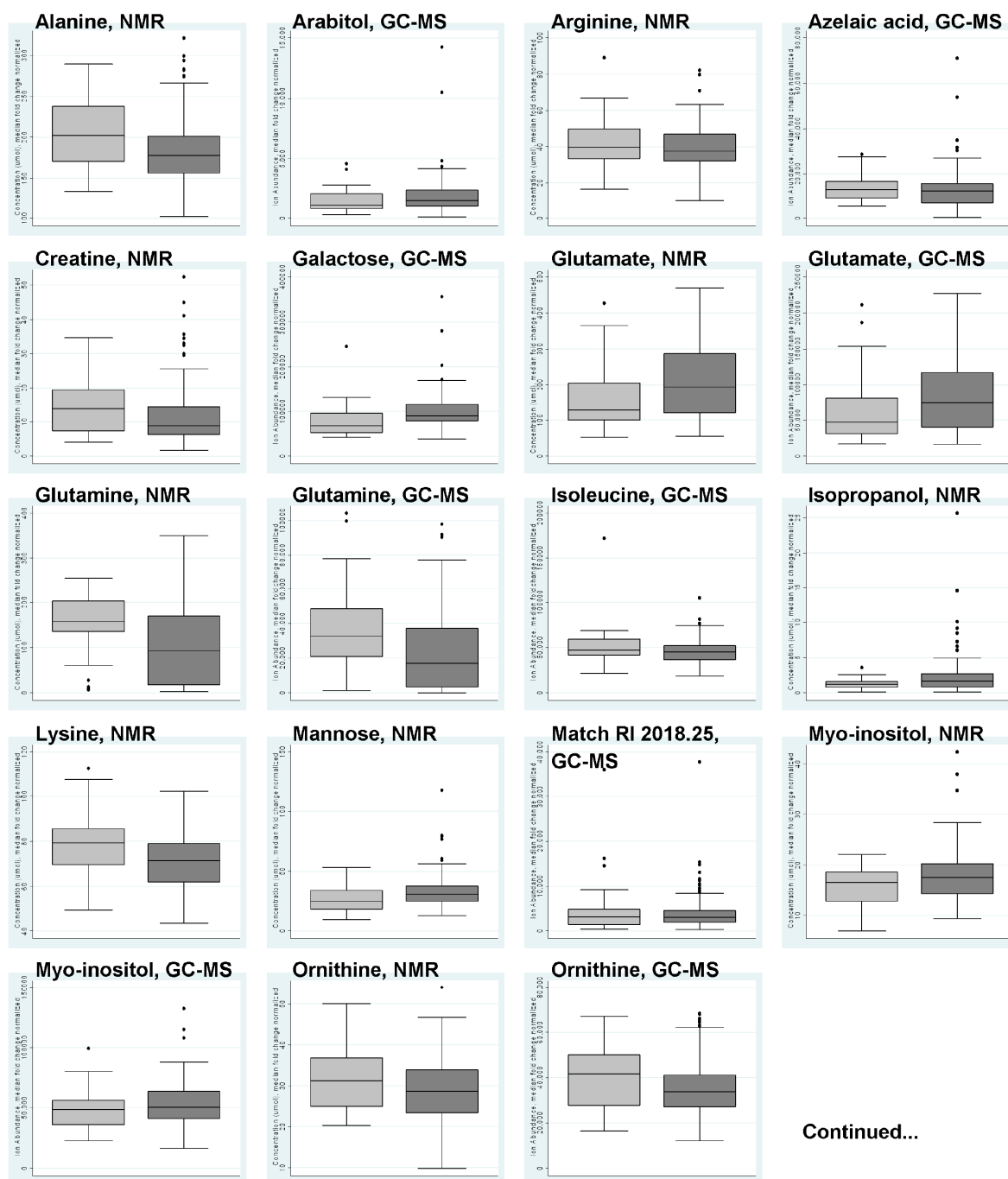
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**Figure S1.** Principal Component Analysis (PCA) Scores Scatter plots for three training and validation set allocations of  $^1\text{H-NMR}$ , GC-MS and combined datasets. All variables are included in the analyses. A, B, and C: three case allocations for  $^1\text{H-NMR}$  data; D, E and F: three case allocations for GC-MS data; G, H and I: three case allocations for combined  $^1\text{H-NMR}$  and GC-MS data. Sample sizes were 80 per allocation. Number of variables in each PCA ( $k$ ) was 83 for  $^1\text{H-NMR}$  spectroscopy; 146 for GC-MS; and 183 for combined. A= number of components.

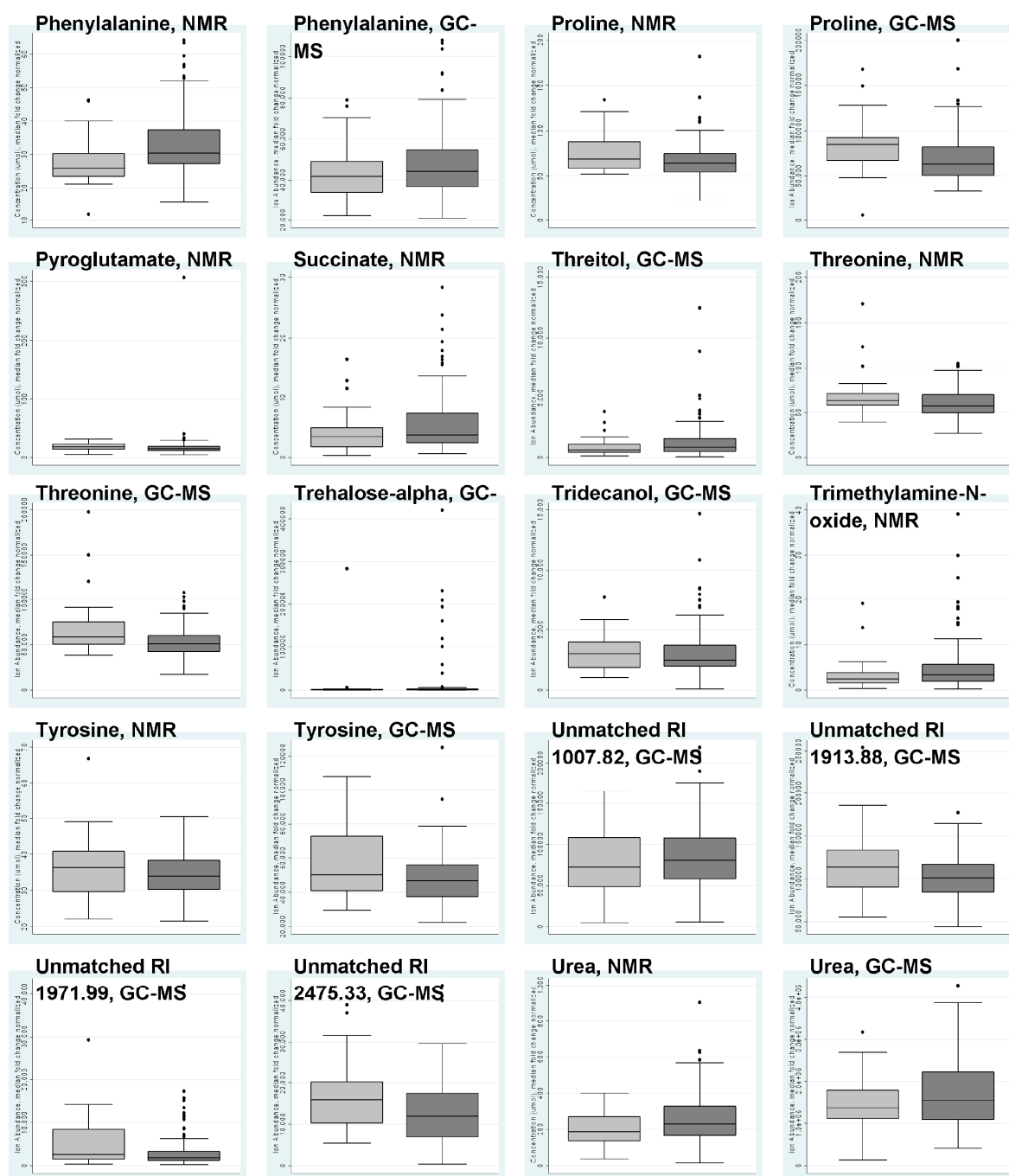


**Figure S2.** Receiver Operating Characteristic (ROC) curve for detection of benign and malignant periampullary lesions.  $^1\text{H-NMR}$ : blue, GC-MS: red, Combined model: black.

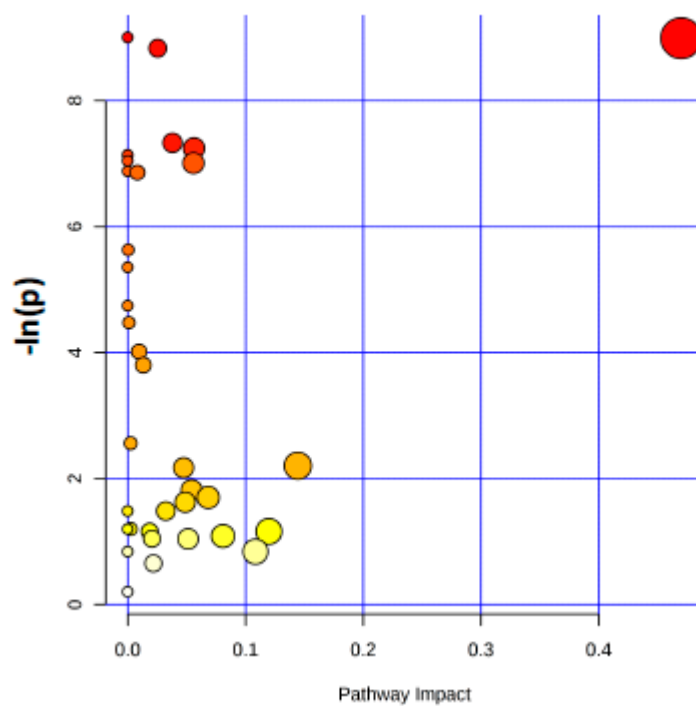


Continued...

Figure S3. Cont.



**Figure S3.** Whisker plots for consistently contributing metabolites from NMR and GC-MS. Whisker box limits are 1st and 3rd quartiles, whisker bar limits are upper and lower adjacent values. Middle line is median. Y-axis displays normalized concentration/ion abundance data: NMR =  $\mu\text{mol}$ , GC-MS = ion abundance. Benign disease: light gray, malignant disease: dark gray.



**Figure S4.** Metaboanalyst 2.0 pathway analysis bubble plot. The plot depicts each pathway's significance (expressed as " $-\ln(p\text{-value})$ " on Y-axis) versus its degree of involvement in the biological process (as identified by "impact" on X-axis).

**Table S1.** Performance measurements in triplicate analysis of <sup>1</sup>H-NMR dataset, 50/50 training/test dataset (*n* = 80/77).

Trial	OPLS-DA: Filtered						OPLS-DA: Minimal <sup>c</sup>									
	Training					Test		Training							Test	
	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	Core CV <sup>c</sup>	AUROC	SE	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	AUROC(i)	Cancer	Non-cancer	AUROC	SE
<b>A</b>	26	0.334	0.174	6.4 × 10 <sup>-4</sup>	0.487	0.71	0.07	13	0.251	0.122	6.6 × 10 <sup>-3</sup>	0.756	Isopropanol Mannose Phenylalanine Succinate TrimethylamineN-oxide TwoHydroxyisobutyrat	Alanine Betaine Glutamine Histidine Lysine Proline Threonine	0.79	0.06
<b>B</b>	28	0.378	0.259	9.8 × 10 <sup>-6</sup>	0.484	0.73	0.07	14	0.308	0.224	6.1 × 10 <sup>-5</sup>	0.756	Mannose MyoInositol Phenylalanine Urea	Creatine Ethanol Glutamine Histidine Lysine Ornithine Proline Pyroglutamate Threonine Xanthine	0.71	0.05
<b>C</b>	24	0.282	0.140	3.3 × 10 <sup>-3</sup>	0.491	0.80	0.05	12	0.230	0.128	5.2 × 10 <sup>-3</sup>	0.756	Choline Isopropanol Mannose Succinate TrimethylamineN-oxide	Alanine Creatine Inosine Lysine Ornithine Pyroglutamate Threonine	0.75	0.06
<i>Average</i>	26	0.331	0.191	1.3 × 10 <sup>-3</sup>		0.75	0.06	13	0.263	0.158	3.8 × 10 <sup>-3</sup>				0.75	0.06

<sup>a</sup> Number of metabolites/features in the filtered (*t*-test *p*-value <0.3) training set

<sup>b</sup> *p*-value for CV-ANOVA testing

<sup>c</sup> Minimal list of metabolites determined by multistep iterative process: selection of metabolites contributing most to class difference by multivariate O2PLS analysis controlling for technical and clinical covariates; then iterative OPLS-DA modeling with sequential exclusion of metabolites based on their contribution to test model parameters- to maximize AUROC.

**Table S2.** Performance measurements in triplicate analysis of GC-MS dataset, 50/50 training/test dataset ( $n = 80/77$ ).

Trial	OPLS-DA: Filtered						OPLS-DA: Minimal <sup>c</sup>									
	Training					Test		Training						Test		
	X <sup>a</sup>	R <sup>2</sup> <sub>Y</sub>	Q <sup>2</sup>	p <sup>b</sup>	Core CV <sup>c</sup>	AUROC	SE	X <sup>a</sup>	R <sup>2</sup> <sub>Y</sub>	Q <sup>2</sup>	p <sup>b</sup>	AUROC(i)	Cancer	Non-cancer	AUROC	SE
A	33	0.440	0.239	$4.8 \times 10^{-5}$	0.736	0.69	0.07	17	0.336	0.165	$1.3 \times 10^{-3}$	0.770	Arabitol5TMS Galactose1MEOX MatchRI170922 Threitol4TMS Trehalosealpha UnmatchedRI11763	Isoleucine2TMS MatchRI129451 Ornithine4TMS Proline2TMS Sorbitol6TMS Threonine3TMS Tridecan1oln1TMS UnmatchedRI16313 UnmatchedRI19719 UnmatchedRI24753 UnmatchedRI28215	0.69	0.07
B	43	0.378	0.258	$1.3 \times 10^{-5}$	0.734	0.52	0.08	21	0.327	0.238	$2.9 \times 10^{-5}$	0.832	Glutamicacid3TMS Inositolmyo6TMS MatchRI201825 Phenylalanine2TMS UnmatchedRI10078 UnmatchedRI11250 UnmatchedRI11396 UnmatchedRI18425 Urea2TMS	AzelaicAcid2TMS GlutamineDL3TMS Glycerol3TMS Octadecadienoic Ornithine4TMS Tridecan1oln1TMS UnmatchedRI11646 UnmatchedRI13319 UnmatchedRI19138 UnmatchedRI19719 UnmatchedRI22199 UnmatchedRI24753	0.54	0.07
C	33	0.348	0.199	$2.6 \times 10^{-4}$	0.784	0.70	0.07	17	0.273	0.162	$1.2 \times 10^{-3}$	0.755	Butanoicacid2am Galactose1MEOX Inositolmyo6TMS Ribitol5TMS Threitol4TMS UnmatchedRI10078 Urea2TMS UnmatchedRI22127	AzelaicAcid2TMS GlutamineDL3TMS Isoleucine2TMS MatchRI201825 Ornithine4TMS Tyrosine3TMS UnmatchedRI19138 UnmatchedRI19736 UnmatchedRI24753	0.67	0.08
Average	36	0.389	0.232	$1.1 \times 10^{-4}$	0.751	0.64	0.07	18	0.312	0.188	$8.4 \times 10^{-4}$	0.786			0.67	0.07

<sup>a</sup> Number of metabolites/features in the filtered ( $t$ -test  $p$ -value  $< 0.3$ ) training set

<sup>b</sup>  $p$ -value for CV-ANOVA testing

<sup>c</sup> Minimal list of metabolites determined by multistep iterative process: selection of metabolites contributing most to class difference by multivariate O2PLS analysis controlling for technical and clinical covariates; then iterative OPLS-DA modeling removing metabolites based on their contribution to predictive modeling in test set (YpredPS and T2PS)

**Table S3.** Performance measurements in triplicate analysis of Combined dataset, 50/50 training/test dataset ( $n = 80/77$ ).

Trial	OPLS-DA: Filtered						OPLS-DA: Minimal <sup>c</sup>									
	Training					Test		Training							Test	
	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	Core CV <sup>c</sup>	AUROC	SE	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	AUROC(i)	Cancer	Non-cancer	AUROC	SE
A	50	0.451	0.238	4.1 × 10 <sup>-5</sup>	-	0.67	0.08	24	0.341	0.177	7.8 × 10 <sup>-4</sup>	0.802	Arabitol5TMS-G Isopropanol-N Mannose-N MatchRI170922-G MyoInositol-N Phenylalanine-C Ribitol5TMS-G Succinate-N Threitol4TMS-G Trehalosealpha-G TwoHydroxyisobutyrate Urea-C	Histidine-C Lysine-N MatchRI129451-G Methionine-C Ornithine-C Proline-C Sorbitol6TMS-G Threonine-C UnmatchedRI16313-G UnmatchedRI22199-G UnmatchedRI24753-G UnmatchedRI28215-G	0.67	0.07
B	62	0.402	0.239	3.7 × 10 <sup>-7</sup>	-	0.63	0.08	26	0.367	0.231	5.2 × 10 <sup>-5</sup>	0.839	Glucuronicacid1M-G Mannose-N MyoInositol-N Phenylalanine-C UnmatchedRI10078-G UnmatchedRI10325-G UnmatchedRI11396-G UnmatchedRI18377-G UnmatchedRI18425-G Urea-C	Arginine-N AzelaicAcid2TMS-G Creatine-N Glutamine-C Glycerol-C Histidine-C Lysine-N Methanol-N Ornithine-C Proline-C UnmatchedRI11646-G UnmatchedRI13319-G UnmatchedRI19736-G UnmatchedRI22199-G UnmatchedRI24753-G Xanthine-N	0.66	0.07

<sup>a</sup> Number of metabolites/features in the filtered ( $t$ -test  $p$ -value <0.3) training set

<sup>b</sup>  $p$ -value for CV-ANOVA testing

<sup>c</sup> Minimal list of metabolites determined by multistep iterative process: selection of metabolites contributing most to class difference by multivariate O2PLS analysis controlling for technical and clinical covariates; then iterative OPLS-DA modeling removing metabolites based on their contribution to predictive modeling in test set (YpredPS and T2PS)



Table S3. Cont.

Trial	OPLS-DA: Filtered						OPLS-DA: Minimal <sup>c</sup>									
	Training					Test		Training					Test			
	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	Core CV <sup>c</sup>	AUROC	SE	X <sup>a</sup>	R2Y	Q2	p <sup>b</sup>	AUROC(i)	Cancer	Non-cancer	AUROC	SE
C	47	0.369	0.219	9.3 × 10 <sup>-5</sup>	-	0.73	0.06	19	0.311	0.204	1.7 × 10 <sup>-4</sup>	0.795	Choline-N Erythritol4TMS-G Galactose1MEOX-G Isopropanol-N Mannose-N MyoInositol-N Phenylalanine-C Ribitol5TMS-G Threitol4TMS-G TrimethylamineNoxide UnmatchedRI22127-G	Arginine-N Creatine-N Inosine-N Lysine-N MatchRI201825-G Threonine-C UnmatchedRI19138-G UnmatchedRI19736-G	0.68	0.07
Average	53	0.407	0.232	4.5 × 10 <sup>-5</sup>		0.68	0.07	23	0.34	0.204	3.3 × 10 <sup>-4</sup>	0.812			0.67	0.07

<sup>a</sup> Number of metabolites/features in the filtered (*t*-test *p*-value <0.3) training set

<sup>b</sup> *p*-value for CV-ANOVA testing

<sup>c</sup> Minimal list of metabolites determined by multistep iterative process: selection of metabolites contributing most to class difference by multivariate O2PLS analysis controlling for technical and clinical covariates; then iterative OPLS-DA modeling removing metabolites based on their contribution to predictive modeling in test set (YpredPS and T2PS)