

Analysis of the Urinary Metabolic Profiles in Irradiated Rats treated with Activated Protein C (APC), a Potential Mitigator of Radiation Toxicity

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Untargeted urine metabolomics using UPLC-QToF-MS

(i). Sample preparation: Urine samples were taken out of $-80\text{ }^{\circ}\text{C}$ and thawed on ice. To $20\text{ }\mu\text{L}$ of urine sample was added $80\text{ }\mu\text{L}$ of chilled extraction buffer prepared by mixing water:acetonitrile (50:50) and containing internal standards (debrisoquine and 4-nitrobenzoic acid). The samples were vortexed and incubated on ice for 20 minutes followed by incubation at $-20\text{ }^{\circ}\text{C}$ for 20 minutes. Finally, the samples were centrifuged at 13000 rpm for 20 minutes at $4\text{ }^{\circ}\text{C}$. The supernatants were transferred to MS vials for LC-MS data acquisition.

(ii). LC methods and data acquisition: $10\text{ }\mu\text{L}$ from each sample was mixed to generate a pooled quality control (QC) sample. The sample queue was randomized to avoid bias. For metabolomics data acquisition, each sample ($1\text{ }\mu\text{L}$) was injected to a $1.7\text{ }\mu\text{m}$, $2.1\text{ mm} \times 50\text{ mm}$ Acquity BEH C18 column (Waters Corporation, MA, USA) using an Acquity UPLC system connected to an electrospray ion source coupled with a quadrupole time-of-flight mass spectrometer (ESI-Q-TOF, Xevo-G2S, Waters Corporation, MA, USA) operating in positive and negative ionization mode. The gradient mobile phases consisted of 100% water with 0.1% formic acid (solvent A), 100% acetonitrile with 0.1% formic acid (solvent B). Each sample injection was run for 11 minutes at a flow rate for $500\text{ }\mu\text{L}/\text{min}$. The LC gradient conditions with a ramp curve of 6 at each step were as follows: Initial – 95% A, 5% B till 0.5 minutes; 4.0 minutes – 80% A, 20% B; 8.0 minutes – 5% A, 95% B till 9.0 minutes; 9.1 minutes – 95% A, 5% B till 11 minutes.

(iii). MS methods: In the MS method, the positive mode had a capillary voltage of 2.5 kV, a sampling cone voltage of 30 V, and a source offset of 80 V. The negative mode had a capillary voltage of 1.0 kV, a sampling cone voltage of 30 V and a source offset of 80 V. The desolvation gas flow was 1000 L/h. and the temperature was set to $500\text{ }^{\circ}\text{C}$. The cone gas flow was 25 L/h, and the source temperature was $120\text{ }^{\circ}\text{C}$. The data were acquired in the sensitivity MS Mode with a scan time of 0.3 seconds, and inter-scan delay at 0.014 seconds. The data were acquired in centroid TOF-MS mode over a mass range from 50 to 1,200 m/z. Accurate mass was maintained by infusing Leucine Enkephalin (556.2771 m/z) in 50% aqueous acetonitrile (0.5 ng/mL) at a rate of $20\text{ }\mu\text{L}/\text{min}$ via the Lockspray interface for real-time mass correction, every 10 seconds. Before and after samples run, a mixture of six standards (acetaminophen: m/z 152.0712 $[\text{M}+\text{H}]^+$ / 150.0555 $[\text{M}-\text{H}]^-$, sulfaguanidine: m/z 215.0603 $[\text{M}+\text{H}]^+$ / 213.0446 $[\text{M}-\text{H}]^-$, sulfadimethoxine: m/z 311.0814 $[\text{M}+\text{H}]^+$ / 309.0658 $[\text{M}-\text{H}]^-$, Val-Tyr-Val: m/z 380.2185 $[\text{M}+\text{H}]^+$ / 378.2029 $[\text{M}-\text{H}]^-$, terfenadine: m/z 472.3216 $[\text{M}+\text{H}]^+$ and leucine-enkephalin: m/z 556.2771 $[\text{M}+\text{H}]^+$ / 554.2615 $[\text{M}-\text{H}]^-$) were run to ensure mass accuracy during data acquisition. Several measures were used to ensure high quality and reproducibility of LC-MS data. The column was conditioned using pooled QC samples, which were injected periodically through the batch to monitor mass accuracy, shifts in retention time and signal intensities as measures of reproducibility. The overlap of QC sample chromatograms (base peak intensity) shows minimal shifts in retention time and consistency in peak intensities throughout the acquisition. Pooled QC samples injected routinely were also used to assess and correct for any analytical variance.

(iv). UPLC-QToF-MS data pre-processing: The MS generated raw data files were first converted into NetCDF files for pre-processing using Waters MassLynx Databridge Software (Waters Corporation). XCMS was used for pre-processing the data files while the Isotopologue Parameter Optimization (IPO) package was used for XCMS parameter optimization.[1] Normalization was performed with internal standards in both positive and negative mode data. The features with more than 20% missing value were also filtered out and the features with less than 20% of missing value were imputed by half of the minimum positive value in the original data. The features with more than 15% of coefficient of variation (CV) were also filtered out. The remaining high-quality features were normalized by QC-RLSC.[2] R package was used to perform multivariate analysis.[3] Statistically significant m/z's with FDR adjusted p -value < 0.05 were run on the UPLC-QToF instrument in the

MS/MS mode. The MS/MS raw data files were converted to NetCDF files using Waters MassLynx Databridge Software, then further converted to MSP file format using an in-house R package. Thereafter, for accurate mass based putative identification of metabolites, we performed database search by matching MS/MS spectra to entries in the NIST 2017 MS/MS database and by applying the online version of CEU Mass Mediator (CMM) which integrated from METLIN, Human Metabolome Database (HMDB) and LIPID MAPS with a ppm error of less than 10.

Targeted urine analysis using 5500 QTRAP

(i). Metabolomics: The targeted metabolomics method was developed in-house to quantitate 270 endogenous molecules using QTRAP® 5500 LC-MS/MS System (Sciex, MA, USA). For the purpose, the sample preparation was kept similar as for untargeted analysis. 5 µL of the prepared sample was injected onto a Kinetex 2.6 µm 100 Å 100 × 2.1 mm (Phenomenex, CA, USA) using SIL-30 AC auto sampler (Shimadzu, Kytoto, Japan) connected with a high flow LC-30AD solvent delivery unit (Shimadzu, Kytoto, Japan) and CBM-20A communication bus module (Shimadzu, Kytoto, Japan) online with QTRAP 5500 (Sciex, MA, USA) operating in positive and negative ion mode. A binary solvent comprising of water with 0.1% formic acid (solvent A) and acetonitrile with 0.1% formic acid (solvent B) was used. The extracted metabolites were resolved at 0.2 mL/min flow rate. The LC gradient conditions were as follows: Initial – 100% A, 0% B for 2.1 minutes; 14 minutes – 5% A, 95% B till 15 minutes; 15.1 minutes – 100% A, 0% B till 22.5 minutes. The auto sampler and oven were kept at 15 °C and 30 °C, respectively. Source and gas setting for the method were as follow: curtain gas = 35, CAD gas = medium, ion spray voltage = 2500 V in positive mode and –4500 V in negative mode, temperature = 400 °C, nebulizing gas = 60 and heater gas = 70.

(ii). Lipidomics: For the purpose, 25 µL of each urine sample was diluted in 125 µL of chilled isopropanol containing internal standards. The samples were vortexed for 1 min and kept on ice for 30 minutes. Samples were incubated at -20 °C for overnight for protein precipitation. The samples were centrifuged at 13,000 rpm for 20 minutes at 4 °C. The supernatant was transferred to MS vial for LC-MS analysis. 10 µL of each prepared sample was mixed to generate the pooled QC sample. 5 µL of the prepared samples were resolved on Xbridge amide 3.5 µm, 4.6 X 100 mm (Waters, MA, USA) column online with a triple quadrupole mass spectrometer (5500 QTRAP, SCIEX, MA, USA) operating in the multiple reaction monitoring (MRM) mode. Each sample was injected using SIL-30 AC auto sampler (Shimadzu, Kyoto, Japan) connected with a high flow LC-30AD solvent delivery unit (Shimadzu, Kyoto, Japan) and CBM-20A communication bus module (Shimadzu, Kyoto, Japan) online with QTRAP 5500 (Sciex, MA, USA) operating in positive and negative ion mode.

Targeted lipidomics method was developed in-house to measure 21 classes of lipid molecules which includes diacylglycerols (DAGs), cholesterol esters (CEs), sphingomyelins (SMs), phosphatidylcholine (PCs), triacylglycerols (TAGs), free fatty acids (FFAs), ceramides (CERs), dihydroceramides (DCERs), hexosylceramide (HCERs), lactosylceramide (LCERs), phosphatidylethanolamine (PEs), lysophosphatidylcholine (LPCs), lysophosphatidylethanolamine (LPEs), phosphatidylinositol (PIs), lysophosphatidylinositol (LPIs), phosphatidylserine (PSs), phosphatidic acid (PAs), lysophosphatidic acid (LPAs), monoacyl glycerol (MAGs), acylcarnitines (ACs) and phosphatidyl glycerols (PGs) using QTRAP® 5500 LC-MS/MS System (Sciex, MA, USA). A binary solvent comprising of acetonitrile/water 95/5 with 10 mM ammonium acetate as solvent A and acetonitrile/water 50/50 with 10 mM ammonium acetate as solvent B, was used for the resolution. Lipids were resolved at 0.7 mL/min flow rate. The LC gradient conditions were as follows: Initial – 100% A, 0% B; 3.0 minutes – 99.9% A, 0.1% B; 6.0 minutes – 94% A, 6% B; 10.0 minutes – 75% A, 25% B; 11.0 minutes - 2% A, 98% B, 13.0 minutes – 0% A, 100% B till 18.6 minutes; 18.7 minutes – 100% A, 0% B till 24 minutes. The auto sampler and oven were kept at 15 °C and 35 °C, respectively.

Source and gas setting were as follow: curtain gas = 30, CAD gas = medium, ion spray voltage = 5.5 kV in positive mode and -4.5 kV in negative mode, temperature = 550 °C, nebulizing gas = 50 and heater gas = 60. The reproducibility and high quality of the LC-MS data was ensured using several measures. The column was conditioned using the pooled QC samples initially and pooled QC samples were also injected periodically (after every 10 sample injections) to monitor shifts in signal intensities and retention time as measures of reproducibility and data quality of the LC-MS data. Pooled QC samples were routinely applied to assess and correct for any analytical variance. We also have blank solvent runs between set of samples (after every 10 samples before and after pooled QC samples) to monitor sample-to-sample carry-over effects. To monitor instrumental variance, we also ran NIST plasma sample (every 20 samples) prepared in the same manner as actual samples.

(iii). Data processing and statistical analysis: The abundance measurement for metabolites were expressed as intensity units that were initially normalized to internal standards and processed using MultiQuant 3.0.3 (Sciex). The data were pre-processed using a signal/noise ratio >20:1 and retention time (RT) tolerance of 5 seconds, after manually checking of metabolites peak by experts to find the reliable features. We also use 20% of missing values in each feature as filter out criteria. Missing values were imputed by half of the minimum positive value in the original data. Thereafter, we used 20% of the coefficient of variation (CV) as our filter criteria to remove any possible noises before data normalization. Analytical drifts (if any) were corrected by quality control based robust LOESS signal correction (QC-RLSC). All the analyses were performed in MetaboAnalyst (V5.0) and R (v 4.0.3). The normalized LC-MS data was log transformed and Pareto scaled. For the 183 samples in the study set, the level of differential expression for each metabolite was calculated using an unpaired t-test, comparing sham vs radiation, and radiation vs radiation plus APC treated samples, constrained by FDR corrected p -value<0.05. MetaboAnalyst (V5.0) and Mummichog analysis Python package v2.0 was used to evaluate the metabolic pathways affected by radiation exposure longitudinally and radioprotective alleviation by APC treatments. Figures were generated with MetaboAnalyst 5.0, GraphPad Prism 7 (GraphPad Software, La Jolla, CA).

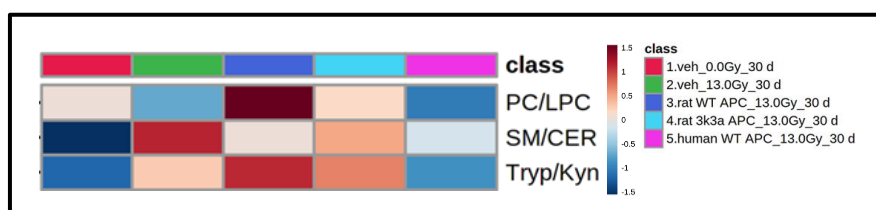
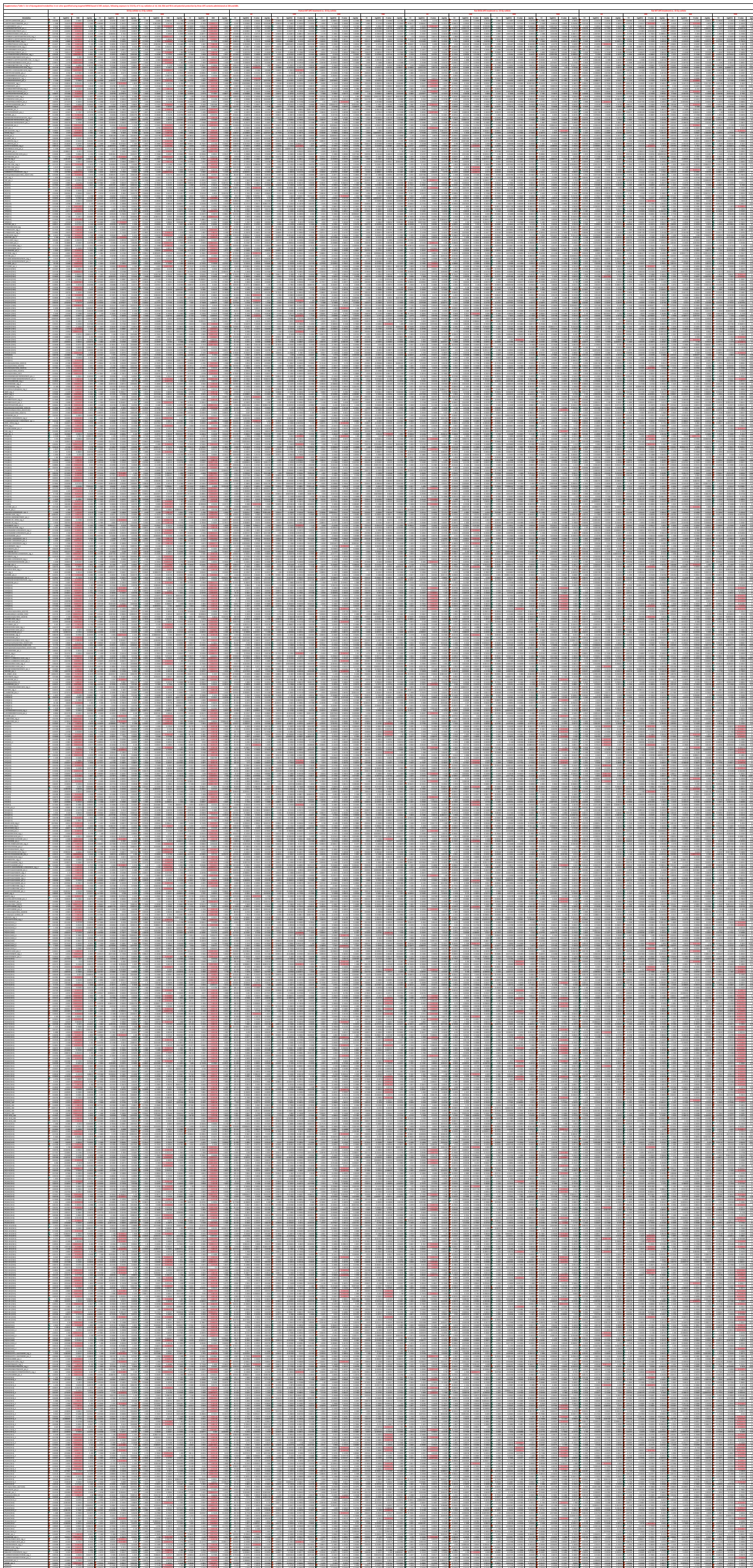


Figure S1. Heatmap showing longitudinal radiation impacts on metabolic ratios for PC/LPC, SM/CER and Trp/Kyn at 30 days post-irradiation.

1. Gowda, H., et al., *Interactive XCMS Online: simplifying advanced metabolomic data processing and subsequent statistical analyses*. *Anal Chem*, 2014. **86**(14): p. 6931-9.
2. Xia, J., et al., *MetaboAnalyst: a web server for metabolomic data analysis and interpretation*. *Nucleic Acids Res*, 2009. **37**(Web Server issue): p. W652-60.
3. Dunn, W.B., et al., *Procedures for large-scale metabolic profiling of serum and plasma using gas chromatography and liquid chromatography coupled to mass spectrometry*. *Nat Protoc*, 2011. **6**(7): p. 1060-83.

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Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region	Country	Region		
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14	14	15	15	16	16	17	17	18	18	19	19	20	20	21	21	22	22	23	23	24	24	25	25	26	26		
27	27	28	28	29	29	30	30	31	31	32	32	33	33	34	34	35	35	36	36	37	37	38	38	39	39		
40	40	41	41	42	42	43	43	44	44	45	45	46	46	47	47	48	48	49	49	50	50	51	51	52	52		
53	53	54	54	55	55	56	56	57	57	58	58	59	59	60	60	61	61	62	62	63	63	64	64	65	65		
66	66	67	67	68	68	69	69	70	70	71	71	72	72	73	73	74	74	75	75	76	76	77	77	78	78		
79	79	80	80	81	81	82	82	83	83	84	84	85	85	86	86	87	87	88	88	89	89	90	90	91	91		
92	92	93	93	94	94	95	95	96	96	97	97	98	98	99	99	100	100	101	101	102	102	103	103	104	104		

Item No.	Part No.	Description	Quantity	Unit	Material	Cost	Remarks
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4	1004
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8	1008
9	1009
10	1010
11	1011
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13	1013
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100	1100



The image displays a large, dense grid of data, likely a spreadsheet or a data table. The grid is composed of many rows and columns, with each cell containing small, illegible text or numbers. The data is presented in a structured format, with vertical lines separating the columns. Several columns are highlighted in red, and some individual cells within these columns are also highlighted in green. The overall appearance is that of a complex data set, possibly representing a large-scale analysis or a detailed report. The grid is oriented vertically on the page.

Supplementary Table 4a. List of dysregulated pathways in rat urine following exposure to 13.0 Gy of X-ray radiation at 1d, 14d, 30d and 90d.

13 Gy vehicle vs. 0 Gy vehicle (p values)				
	d1	d14	d30	d90
Alanine, aspartate and glutamate metabolism	1.4347E-07	-	0.0036354	0.00003939
alpha-Linolenic acid metabolism	0.00041387	0.049357	-	0.00029328
Amino sugar and nucleotide sugar metabolism	-	-	-	0.030661
Aminoacyl-tRNA biosynthesis	0.000018211	0.00002466	0.00035083	0.00077749
Arginine and proline metabolism	0.00023656	0.0032839	0.013788	0.00053236
Arginine biosynthesis	1.3023E-06	-	0.0015199	0.000010228
Biosynthesis of unsaturated fatty acids	8.1909E-08	-	-	0.000025722
Butanoate metabolism	0.0031336	-	-	-
Citrate cycle (TCA cycle)	0.00031864	-	0.039332	0.00016591
Cysteine and methionine metabolism	0.0018492	-	-	0.018087
Glutathione metabolism	0.00056426	0.021712	-	0.0080464
Glycerolipid metabolism	-	-	-	0.012418
Glycerophospholipid metabolism	0.0086389	0.00021965	-	0.00047111
Glycine, serine and threonine metabolism	0.00036892	-	0.035851	0.00016642
Glycolysis / Gluconeogenesis	0.035989	-	-	0.0054767
Glyoxylate and dicarboxylate metabolism	0.00028559	-	-	0.00012798
Linoleic acid metabolism	-	0.01923	-	-
Pantothenate and CoA biosynthesis	0.0095811	0.01025	-	0.0061964
Pentose phosphate pathway	0.00061984	-	-	0.011979
Phenylalanine metabolism	0.031028	-	-	-
Phenylalanine, tyrosine and tryptophan biosynthesis	0.0014313	-	-	0.023581
Purine metabolism	6.4054E-09	-	0.00011953	4.7464E-08
Pyrimidine metabolism	1.8942E-10	0.040405	9.0641E-06	4.5175E-08
Pyruvate metabolism	0.018194	-	-	0.0022031
Riboflavin metabolism	0.028684	-	-	-
Sphingolipid metabolism	2.8286E-06	0.000041827	-	1.5317E-06
Taurine and hypotaurine metabolism	0.016123	-	-	0.012156
Valine, leucine and isoleucine biosynthesis	0.000088649	0.000025234	-	0.0010089
Valine, leucine and isoleucine degradation	-	0.0038086	-	0.013343
Aminosugars metabolism	-	0.007394337	0.015544912	-
Androgen and estrogen biosynthesis and metabolism	0.037559869	-	-	0.013024116
Ascorbate (Vitamin C) and Aldarate Metabolism	-	-	0.043357701	0.000168053
Beta-Alanine metabolism	-	0.017393496	-	-
Bile acid biosynthesis	-	-	-	0.007814469
Biopterin metabolism	-	0.026048231	-	-
Blood Group Biosynthesis	-	0.049827746	0.040836904	-
C21-steroid hormone biosynthesis and metabolism	-	0.002268717	-	8.40266E-05
Carnitine shuttle	-	-	-	0.014452567
Drug metabolism - cytochrome P450	0.047727082	-	0.005629779	-
Drug metabolism - other enzymes	-	0.049827746	0.039744559	-
Glutamate metabolism	-	0.048819427	-	-
Glycosphingolipid biosynthesis - ganglioseries	-	0.049827746	-	-
Glycosphingolipid biosynthesis - lactoseries	-	0.049827746	0.040836904	-
Glycosphingolipid biosynthesis - neolactoseries	-	0.049827746	0.040836904	-
Glycosphingolipid metabolism	-	0.048819427	-	-
Histidine metabolism	-	0.017393496	-	-
Keratan sulfate biosynthesis	-	0.049827746	0.040836904	-
Methionine and cysteine metabolism	-	-	-	0.028569028
Nitrogen metabolism	-	0.049827746	-	-
O-Glycan biosynthesis	-	0.049827746	0.040836904	-
Porphyryn metabolism	-	0.016385178	-	0.028569028
Putative anti-Inflammatory metabolites formation from EPA	-	0.017393496	-	-
Sialic acid metabolism	0.025544072	-	-	-
Squalene and cholesterol biosynthesis	-	0.030249559	-	-
Tryptophan metabolism	0.004033275	-	-	-
Tyrosine metabolism	0.001764558	0.031341904	0.001092345	-
Urea cycle/amino group metabolism	0.056801949	-	-	-
Vitamin B3 (nicotinate and nicotinamide) metabolism	-	0.049827746	-	-
Vitamin B6 (pyridoxine) metabolism	-	-	0.015544912	-

Supplementary Table 4b. List showing potential restoration of biological pathways in rat urine after APC (human WT, Rat 3K3A and rat WT) treatment at 24h and 48h post irradiation to 13.0 Gy of X-ray radiation at 1d, 14d, 30d and 90d.

	Human WT APC treatment vs. 13 Gy vehicle (p values)			Rat 3k3a APC treatment vs. 13 Gy vehicle (p values)			Rat WT APC treatment vs. 13 Gy vehicle (p values)		
	d14	d30	d90	d14	d30	d90	d14	d30	d90
1- and 2-Methylnaphthalene degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
3-Chloroacrylic acid degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
3-oxo-10R-octadecatrienoate beta-oxidation	0.00487354	0.018401815	0.043777834	-	0.045458365	0.022939249	-	0.034282833	-
Alanine and Aspartate Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Alkaloid Biosynthesis II	0.00487354	0.024787833	0.04688616	-	0.045458365	0.022939249	-	0.048147215	-
alpha-Linolenic acid metabolism	0.03316	0.04129	0.03316	0.03316	0.049357	0.0054168	-	0.03316	-
Aminocycl-TRNA biosynthesis	-	-	-	-	-	-	0.04129	-	0.0054168
Aminosalicylic acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.036383497	-	-
Androgen and estrogen biosynthesis and metabolism	0.00487354	-	0.04688616	0.023611461	0.045458365	0.022939249	-	0.02218301	0.035459205
Arachidonic acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Arginine and Proline Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Ascorbate (Vitamin C) and Aldarate Metabolism	0.00487354	0.01462062	0.04688616	-	0.045458365	0.009495	-	0.004453407	-
Ascorbate and aldarate metabolism	-	0.025574	-	-	-	-	-	-	-
Aspartate and asparagine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Atrazine degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Benzoate degradation via CoA ligation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Beta-Alanine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Bile acid biosynthesis	0.00487354	-	0.04688616	0.000756239	0.045458365	0.022939249	-	-	0.002100664
Biotin metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Blood Group Biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Butanoate metabolism	0.00487354	0.04898748	0.04688616	-	0.045458365	0.022939249	-	-	-
C21-steroid hormone biosynthesis and metabolism	0.00487354	-	0.036719603	0.002016637	0.045458365	0.022939249	-	0.000504159	0.046466683
C5- Branched dibasic acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Caffeine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Carbon fixation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Carnitine shuttle	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.046382657	-	-
Chondroitin sulfate degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.021174691	-	-
CoA Catabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
D4&E4-neuroprostanes formation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
De novo fatty acid biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	0.008654735
Dimethyl branched-chain fatty acid mitochondrial beta-oxidation	0.00487354	0.017141417	0.04688616	-	0.045458365	0.022939249	-	-	-
Di-unsaturated fatty acid beta-oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Drug metabolism - cytochrome P450	0.00487354	-	0.000504159	0.044281993	0.045458365	0.022939249	-	-	-
Drug metabolism - other enzymes	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Dynorphin metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Electron transport chain	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Fatty acid activation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	0.002100664
Fatty Acid Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Fatty acid oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Fatty acid oxidation, peroxisome	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Fructose and mannose metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Galactose metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.047895135	-	-
Geraniol degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glutamate metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glutathione Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycerolipid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycerophospholipid metabolism	0.0030573	0.00011161	0.000045368	0.000045368	0.0074218	0.0005553	0.00011161	0.000045368	0.00059553
Glycine, serine, alanine and threonine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycolysis and Gluconeogenesis	0.00487354	0.018821948	0.04688616	-	0.045458365	0.022939249	-	0.032014116	-
Glycosaminoglycan degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycosphingolipid biosynthesis - ganglioseres	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycosphingolipid biosynthesis - globoseries	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycosphingolipid biosynthesis - lactoseries	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycosphingolipid biosynthesis - neolactoseries	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glycosphingolipid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.036383497	0.035677	0.042433409
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	0.00487354	0.044409	0.04688616	0.035677	0.045458365	0.022939249	0.044409	0.035677	-
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Glyoxylate and Dicarbonylate Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Heparan sulfate biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Heparan sulfate degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.021174691	-	-
Hexose phosphorylation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Histidine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Hyaluron Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Keratan sulfate biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Keratan sulfate degradation	0.00487354	-	0.043777834	-	0.045458365	0.022939249	0.015796992	-	-
Leukotriene metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Limone and pinene degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Linololate metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Linoleic acid metabolism	0.00487354	0.016046	0.04688616	0.012853	0.045458365	0.022939249	0.016046	0.012853	0.025574
Lipoate metabolism	0.00487354	0.017141417	0.04688616	-	0.045458365	0.022939249	-	-	-
Lysine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Methionine and cysteine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Mono-unsaturated fatty acid beta-oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
N-Glycan Biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.036383497	-	-
N-Glycan Degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Nicotinate and nicotinamide metabolism	0.00487354	-	0.04688616	-	0.045458365	0.038188	0.04752	-	0.038188
Nitrogen metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Nucleotide Sugar Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.007898496	-	-
O-Glycan biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Omega-3 fatty acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	0.034871019
Omega-6 fatty acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Parathio degradation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Pentose and Glucuronate Interconversions	0.00487354	0.024787833	0.04688616	-	0.045458365	0.022939249	-	0.048147215	-
Pentose phosphate pathway	0.00487354	0.037475842	0.04688616	-	0.045458365	0.022939249	-	-	-
Phenylalanine metabolism	-	0.031885	-	-	-	-	-	-	-
Phosphatidylinositol phosphate metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Phytanic acid peroxisomal oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Polyunsaturated fatty acid biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Porphyrin metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Propanoate metabolism	0.00487354	0.037307789	0.04688616	-	0.045458365	0.022939249	-	-	-
Prostaglandin formation from arachidonate	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Prostaglandin formation from dihomo gamma-linoleic acid	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Proteoglycan biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Purine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	0.01462062	-	-
Putative anti-inflammatory metabolites formation from EPA	0.00487354	0.037307789	0.04688616	0.036407391	0.045458365	0.022939249	-	-	0.010419292
Pyrimidine metabolism	0.00487354	0.047229222	0.04688616	-	0.045458365	0.022939249	0.00487354	-	-
Pyruvate Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
R Group Synthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Riboflavin metabolism	0.00487354	-	0.012093	-	0.045458365	0.012093	-	-	0.012093
ROS Detoxification	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Saturated fatty acids beta-oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Selenoamino acid metabolism	0.00487354	-	0.020166373	-	0.045458365	0.022939249	-	-	-
Sialic acid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Sphingolipid metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Squalene and cholesterol biosynthesis	0.00487354	-	0.02636417	0.017477523	0.045458365	0.022939249	-	0.034282833	-
Starch and Sucrose Metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
TCA cycle	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Trihydroxyprostanoyl-CoA beta-oxidation	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Tryptophan metabolism	0.00487354	0.020502479	0.04688616	-	0.045458365	0.022939249	-	-	-
Tyrosine metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Ubiquinone Biosynthesis	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Urea cycle/ amino group metabolism	0.00487354	-	0.04688616	-	0.045458365	0.022939249	-	-	-
Valine,									