

Supplemental Table 1. Complete list of NHP samples and grouping included in this study. Mesenteric Lymph Node (MLN) were harvested from each animal for analysis.

Supplemental Figure S1: HPLC-MS^E Base Peak Chromatogram for a lipid extract from MLN before exposure to irradiation in positive ion mode.

Supplemental Figure S2: HPLC-MS^E Base Peak Chromatogram for a lipid extract from MLN before exposure to irradiation in negative ion mode.

Supplemental Figure S3: Expression of proteins most changed in MLN after radiation. LC-MS/MS proteomic analysis of NHP after 12 Gy PBI/BM2.5. Minimum 2-fold change of expression for at least 3 time points and FDR adjusted ANOVA p-value <0.05 were criteria for inclusion.

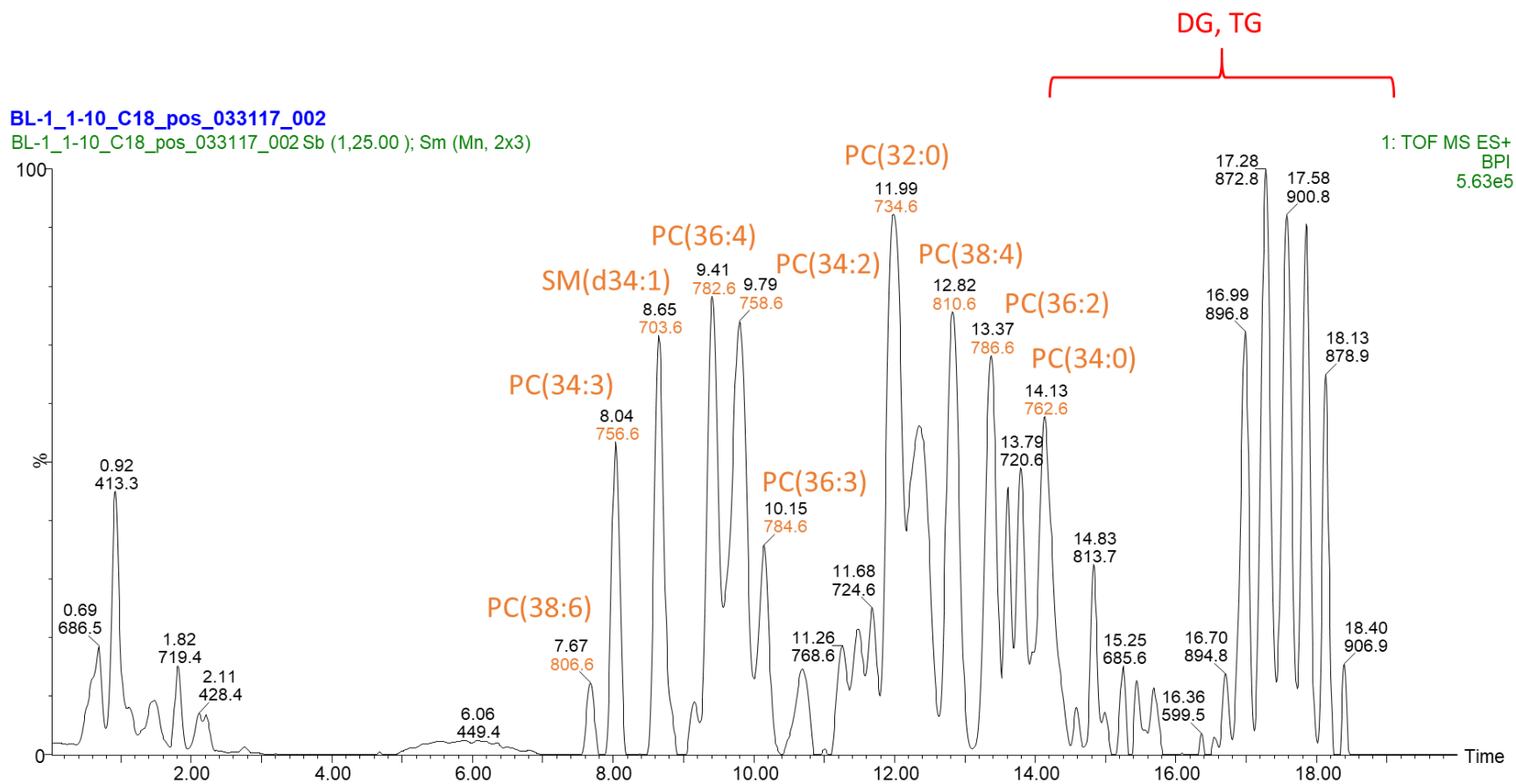
Supplementary Table 2: Lipids significantly changed by radiation in the Mesenteric Lymph Node in negative ion mode HPLC-MSE. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3. SD=standard deviation, n.d.= not detected, *not calculable, under limit of detection in Day 4.

Supplementary Table 3: Top 100 (according to p-value) Lipids significantly changed by radiation in the Mesenteric Lymph Node in positive ion mode HPLC-MSE. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3. SD=standard deviation \$ Isobaric ions which co-elute and were not distinguished

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Fisher's exact test p-value <0.05.

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Label	Type	Day	Animal #
Day 0 (Baseline)	Baseline*	0	RA0876
	Baseline*	0	RA0879
	Baseline*	0	RA088-RLL3
	Baseline	0	RA0147
Day 4	Scheduled*	4	RA0191
	Scheduled*	4	RA0261
	Scheduled*	4	RA0827
Day 8	Scheduled*	8	RA0231
	Scheduled*	8	RA0398
	Scheduled*	8	RA0841
	Scheduled	8	RA0878
Day 11	Scheduled	11	RA0432
	Scheduled	11	RA0869
	Scheduled	11	RA0871
Day 15	Scheduled	15	RA0414
	Scheduled	15	RA0838
	Scheduled	15	RA0868
	Scheduled	15	RA0873
Day 21	Scheduled*	21	RA0863
	Scheduled*	21	RQ9724
	Scheduled*	22	RA0847

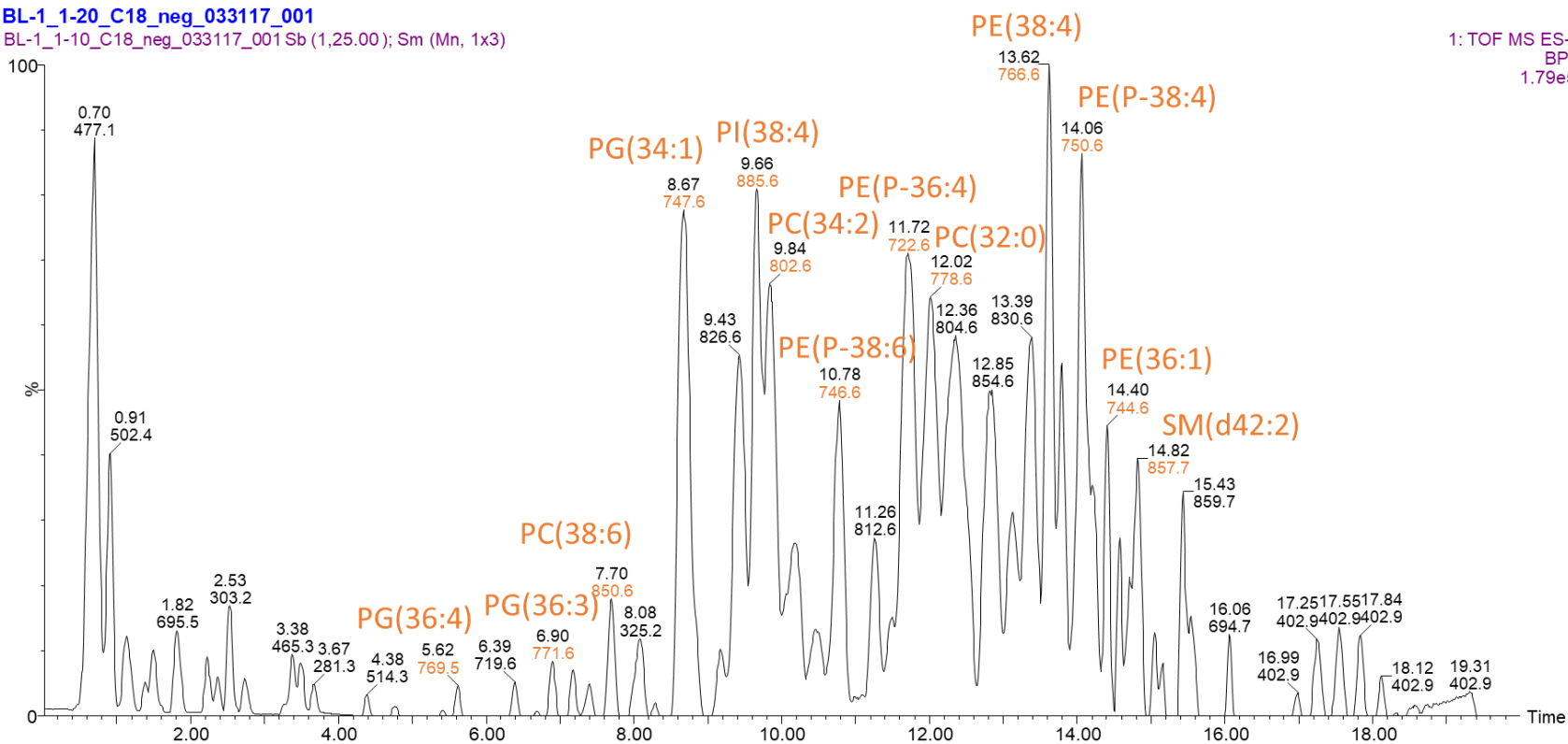


Supplemental Figure S1: HPLC-MS^E Base Peak Chromatogram for a lipid extract from MLN before exposure to irradiation in positive ion mode.

BL-1_1-20_C18_neg_033117_001

BL-1_1-10_C18_neg_033117_001 Sb (1,25.00); Sm (Mn, 1x3)

1: TOF MS ES-
BPI
1.79e5



Supplemental Figure S2: HPLC-MS^E Base Peak Chromatogram for a lipid extract from MLN before exposure to irradiation in negative ion mode.

Supplementary Table 2: Lipids significantly changed by radiation in the Mesenteric Lymph Node in negative ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(min)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
1	279.2332	279.2329	1.1	FA(18:2)	C18H31O2	[M-H]-	2.73	0.036	2.7	Day 4	405.1	168.0	1081.5	20.8
2	281.2494	281.2486	2.8	FA(18:1)	C18H33O2	[M-H]-	3.68	0.016	4.1	Day 4	353.9	112.3	1459.2	423.6
3	297.2444	297.2435	3.0	FA(18:1(OH))	C18H33O3	[M-H]-	1.22	0.000	13.4	Day 4	9.1	1.3	121.7	17.3
4	299.2602	299.2591	3.7	FA(18:0(OH))	C18H35O3	[M-H]-	1.53	0.006	95.2	Day 4	5.1	2.9	480.8	462.3
5	303.234	303.2329	3.6	FA(20:4)	C20H31O2	[M-H]-	2.53	0.033	2.5	Baseline	1015.2	247.0	398.4	152.5
6	329.2489	329.2486	0.9	FA(22:5)	C22H33O2	[M-H]-	2.66	0.007	27.2	Baseline	40.2	17.5	1.5	1.2
7	331.2648	331.2642	1.8	FA(22:4)	C22H35O2	[M-H]-	3.47	0.020	16.5	Baseline	54.3	21.4	3.3	2.5
8	464.3164	464.3146	3.9	LPE(P-18:0)	C23H47NO6P	[M-H]-	2.78	0.004	2.0	Day 4	329.5	53.1	673.0	40.3
9	480.312	480.3095	5.2	LPE(18:0)	C23H47NO7P	[M-H]-	1.50	0.031	1.7	Day 4	528.7	44.9	904.8	181.9
10	494.3274	494.3252	4.5	LPE(19:0)	C24H49NO7P	[M-H]-	1.82	0.026	4.1	Day 4	40.7	6.3	168.1	92.4
11	500.2803	500.2782	4.2	LPE(20:4)	C25H43NO7P	[M-H]-	1.17	0.019	3.4	Baseline	633.5	274.2	188.6	16.1
12	504.3119	504.3095	4.8	LPE(20:2)	C25H47NO7P	[M-H]-	1.15	0.033	2.8	Baseline	170.6	51.1	61.7	16.1
13	508.3427	508.3408	3.7	LPE(20:0)	C25H51NO7P	[M-H]-	2.23	0.016	1.8	Day 4	401.8	52.2	706.7	107.0
14	528.3108	528.3095	2.5	LPE(22:4)	C27H47NO7P	[M-H]-	1.11	0.003	97.2	Baseline	148.7	90.4	1.5	1.2
15	540.3332	540.3307	4.6	LPC(16:0)	C25H51NO9P	[M+Formate]-	1.38	0.033	2.1	Baseline	476.9	109.6	226.0	53.2
16	540.3335	540.3307	5.2	LPC(16:0)	C25H51NO9P	[M+Formate]-	1.50	0.024	2.0	Day 4	1538.8	234.2	3100.1	727.0
17	554.3486	554.3463	4.1	LPC(17:0)	C26H53NO9P	[M+Formate]-	1.82	0.028	4.1	Day 4	197.8	25.1	813.3	460.4
18	568.3653	568.362	5.8	LPC(18:0)	C27H55NO9P	[M+Formate]-	2.22	0.025	1.8	Day 4	1638.8	157.9	3027.5	696.6
19	588.3335	588.3307	4.8	LPC(20:4)	C29H51NO9P	[M+Formate]-	1.11	0.010	26.3	Baseline	885.8	457.9	33.7	23.9
20	590.3476	590.3463	2.2	LPC(20:3)	C29H53NO9P	[M+Formate]-	1.29	0.001	NC*	Baseline	36.8	22.8	n.d.	NC*
21	662.5749	662.5729	3.0	Cer(d40:3)	C41H76NO5	[M+Formate]-	14.41	0.048	9.7	Baseline	123.3	2.7	12.7	18.0
22	674.5164	674.513	5.0	PE(P-32:0)	C37H73NO7P	[M-H]-	13.93	0.016	1.7	Baseline	532.9	42.3	307.5	55.6
23	684.462	684.461	1.5	PE(32:3)	C37H67NO8P	[M-H]-	0.69	0.033	13.3	Day 4	4024.9	1010.7	53361.4	44852.3
24	690.6054	690.6042	1.7	Cer(d42:3)	C43H80NO5	[M+Formate]-	15.04	0.030	2.8	Baseline	2524.5	311.3	899.5	463.1
25	698.5151	698.513	3.0	PE(P-34:2)	C39H73NO7P	[M-H]-	12.38	0.000	2.5	Baseline	2444.5	209.5	975.8	20.9
26	704.5257	704.5236	3.0	PE(33:0)	C38H75NO8P	[M-H]-	10.37	0.000	214.3	Baseline	90.0	23.8	0.4	0.6
27	704.5612	704.5599	1.8	PE(O-34:0)	C39H79NO7P	[M-H]-	14.78	0.007	6.4	Baseline	177.1	39.2	27.7	14.7

Supplementary Table 2: Lipids significantly changed by radiation in the Mesenteric Lymph Node in negative ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(min)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
28	716.5271	716.5236	4.9	PE(34:1)	C39H75NO8P	[M-H]-	9.22	0.046	16.2	Baseline	313.5	142.7	19.4	27.4
29	720.4989	720.4973	2.2	PE(P-36:5)	C41H71NO7P	[M-H]-	9.59	0.019	5.0	Baseline	946.2	209.5	188.3	95.0
30	723.5017	723.497	6.5	PA(38:4)	C41H72O8P	[M-H]-	10.09	0.032	4.1	Baseline	147.9	14.6	36.1	22.1
31	724.5316	724.5286	4.1	PE(P-36:3)	C41H75NO7P	[M-H]-	12.38	0.006	4.3	Baseline	3105.7	423.6	726.9	290.6
32	730.5783	730.5756	3.7	PE(P-36:0)	C41H81NO7P	[M-H]-	13.85	0.037	3.8	Baseline	512.0	130.7	133.4	63.9
33	734.5364	734.5341	3.1	PC(P-30:0)	C39H77NO9P	[M+Formate]-	9.86	0.026	4.1	Baseline	920.5	236.0	224.1	93.8
34	742.5435	742.5392	5.8	PE(36:2)	C41H77NO8P	[M-H]-	13.79	0.049	1.5	Day 4	14506.0	1071.9	21411.6	3717.8
35	744.565	744.5631	2.6	HexCer(d34:1)	C41H78NO10	[M+Formate]-	9.87	0.011	3.4	Baseline	7124.5	1110.9	2080.1	662.3
36	746.5151	746.513	2.8	PE(P-38:6)	C43H73NO7P	[M-H]-	9.52	0.021	2.5	Baseline	879.8	33.5	346.6	116.2
37	747.5204	747.5181	3.1	PG(34:1)	C40H76O10P	[M-H]-	9.97	0.002	4.0	Baseline	2555.2	365.9	639.0	166.9
38	748.5315	748.5286	3.9	PE(P-38:5)	C43H75NO7P	[M-H]-	11.39	0.004	6.3	Baseline	2763.7	192.9	437.5	183.5
39	748.532	748.5286	4.5	PE(P-38:5)	C43H75NO7P	[M-H]-	13.25	0.041	1.8	Baseline	3851.8	785.2	2116.2	361.6
40	749.5846	749.5814	4.3	SM(d34:0)	C40H82N2O8P	[M+Formate]-	9.82	0.038	2.2	Day 4	1210.2	188.8	2697.5	823.8
41	750.5466	750.5443	3.1	PE(P-38:4)	C43H77NO7P	[M-H]-	12.56	0.004	6.2	Baseline	5549.8	978.6	891.2	387.6
42	752.5638	752.5599	5.2	PE(P-38:3)	C43H79NO7P	[M-H]-	13.95	0.021	3.2	Baseline	3400.7	1022.1	1066.9	269.9
43	762.5108	762.5079	3.8	PE(38:6)	C43H73NO8P	[M-H]-	8.33	0.008	3.2	Baseline	957.5	60.8	298.0	98.6
44	764.5248	764.5236	1.6	PE(38:5)	C43H75NO8P	[M-H]-	10.96	0.020	72.4	Baseline	359.1	341.5	5.0	3.7
45	764.526	764.5236	3.1	PE(38:5)	C43H75NO8P	[M-H]-	11.42	0.026	3.8	Baseline	1401.3	292.6	369.3	180.1
46	768.5566	768.5549	2.2	PE(38:3)	C43H79NO8P	[M-H]-	10.76	0.012	4.5	Baseline	288.7	85.0	64.3	19.7
47	768.5584	768.5549	4.6	PE(38:3)	C43H79NO8P	[M-H]-	14.27	0.034	20.1	Baseline	247.6	121.2	12.3	16.1
48	769.5045	769.5025	2.6	PG(36:4)	C42H74O10P	[M-H]-	6.67	0.020	25.8	Baseline	141.4	43.8	5.5	7.7
49	772.5884	772.5862	2.8	PE(38:1)	C43H83NO8P	[M-H]-	13.43	0.028	2.7	Baseline	448.8	127.1	164.0	43.4
50	773.5354	773.5338	2.1	PG(36:2)	C42H78O10P	[M-H]-	10.53	0.038	17.5	Baseline	168.8	57.3	9.6	7.5
51	775.6002	775.5971	4.0	SM(d36:1)	C42H84N2O8P	[M+Formate]-	11.95	0.006	2.0	Day 4	2342.0	474.3	4739.2	167.9
52	776.5621	776.5599	2.8	PE(P-40:5)	C45H79NO7P	[M-H]-	14.36	0.036	1.6	Baseline	1698.6	180.1	1092.5	198.0
53	776.5631	776.5599	4.1	PE(P-40:5)	C45H79NO7P	[M-H]-	12.79	0.040	15.5	Baseline	260.1	56.7	16.8	20.0
54	777.5489	777.544	6.3	PA(42:5)	C45H78O8P	[M-H]-	9.53	0.040	5.2	Baseline	349.3	160.4	67.4	45.8
55	790.5414	790.5392	2.8	PE(40:6)	C45H77NO8P	[M-H]-	11.05	0.000	466.3	Baseline	309.0	81.4	0.7	0.9
56	790.5418	790.5392	3.3	PE(40:6)	C45H77NO8P	[M-H]-	7.72	0.032	3.0	Baseline	388.2	67.2	127.8	52.3

Supplementary Table 2: Lipids significantly changed by radiation in the Mesenteric Lymph Node in negative ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(min)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
57	790.6001	790.5967	4.3	PC(P-34:0)	C43H85NO9P	[M+Formate]-	13.85	0.021	2.1	Baseline	5758.1	1467.2	2729.3	84.9
58	796.5162	796.5134	3.5	PC(34:5)	C43H75NO10P	[M+Formate]-	8.15	0.006	49.7	Baseline	110.7	12.2	2.2	3.2
59	800.5469	800.5447	2.7	PC(34:3)	C43H79NO10P	[M+Formate]-	7.56	0.030	3.2	Baseline	391.3	147.1	121.3	29.7
60	800.5481	800.5447	4.2	PC(34:3)	C43H79NO10P	[M+Formate]-	7.99	0.033	24.2	Baseline	578.0	51.9	23.9	27.8
61	803.6309	803.6284	3.1	SM(d38:1)	C44H88N2O8P	[M+Formate]-	14.14	0.017	2.9	Day 4	654.1	266.0	1880.0	278.5
62	810.53	810.529	1.2	PS(38:4)	C44H77NO10P	[M-H]-	13.79	0.046	2.9	Day 4	130.5	16.9	383.8	164.4
63	818.5929	818.5916	1.6	PS(38:0)	C44H85NO10P	[M-H]-	13.75	0.044	2.0	Baseline	413.7	34.1	205.2	64.0
64	824.5464	824.5447	2.1	PC(36:5)	C45H79NO10P	[M+Formate]-	6.61	0.006	58.5	Baseline	80.5	39.9	1.4	1.9
65	824.5476	824.5447	3.5	PC(36:5)	C45H79NO10P	[M+Formate]-	7.77	0.010	2.9	Baseline	961.4	206.0	330.3	81.8
66	828.5787	828.576	3.3	PC(36:3)	C45H83NO10P	[M+Formate]-	10.74	0.033	1.9	Baseline	6971.9	1513.7	3710.0	562.1
67	831.6623	831.6597	3.1	SM(d40:1)	C46H92N2O8P	[M+Formate]-	14.86	0.020	1.9	Day 4	5236.9	855.3	9989.9	1875.0
68	838.5643	838.5603	4.8	PS(40:4)	C46H81NO10P	[M-H]-	11.82	0.033	16.5	Baseline	137.4	49.6	8.3	11.7
69	838.6003	838.5967	4.3	PC(P-38:4)	C47H85NO9P	[M+Formate]-	13.80	0.037	3.1	Day 4	406.8	258.0	1256.9	153.2
70	840.5782	840.576	2.6	PS(40:3)	C46H83NO10P	[M-H]-	11.06	0.010	3.3	Baseline	902.7	221.7	274.0	69.1
71	850.5629	850.5604	2.9	PC(38:6)	C47H81NO10P	[M+Formate]-	7.73	0.003	1.6	Baseline	5060.1	477.6	3107.8	128.8
72	852.5773	852.576	1.5	PC(38:5)	C47H83NO10P	[M+Formate]-	10.18	0.019	123.8	Baseline	78.2	84.1	0.6	0.9
73	852.5778	852.576	2.1	PC(38:5)	C47H83NO10P	[M+Formate]-	10.57	0.046	5.5	Baseline	873.2	289.0	159.5	94.3
74	852.6601	852.657	3.6	HexCer(d42:3)	C49H90NO10	[M+Formate]-	14.50	0.009	86.2	Baseline	569.6	107.7	6.6	9.3
75	854.593	854.5917	1.5	PC(38:4)	C47H85NO10P	[M+Formate]-	10.66	0.008	7.7	Baseline	2036.5	258.3	265.7	128.2
76	854.6758	854.6727	3.6	HexCer(d42:2)	C49H92NO10	[M+Formate]-	15.02	0.025	6.6	Baseline	1823.7	429.0	275.3	223.7
77	859.5377	859.5342	4.1	PI(36:3)	C45H80O13P	[M-H]-	8.10	0.009	35.0	Baseline	67.6	18.0	1.9	2.7
78	859.6931	859.691	2.4	SM(d42:1)	C48H96N2O8P	[M+Formate]-	15.43	0.018	1.4	Day 4	7442.3	531.8	10415.9	1053.8
79	862.6552	862.6543	1.0	PC(38:0)	C47H93NO10P	[M+Formate]-	14.76	0.045	8.9	Baseline	25.5	12.2	2.9	4.0
80	876.5767	876.576	0.8	PC(40:7)	C49H83NO10P	[M+Formate]-	8.33	0.010	45.7	Baseline	138.0	43.9	3.0	4.3
81	878.5943	878.5917	3.0	PC(40:6)	C49H85NO10P	[M+Formate]-	10.21	0.000	14.7	Baseline	968.9	190.0	65.9	12.4
82	880.6109	880.6073	4.1	PC(40:5)	C49H87NO10P	[M+Formate]-	13.05	0.024	3.0	Baseline	1471.4	480.6	491.0	162.7
83	882.6244	882.623	1.6	PC(40:4)	C49H89NO10P	[M+Formate]-	13.87	0.001	NC*	Baseline	58.4	30.9	n.d.	NC*
84	883.6933	883.691	2.6	SM(d44:3)	C50H96N2O8P	[M+Formate]-	14.89	0.000	NC*	Baseline	54.6	23.5	n.d.	NC*
85	929.552	929.5526	0.6	PIP(P-36:0)	C45H87O15P2	[M-H]-	13.31	0.035	19.9	Baseline	205.8	120.4	10.3	14.6

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	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(min)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
86	979.5673	979.5682	0.9	PIP(P-40:3)	C49H89O15P2	[M-H]-	10.85	0.001	355.4	Baseline	225.6	168.5	0.6	0.9
87	1447.9686	1447.9649	2.6	CL(72:8)	C81H141O17P2	[M-H]-	16.34	0.027	23.9	Baseline	300.6	58.1	12.6	17.8

Supplementary Table 2: Lipids significantly changed by radiation in the Mesenteric Lymph Node in negative ion mode HPLC-MSE. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, SD=standard deviation n=3.*not calculable, under limit of detection at Day 4. n.d.= not detected

Supplementary Table 3: Top 100 (according to p-value) Lipids significantly changed by radiation in the Mesenteric Lymph Node in positive ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(mi n)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
1	467.4095	467.4095	0	MG(26:2)	C29H55O4	[M+H] ⁺	15.96	0.0058	17.73	Day 4	21.5	13.1	381.5	182.2
2	520.3413	520.3398	2.9	LPC(18:2)	C26H51NO7P	[M+H] ⁺	1.15	0.0057	2.14	Baseline	7198.8	986.9	3356.1	485.1
3	544.3418	544.3398	3.7	LPC(20:4)	C28H51NO7P	[M+H] ⁺	1.12	0.005	7.43	Baseline	6073.8	2132.7	817	339.7
4	546.3598	546.3554	8.1	LPC(20:3)	C28H53NO7P	[M+H] ⁺	1.28	0.0034	4.72	Baseline	839.9	263.8	178	27.3
5	738.5264	738.5279	2	PG(32:1)	C38H77NO10P	[M+NH4] ⁺	9.86	0.005	21.11	Baseline	386.6	189.1	18.3	13.2
6	746.508	746.5095	2	PE(P-36:4)	C41H74NO7PNa	[M+Na] ⁺	14.01	0.0066	2.28	Baseline	915.4	129.2	401.8	66
7	774.5421	774.5408	1.7	PE(P-38:4)	C43H78NO7PNa	[M+Na] ⁺	13.82	0.0084	1.68	Baseline	2696.2	400.9	1600.9	54
8	832.6444	832.6449	0.6	TG(50:10)	C53H86NO6	[M+NH4] ⁺	14.49	0.0011	2.8	Baseline	277.7	39.4	99.2	10.1
9 ^s	834.601	834.6008	0.2	PC(40:6)\$	C48H85NO8P	[M+H] ⁺	10.19	0.0093	4.73	Baseline	50218	9839	10622	4945.2
		834.5983	3.2	PC(38:3)\$	C46H86NO8PNa	[M+Na] ⁺								
10 ^s	836.6136	836.6164	3.3	PC(40:5)\$	C48H87NO8P	[M+H] ⁺	11.53	0.0071	11.69	Baseline	4205.3	1580.3	359.8	215.3
		836.614	0.5	PC(38:2)\$	C46H88NO8PNa	[M+Na] ⁺								
11	843.7775	843.7776	0.1	DG(50:0)	C53H104O5Na	[M+Na] ⁺	18.5	0.0091	17.28	Day 4	267.1	237.9	4616.1	1409.4
12	850.5721	850.5709	1.4	SHexCer(t38:2)	C44H84NO12S	[M+H] ⁺	13.79	0.0081	2.15	Baseline	1376.1	214.4	638.9	97.5
13	852.8022	852.8014	0.9	TG(50:0)	C53H106NO6	[M+NH4] ⁺	18.1	0.0011	17.71	Day 4	1917.8	604.6	33970	12147.5
14	859.7754	859.7749	0.6	TG(52:2)	C55H103O6	[M+H] ⁺	17.79	0.0029	1.97	Day 4	3582.7	503.6	7048.7	145
15	864.8019	864.8014	0.6	TG(51:1)	C54H106NO6	[M+NH4] ⁺	17.93	0.0021	2.53	Day 4	29830	4149.2	75609	8878.4
16	871.808	871.8089	1	DG(52:0)	C55H108O5Na	[M+Na] ⁺	18.76	0.0003	54.12	Day 4	40	13.3	2166.7	676.1
17	873.7295	873.7306	1.3	DG(53:6)	C56H98O5Na	[M+Na] ⁺	18.09	0.0013	16.96	Day 4	33.7	7.8	572.3	265.3
18	874.7848	874.7858	1.1	TG(52:3)	C55H104NO6	[M+NH4] ⁺	17.91	0.0042	2.19	Day 4	530.3	91.1	1161.3	113
19	877.8735	877.8735	0	CE(34:0)	C61H113O2	[M+H] ⁺	18.99	0.0004	236	Day 4	0.9	0.8	224	110.8
20	880.8342	880.8327	1.7	TG(52:0)	C55H110NO6	[M+NH4] ⁺	18.37	0.0007	37.1	Day 4	2333.1	816	86566	26373.8
21	888.8367	888.8378	1.2	DG(54:3)	C57H110NO5	[M+NH4] ⁺	18.24	0.0071	5.44	Day 4	3118.8	1420	16975	3380.1
22	892.7393	892.7388	0.6	TG(54:8)	C57H98NO6	[M+NH4] ⁺	16.62	0.0006	1.95	Day 4	2037.7	74.2	3971.9	351.4

Supplementary Table 3: Top 100 (according to p-value) Lipids significantly changed by radiation in the Mesenteric Lymph Node in positive ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(mi n)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
23	892.8316	892.8327	1.2	TG(53:1)	C56H110NO6	[M+NH4] +	18.22	0.0018	3.74	Day 4	14351	3717.1	53644	2741.2
24	897.823	897.8245	1.7	DG(54:1)	C57H110O5Na	[M+Na]+	18.74	0.0049	9.71	Day 4	594	197.1	5765	2010.7
25 ^s	899.8088	899.8062	2.9	TG(55:3)\$	C58H107O6	[M+H]+	18.49	0.004	7.01	Day 4	185	75.6	1296.2	91.6
		899.8038	5.6	TG(53:0)\$	C56H108O6Na	[M+Na]+								
26	901.7641	901.7619	2.4	DG(55:6)	C58H102O5Na	[M+Na]+	18.36	0.0014	6.83	Day 4	426.4	84.4	2913.2	726.7
27 ^s	905.7551	905.7593	4.6	TG(56:7)\$	C59H101O6	[M+H]+	17.11	0.0049	2.66	Day 4	896.1	74	2388.1	543.9
		905.7568	1.9	TG(54:4)\$	C57H102O6Na	[M+Na]+								
28	908.7711	908.7701	1.1	TG(55:7)	C58H102NO6	[M+NH4] +	17.31	0.0095	3.01	Day 4	115.4	35.6	347.8	60.6
29	908.8644	908.864	0.4	TG(54:0)	C57H114NO6	[M+NH4] +	18.62	0.0023	28.97	Day 4	1511.5	666.3	43780	16823.6
30	918.8474	918.8484	1.1	TG(55:2)	C58H112NO6	[M+NH4] +	18.2	0.0064	2.88	Day 4	15569	2559.9	44783	9662.2
31	920.8627	920.864	1.4	TG(55:1)	C58H114NO6	[M+NH4] +	18.48	0.0053	3.96	Day 4	4052.1	1067.2	16060	3601.2
32	924.8024	924.8014	1.1	TG(56:6)	C59H106NO6	[M+NH4] +	17.4	0.0029	2.04	Day 4	72229	4540.3	147413	19574
33	926.8184	926.8171	1.4	TG(56:5)	C59H108NO6	[M+NH4] +	17.72	0.0048	2.53	Day 4	24903	5645.4	62894	4645.4
34	934.8805	934.8797	0.9	TG(56:1)	C59H116NO6	[M+NH4] +	18.61	0.0077	10.11	Day 4	6931.4	3058.1	70065	31626.8
35 ^s	941.8483	941.8532	5.2	TG(58:3)\$	C61H113O6	[M+H]+	18.86	0.0055	7.11	Day 4	197	23.8	1400.5	670.2
		941.8507	2.5	TG(56:0)\$	C59H114O6Na	[M+Na]+								
36	944.7695	944.7701	0.6	TG(58:10)	C61H102NO6	[M+NH4] +	16.88	0.0025	4.17	Day 4	372.8	75.3	1555.4	289.9
37	952.8324	952.8327	0.3	TG(58:6)	C61H110NO6	[M+NH4] +	17.89	0.008	3.37	Day 4	1597.3	595.8	5376.6	505.2
38	952.833	952.8327	0.3	TG(58:6)	C61H110NO6	[M+NH4] +	17.69	0.0054	2.55	Day 4	26687	5514.8	68029	8600.1
39	954.8479	954.8484	0.5	TG(58:5)	C61H112NO6	[M+NH4] +	17.92	0.0019	3.61	Day 4	9689.9	2099.3	34972	4124.4
40	964.922	964.9266	4.8	TG(58:0)	C61H122NO6	[M+NH4] +	18.38	0.0089	20.64	Day 4	33.3	19.5	688.3	323.1
41	968.7685	968.7701	1.7	TG(60:12)	C63H102NO6	[M+NH4] +	16.58	0.0039	9.51	Day 4	99.7	38.9	948.8	254.5
42	970.7841	970.7858	1.8	TG(60:11)	C63H104NO6	[M+NH4] +	16.88	0.0093	5.17	Day 4	426.9	174.9	2208.8	435.2
43	972.8004	972.8014	1	TG(60:10)	C63H106NO6	[M+NH4] +	17.22	0.0016	9.9	Day 4	11.8	5.6	116.6	8.9

Supplementary Table 3: Top 100 (according to p-value) Lipids significantly changed by radiation in the Mesenteric Lymph Node in positive ion mode HPLC-MS^E. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3.

	Input Mass	Matched Mass	ppm	Name	Formula	Ion	tR(mi n)	Anova (p)	Max Fold Change	Highest Mean	Baseline		Day 4	
											Mean	SD	Mean	SD
44	974.8151	974.8171	2.1	TG(60:9)	C63H108NO6	[M+NH4] +	17.33	0.0046	4.12	Day 4	730.8	227.5	3010	502.1
45	976.8311	976.8327	1.6	TG(60:8)	C63H110NO6	[M+NH4] +	17.59	0.0094	5.36	Day 4	362.8	142.4	1944.1	701.6
46	976.9246	976.9266	2	TG(59:1)	C62H122NO6	[M+NH4] +	18.95	0.0087	19.19	Day 4	185.6	69.7	3560	2325.6
47	977.7564	977.7568	0.4	TG(60:10)	C63H102O6Na	[M+Na] ⁺	17.01	0.0087	3.34	Day 4	1155.6	366.7	3856.7	562
48	980.8622	980.864	1.8	TG(60:6)	C63H114NO6	[M+NH4] +	17.94	0.0053	4.39	Day 4	1673.3	403	7354	1974.1
49	982.8777	982.8797	2	TG(60:5)	C63H116NO6	[M+NH4] +	18.19	0.007	8.26	Day 4	654.4	223.3	5402.6	2535.4
50	983.8379	983.8402	2.3	DG(61:7)	C64H112O5Na	[M+Na] ⁺	18.83	0.0044	11.67	Day 4	150.2	42.6	1752.8	829.9
51	996.8913	996.8953	4	TG(61:5)	C64H118NO6	[M+NH4] +	17.7	0.0011	2.24	Day 4	201.3	17.3	451.8	49.7
52	1010.906 8	1010.911	4.2	TG(62:5)	C65H120NO6	[M+NH4] +	17.72	0.0011	2.88	Day 4	240.3	40.6	691.8	48.3
53	1010.907 6	1010.911	3.4	TG(62:5)	C65H120NO6	[M+NH4] +	18.54	0.0054	16.73	Day 4	132.5	55.5	2215.9	1306.3

Supplementary Table 3: Top 100 (according to p-value) Lipids significantly changed by radiation in the Mesenteric Lymph Node in positive ion mode HPLC-MSE. NHP were exposed to 12 Gy PBI/BM2.5. Lipids assayed at both time points: Day 0 (baseline), n=3 and Day 4, n=3. SD=standard deviation \$ Isobaric ions which co-elute and were not distinguished

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
EIF2 Signaling	7.94E-31	-4.8	ACTB,ACTG2,AGO3,EIF1AY,EIF2A,EIF2S1,EIF2S2,EIF2S3,EIF3B,EIF3C,EIF3D,EIF3E,EIF3F,EIF3G,EIF3H,EIF3I,EIF3J,EIF3K,EIF3L,EIF3M,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF5,FAU,HRAS,MAP2K1,MAPK1,MAPK3,PAIP1,PIK3C2B,PIK3CA,PPP1CA,PPP1CB,PPP1CC,PTBP1,RPL10,RPL10A,RPL12,RPL13,RPL13A,RPL18A,RPL22,RPL23,RPL24,RPL26L1,RPL27,RPL27A,RPL28,RPL31,RPL32,RPL35,RPL4,RPL7,RPL7A,RPL8,RPLP1,RPLP2,RPS10,RPS11,RPS13,RPS14,RPS15,RPS16,RPS19,RPS20,RPS23,RPS28,RPS4Y1,RPS5,RPS6,RPS7,RPS9,SHC1
Regulation of eIF4 and p70S6K Signaling	2.00E-20	0.0	AGO3,EIF1AY,EIF2A,EIF2S1,EIF2S2,EIF2S3,EIF3B,EIF3C,EIF3D,EIF3E,EIF3F,EIF3G,EIF3H,EIF3I,EIF3J,EIF3K,EIF3L,EIF3M,EIF4A3,EIF4E,EIF4G1,EIF4G2,FAU,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK14,MAPK3,PAIP1,PIK3C2B,PIK3CA,PPP2R5A,PPP2R5D,RPS10,RPS11,RPS13,RPS14,RPS15,RPS16,RPS19,RPS20,RPS23,RPS28,RPS4Y1,RPS5,RPS6,RPS7,RPS9,SHC1
Protein Ubiquitination Pathway	1.00E-18		CBL,CRYAB,CUL1,DNAJB6,DNAJC1,DNAJC14,DNAJC9,ELOC,HLAB,HSP90AB1,HSPA12A,HSPA4,HSPA9,HSPB1,HSPD1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMB10,PSMB2,PSMB3,PSMB4,PSMB8,PSMB9,PSMC3,PSMC4,PSMC5,PSMD1,PSMD10,PSMD11,PSMD14,PSMD2,PSMD4,PSMD5,PSMD6,PSMD7,PSME1,PSME2,SGUT1,THOP1,UBA1,UBE2D2,UBE2H,UBE2L3,UBE2N,UBE4A,UBE4B,UCHL3,UCHL5,USO1,USP10,USP13,USP14,USP2,USP39,USP4,USP43,USP45,USP47,USP5,USP7
mTOR Signaling	1.26E-13	-2.4	EIF3B,EIF3C,EIF3D,EIF3E,EIF3F,EIF3G,EIF3H,EIF3I,EIF3J,EIF3K,EIF3L,EIF3M,EIF4A3,EIF4E,EIF4G1,EIF4G2,FAU,HRAS,MAPK1,MAPK3,PIK3C2B,PIK3CA,PPP2R5A,PPP2R5D,PRKAA1,PRKCB,PRKCD,PRKCH,RHOG,RHOT1,RHOT2,RPS10,RPS11,RPS13,RPS14,RPS15,RPS16,RPS19,RPS20,RPS23,RPS28,RPS4Y1,RPS5,RPS6,RPS6KA3,RPS6KA5,RPS7,RPS9
Systemic Lupus Erythematosus Signaling	1.00E-12		C5,C6,C8B,C8G,C9,CAMK4,CBL,CD247,CD2BP2,CD3D,CD3E,EFTUD2,HLAB,HNRNPA2B1,HNRNPC,HRAS,KNG1,LSM12,LSM2,LSM4,LYN,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PPIH,PRPF19,PRPF31,PRPF38A,PRPF40A,PRPF4B,PRPF8,PTPN6,SF3B4,SNRNP200,SNRNP35,SNRNP40,SNRNP70,SNRPA,SNRPA1,SNRPB2,SNRPD1,SNRPD2,SNRPD3,SNRPE,SNRPF,SNRPN,SNU13
Acute Phase Response Signaling	1.26E-12	1.7	A2M,AGT,AMBP,APCS,APOA2,C3,C4A/C4B,C4BPA,C4BPB,C5,C9,CP,CRP,F2,FGB,FGG,FTL,HNRNPK,HP,HPX,HRAS,IKBKB,ITIH2,ITIH3,ITIH4,LBP,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,ORM1,PIK3CA,PLG,SAA1,SERPINA1,SERPINA3,SERPIND1,SERPINF2,SERPING1,SHC1
Complement System	1.82E-10	1.7	C1QBP,C1QC,C3,C4A/C4B,C4BPA,C4BPB,C5,C5AR1,C6,C8B,C8G,C9,CFD,CR1,CR2,MASP1,SERPING1

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
Actin Cytoskeleton Signaling	2.63E-10	-1.1	ACTB,ACTG2,ACTR2,APC2,ARHGEF12,ARHGEF6,ARHGEF7,ARPC1B,ARPC2,CFL1,CFL2,CSK,CYFIP2,DIAPH1,EZR,F2,FGF2,FLNA,GNA13,HRAS,ITGA5,ITGB1,KNG1,LBP,MAP2K1,MAPK1,MAPK3,MSN,MYH11,MYH6,NCKAP1L,PAK2,PFN1,PFN2,PIK3C2B,PIK3CA,PIP4K2A,PPP1CB,Ppp1r12b,RAC2,RAC3,SHC1,VCL,WAS,WASF2,WASL
Actin Cytoskeleton Signaling	2.63E-10	-1.1	ACTB,ACTG2,ACTR2,APC2,ARHGEF12,ARHGEF6,ARHGEF7,ARPC1B,ARPC2,CFL1,CFL2,CSK,CYFIP2,DIAPH1,EZR,F2,FGF2,FLNA,GNA13,HRAS,ITGA5,ITGB1,KNG1,LBP,MAP2K1,MAPK1,MAPK3,MSN,MYH11,MYH6,NCKAP1L,PAK2,PFN1,PFN2,PIK3C2B,PIK3CA,PIP4K2A,PPP1CB,Ppp1r12b,RAC2,RAC3,SHC1,VCL,WAS,WASF2,WASL
Intrinsic Prothrombin Activation Pathway	3.31E-09	2.5	COL18A1,COL1A1,COL1A2,COL2A1,COL3A1,F12,F13A1,F2,F9,FGB,FGG,KNG1,PROS1,SERPINC1
CD28 Signaling in T Helper Cells	4.07E-09	-3.1	ACTR2,ARPC1B,ARPC2,CAMK4,CD247,CD3D,CD3E,CSK,FYN,GRAP2,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,IKBKB,MAP2K1,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PPP3CA,PPP3CB,PTPN6,SYK,WAS,ZAP70
Calcium-induced T Lymphocyte Apoptosis	4.68E-09	-4.5	ATP2A3,CAMK4,CD247,CD3D,CD3E,EP300,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,PLCG1,PPP3CA,PPP3CB,PRKCB,PRKCD,PRKCH,ZAP70
Coagulation System	7.08E-09	-0.3	A2M,F12,F13A1,F2,F9,FGB,FGG,KNG1,PLG,PROS1,SERPINA1,SERPINA5,SERPINC1,SERPIND1,SERPINF2
RAN Signaling	2.34E-08		CSE1L,IPO5,KPNA4,KPNB1,RAN,RANBP1,RANBP2,RANGAP1,TNPO1,XPO1
Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	3.80E-08	-3.7	ACTB,ACTG2,ACTR2,ARF6,ARPC1B,ARPC2,CBL,EZR,FYB1,FYN,LYN,MAPK1,MAPK3,MYO5A,NCF1,PLCG1,PRKCB,PRKCD,PRKCH,PTK2B,RAC2,RAC3,SYK,WAS
Agrin Interactions at Neuromuscular Junction	6.31E-08	-0.7	ACTB,ACTG2,AGRN,ARHGEF6,ARHGEF7,ERBB3,GABPA,HRAS,ITGA1,ITGA5,ITGA6,ITGB1,LAMB1,LAMC1,MAPK1,MAPK3,PAK2,PKLR,RAC2,RAC3
Integrin Signaling	6.92E-08	-1.3	ACTB,ACTG2,ACTR2,ARF6,ARHGEF7,ARPC1B,ARPC2,CAV1,FYN,HRAS,ITGA1,ITGA5,ITGA6,ITGAV,ITGB1,ITGB4,MAP2K1,MAPK1,MAPK3,NEDD9,PAK2,PFN1,PFN2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PPP1CB,Ppp1r12b,RAC2,RAC3,RHOG,RHOT1,RHOT2,SHC1,SPAN3,VCL,WAS,WASL,WIPF1

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
PKC θ Signaling in T Lymphocytes	7.41E-08	-3.9	CD247,CD3D,CD3E,FYN,GRAP2,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,HRAS,IKBKB,MAP3K6,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PPP3CA,PPP3CB,RAC2,RAC3,ZAP70
Nur77 Signaling in T Lymphocytes	1.20E-07		CAMK4,CASP3,CD247,CD3D,CD3E,EP300,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,MAP2K5,PPP3CA,PPP3CB,SIN3A
Role of NFAT in Regulation of the Immune Response	1.86E-07	-4.7	BTK,CAMK4,CD247,CD3D,CD3E,ELP1,FYN,GNA13,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,HRAS,IKBKB,LYN,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,RACK1,SYK,XPO1,ZAP70
Antigen Presentation Pathway	2.24E-07		CD74,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DPA1,HLA-DQA1,HLA-DRA,HLA-DRB5,NLRC5,PSMB8,PSMB9,TAPBP
Phospholipase C Signaling	3.16E-07	-4.0	ADCY10,ARHGEF12,ARHGEF2,ARHGEF6,ARHGEF7,BTK,CAMK4,CD247,CD3D,CD3E,EP300,FYN,GNA13,GRAP2,HRAS,ITGA5,ITGB1,LYN,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PLCB3,PLCG1,PLCG2,PPP1CB,PPP1R12B,PPP3CA,PPP3CB,PRKCB,PRKCD,PRKCH,ACK1,RHOG,RHOT1,RHOT2,RPS6KA3,SHC1,SYK,ZAP70
tRNA Charging	3.24E-07		CARS1,DARS1,DARS2,EPRS1,FARSA,FARSB,HARS2,IARS1,MARS1,NARS1,QARS1,RARS1,VAR1,YARS1
Regulation of Actin-based Motility by Rho	4.79E-07	-2.4	ACTB,ACTG2,ACTR2,ARPC1B,ARPC2,CFL1,ITGA5,ITGB1,PAK2,PFN1,PFN2,PIP4K2A,PPP1CB,PPP1R12B,RAC2,RAC3,RHOG,RHOT1,RHOT2,WAS,WASL,WIPF1
LXR/RXR Activation	5.50E-07	4.6	A1BG,ACACA,AGT,AMBP,APOA2,APOB,APOD,APOE,C3,C4A/C4B,C9,CLU,GC,HPX,ITIH4,KNG1,LBP,LYZ,NFKB1,NFKB2,NR1H2,ORM1,SAA1,SERPINA1,SERPINF2,VTN
Signaling by Rho Family GTPases	6.92E-07	-3.0	ACTB,ACTG2,ACTR2,ARHGEF12,ARHGEF2,ARHGEF6,ARHGEF7,ARPC1B,ARPC2,CDH13,CFL1,CFL2,CLIP1,EZR,GFAP,GNA13,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,MSN,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,PIP4K2A,PKN1,PPP1R12C,PTK2B,RACK1,RHOG,RHOT1,RHOT2,SEPTIN1,SEPTIN6,STMN1,WAS,WASL,WIPF1
T Cell Receptor Signaling	9.33E-07		BTK,CAMK4,CBL,CD247,CD3D,CD3E,CD8A,CSK,FYN,GRAP2,HRAS,IKBKB,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PPP3CA,PPP3CB,PTPN7,ZAP70
Cdc42 Signaling	1.41E-06	-0.7	ACTR2,APC2,ARHGEF6,ARPC1B,ARPC2,CD247,CD3D,CD3E,CFL1,CFL2,CLIP1,DIAPH1,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DPA1,HLA-DQA1,HLA-DRA,HLA-DRB5,ITGA5,ITGB1,MAPK1,MAPK14,PAK2,PPP1CB,PPP1R12B,WAS,WASL,WIPF1

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	1.55E-06	-0.5	APOA2,APOB,APOD,APOE,CLU,IKBKB,LYZ,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,NCF1,NFKB1,NFKB2,ORM1,PIK3C2B,PIK3CA,PLCG1,PLCG2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PRKCB,PRKCD,PRKCH,PTPN6,RHOG,RHOT1,RHOT2,SERPIN1A1
iCOS-iCOSL Signaling in T Helper Cells	2.29E-06	-3.3	CAMK4,CD247,CD3D,CD3E,CSK,GRAP2,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,IKBKB,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PLEKHA2,PPP3CA,PPP3CB,SHC1,ZAP70
Virus Entry via Endocytic Pathways	3.72E-06		ACTB,ACTG2,CAV1,DNM2,FLNA,FYN,HLA-B,HRAS,ITGA1,ITGA5,ITGA6,ITGB1,ITGB4,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,RAC2,RAC3
FXR/RXR Activation	4.17E-06		A1BG,ABCC2,AGT,AMBP,APOA2,APOB,APOD,APOE,C3,C4A/C4B,C9,CLU,CYP27A1,FOXO1,GC,HPX,ITIH4,KNG1,ORM1,PKLR,SAA1,SERPINA1,SERPINF2,SLC22A7,VTN
FAK Signaling	8.13E-06		ACTB,ACTG2,ARHGEF6,ARHGEF7,CSK,FYN,GIT2,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,TNS1,VCL,WAS
ERK/MAPK Signaling	8.32E-06	-1.5	EIF4E,ELF1,EP300,FYN,HRAS,HSPB1,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PRKAR1A,PRKCB,PRKCD,PTK2B,RAC2,RAC3,RPS6KA5,SHC1,YWHAB,YWHAH,YWHAZ
p70S6K Signaling	8.51E-06	-1.7	AGT,BTK,EEF2,F2,HRAS,LYN,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP2R5A,PPP2R5D,PRKCB,PRKCD,PRKCH,RPS6,SHC1,SYK,YWHAB,YWHAH,YWHAZ
VEGF Signaling	1.55E-05	-0.8	ACTB,ACTG2,EIF1AY,EIF2S1,EIF2S2,EIF2S3,ELAVL1,FOXO1,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PTK2B,PTPN6,SHC1,VCL
PI3K Signaling in B Lymphocytes	1.78E-05	-2.6	BTK,C3,CAMK4,CBL,CR2,FYN,HRAS,IKBKB,LYN,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3AP1,PIK3CA,PLCB3,PLCG1,PLCG2,PLEKHA2,PPP3CA,PPP3CB,PRKCB,SYK
RhoGDI Signaling	2.34E-05	2.1	ACTB,ACTG2,ACTR2,ARHGAP4,ARHGEF12,ARHGEF2,ARHGEF6,ARHGEF7,ARPC1B,ARPC2,CD44,CDH13,CFL1,CFL2,EP300,EZR,GNA13,ITGA5,ITGB1,MSN,PAK2,PIP4K2A,PPP1R12C,RACK1,RHOG,RHOT1,RHOT2,WASF2,WASL
Role of Tissue Factor in Cancer	2.40E-05		CASP3,CFL1,CFL2,EIF4E,F2,FGB,FGG,FYN,GNA13,HRAS,ITGA6,ITGAV,ITGB1,LYN,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PTK2B,RPS6KA3,RPS6KA5,STAT5A
Mechanisms of Viral Exit from Host Cells	2.45E-05		ACTB,ACTG2,CHMP2A,CHMP4A,CHMP4B,LMNB1,PDCD6IP,PRKCB,PRKCD,PRKCH,SH3GLB2,XPO1

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Canonical Pathways	p-value	z-score	Proteins
B Cell Receptor Signaling	3.24E-05	-3.3	APBB1IP,BTK,CAMK4,CFL1,CFL2,CSK,EP300,FOXO1,HRAS,IKKBK B,LYN,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3AP1,PIK3C2B,PIK3CA,PLCG2,PPP3CA,PPP3CB,PRKCB,PTK2B,PTPN6,RAC2,SHC1,SYK
NF-κB Activation by Viruses	4.27E-05	-0.9	CR2,ELP1,HRAS,IKKBK,ITGA1,ITGA5,ITGA6,ITGAV,ITGB1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH
Telomere Extension by Telomerase	4.27E-05		HNRNPA2B1,MRE11,RAD50,TERF2,TERF2IP,XRCC5,XRCC6
D-myo-inositol-5-phosphate Metabolism	4.37E-05		DOT1L,DUSP28,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PIP4K2A,PLCB3,PLCG1,PLCG2,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
Clathrin-mediated Endocytosis Signaling	4.47E-05		ACTB,ACTG2,ACTR2,APOA2,APOB,APOD,APOE,ARF6,ARPC1B,ARPC2,CBL,CLU,CSNK2A2,DAB2,DNM2,F2,FGF2,ITGA5,ITGB1,ITGB4,LYZ,MYO1E,ORM1,PIK3C2B,PIK3CA,PPP3CA,PPP3CB,SERPINA1,SH3GLB2,SH3KBP1,WASL
Granzyme A Signaling	4.68E-05		ANP32A,APEX1,EP300,H1-10,H1-3,H1-4,HMGB2,SET
Erythropoietin Signaling	4.79E-05		CBL,HRAS,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTPN6,SHC1,STAT5A
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	4.79E-05		CAMK4,CD247,CD3D,CD3E,FYN,HRAS,IKKBK,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PLCG1,PLCG2,PPP3CA,PPP3CB,ZAP70
Androgen Signaling	5.01E-05	-2.1	CAMK4,EP300,GNA13,GTF2B,HSPA4,MAPK1,MAPK3,NFKB1,NFKB2,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1,SHC1,TGFB11I
Purine Nucleotides De Novo Biosynthesis II	5.13E-05		ADSS2,ATIC,GART,GMPS,IMPDH1,IMPDH2
Neuregulin Signaling	5.89E-05	-2.1	DCN,ERBB3,HRAS,HSP90AB1,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTEN,PTPN6,PTPN7,PTPN8,PTPN9,PTPN10,PTPN11,PTPN12,PTPN13,PTPN14,PTPN15,PTPN16,PTPN17,PTPN18,PTPN19,PTPN20,PTPN21,PTPN22,PTPN23,PTPN24,PTPN25,PTPN26,PTPN27,PTPN28,PTPN29,PTPN30,PTPN31,PTPN32,PTPN33,PTPN34,PTPN35,PTPN36,PTPN37,PTPN38,PTPN39,PTPN40,PTPN41,PTPN42,PTPN43,PTPN44,PTPN45,PTPN46,PTPN47,PTPN48,PTPN49,PTPN50,PTPN51,PTPN52,PTPN53,PTPN54,PTPN55,PTPN56,PTPN57,PTPN58,PTPN59,PTPN60,PTPN61,PTPN62,PTPN63,PTPN64,PTPN65,PTPN66,PTPN67,PTPN68,PTPN69,PTPN70,PTPN71,PTPN72,PTPN73,PTPN74,PTPN75,PTPN76,PTPN77,PTPN78,PTPN79,PTPN80,PTPN81,PTPN82,PTPN83,PTPN84,PTPN85,PTPN86,PTPN87,PTPN88,PTPN89,PTPN90,PTPN91,PTPN92,PTPN93,PTPN94,PTPN95,PTPN96,PTPN97,PTPN98,PTPN99,PTPN100
Glycolysis I	5.89E-05		ALDOA,ENO1,ENO2,GAPDH,GAPDHS,PFKL,PGK1,PGK2,PKLR
Gluconeogenesis I	5.89E-05		ALDOA,ENO1,ENO2,GAPDH,GAPDHS,MDH1,ME2,PGK1,PGK2

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Canonical Pathways	p-value	z-score	Proteins
Paxillin Signaling	6.61E-05	-1.2	ACTB,ACTG2,ARF6,ARHGEF6,ARHGEF7,CSK,GIT2,HRAS,ITGA1,ITGA5,ITGA6,ITGAV,ITGB1,ITGB4,MAPK1,MAPK14,PAK2,PIK3C2B,PIK3CA,PTK2B,VCL
Granzyme B Signaling	7.08E-05	-1.1	BID,CASP3,DFFA,GZMB,LMNB1,PARP1,PRKDC
Extrinsic Prothrombin Activation Pathway	7.08E-05		F12,F13A1,F2,FGB,FGG,PROS1,SERPINC1
NRF2-mediated Oxidative Stress Response	7.41E-05	-3.0	ABCC2,ACTB,ACTG2,CCT7,CUL3,DNAJA4,DNAJB6,DNAJC1,DNAJC14,DNAJC9,EP300,FTL,GCLC,HRAS,MAP2K1,MAP2K5,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH,SOD3,SQSTM1,STIP1,TXNRD1,UBE2K,USP14
Thrombin Signaling	7.94E-05	-3.3	ADCY10,ARHGEF12,ARHGEF2,ARHGEF6,CAMK1D,CAMK4,F2,GNA13,HRAS,IKBKB,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP1CB,PPP1R12B,PRKCB,PRKCD,PRKCH,RACK1,RHOG,RHOT1,RHOT2,SHC1
Rac Signaling	1.12E-04	-2.7	ACTR2,ANK1,ARPC1B,ARPC2,CD44,CFL1,CFL2,CYFIP2,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,PIP4K2A,PTK2B
Oxidative Phosphorylation	1.17E-04		COX4I1,COX6B1,COX6C,COX7B,COX8A,NDUFA10,NDUFA12,NDUFA2,NDUFA4,NDUFA8,NDUFA9,NDUFB11,NDUFB3,NDUFB4,NDUFS1,NDUFS4,NDUFS7,NDUFS8,UQCRC1,UQCRCF5
3-phosphoinositide Biosynthesis	1.29E-04		CDIPT,DOT1L,DUSP28,ERBB3,FYN,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PIK3AP1,PIK3C2B,PIK3CA,PIP4K2A,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
Type I Diabetes Mellitus Signaling	1.32E-04	-0.9	BID,CASP3,CD247,CD3D,CD3E,GZMB,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,HSPD1,IKBKB,MAPK1,MAPK14,NFKB1,NFKB2
Glucocorticoid Receptor Signaling	1.41E-04		A2M,ACTB,AGT,CD247,CD3D,CD3E,EP300,FGG,FKBP4,GTF2B,HMGB1,HRAS,HSP90AB1,HSPA4,HSPA9,IKBKB,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NR3C2,PIK3C2B,PIK3CA,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,PPP3CA,PPP3CB,PRKAA1,SHC1,SMARCC2,SMARCE1,STAT5A,SUMO1,TAF3,YWHAH
Renin-Angiotensin Signaling	1.62E-04	-2.4	ADCY10,AGT,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH,PTK2B,PTPN6,SHC1
Actin Nucleation by ARP-WASP Complex	1.62E-04	-2.3	ACTR2,ARPC1B,ARPC2,HRAS,ITGA5,ITGB1,PPP1R12C,RHOG,RHOT1,RHOT2,WAS,WASL,WIPF1

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Canonical Pathways	p-value	z-score	Proteins
Caveolar-mediated Endocytosis Signaling	1.62E-04		ACTB,ACTG2,CAV1,COPE,DNM2,FLNA,FYN,HLA-B,ITGA1,ITGA5,ITGA6,ITGAV,ITGB1,ITGB4,PTPN1
Chemokine Signaling	1.62E-04	-1.8	CAMK1D,CAMK4,CFL1,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PLCB3,PLCG1,PLCG2,PPP1CB,Ppp1r12b,PRKCB,PTK2B
fMLP Signaling in Neutrophils	1.82E-04	-3.1	ACTR2,ARPC1B,ARPC2,CAMK4,HRAS,MAP2K1,MAPK1,MAPK3,NCF1,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PPP3CA,PPP3CB,PRKCB,PRKCD,PRKCH,RACK1,WAS
Breast Cancer Regulation by Stathmin1	1.86E-04		ADCY10,ARHGEF12,ARHGEF2,ARHGEF6,ARHGEF7,CAMK1D,CAMK4,GNA13,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCB3,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1,SHC1,STMN1,TUBA1B,TUBA4A
G Beta Gamma Signaling	1.95E-04	-2.0	ARHGEF6,BTK,CAV1,CAV2,DNM2,GNA13,HRAS,MAPK1,MAPK3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1,SHC1
Natural Killer Cell Signaling	2.04E-04		CD247,FYN,HRAS,MAP2K1,MAPK1,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTPN6,RAC2,RAC3,SH2D1A,SHC1,SYK,ZAP70
RhoA Signaling	2.04E-04	-2.8	ACTB,ACTG2,ACTR2,ARHGAP4,ARHGEF12,ARPC1B,ARPC2,CFL1,CFL2,EZR,GNA13,MSN,PFN1,PFN2,PIP4K2A,PKN1,PPP1CB,Ppp1r12b,PTK2B,SEPTIN1,SEPTIN6
Superpathway of Inositol Phosphate Compounds	2.24E-04		CDIPT,DOT1L,DUSP28,ERBB3,FYN,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PIK3AP1,PIK3C2B,PIK3CA,PIP4K2A,PLCB3,PLCG1,PLCG2,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
Apoptosis Signaling	2.24E-04	2.2	ACIN1,BID,CASP3,CASP7,DFFA,HRAS,IKBKB,LMNA,MAP2K1,MAPK1,MAPK3,NAIP,NFKB1,NFKB2,PARP1,PLCG1,PLCG2
Gαq Signaling	2.57E-04	-3.3	BTK,CAMK4,CSK,GRK2,IKBKB,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,PRKCB,PRKCD,PRKCH,PTK2B,RACK1,RHOG,RHOT1,RHOT2
DNA Double-Strand Break Repair by Non-Homologous End Joining	2.75E-04		MRE11,PARP1,PRKDC,RAD50,XRCC5,XRCC6
Tec Kinase Signaling	2.82E-04	-3.3	ACTB,ACTG2,BTK,FYN,GNA13,GTF2I,ITGA5,ITGB1,LYN,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTK2B,RACK1,RHOG,RHOT1,RHOT2,STAT5A,WAS
CDK5 Signaling	2.82E-04	1.0	ADCY10,HRAS,ITGA6,ITGB1,LAMB1,LAMC1,MAP2K1,MAPK1,MAPK14,MAPK3,NTRK2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PRKAR1A

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Canonical Pathways	p-value	z-score	Proteins
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	2.95E-04		DOT1L,DUSP28,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	2.95E-04		DOT1L,DUSP28,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
Leukocyte Extravasation Signaling	3.39E-04	-2.4	ACTB,ACTG2,ARHGAP4,BTK,CD44,CTNNA3,EZR,ITGA1,ITGA5,ITGA6,ITGB1,MAPK1,MAPK14,MSN,NCF1,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTK2B,RAC2,SIPA1,TIMP3,VCL,WAS,WASL,WIPF1
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	3.55E-04	1.4	BID,CASP3,CASP7,CD247,CD3D,CD3E,DFFA,GZMB,HLA-B
DNA Methylation and Transcriptional Repression Signaling	3.72E-04		CHD3,MECP2,MTA2,RBBP4,RBBP7,SAP18,SIN3A
PTEN Signaling	3.98E-04	0.5	CASP3,CBL,CSNK2A2,FOXO1,HRAS,IKBKB,ITGA5,ITGB1,MAGI3,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,NTRK2,PIK3CA,RAC2,RAC3,SHC1,YWHAH
Remodeling of Epithelial Adherens Junctions	4.17E-04	-2.4	ACTB,ACTG2,ACTR2,ARF6,ARPC1B,ARPC2,CLIP1,DNM2,HGF,MAPRE1,MAPRE2,TUBA1B,TUBA4A,VCL
Neuroprotective Role of THOP1 in Alzheimer's Disease	4.79E-04		AGT,ECE1,HLA-B,IDE,KNG1,NFYA,PLG,PRKAR1A,SERPINA3,THOP1
14-3-3-mediated Signaling	5.01E-04	-2.5	CBL,FOXO1,GFAP,HRAS,MAP2K1,MAPK1,MAPK3,PDCD6IP,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,TUBA1B,TUBA4A,YWHAB,YWHAH,YWHAZ
HIPPO signaling	5.25E-04	0.9	AJUBA,CD44,CUL1,ITCH,LATS1,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,STK4,TP53BP2,YWHAB,YWHAH,YWHAZ
Sumoylation Pathway	5.62E-04	0.6	CTBP1,EP300,ISG20,NFKB1,NFKB2,PCNA,PML,RAN,RANBP2,RANBP1,RFC2,RFC4,RHOG,RHOT1,RHOT2,SUMO1,UBA2
Mismatch Repair in Eukaryotes	6.46E-04		FEN1,MSH3,MSH6,PCNA,RFC2,RFC4

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
PI3K/AKT Signaling	6.92E-04	-1.6	CDC37,EIF4E,FOXO1,HRAS,HSP90AB1,IKBKB,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3CA,PPP2R5A,PPP2R5D,SHC1,YWHAB,YWHAH,YWHAZ
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	6.92E-04	1.0	CUL1,EP300,PPM1D,PRKDC,TOP2A,TOP2B,TRIP12,WEE1,YWHAB,YWHAH,YWHAZ
Mitochondrial Dysfunction	7.24E-04		CASP3,COX4I1,COX6B1,COX6C,COX7B,COX8A,GPX4,HSD17B10,NDUFA10,NDUFA12,NDUFA2,NDUFA4,NDUFA8,NDUFA9,NDUFB11,NDUFB3,NDUFB4,NDUFS1,NDUFS4,NDUFS7,NDUFS8,PSEN1,RHOT2,UQCRC1,UQCRFS1
Thrombopoietin Signaling	7.59E-04	-1.9	HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,SHC1,STAT5A
NGF Signaling	8.51E-04	-2.1	EP300,HRAS,IKBKB,MAP2K1,MAP3K6,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCD,RHOG,RPS6KA3,RPS6KA5,SHC1,SMPD3
Germ Cell-Sertoli Cell Junction Signaling	8.51E-04		A2M,ACTB,ACTG2,CFL1,CFL2,HRAS,ITGA6,ITGB1,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,PAK2,PIK3C2B,PIK3CA,RAC2,RAC3,RHOG,RHOT1,RHOT2,TUBA1B,TUBA4A,VCL,WASL
IL-3 Signaling	9.33E-04	-1.8	FOXO1,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PPP3CA,PPP3CB,PRKCB,PRKCD,PRKCH,PTPN6,SHC1,STAT5A
Prolactin Signaling	9.33E-04	-2.1	EP300,FYN,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,SHC1,STAT5A
PAK Signaling	1.02E-03	-1.3	ARHGEF6,ARHGEF7,CASP3,CFL1,CFL2,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,PAK2,PIK3C2B,PIK3CA,PTK2B,SHC1,WASL
Fc Epsilon RI Signaling	1.05E-03	-3.3	BTK,FYN,GRAP2,HRAS,LYN,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,RAC2,RAC3,SYK
Aldosterone Signaling in Epithelial Cells	1.07E-03	-1.4	CRYAB,DNAJB6,DNAJC1,DNAJC14,DNAJC9,HSP90AB1,HSPA12A,HSPA4,HSPA9,HSPB1,HSPD1,MAP2K1,MAPK1,MAPK3,NR3C2,PIK3C2B,PIK3CA,PIP4K2A,PLCB3,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH
3-phosphoinositide Degradation	1.12E-03		DOT1L,DUSP28,MTMR7,NT5C,NUDT2,NUDT3,NUDT9,PPP1CA,PPP1CC,PPP1R12C,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP4C,PTPN1,PTPN6,PTPN7,SACM1L,SET,TNS3,UBLCP1,WBP11
IL-15 Signaling	1.15E-03		HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG1,RAC3,SHC1,STAT5A,SYK

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5

Canonical Pathways	p-value	z-score	Proteins
ILK Signaling	1.15E-03	-1.0	ACTB,ACTG2,ARHGEF6,CASP3,CFL1,CFL2,EP300,FERMT2,FLNA,ITGB1,ITGB4,MAPK1,MAPK3,MYH11,MYH6,NFKB1,NFKB2,PIK3C2B,PIK3CA,PPP2R5A,PPP2R5D,RHOG,RHOT1,RHOT2,RPS6KA5,TGFB1I1,VCL
Synaptic Long Term Potentiation	1.15E-03	-1.4	CAMK4,EP300,HRAS,MAP2K1,MAPK1,MAPK3,PLCB3,PLCG1,PLCG2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH
CCR5 Signaling in Macrophages	1.35E-03		CAMK4,CD247,CD3D,CD3E,MAPK1,MAPK14,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTK2B,RACK1
Semaphorin Signaling in Neurons	1.38E-03		ARHGEF12,CFL1,CFL2,FYN,ITGB1,MAPK1,MAPK3,PAK2,RHOG,RHOT1,RHOT2
Cell Cycle Control of Chromosomal Replication	1.38E-03		MCM3,MCM6,MCM7,PCNA,POLA1,RPA2,RPA3,TOP2A,TOP2B
4-1BB Signaling in T Lymphocytes	1.41E-03	-2.1	ELP1,IKBKB,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2
Gap Junction Signaling	1.48E-03		ACTB,ACTG2,ADCY10,CAV1,DBN1,GUCY1B1,HRAS,MAP2K1,MAP2K5,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH,TUBA1B,TUBA4A
Glioma Invasiveness Signaling	1.55E-03	-0.8	CD44,HRAS,ITGAV,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLG,RHOG,RHOT1,RHOT2,TIMP3,VTN
Hereditary Breast Cancer Signaling	1.58E-03		ACTB,EP300,H2AX,HRAS,MRE11,MSH6,NPM1,PIK3C2B,PIK3CA,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,RAD50,RAD51,RFC2,RFC4,SMARCC2,SMARCE1,WEE1
Superpathway of Methionine Degradation	1.78E-03		AHCYL1,GOT2,MAT2B,MCEE,MGMT,PCCB,PRMT1,PRMT5
ATM Signaling	1.91E-03	-1.0	BID,CBX3,CBX5,EP300,H2AX,MAPK14,MRE11,PPM1D,RAD50,RAD51,SMC1A,SMC3,TRIM28,USP7
IL-4 Signaling	1.95E-03		FCER2,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,HRAS,NR3C2,PIK3C2B,PIK3CA,PTPN6,SHC1
ErbB Signaling	2.00E-03		ERBB3,FOXO1,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,SHC1
ErbB4 Signaling	2.04E-03	-1.7	HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PSEN1,SHC1

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Canonical Pathways	p-value	z-score	Proteins
CREB Signaling in Neurons	2.04E-03	-1.7	ADCY10,CAMK4,EP300,GNA13,GTF2B,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1,SHC1
Growth Hormone Signaling	2.14E-03	-1.6	A2M,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,PTPN6,RPS6KA3,RPS6KA5,STAT5A
CTLA4 Signaling in Cytotoxic T Lymphocytes	2.19E-03		AP1M1,CD247,CD3D,CD3E,CD8A,FYN,GRAP2,HLA-B,PIK3C2B,PIK3CA,PLCG1,PPP2R5A,PPP2R5D,PTPN6,SYK,ZAP70
IL-12 Signaling and Production in Macrophages	2.24E-03		APOA2,APOB,APOD,APOE,CLU,EP300,IKBKB,LYZ,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,ORM1,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH,SERPINA1
DNA Double-Strand Break Repair by Homologous Recombination	2.40E-03		ATRX,MRE11,POLA1,RAD50,RAD51
Purine Nucleotides Degradation II (Aerobic)	2.45E-03		ADA,ADA2,IMPDH1,IMPDH2,NT5C,NT5C2
Pyridoxal 5'-phosphate Salvage Pathway	2.45E-03		GRK6,MAP2K1,MAP3K6,MAPK1,MAPK3,PAK2,PDXK,PKN1,PRKAA1,PRKCD,PRKCH,PRPF4B
Cancer Drug Resistance By Drug Efflux	2.57E-03		ABCC10,ABCC2,FOXO1,HRAS,MAP2K1,MAPK1,MAPK3,NFKB1,PIK3CA,YBX1
Cholecystokinin/Gastrin-mediated Signaling	2.69E-03	-2.0	GNA13,HRAS,MAP2K1,MAP2K5,MAPK1,MAPK14,MAPK3,PLCB3,PRKCB,PRKCD,PRKCH,PTK2B,RHOG,RHOT1,RHOT2,SHC1
Death Receptor Signaling	2.75E-03	-1.3	ACIN1,ACTB,ACTG2,BID,CASP3,CASP7,DFFA,HSPB1,IKBKB,LMNA,NAIP,NFKB1,NFKB2,PARP1,PARP4
PPAR α /RXR α Activation	2.75E-03	1.1	ADCY10,ADIPOQ,AIP,APOA2,CAND1,CKAP5,EP300,GOT2,HRAS,HSP90AB1,IKBKB,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PLCB3,PLCG1,PLCG2,PRKAA1,PRKAR1A,PRKCB,SHC1
UVB-Induced MAPK Signaling	2.82E-03		EIF4E,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH,RPS6KA3,RPS6KA5

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Canonical Pathways	p-value	z-score	Proteins
UVC-Induced MAPK Signaling	2.95E-03	-1.7	HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PRKCB,PRKCD,PRKCH, SMPD3
Huntington's Disease Signaling	3.09E-03	0.3	CASP3,CASP7,DNM2,EP300,GLS,HRAS,HSPA4,HSPA9,MAPK1,MAPK3,NAPB,NSF,PIK3C2B,PIK3CA,PLCB3,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,PRKCB,PRKCD,PRKCH,PSME1,PSME2,PSMF1,RACK1,SHC1,SIN3A,TCERG1
Dendritic Cell Maturation	3.24E-03	-1.8	COL18A1,COL1A1,COL1A2,COL2A1,COL3A1,EP300,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5,IKBKB,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2
B Cell Development	3.24E-03		HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5
FLT3 Signaling in Hematopoietic Progenitor Cells	3.39E-03	-2.1	CBL,EIF4E,EP300,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,RPS6KA3,RPS6KA5,SHC1,STAT5A
Phagosome Formation	3.39E-03		FCER2,ITGA5,ITGB1,MARCO,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,RHOG,RHOT1,RHOT2,SYK,TLR5,VTN
Axonal Guidance Signaling	3.47E-03		ACTR2,ADAM22,ARHGEF12,ARHGEF6,ARHGEF7,ARPC1B,ARPC2,CFL1,CFL2,EIF4E,FYN,GLI1,GNA13,HRAS,ITGA5,ITGB1,LNPEP,MAP2K1,MAPK1,MAPK3,NTRK2,PAK2,PFN1,PFN2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH,PSMD14,RAC2,RAC3,RACK1,SEMA3E,SEMA4F,SEMA4G,SEMA6C,SHC1,TUBA1B,TUBA4A,WAS,WASL,WIPF1
Tetrahydrofolate Salvage from 5,10-methylenetetrahydrofolate	3.55E-03		GART,MTHFD1,MTHFD1L
Nitric Oxide Signaling in the Cardiovascular System	3.55E-03	-2.2	ATP2A3,CAMK4,CAV1,GUCY1B1,HSP90AB1,KNG1,MAP2K1,MAPK1,MAPK3,PDE3B,PIK3C2B,PIK3CA,PRKAA1,PRKAR1A,PRKCB,PRKCD,PRKCH
Melanocyte Development and Pigmentation Signaling	3.72E-03	-1.3	ADCY10,EP300,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKAR1A,PTPN6,RPS6KA3,RPS6KA5,SHC1
LPS-stimulated MAPK Signaling	3.80E-03	-1.9	HRAS,IKBKB,LBP,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH

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Canonical Pathways	p-value	z-score	Proteins
Xenobiotic Metabolism Signaling	3.89E-03		ABCC2,AIP,ALDH16A1,ALDH1B1,ALDH5A1,ALDH9A1,CAMK1D,CAMK4,CES5A,CUL3,EP300,FTL,GCLC,HRAS,HSP90AB1,IL4I1,MAP2K1,MAP2K5,MAP3K6,MAPK1,MAPK14,MAPK3,MGMT,NFKB1,NFKB2,PIK3C2B,PIK3CA,PPP2R5A,PPP2R5D,PRKCB,PRKCD,PRKCH,SOD3,SUMO1
Molecular Mechanisms of Cancer	3.89E-03		ADCY10,ARHGEF12,ARHGEF2,ARHGEF6,ARHGEF7,BID,CASP3,CASP7,CBL,EP300,FOXO1,FYN,GLI1,GNA13,HAT1,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK14,MAPK3,NAIP,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,PLCB3,PRKAR1A,PRKCB,PRKCD,PRKCH,PRKDC,PSEN1,RAC2,RAC3,RHOG,RHOT1,RHOT2,SHC1,SIN3A
CD40 Signaling	4.17E-03	-0.8	ELP1,FCER2,IKBKB,MAP2K1,MAP2K5,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,TNFAIP3
Pentose Phosphate Pathway	4.27E-03		PGLS,RPE,RPIA,TALDO1
OX40 Signaling Pathway	5.25E-03	0.4	CD247,CD3D,CD3E,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DPA1,HLA-DQA1,HLA-DRA,HLA-DRB5,NFKB1,NFKB2
Melatonin Signaling	5.25E-03	-1.7	CAMK4,MAP2K1,MAP2K5,MAPK1,MAPK3,PLCB3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH
Uridine-5'-phosphate Biosynthesis	5.37E-03		CAD,UMPS
Estrogen Receptor Signaling	5.75E-03		CTBP1,DDX5,EP300,GTF2B,HRAS,MAP2K1,MAPK1,MAPK3,POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,PRKDC,SHC1,SPEN,TAF3,THRAP3
Macropinocytosis Signaling	5.89E-03	-2.1	ARF6,HGF,HRAS,ITGA5,ITGB1,ITGB4,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH
Methionine Degradation I (to Homocysteine)	6.17E-03		AHCYL1,MAT2B,MGMT,PRMT1,PRMT5
RAR Activation	6.31E-03		ACTB,ADCY10,CSK,CSNK2A2,EP300,MAP2K1,MAPK1,MAPK14,NFKB1,NFKB2,PARP1,PIK3CA,PML,PRKAR1A,PRKCB,PRKCD,PRKCH,PRMT1,PSMC5,RPL7A,SMARCC2,SMARCE1,SNW1,STAT5A
Glioma Signaling	6.46E-03	-2.1	CAMK1D,CAMK4,HRAS,IDH2,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,SHC1,SIN3A
IL-2 Signaling	6.46E-03	-1.3	CSNK2A2,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PTK2B,SHC1,STAT5A,SYK
Autoimmune Thyroid Disease Signaling	6.46E-03		GZMB,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5

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Canonical Pathways	p-value	z-score	Proteins
Ephrin B Signaling	6.46E-03	-0.3	CAP1,CBL,CFL1,CFL2,GNA13,HNRNP,K,HRAS,MAPK1,MAPK3,RAC2,RAC3,RACK1
GM-CSF Signaling	6.46E-03	-1.3	HRAS,LYN,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PPP3CA,PPP3CB,PRKCB,RACK1,SHC1
Tumoricidal Function of Hepatic Natural Killer Cells	6.61E-03	0.4	BID,CASP3,CASP7,DFFA,GZMB,LYVE1
Pentose Phosphate Pathway (Non-oxidative Branch)	6.61E-03		RPE,RPIA,TALDO1
CCR3 Signaling in Eosinophils	6.76E-03		CAMK4,CFL1,CFL2,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCB3,PPP1CB,Ppp1r12b,PRKCB,PRKCD,PRKCH,RACK1
RANK Signaling in Osteoclasts	6.76E-03	-2.3	CAMK4,CBL,IKBKB,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PPP3CA,PPP3CB,PTK2B
Corticotropin Releasing Hormone Signaling	6.92E-03	-2.5	ADCY10,CAMK4,EP300,GLI1,GUCY1B1,KRT1,MAP2K1,MAPK1,MAPK14,MAPK3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH
JAK/Stat Signaling	7.24E-03	-1.4	HRAS,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIAS3,PIK3C2B,PIK3CA,PTPN1,PTPN6,SHC1,STAT5A
Insulin Receptor Signaling	7.24E-03	-2.5	ACLY,CBL,EIF4E,FOXO1,FYN,HRAS,MAP2K1,MAPK1,MAPK3,PD3B,PIK3C2B,PIK3CA,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PRKAR1A,PTPN1,SHC1
UVA-Induced MAPK Signaling	7.41E-03	-2.1	CASP3,HRAS,MAPK1,MAPK14,MAPK3,PARP1,PARP4,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,RPS6KA3,RPS6KA5,SMPD3
Graft-versus-Host Disease Signaling	7.41E-03		GZMB,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DQA1,HLA-DRA,HLA-DRB5
P2Y Purigenic Receptor Signaling Pathway	7.76E-03	-2.2	ADCY10,EP300,HRAS,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1
Sphingosine-1-phosphate Signaling	8.32E-03	-1.5	ADCY10,ASAH1,CASP3,CASP7,GNA13,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PTK2B,RHOG,RHOT1,RHOT2,SMPD3

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Canonical Pathways	p-value	z-score	Proteins
TNFR1 Signaling	8.51E-03	-1.4	BID,CASP3,CASP7,IKBKB,NAIP,NFKB1,NFKB2,PAK2,TNFAIP3
Ephrin Receptor Signaling	8.71E-03	-2.5	ACTR2,ARPC1B,ARPC2,CFL1,CFL2,EP300,FYN,GNA13,HRAS,ITGA5,ITGB1,MAP2K1,MAPK1,MAPK3,PAK2,RAC2,RAC3,RACK1,SHC1,WAS,WASL,WIPF1
Protein Kinase A Signaling	8.71E-03	-2.3	ADCY10,AKAP12,AKAP9,APEX1,CAMK4,DUSP3,EP300,FLNA,GN A13,H1-10,H1-3,H1-4,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PDE12,PDE3B,PDE6C,PDE8A,PLCB3,PLCG1,PLCG2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH,PTK2B,PTPN1,PTPN6,PTPN7,RACK1,YWHAB,YWHAH,YWHAZ
BER pathway	8.91E-03		APEX1,FEN1,PARP1,PCNA
eNOS Signaling	9.55E-03	-1.7	ADCY10,CAMK4,CASP3,CAV1,CCNA2,DNM2,GUCY1B1,HSP90A B1,HSPA4,HSPA9,KNG1,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKAA1,PRKAR1A,PRKCB,PRKCD,PRKCH
HGF Signaling	9.77E-03	-1.3	ELF1,HGF,HRAS,ITGA5,ITGB1,MAP2K1,MAP3K6,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH
Th1 Pathway	9.77E-03	-2.8	CD247,CD3D,CD3E,CD8A,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DPA1,HLA-DQA1,HLA-DRA,HLA-DRB5,LGALS9,NFKB1,PIK3C2B,PIK3CA,PSEN1
Cysteine Biosynthesis III (mammalia)	1.02E-02		AHCYL1,MAT2B,MGMT,PRMT1,PRMT5
Oncostatin M Signaling	1.05E-02	-0.4	HRAS,MAP2K1,MAPK1,MAPK3,SHC1,STAT5A,TIMP3
TWEAK Signaling	1.05E-02	-1.1	BID,CASP3,CASP7,IKBKB,NAIP,NFKB1,NFKB2
α -Adrenergic Signaling	1.07E-02	-1.7	ADCY10,CAMK4,HRAS,MAP2K1,MAPK1,MAPK3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1
Role of BRCA1 in DNA Damage Response	1.10E-02		ACTB,ATRIP,BABAM1,MRE11,MSH6,RAD50,RAD51,RFC2,RFC4,SMARCC2,SMARCE1,UIMC1
Adenine and Adenosine Salvage III	1.10E-02		ADA,ADA2,HPRT1

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Canonical Pathways	p-value	z-score	Proteins
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	1.15E-02	-0.7	C1QC,C3,C5,C5AR1,DDX58,EIF2S1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PLCG2,PRKCB,PRKCD,PRKCH,SYK,TLR5
Atherosclerosis Signaling	1.15E-02		APOA2,APOB,APOD,APOE,CLU,COL18A1,COL1A1,COL1A2,COL2A1,COL3A1,GLG1,LYZ,NFKB1,NFKB2,ORM1,PAFAH1B1,SERPINA1
Cardiac β -adrenergic Signaling	1.15E-02	0.5	ADCY10,AKAP12,AKAP9,APEX1,ATP2A3,GRK2,PDE12,PDE3B,PDE6C,PDE8A,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PRKAR1A,RACK1
IL-6 Signaling	1.15E-02	0.0	A2M,COL1A1,CRP,CSNK2A2,HRAS,HSPB1,IKBKB,LBP,MAP2K1,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,SHC1
AMPK Signaling	1.15E-02	-1.2	ACACA,ACTB,ADIPOQ,AK2,CAB39,CCNA2,EEF2,ELAVL1,EP300,FOXO1,MAPK1,MAPK14,PFKL,PIK3C2B,PIK3CA,PPM1D,PPM1G,PPP2R5A,PPP2R5D,PRKAA1,PRKAR1A,SMARCC2,SMARCE1
IL-17A Signaling in Fibroblasts	1.23E-02		IKBKB,LCN2,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2
Nucleotide Excision Repair Pathway	1.23E-02		POLR2A,POLR2B,POLR2C,POLR2E,POLR2I,RPA2,RPA3
CD27 Signaling in Lymphocytes	1.26E-02	-0.3	BID,CASP3,ELP1,IKBKB,MAP2K1,MAP2K5,MAP3K6,NFKB1,NFKB2
GNRH Signaling	1.32E-02	-1.2	ADCY10,DNM2,EP300,HRAS,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PAK2,PLCB3,PRKAR1A,PRKCB,PRKCD,PRKCH
Role of IL-17F in Allergic Inflammatory Airway Diseases	1.35E-02	-2.1	EP300,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,RPS6KA3,RPS6KA5
FGF Signaling	1.38E-02	-1.4	EP300,FGF2,HGF,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PLCG1,PTPN6,RPS6KA5
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1.51E-02		A2M,AGT,COL15A1,COL18A1,COL19A1,COL1A1,COL1A2,COL2A1,COL3A1,COL4A1,COL4A2,COL5A2,COL6A2,COL6A3,ECE1,FGF2,HGF,LBP,MYH11,MYH6,NFKB1,NFKB2
Dopamine-DARPP32 Feedback in cAMP Signaling	1.51E-02	-1.1	ADCY10,ATP2A3,CAMK4,EP300,GUCY1B1,PLCB3,PLCG1,PLCG2,PPP1CA,PPP1CB,PPP1CC,PPP1R7,PPP2R5A,PPP2R5D,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH

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Canonical Pathways	p-value	z-score	Proteins
Diphthamide Biosynthesis	1.51E-02		DPH6,EEF2
S-methyl-5-thio- α -D-ribose 1-phosphate Degradation	1.51E-02		ADI1,MRI1
D-glucuronate Degradation I	1.51E-02		CRYL1,DCXR
Telomerase Signaling	1.55E-02	-1.2	DKC1,ELF1,HRAS,HSP90AB1,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PPP2R5A,PPP2R5D,SHC1,TERF2,TERF2IP,TPP1
Urate Biosynthesis/Inosine 5'-phosphate Degradation	1.58E-02		IMPDH1,IMPDH2,NT5C,NT5C2
Inflammasome pathway	1.58E-02	-2.0	AIM2,NAIP,NEK7,NFKB1,NFKB2
Reelin Signaling in Neurons	1.66E-02		APOE,ARHGEF12,ARHGEF2,ARHGEF6,FYN,ITGA1,ITGA5,ITGA6,ITGB1,LYN,PAFAH1B1,PIK3C2B,PIK3CA
Purine Ribonucleosides Degradation to Ribose-1-phosphate	1.66E-02		ADA,ADA2,PGM2
HMGB1 Signaling	1.74E-02	-2.7	AGER,HAT1,HMGB1,HRAS,MAP2K1,MAP2K5,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,RBBP7,RHOG,RHOT1,RHOT2
IL-8 Signaling	1.82E-02	-3.1	CR2,GNA13,HRAS,IKBKB,ITGAV,MAP2K1,MAPK1,MAPK3,NFKB1,PAK2,PIK3C2B,PIK3CA,PRKCB,PRKCD,PRKCH,PTK2B,RAB11FIP2,RAC2,RAC3,RACK1,RHOG,RHOT1,RHOT2
Antioxidant Action of Vitamin C	1.82E-02	2.1	GLRX,IKBKB,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PAFAH1B1,PLCB3,PLCG1,PLCG2,SLC2A3,STAT5A,TXNRD1
TREM1 Signaling	2.04E-02	-0.3	ITGA5,ITGB1,MAPK1,MAPK3,NFKB1,NFKB2,NLRC5,PLCG1,PLCG2,STAT5A,TLR5
Leptin Signaling in Obesity	2.09E-02	-1.1	ADCY10,FOXO1,MAP2K1,MAPK1,MAPK3,PDE3B,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PRKAR1A
Regulation of Cellular Mechanics by Calpain Protease	2.19E-02	-0.4	CAST,CCNA2,EZR,HRAS,ITGA5,ITGB1,MAPK1,MAPK3,VCL

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Canonical Pathways	p-value	z-score	Proteins
Neurotrophin/TRK Signaling	2.24E-02	-0.6	EP300,HRAS,MAP2K1,MAP2K5,MAPK1,MAPK3,NTRK2,PIK3C2B,PIK3CA,PLCG1,SHC1
Lymphotoxin β Receptor Signaling	2.34E-02	-1.4	CASP3,ELP1,EP300,IKBKB,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA
Leucine Degradation I	2.34E-02		BCAT1,BCAT2,MCCC2
Angiopoietin Signaling	2.45E-02	-1.0	DOK2,ELP1,FOXO1,HRAS,IKBKB,NFKB1,NFKB2,PAK2,PIK3C2B,PIK3CA,STAT5A
Role of PKR in Interferon Induction and Antiviral Response	2.45E-02		BID,CASP3,EIF2S1,IKBKB,MAPK14,NFKB1,NFKB2
Role of NFAT in Cardiac Hypertrophy	2.45E-02	-0.4	ADCY10,CAMK1D,CAMK4,EP300,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,PRKAR1A,PRKCB,PRKCD,PRKCH,RACK1,SHC1
EGF Signaling	2.57E-02	-1.3	CSNK2A2,HRAS,MAP2K1,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PLCG1,SHC1
Th2 Pathway	2.63E-02	-1.4	CD247,CD3D,CD3E,HLA-B,HLA-DMA,HLA-DMB,HLA-DOA,HLA-DOB,HLA-DPA1,HLA-DQA1,HLA-DRA,HLA-DRB5,IKZF1,NFKB1,PIK3C2B,PIK3CA,PSEN1,STAT5A
VEGF Family Ligand-Receptor Interactions	2.69E-02	-1.7	HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,PRKCD,PRKCH,SHC1
ErbB2-ErbB3 Signaling	2.82E-02	-1.3	ERBB3,FOXO1,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,SHC1,STAT5A
Methylmalonyl Pathway	2.95E-02		MCEE,PCCB
MIF-mediated Glucocorticoid Regulation	3.09E-02	-1.6	CD74,MAPK1,MAPK3,MIF,NFKB1,NFKB2
PDGF Signaling	3.09E-02	-1.7	CAV1,CSNK2A2,HRAS,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PLCG1,PLCG2,PRKCB,SHC1
Adenosine Nucleotides Degradation II	3.16E-02		ADA,ADA2,NT5C,NT5C2
CXCR4 Signaling	3.39E-02	-2.7	ADCY10,ELMO1,GNA13,HRAS,LYN,MAP2K1,MAPK1,MAPK3,PAK2,PIK3C2B,PIK3CA,PLCB3,PRKCB,PRKCD,PRKCH,RACK1,RHO G,RHOT1,RHOT2

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Canonical Pathways	p-value	z-score	Proteins
Acute Myeloid Leukemia Signaling	3.39E-02	-1.3	HRAS,IDH2,MAP2K1,MAP2K5,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,PML,STAT5A
Inhibition of Angiogenesis by TSP1	3.55E-02	-2.0	CASP3,FYN,GUCY1B1,HSPG2,MAPK1,MAPK14
Sertoli Cell-Sertoli Cell Junction Signaling	3.72E-02		A2M,ACTB,ACTG2,ADCY10,GUCY1B1,HRAS,ITGA5,ITGB1,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,PRKAR1A,SPTA1,TUBA1B,TUBA4A,VCL,WAS,YBX3
Tight Junction Signaling	3.72E-02		ACTB,ACTG2,ARHGEF2,CASK,CPSF3,CSTF2,MYH11,MYH6,NAPB,NFKB1,NFKB2,NSF,NUDT21,PPP2R5A,PPP2R5D,PRKAR1A,SAFB,VCL,YBX3
FcγRIIB Signaling in B Lymphocytes	3.80E-02	-1.4	BTK,HRAS,LYN,PIK3C2B,PIK3CA,PLCG2,SHC1,SYK
PPAR Signaling	3.89E-02	1.7	AIP,EP300,HRAS,HSP90AB1,IKBKB,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,SHC1,STAT5A
Cardiac Hypertrophy Signaling	3.89E-02	-2.3	ADCY10,ADSS2,CAMK4,EIF4E,EP300,GNA13,HRAS,HSPB1,MAP2K1,MAP3K6,MAPK1,MAPK14,MAPK3,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PPP3CA,PPP3CB,PRKAR1A,RACK1,RHOG,RHOT1,RHOT2
Neuropathic Pain Signaling In Dorsal Horn Neurons	3.89E-02	-2.1	CAMK1D,CAMK4,MAPK1,MAPK3,NTRK2,PIK3C2B,PIK3CA,PLCB3,PLCG1,PLCG2,PRKAR1A,PRKCB,PRKCD,PRKCH
ERK5 Signaling	3.98E-02	-2.3	EP300,GNA13,HRAS,MAP2K5,RPS6KA3,RPS6KA5,YWHAB,YWHAH,YWHAZ
iNOS Signaling	3.98E-02	-2.2	CAMK4,IKBKB,LBP,MAPK1,MAPK14,NFKB1,NFKB2
Prostate Cancer Signaling	4.17E-02		EP300,FOXO1,HRAS,HSP90AB1,MAP2K1,MAPK1,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,SIN3A
PEDF Signaling	4.27E-02	-0.9	CASP7,HRAS,IKBKB,MAPK1,MAPK14,MAPK3,NFKB1,NFKB2,PIK3C2B,PIK3CA,WASF2
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	4.37E-02		CDIPT,PIP4K2A,PLCB3,PLCG1,PLCG2

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Canonical Pathways	p-value	z-score	Proteins
Salvage Pathways of Pyrimidine Ribonucleotides	4.47E-02		CMPK2,GRK6,MAP2K1,MAP3K6,MAPK1,MAPK3,PAK2,PKN1,PRKAA1,PRKCD,PRKCH,PRPF4B
CMP-N-acetylneuraminat e Biosynthesis I (Eukaryotes)	4.68E-02		NAGK,NANS
2-oxobutanoate Degradation I	4.68E-02		MCEE,PCCB
Folate Polyglutamylatio n	4.68E-02		MTHFD1,MTHFD1L
IGF-1 Signaling	4.68E-02	-1.0	CSNK+A228:G240,MAP2K1,MAPK1,MAPK3,PIK3C2B,PIK3CA,PRKAR1A,SHC1,YWHAB,YWHAH,YWHAZ

Supplementary Table 4: Canonical pathways altered by radiation. Criteria for pathway changes were non-zero absolute activation z-score and Benjamini-Hochberg corrected Fisher's exact test p-value <0.05. Derived from LC-MS/MS proteomic analysis of NHP MLN extract after 12 Gy PBI/BM2.5