

Simvastatin Attenuates Radiation-Induced Murine Lung Injury and Dysregulated Lung Gene Expression

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Online Data Supplement

Supplemental Table 1: Gene filtering criteria and results by significant analysis of microarray

Gene List*	2-group comparison	Delta	FDR%	Fold	Probe sets	Up	Down
1	Radiation vs Control	15	3.8	2.0	3224	677	2547
2	Radiation-Simva vs Radiation	15	4.5	2.0	3037	2560	477
3	Radiation- Simva vs Simva	15	3.0	2.0	933	461	472

* Gene list 1, 2 and 3 are the microarray result of 6 wks observation (GEO accession number GSE14431). The full lists of genes can be found in website <http://phenos.bsd.uchicago.edu/publication/Radiation-Simvastatin>.

Supplemental Table 2: Biological process enriched with genes repressed by irradiation and reversed by simvastatin

GO ID - Function Name	Gene List 1		Gene List 2	
	#	<i>q</i> -value	#	<i>q</i> -value
GO:0006511 ubiquitin-dependent protein catabolic process	22	1.6E-03	17	4.5E-02
GO:0006350 Transcription	156	5.5E-04	125	8.2E-03
GO:0006397 mRNA processing	41	3.1E-07	31	8.2E-03
GO:0007186 GPCR protein signaling pathway	12	1.9E-03	8	8.4E-03
GO:0006355 regulation of transcription, DNA-dependent	144	8.4E-03	136	4.5E-02
GO:0016568 chromatin modification	25	1.9E-03	19	4.8E-02
GO:0008380 RNA splicing	31	3.1E-05	24	1.7E-02
GO:0008152 metabolic process	-----	NS	15	1.3E-02
GO:0007242 intracellular signaling cascade	-----	NS	36	1.7E-02
GO:0006468 protein amino acid phosphorylation	-----	NS	31	1.4E-02

Differentially expressed genes in Gene list 1 and 2 were identified by Significant Analysis of Microarray described in Supplemental Table 1. The genes downregulated by irradiation in Gene list 1 or the genes upregulated by simvastatin in Gene list 2 were uploaded into Onto-Express software to identify overrepresented Gene Ontology (GO) categories. The significance is set at *q*-value < 0.05 with more than 6 genes in the biological process (see Methods). *: *p*-value adjusted by Benjamini-Hochberg approach to control multiple test.

Supplemental Table 3: PubMed database blast (PubMatrix) of potential gene/protein RILI interactome components.

Pubmatrix	Radiation	irradiation	X-ray	pulmonary fibrosis	Radiation pneumonitis
CDC2a	0	1	0	0	0
ccna2	2	3	1	0	0
syk	22	23	19	1	0
fcer1g	1	1	0	0	0
vav3	0	0	0	0	0
CD44	145	194	28	22	2
mmp9	12	13	11	6	0
itgam	99	110	17	11	0

PubMatrix analysis of selected prioritized interactome genes/proteins depicted in Figure 4B. These interacting proteins were blasted against PubMatrix headers reflecting radiation responses. The majority of these genes reflect involvement in normal cellular responses to radiation.