

Table S1. Sequences of primers used for quantitative PCR reactions.

Gene name	Primer sequence (5'-3')	Product size (bp)
<i>β-actin</i> F	ACCCTAAGGCCAACCGTGAA	193
<i>β-actin</i> R	ATGGCGTGAGGGAGAGCATAG	
<i>IL-18</i> F	CAGGCCTGACATCTTCTGCAA	105
<i>IL-18</i> R	TCTGACATGGCAGCCATTGT	
<i>HIF-1α</i> F	TCCATGTGACCATGAGGAAA	160
<i>HIF-1α</i> R	CTTCCACGTTGCTGACTTGA	
<i>IL-1β</i> F	TGAAGCAGCTATGGCAACTG	183
<i>IL-1β</i> R	TTGTTGATGT GCTGCTGTGA	
<i>IL-6</i> F	AGTTGCCTTCTTGGGACTGA	159
<i>IL-6</i> R	TCCACGATTTCCCAGAGAAC	
<i>PCK1</i> F	CTGCATAACGGTCTGGACTTC	159
<i>PCK1</i> R	CAGCAACTGCCCCGTACTCC	
<i>G6pc</i> F	CGACTCGCTATCTCCAAGTGA	173
<i>G6pc</i> R	GTTGAACCAGTCTCCGACCA	
<i>Fbp1</i> F	CACCGCGATCAAAGCCATCT	161
<i>Fbp1</i> R	AGGTAGCGTAGGACGACTTCA	
<i>PC</i> F	CTGAAGTTCCAAACAGTTCGAGG	162
<i>PC</i> R	CGCACGAAACACTCGGATG	

Figure S1. The SUVmean and SUVmax values measured in the left hepatic parenchyma on the first and third post-irradiation days. There was no significant increased FDG uptake between RT (n=6) group and no-RT (n=6) group in post-irradiation days.

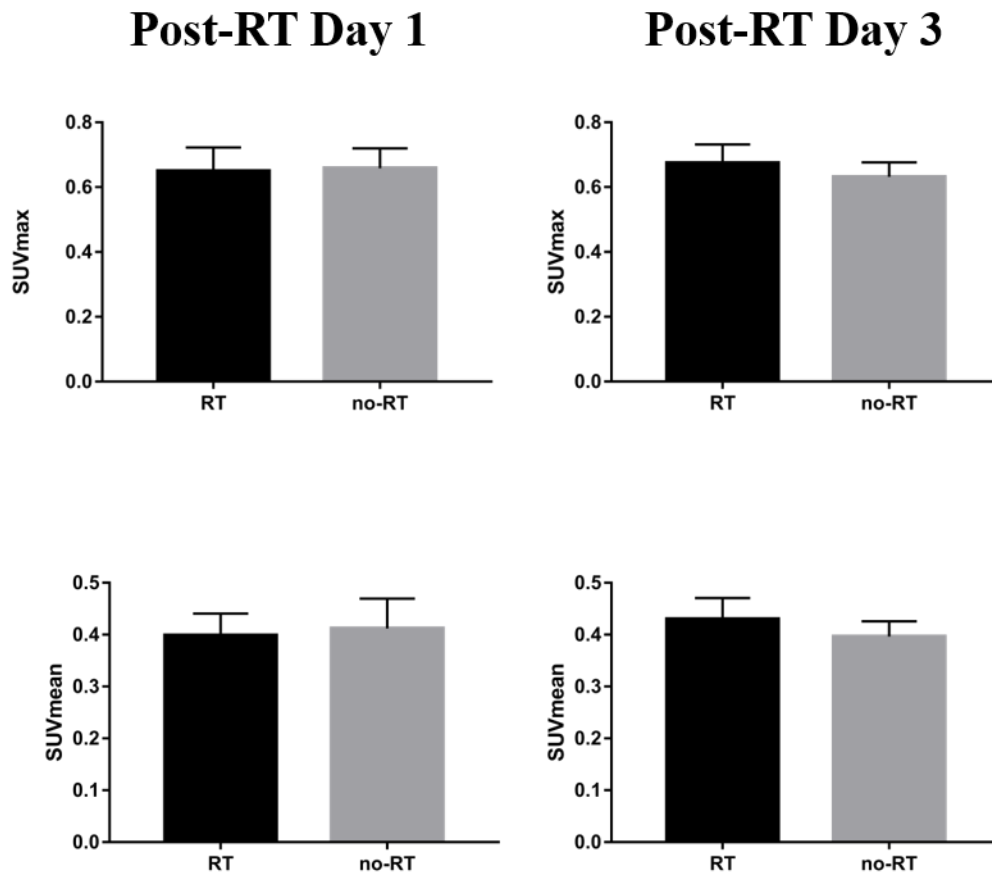


Figure S2. The comparison of FDG uptake expressed as the ratio of right to left lobes in tumor-free animals with and without irradiation after 3 day RT. In experiments conducted in tumor-free animals, the right-to-left ratio of ^{18}F -FDG uptake in the liver parenchyma measured on post-RT day 3 was 1.13-fold higher in the RT (n=4) group compared with the no-RT (n=4) group (1.11 ± 0.10 *versus* 0.98 ± 0.03 , respectively, $p < 0.05$).

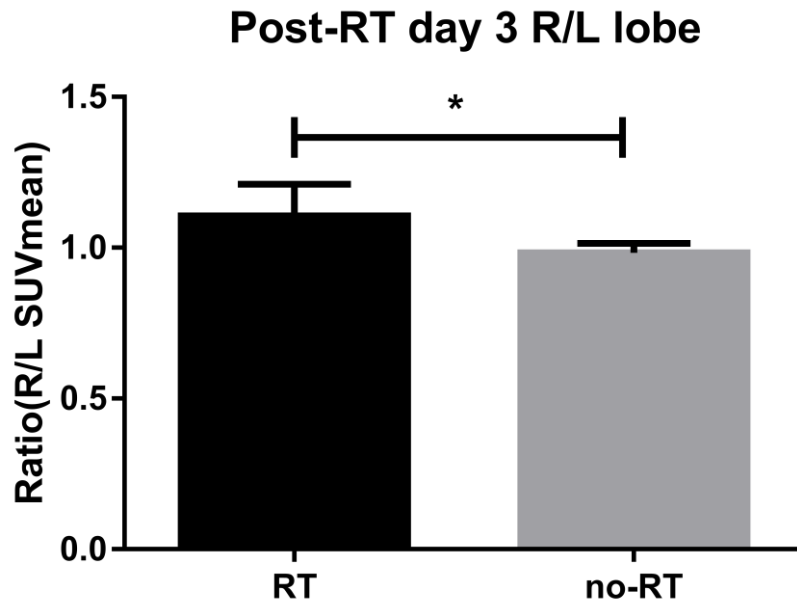


Figure S3. Lymphocytes and macrophages subpopulations within liver parenchyma identified using CD8, F4/80 and CD68 immunohistochemical staining. Representative section of right liver parenchyma stained with (a) CD8, F4/80, and CD68 on post-RT day 1 in the RT group, compared to the no-RT group. (b) CD8, F4/80, and CD68 on post-RT day 3 in the RT group, compared to the no-RT group. Nonetheless, there was no significant expansion of CD8⁺ T cells as well as of the F4/80⁺ or CD68⁺ macrophage populations in liver tissues on post-RT days 1 and 3

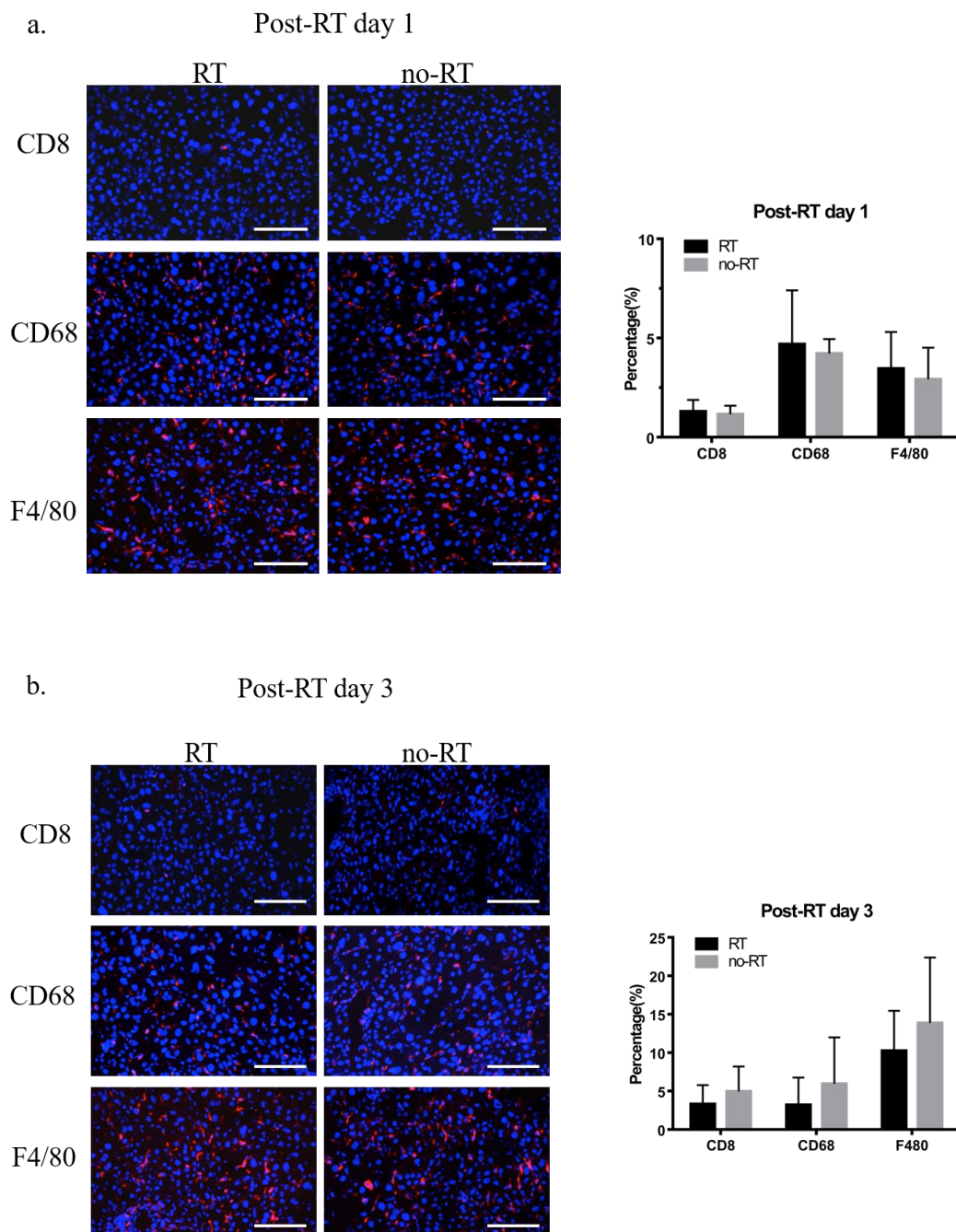


Figure S4. Expression levels of genes encoding for pro-inflammatory cytokines in the RT and no-RT groups on the first and third post-irradiation days (left lobe of the liver). On the first post-irradiation day, the expression levels of the IL-18 and IL-6 genes (expressed as fold-change) were significantly increased in the RT group – but not in the no-RT group. On the third post-irradiation day, the expression levels of the IL-1 β , HIF-1 α , and IL-6 genes (expressed as fold-change) were significantly increased in the RT group – but not in the no-RT group.

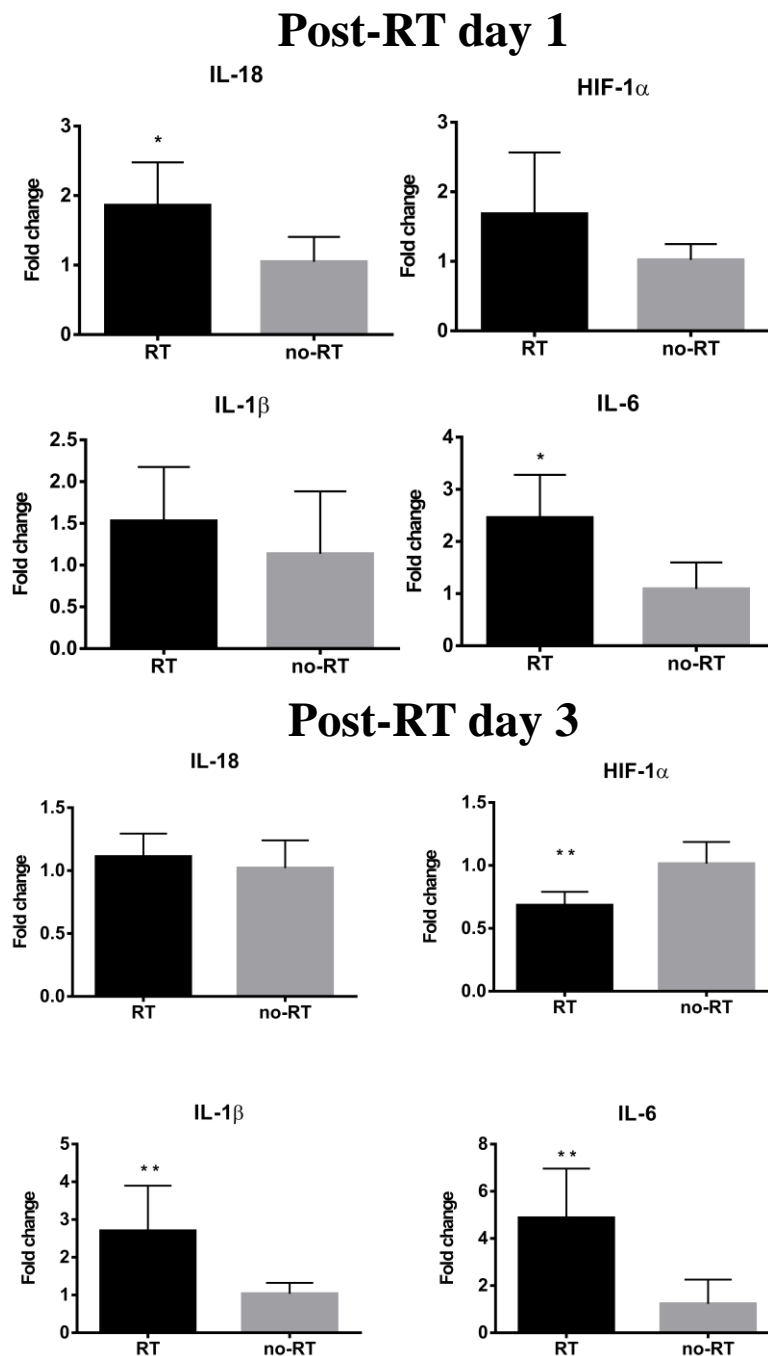


Figure S5. The extent of liver damage was assessed by measuring serum levels of AST, ALT, and albumin on the first and third post-irradiation days. Compared with control animals (n=3), the presence of experimental tumors resulted in increased ALT (36.4 ± 11.00 versus 52.67 ± 8.08 IU/L, respectively, $p = 0.021$) and albumin levels. However, ALT, AST and albumin levels did not show significant differences in the RT (n=3) and no-RT (n=3) groups on post-RT neither day 1 nor day 3.

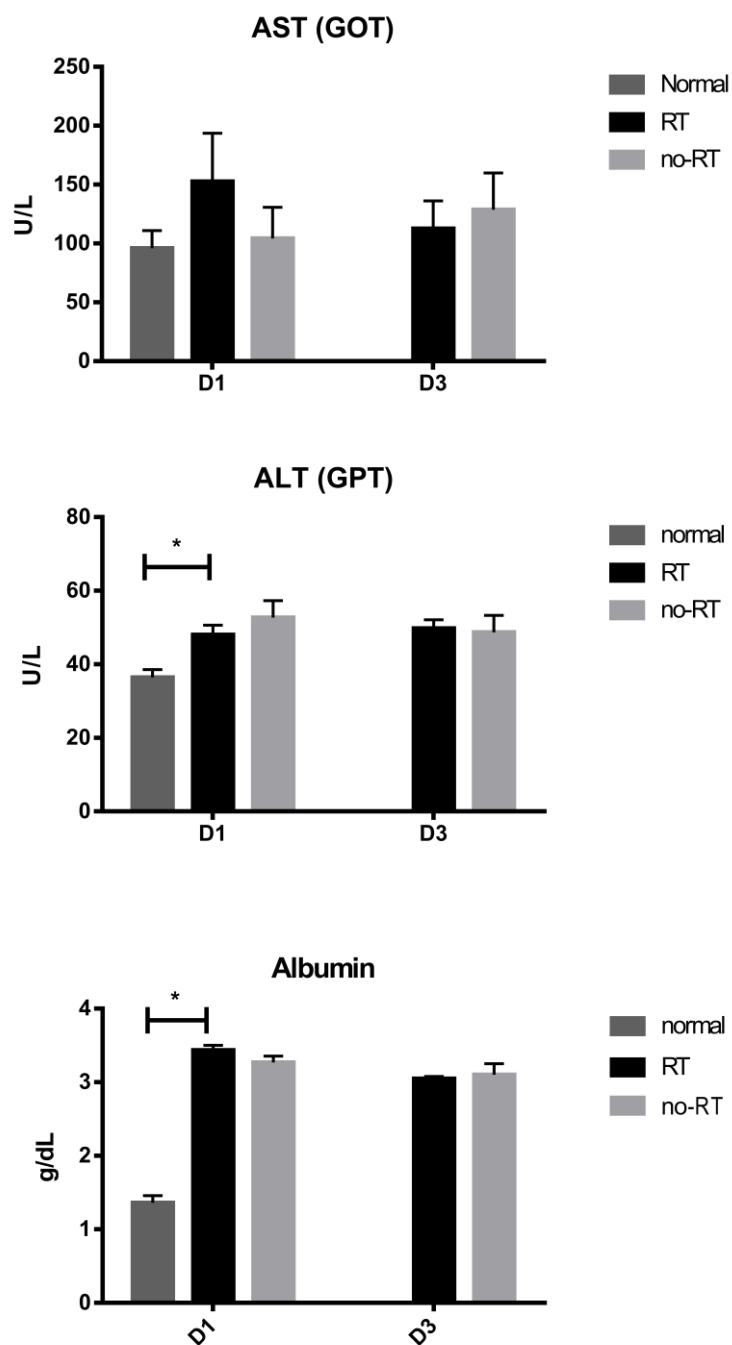


Table S2. Predicted (MetaboAnalyst 3.0) alterations in metabolic pathways in the right and left lobes of the liver on the first and third post-irradiation days

<i>Region</i>	<i>Metabolic pathway</i>	<i>P</i>
<u>Post-RT day 1</u>		
Right lobe	Starch and sucrose metabolism	<0.001
	Galactose metabolism	<0.001
	Neomycin, kanamycin, and gentamicin biosynthesis	0.005
Left lobe	Galactose metabolism	0.008
	Alanine, aspartate, and glutamate metabolism	0.009
	Neomycin, kanamycin, and gentamicin biosynthesis	0.01
<u>Post-RT day 3</u>		
Right lobe	Glycine, serine, and threonine metabolism	<0.001
	Arginine and proline metabolism	0.003
	Alanine, aspartate, and glutamate metabolism	0.02
	Glyoxylate and dicarboxylate metabolism	0.025
	Nitrogen metabolism	0.047
	D-glutamine and D-glutamate metabolism	0.047
Left lobe	Glycine, serine, and threonine metabolism	<0.001
	Tricarboxylic acid cycle	0.003
	Alanine, aspartate, and glutamate metabolism	0.007
	Riboflavin metabolism	0.018