Fig. S1. Power analysis for discovering differentially expressed genes between various types of HCC and normal liver. Samples from Fe and Si radiation were pooled or un-pooled in high-LET radiation group. The analysis was performed with fdr < 0.1 and using proposed algorithm by Liu and Hwang 2007. Vertical line indicated 34 which is the samples size of our dataset. π_0 values are the estimated proportions of genes that are not changed.
Reference:

Liu, P. and Hwang, J.T. (2007) Quick calculation for sample size while controlling false discovery rate with application to microarray analysis. *Bioinformatics*, **23**, 739-746.

a

	Fe HCC	Si HCC	γ-ray HCC	Spontaneous HCC
Cellular Immune Response				
Humoral Immune Response				
Cytokine Signaling				
Pathogen-Influenced Signaling				
Cell Cycle Regulation				
Cellular Stress and Injury				
Proliferation and Development				
Transcriptional Regulation				
Intracellular and Second Messenger Signaling				
Apoptosis				
Nuclear Receptor Signaling				
Xenobiotic Metabolism				

Mean Z-score
-2.28   0.00   2.28

b

	Fe HCC	Si HCC	γ-ray HCC	Spontaneous HCC
PI3K/AKT Signaling				
PTEN Signaling				
mTOR Signaling				
EGF Signaling				
ERK/MAPK Signaling				
STAT3 Pathway				

Z-score
-2.71   0.00   2.71

c

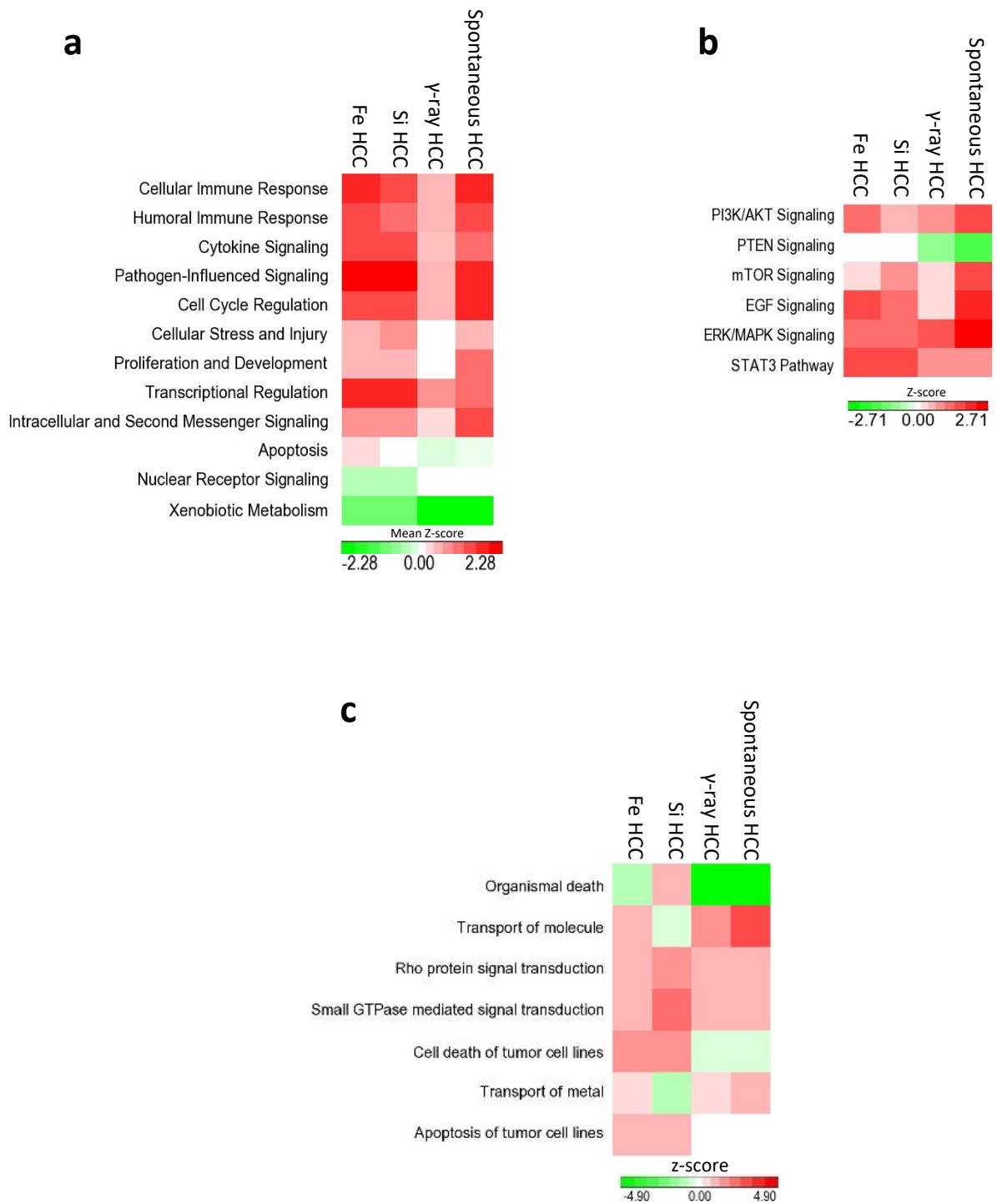|	Fe HCC	Si HCC	γ-ray HCC	Spontaneous HCC
Organismal death				
Transport of molecule				
Rho protein signal transduction				
Small GTPase mediated signal transduction				
Cell death of tumor cell lines				
Transport of metal				
Apoptosis of tumor cell lines				

z-score
-4.90   0.00   4.90

Fig. S2. Z-scores of signaling pathways were plotted as heatmaps from different types of HCC. High-LET HCC samples were divided into Fe and Si induced HCC groups. A. averaged z-scores of all pathways within each functional category. A) positive z-score indicates activation; a negative z-score indicates suppression. B) Signaling pathways known to be associated with human HCC also changed in mouse HCC models. Z-scores representing activation (positive) or suppression (negative) of the pathways were shown as a heatmap. C) Gene functional analysis of mR-HCC genes showed significantly enriched functional groups associated with the gene set.