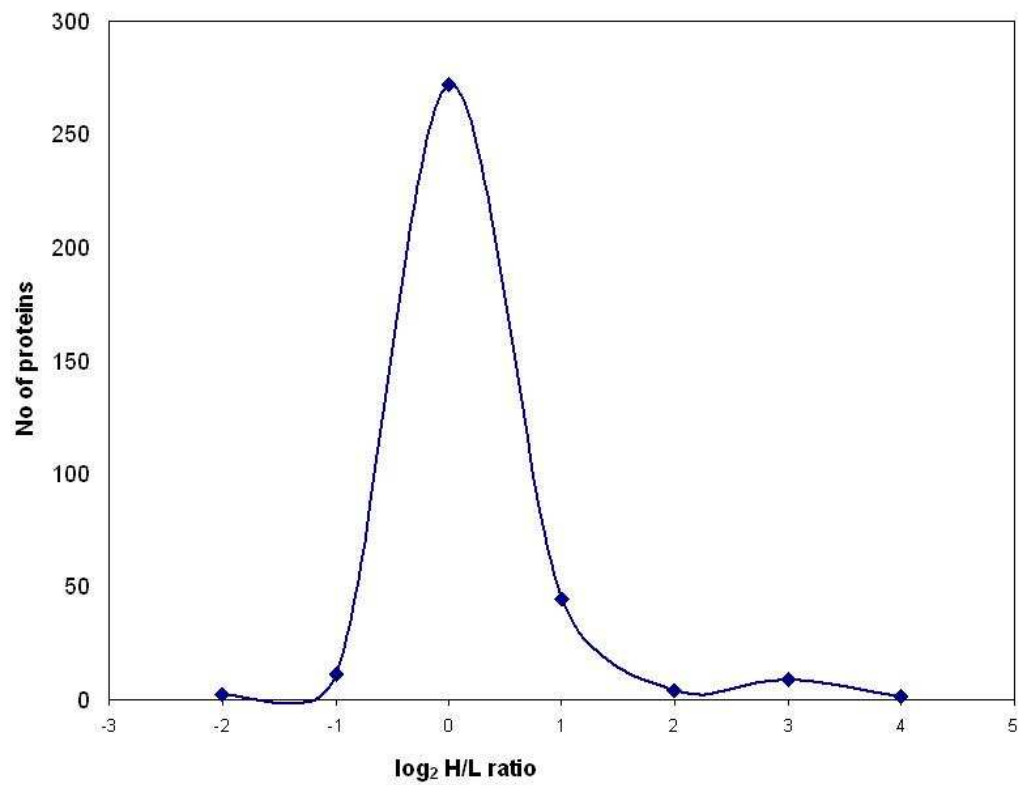
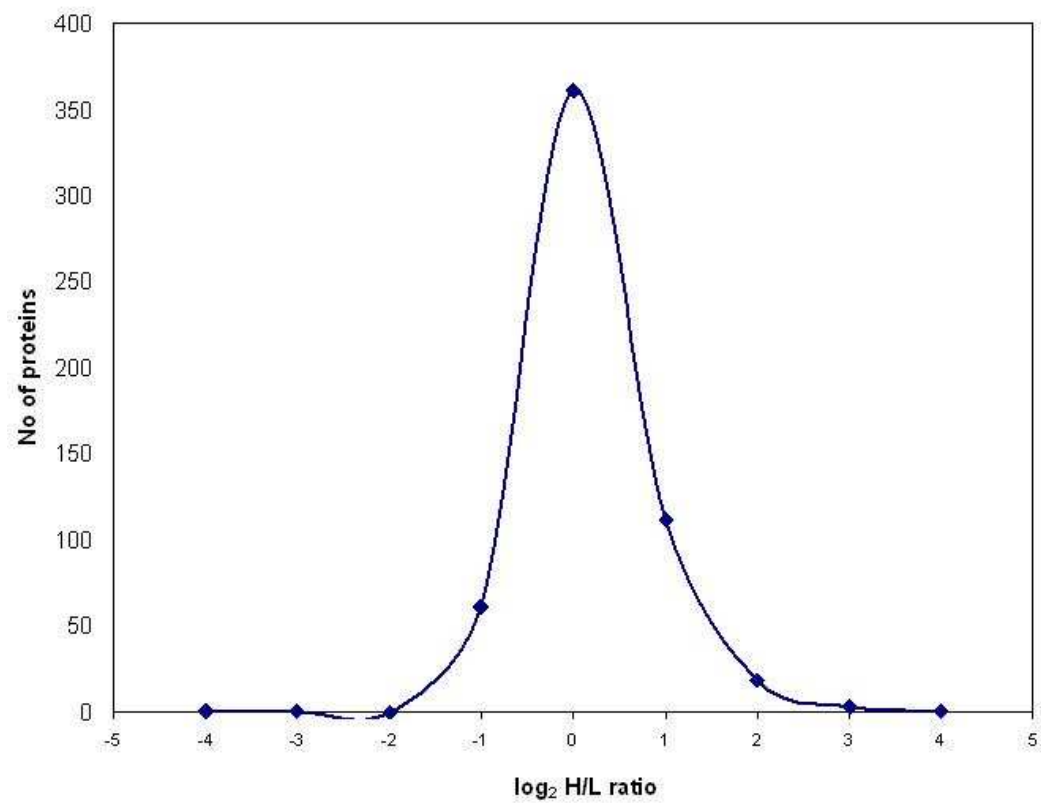


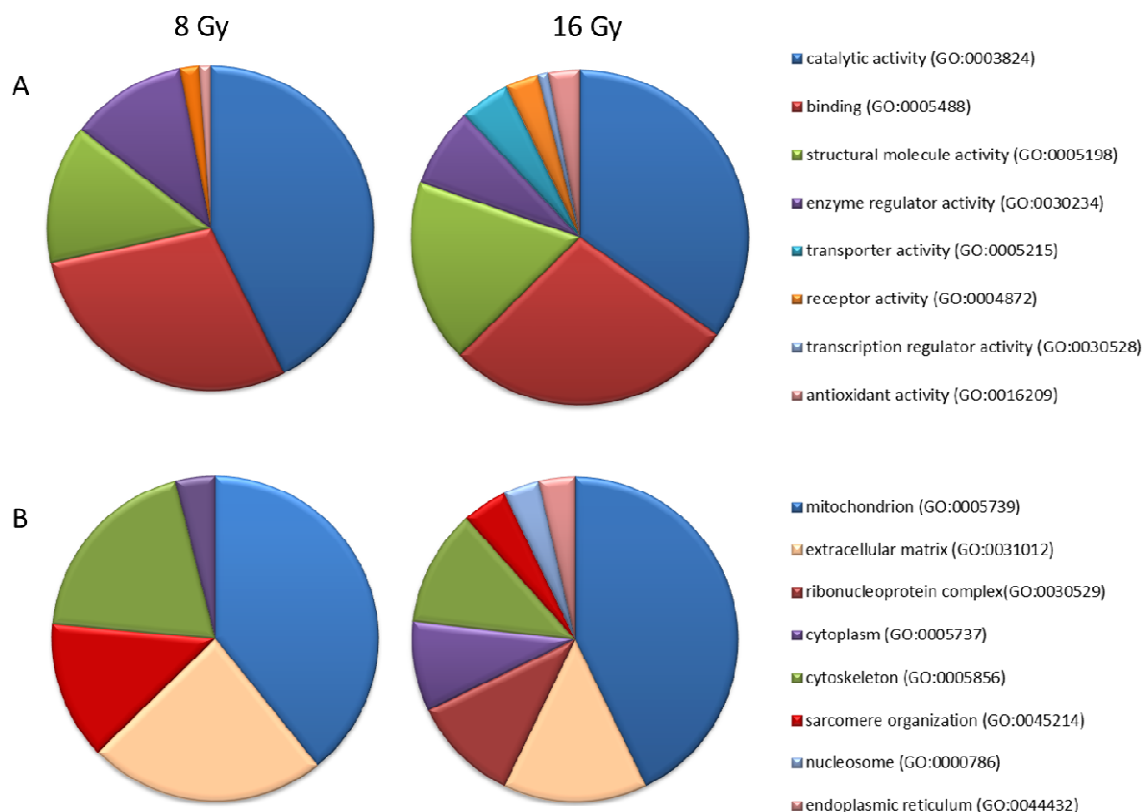
### Supporting Figures:



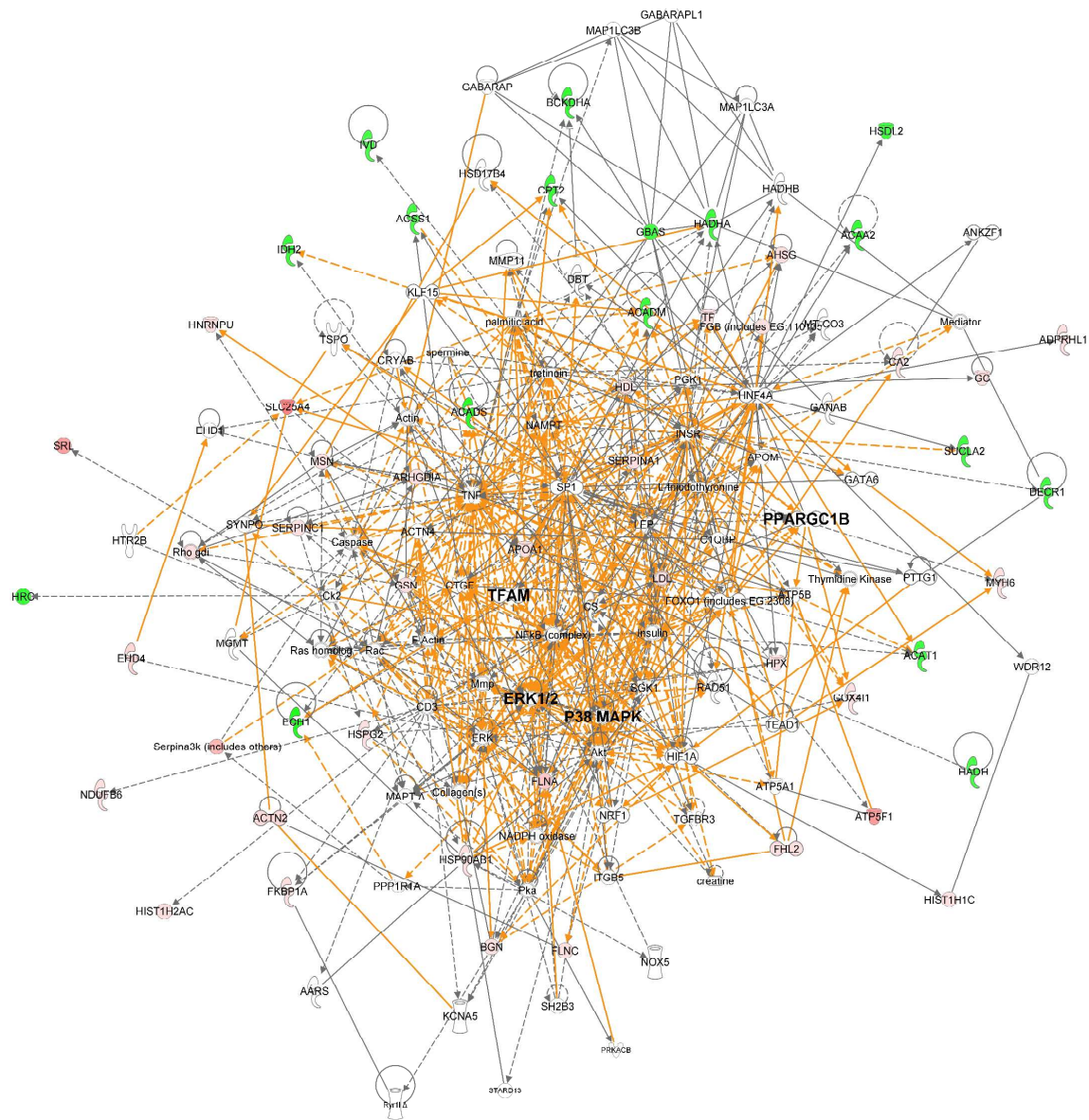
**Figure S1. Lognormal distribution of the quantified proteins based on the variability at the heart proteome after 8 Gy.** Fold changes (H/L ratio) of all identified proteins were log<sub>2</sub> transformed and binned into indicated intervals. Normalization factor:  $1.004 \pm 0.173$



**Figure S2. Lognormal distribution of the quantified proteins based on the variability at the heart proteome after 16 Gy.** Fold changes (H/L ratio) of all identified proteins were log<sub>2</sub> transformed and binned into indicated intervals. Normalization factor:  $0.82 \pm 0.078$

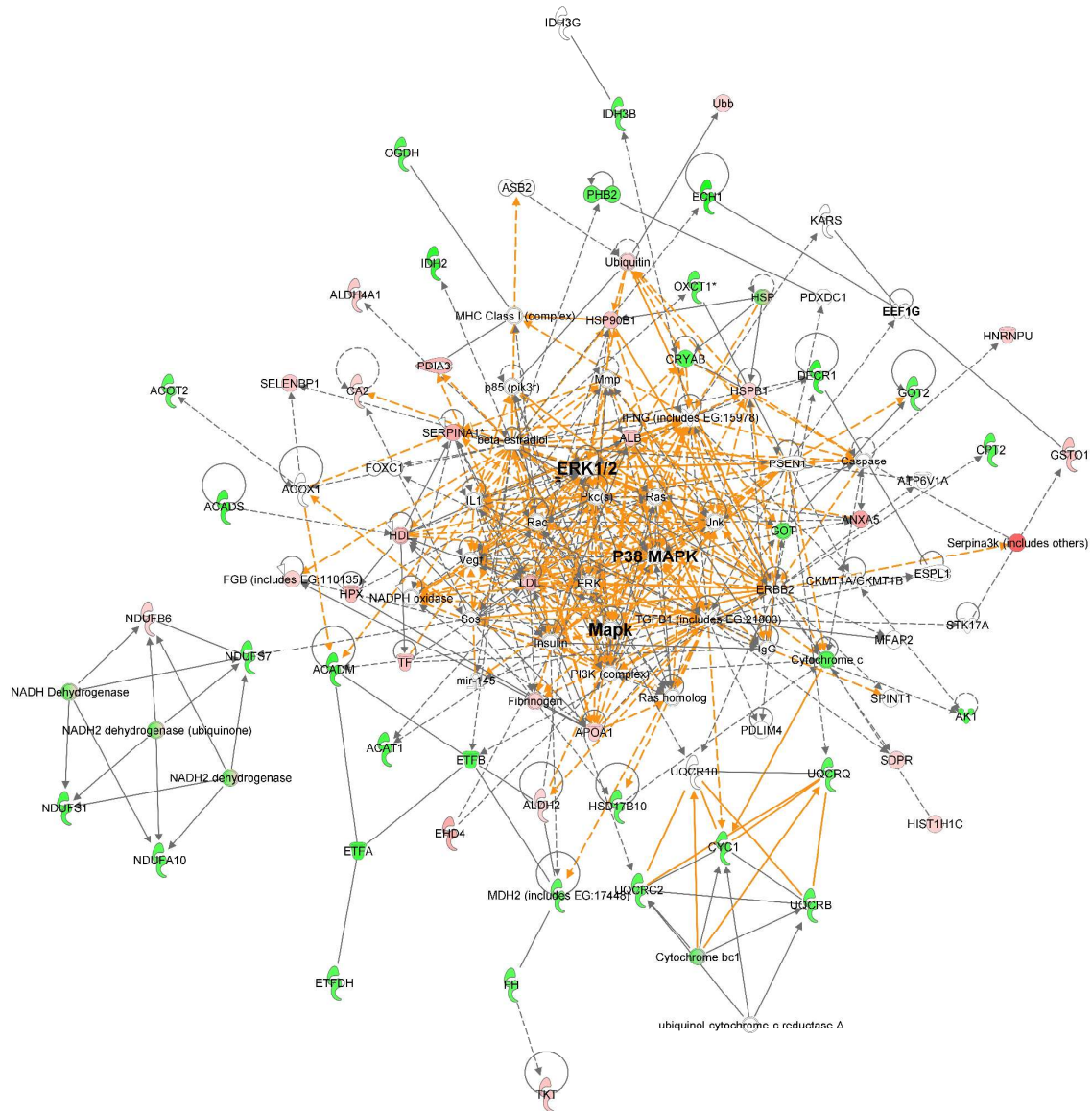


**Figure S3.** Gene ontology (GO) analysis of significantly differentially regulated proteins. The most radiation-responsive GO categories “Molecular function” (A), and “Cellular compartment” (B) using the PANTHER (<http://www.pantherdb.org>) and DAVID bioinformatics tools (<http://www.david.niaid.nih.gov>) are shown. Catalytic activity and binding were the most altered cellular functions by ionizing radiation. The mitochondrial proteins were the most affected protein class.



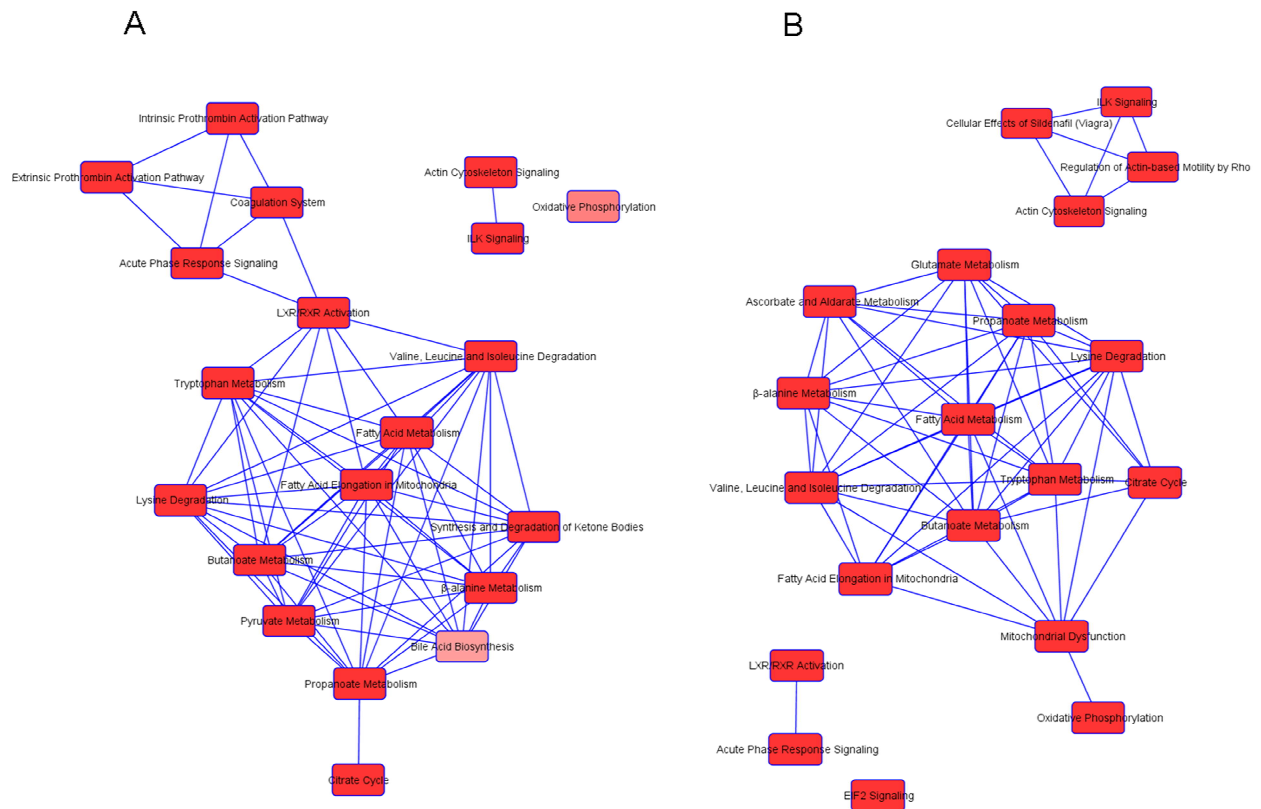
**Figure S4. Graphical representation of the merged of the most significant protein interaction network after 8 Gy using Ingenuity Pathway Analysis of differentially regulated proteins.** All significantly deregulated proteins identified by ICPL were imported into the Ingenuity Pathway Analysis. The up-regulated proteins are marked in red and the down-regulated in green. The nodes represent proteins that are connected with one or several arrows; the solid arrows represent direct interactions and the dotted arrows indirect interactions; direct and predicted protein interactions were searched for (<http://www.INGENUITY.com>).



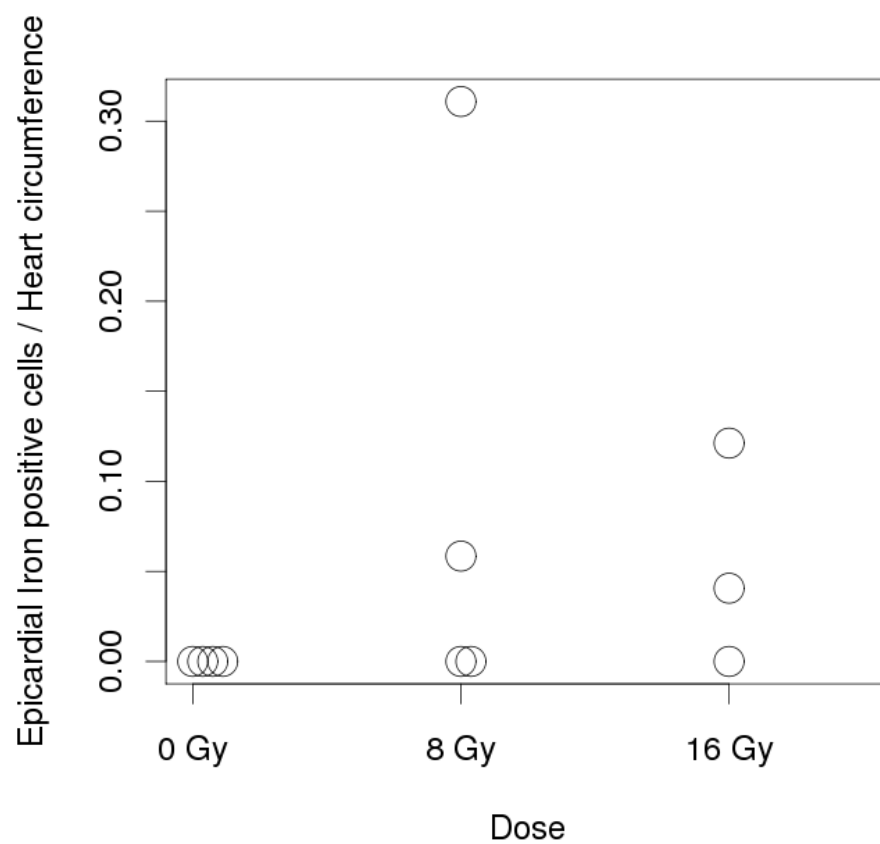


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**Figure S5. Graphical representation of the merged of the most significant protein interaction network after 16 Gy using Ingenuity Pathway Analysis of differentially regulated proteins.** All significantly deregulated proteins identified by ICPL were imported into the Ingenuity Pathway Analysis. The up-regulated proteins are marked in red and the down-regulated in green. The nodes represent proteins that are connected with one or several arrows; the solid arrows represent direct interactions and the dotted arrows indirect interactions; direct and predicted protein interactions were searched for (<http://www.INGENUITY.com>).



**Figure S6. Graphical representation of 20 top canonical pathway networks representing significantly deregulated proteins after 8 Gy (A) and 16 Gy (B).** Compiling of top 20 significant canonical pathways of the significantly deregulated proteins showed overlapping and interconnected pathways mainly involved in metabolic activity and cytoskeletal organization.



**Figure S7. Number of epicardial iron positive cells in control and irradiated hearts.** The number of iron positive cells were counted and normalized to heart area in irradiated and control mice. (Kruskal-Wallis rank sum test).