**Analysis of lncRNA-miRNA-mRNA expression pattern in heart tissue after total body irradiation in a mouse model**

**Supplemental Table Legends**

**Supplemental Table S1: Differentially expressed genes at each dose compared to controls.** Each tab corresponds to a specific dose. Columns B through G list the Agilent probe ID, systematic name (ID of target sequence designed to hybridize with the Agilent probe), p-value, Benjamini-Hochberg adjusted p-value, B statistic (log of the odds that the gene is differentially expressed), and the average log2Fold Change (FC) across samples exposed to the dose, respectively. Probes are listed in order of decreasing significance.

**Supplemental Table S2: Top 20 most significantly up- and down-regulated mRNAs that showed a linear trend across all doses.** Tables of up-regulated (A) and down-regulated (B) linear, or dose-responsive, mRNAs. Gene symbol, systematic name, Benjamini-Hochberg adjusted p-value, B statistic, and the average log2FC across all doses are shown in each table. Genes are listed in order of decreasing significance.

**Supplemental Table S3: Differentially expressed lncRNAs at each dose compared to controls.** Each tab corresponds to a specific dose. Columns B through G list the Agilent probe ID, systematic name, p-value, Benjamini-Hochberg adjusted p-value, B statistic, and the average log2FC across samples exposed to the dose, respectively. Probes are listed in order of decreasing significance.

**Supplemental Table S4: Significantly up- and down-regulated lncRNAs that showed a linear trend across all doses.** Table of up- and down-regulated linear, or dose-responsive, lncRNAs. lncRNA symbol (if annotated), systematic name, Benjamini-Hochberg adjusted p-value, B statistic, and the average log2FC across all doses are shown in each table. For unannotated lncRNAs, a BLAT analysis was performed using ensmbl.org and the overlapping transcript, if any, was listed in the table. The asterisk (\*) denotes the transcripts identified through BLAT. lncRNAs are listed in order of decreasing significance.

**Supplemental Table S5: Differentially expressed miRNAs at each dose compared to controls.** Each tab corresponds to miRNAs that were significantly differentially expressed at the specific dose. Columns B through G list the Agilent probe ID, systematic name, p-value, Benjamini-Hochberg adjusted p-value, B statistic, and the average log2FC across samples exposed to the dose, respectively. Probes are listed in order of decreasing significance.

**Supplemental Table S6: Top 20 most significant miRNAs that showed a linear trend across all doses.** Table of up-regulated linear, or dose-responsive, miRNAs. lncRNA symbol (if annotated), systematic name, Benjamini-Hochberg adjusted p-value, B statistic, and the average log2FC across all doses are shown in each table. For unannotated lncRNAs, a BLAT analysis was performed using ensmbl.org and the overlapping transcript, if any, was listed in the table. The asterisk (\*) denotes the transcripts identified through BLAT. lncRNAs are listed in order of decreasing significance.

**Supplemental Table S7: Differentially expressed genes with involvement in the most activated and most deactivated pathways.** A list of differentially expressed genes and the corresponding log2FC at each dose are included in each tab. The 78 genes in the activated pathways are listed in the first tab, and the 79 genes in the deactivated pathways are listed in the second tab.

**Supplemental Table S8:** **Top 20 probes differentially expressed in this study compared to whole blood from the same animals and human coronary artery endothelial cells.** The most significant 20 genes regulated in a dose dependent manner in the heart samples were compared to differentially expressed genes from whole blood collected from the same animals at 48h and compared to human coronary artery endothelial cells 24h after exposure to 10 Gy irradiation.