

B.

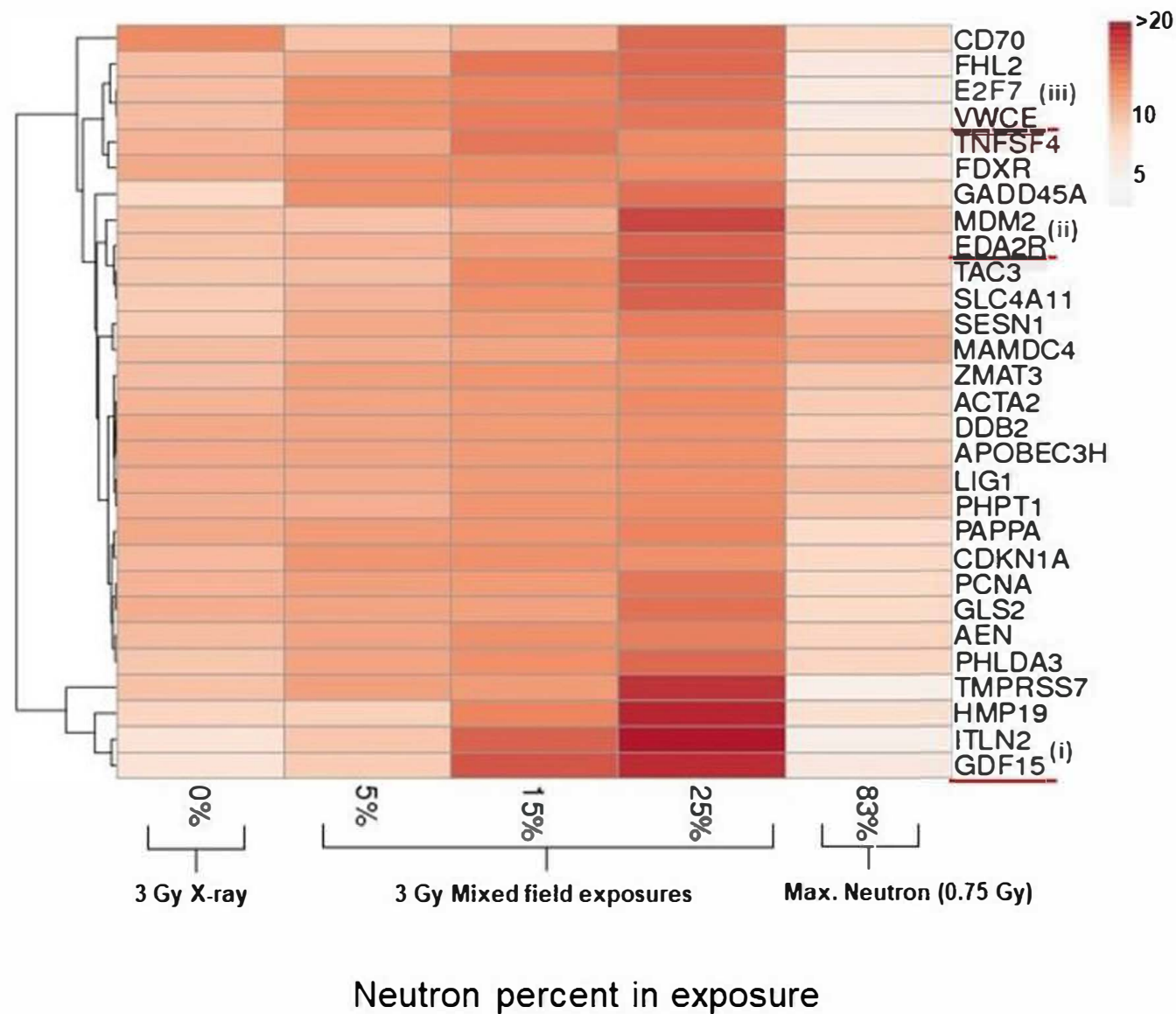
	3 Gy X-ray	3 Gy Mixed field exposures			Max. Neutron (0.75 Gy)
Neutron percent	0%	5%	15%	25%	83%
Number of Unique genes	75	84	159	309	140
IPA analysis of top significant canonical pathways (P-value)	<ul style="list-style-type: none"> Parkinson's signaling (1.27E-03) Amino acids Metabolism (3.28E-02) Calcium Metabolism (1.48E-02) 	<ul style="list-style-type: none"> Amino acids Metabolism (4.92E-03) Notch Signaling (3.95E-03) Glucose Metabolism (1.1E-02) Protein Citrulation (1.22E-02) 	<ul style="list-style-type: none"> Crosstalk between Dendritic cells and Natural Killer cells (7.22E-03) Negative Regulation T-cell signaling (1.3E-03) Death Receptor Signaling (8.15E-03) G-protein mediated signaling (1.43E-02) 	<ul style="list-style-type: none"> Natural Killer-cell Signaling (7.64E-04) Negative regulation of T-cell Signaling (2.03E-04) Innate Immunity (1.21E-02) Communication between Innate and adaptive immune cells (1.02E-02) 	<ul style="list-style-type: none"> Amino acid metabolism (9.50E-03) Hormone mediated signaling (1.53E-02) NAD Biosynthesis (1.01E-02)

Supplementary File S1. Unique differentially expressed genes across all exposures.

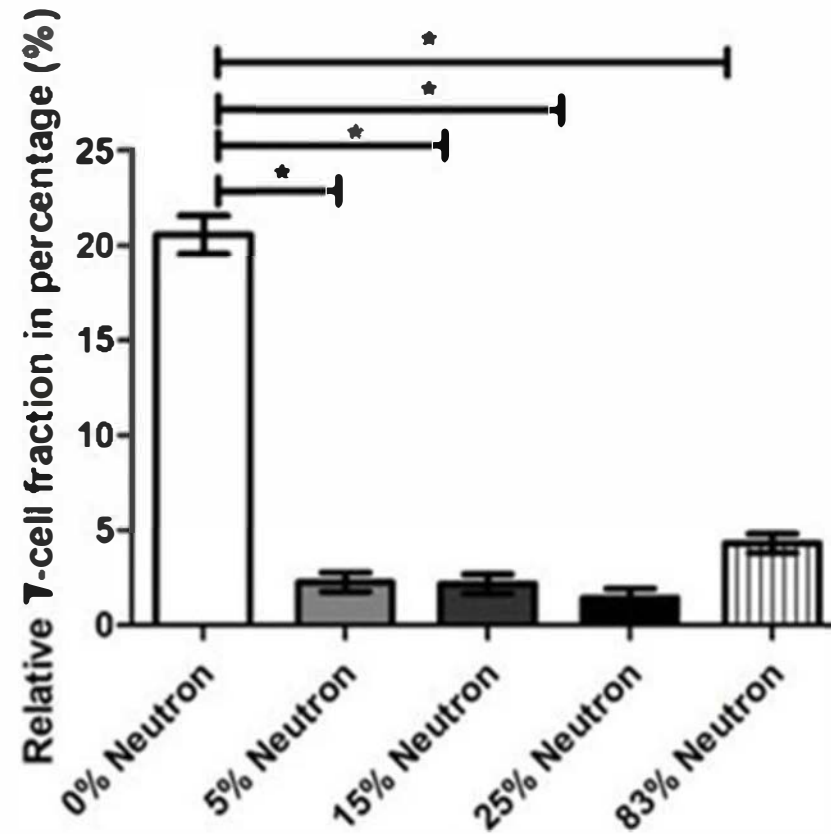
A. Number of unique differentially expressed genes at different neutron exposures (Figure 1A)

B. Table indicating top significant canonical pathways based on P-values (IPA analysis) associated with each set of unique genes for individual exposures (columns are color coded according to neutron percent as shown in A).

C. Unique Differentially expressed Genes involved in T-cell signaling plotted on the basis of p-value (-log) at different neutron exposures. T-cell signaling was not identified as a canonical pathway in the unique gene set at 0% Neutron (3 Gy x-ray). The pathway is not significant at 5% and 83% Neutron exposures.



Supplementary File S2. Genes showing increased expression with increasing neutron percent in the exposures. The expression level at 83% neutron (max. 0.75 Gy) has been added for comparison. Heat map of expression of p53 responsive genes which showed increased trend of expression with increasing neutron percent in mixed field exposures from 0%-25% as observed in microarray. The color indicate fold change compared to controls (non-exposed). Each column represents average of 5 individuals per radiation category. Genes with red underline are validated using qRT-PCR(Figure 2)



Supplementary File S3. Using CIBERSORT tool (reference 37) differentially expressed genes ($P < 0.001$) at each neutron-photon exposure were compared with the expression levels of a standard matrix of blood-cell marker genes to calculate relative percentages of blood cell sub-types contributing to the overall profile. The bars indicate mean T-cell fractions from 5 different individual samples for each neutron exposure. The estimated percentage of other cell types in the blood had poor statistical confidence ($p > 0.05$), and thus not included in the analysis. Error bars indicate \pm SD ($n=5$). * Significant at $P < 0.05$ using T-test compared to 0%Neutron (3 Gy x-ray). The T-cell fraction (percentage%) is relative to the levels in controls.