

Supplementary Figures

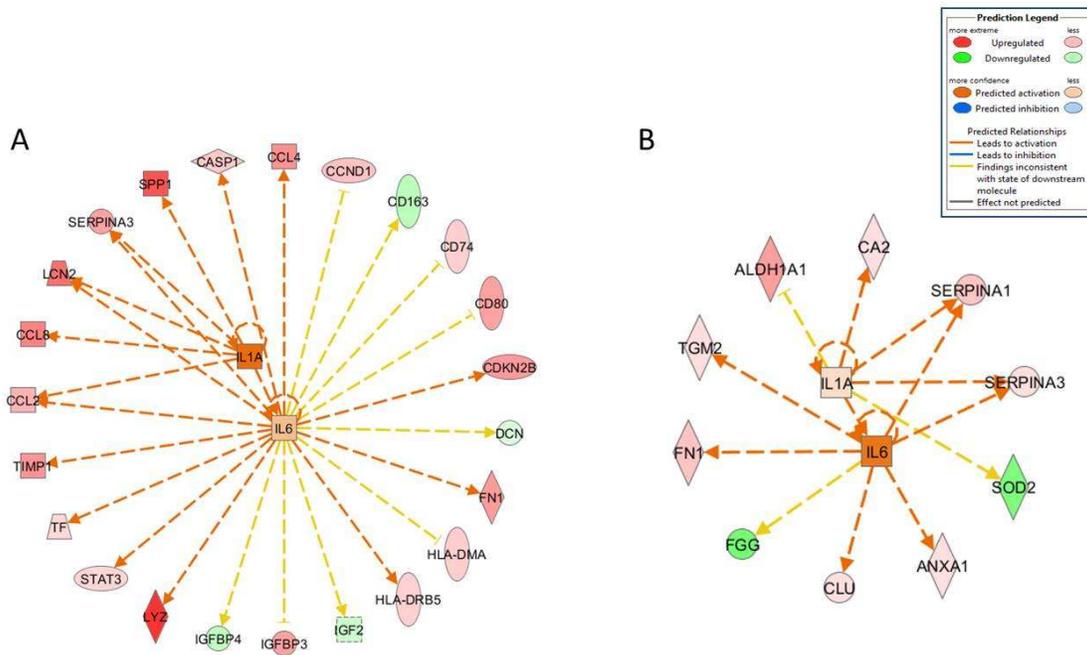


Figure S1. IPA of transcriptomics and proteomics upstream regulators.

Graphical representation of the interleukin-related gene and protein networks in the transcriptome (A) and proteome (B) profiles in irradiated heart (<http://www.INGENUITY.com>). The up-regulated genes and proteins are marked in red and the down-regulated in green. The nodes in orange represent upstream regulators. The gene and protein IDs are given in Tables S2 and S6, respectively.

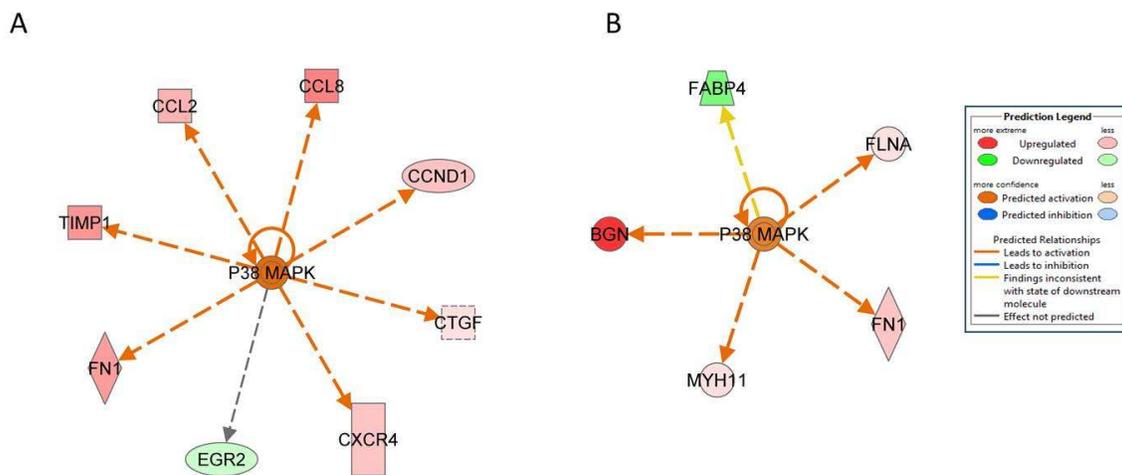


Figure S2. IPA of transcriptomics and proteomics upstream regulators.

Graphical representation of the p38 related gene and protein networks in the transcriptome (A) and proteome (B) profiles in irradiated heart (<http://www.INGENUITY.com>). The up-regulated genes and proteins are marked in red and the down-regulated in green. The nodes in orange represent upstream regulators. The protein and gene IDs are given in Tables S2 and S6, respectively.

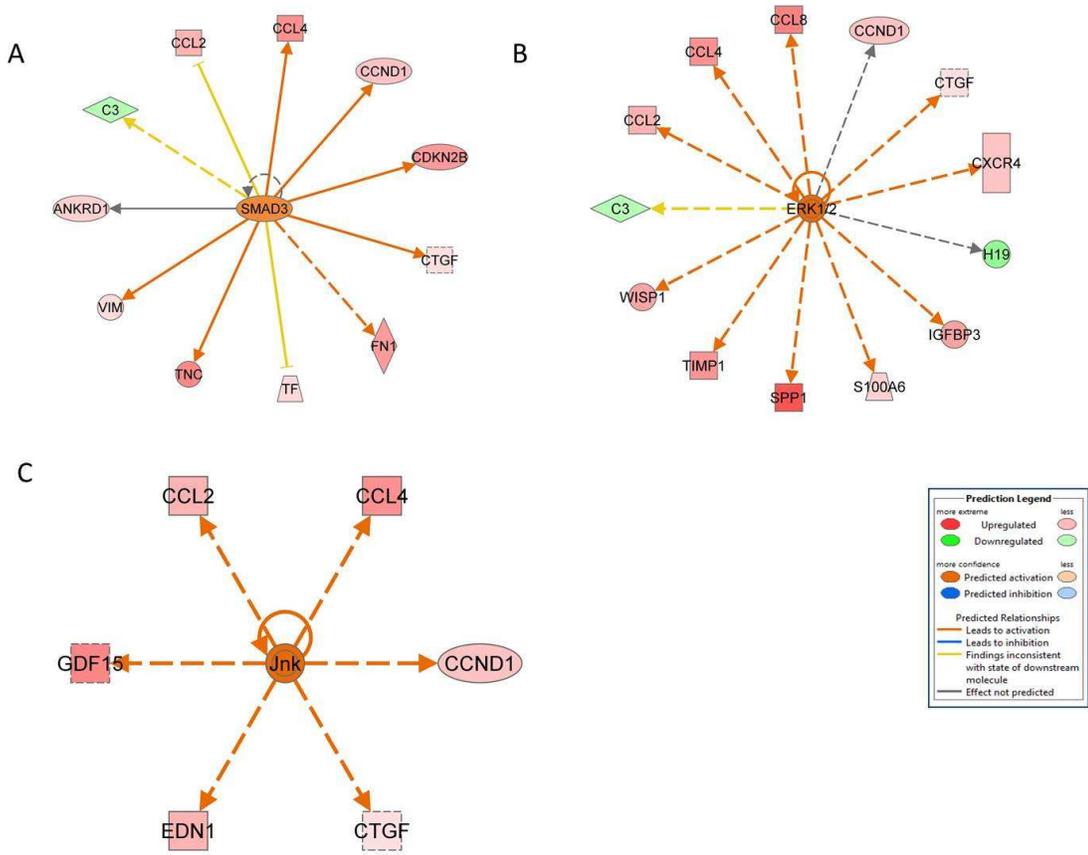


Figure S3. IPA of transcriptomics upstream regulators. Graphical representation of the deregulated TGF beta-related gene networks with their upstream transcriptional regulators *Smad3* (A), ERK 1/2 (*Mapk3/1*) (B) and JNK (*Mapk8*) (C) after irradiation (<http://www.INGENUITY.com>). The up-regulated genes are marked in red and the down-regulated in green. The nodes in orange represent upstream regulators. The gene IDs are given in Table S2.

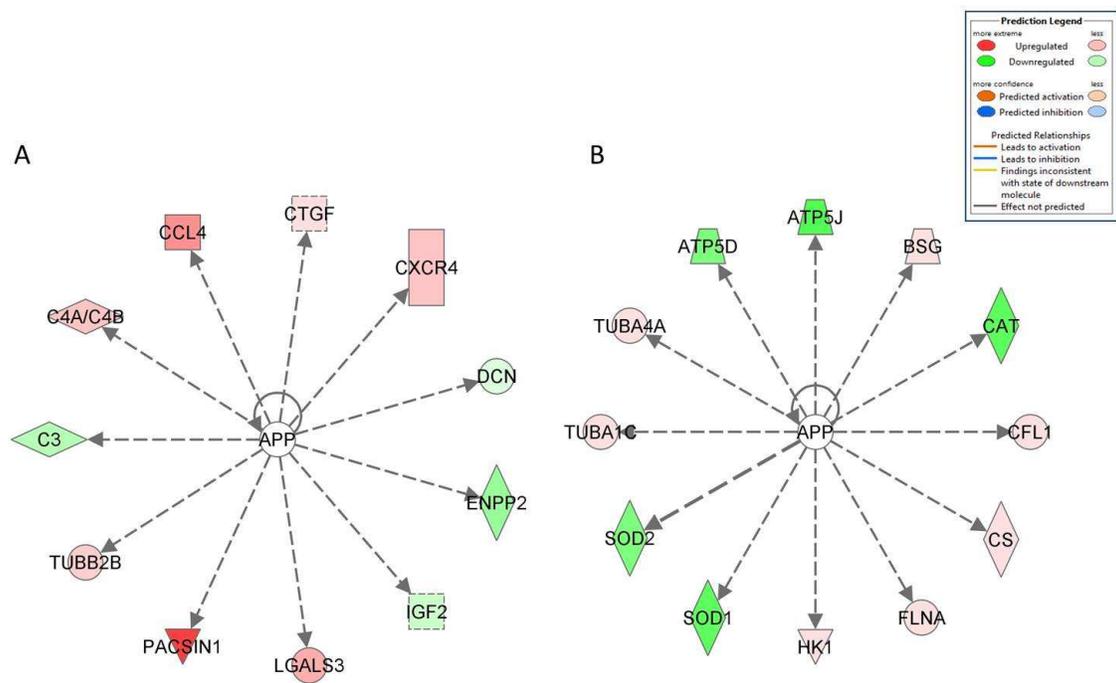


Figure S4. IPA of transcriptomics and proteomics upstream regulators.

Graphical representation of the APP-related gene and protein networks in the transcriptome (A) and proteome (B) profiles in irradiated heart (<http://www.INGENUITY.com>). The up-regulated proteins are marked in red and the down-regulated in green. The node in white represent upstream regulator (APP). The gene protein IDs are given in Tables S2 and S7, respectively.