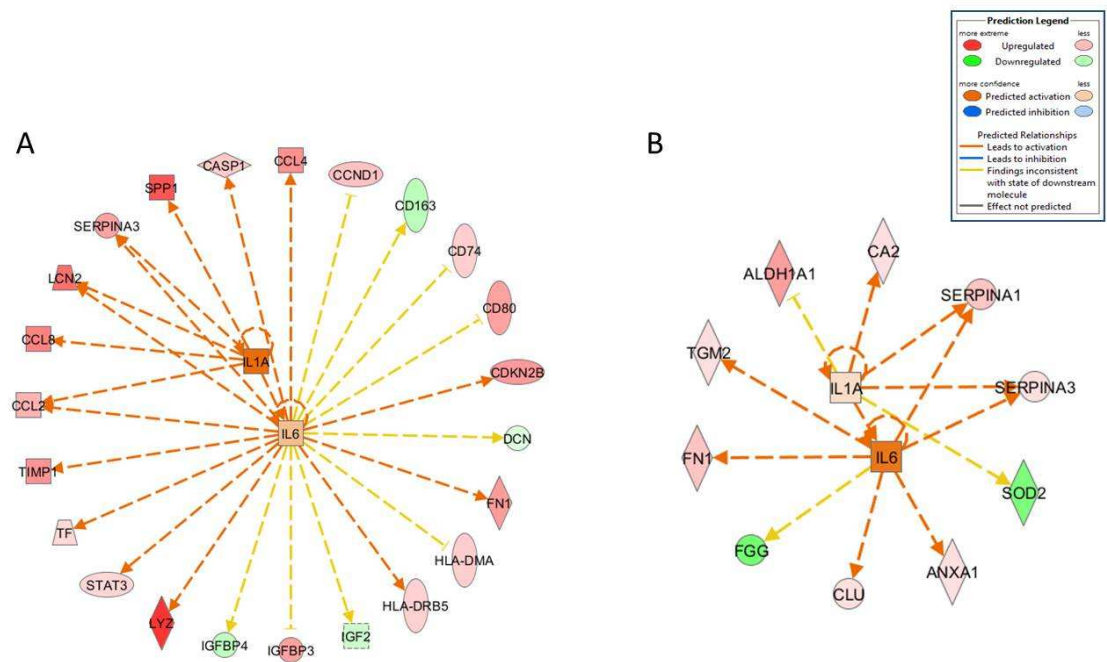
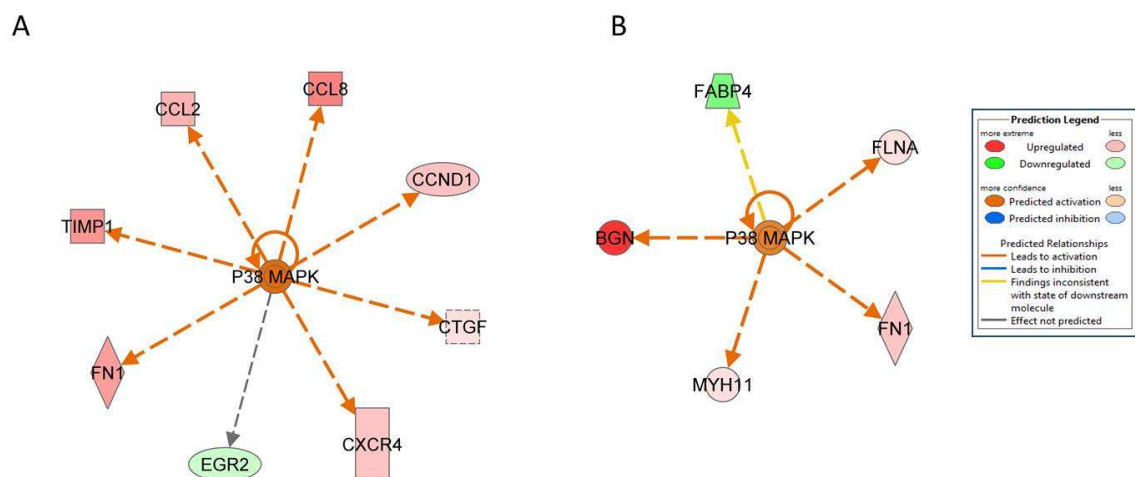


# Supplementary Figures



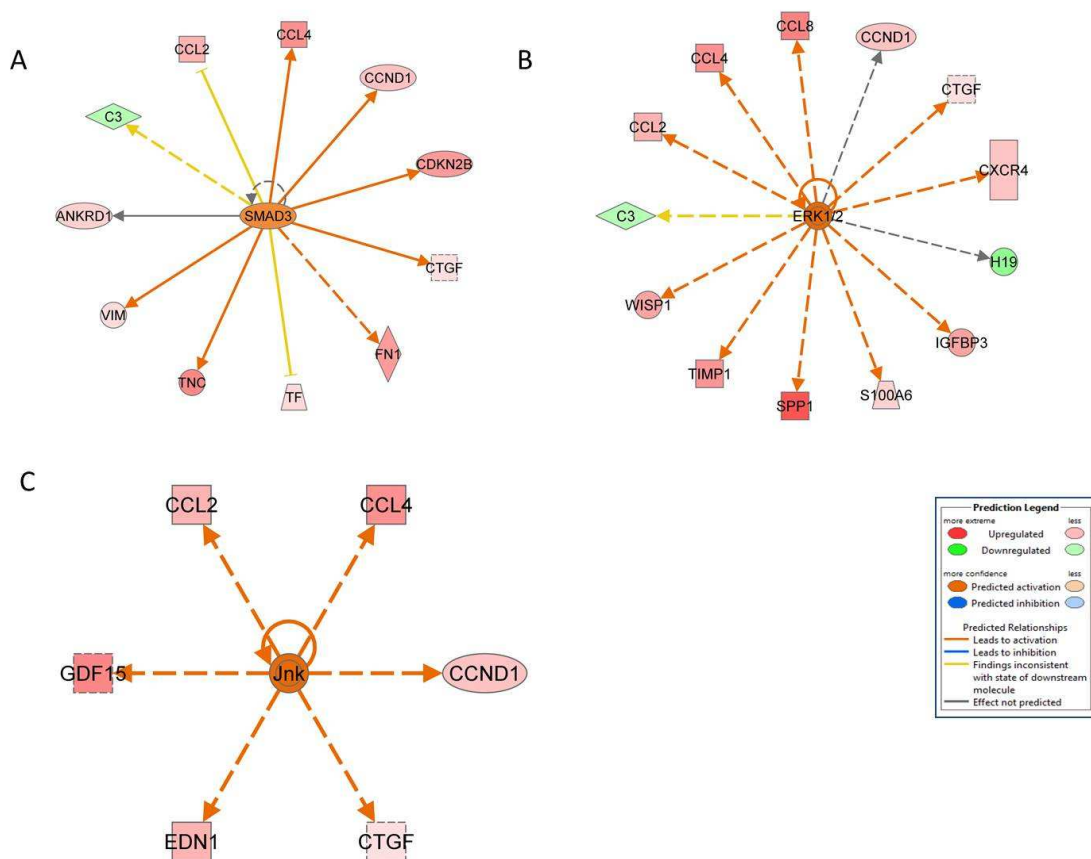
**Figure S1. IPA of transcriptomics and proteomics upstream regulators.**

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.

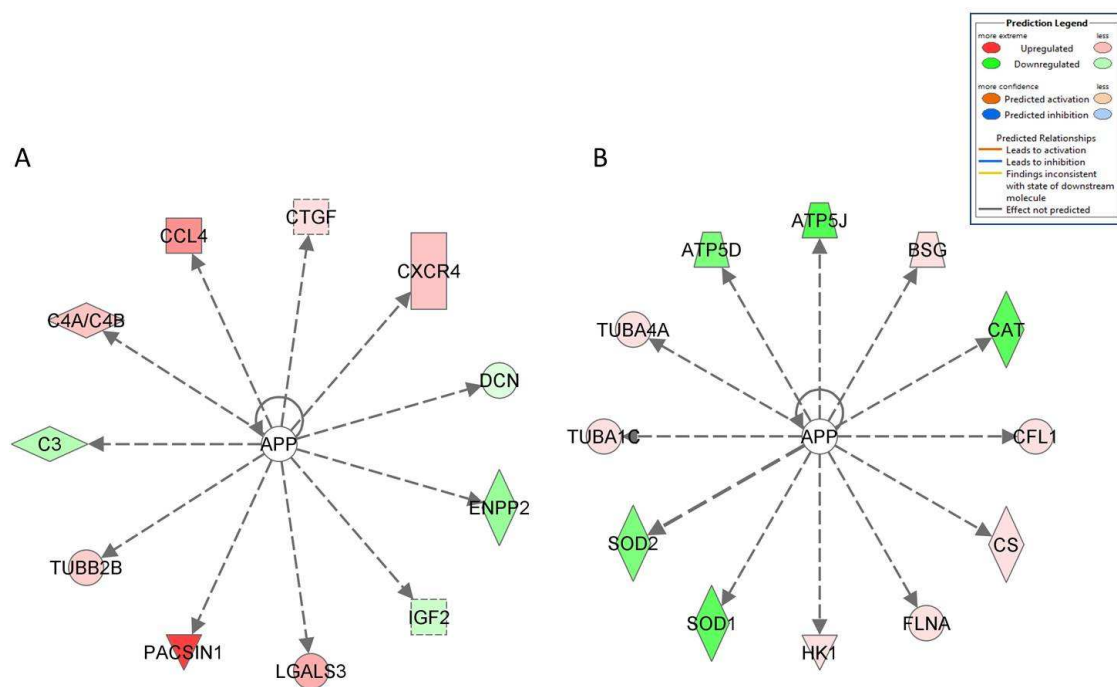


**Figure S2. IPA of transcriptomics and proteomics upstream regulators.**

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.