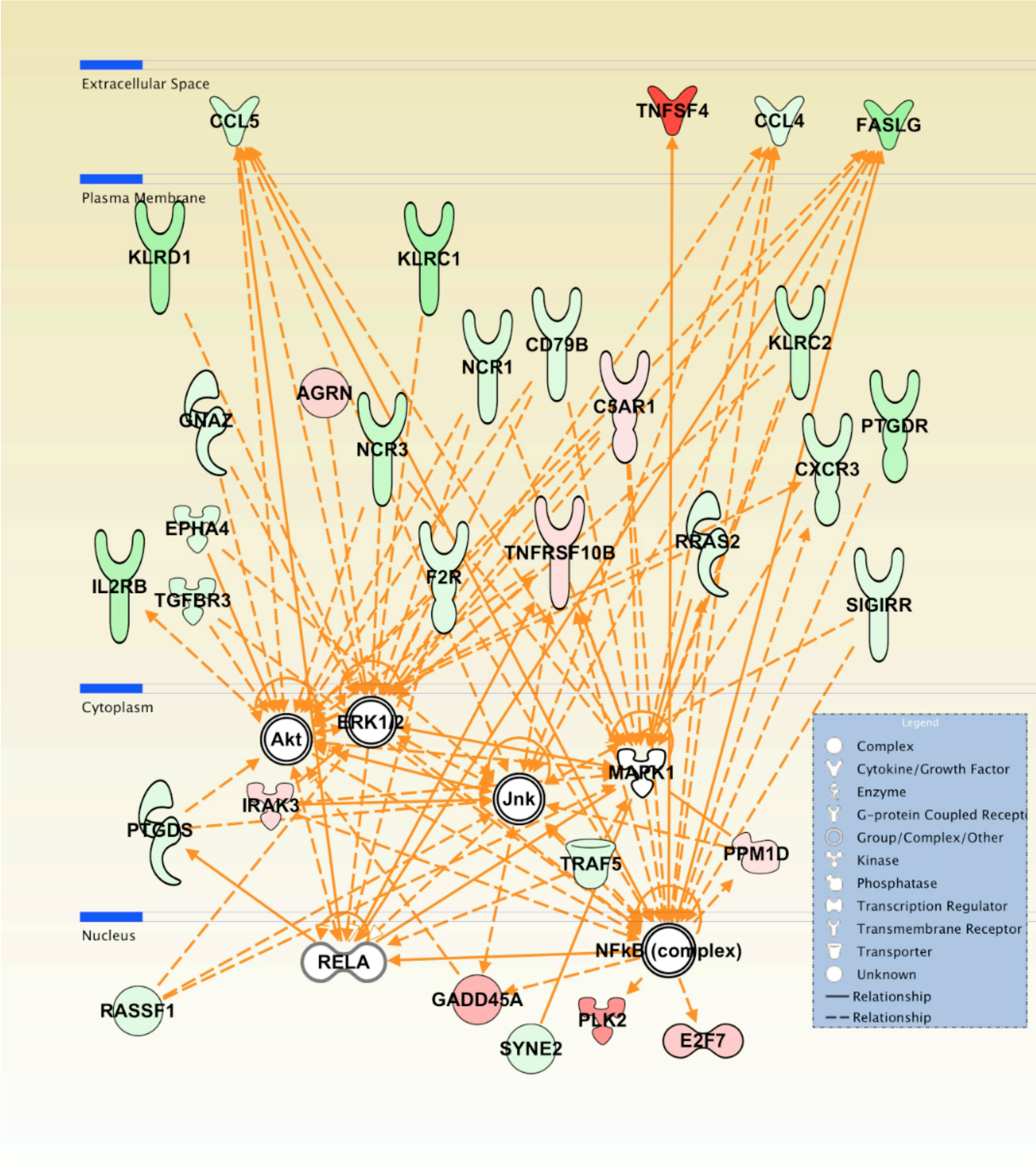
IPA Network Analysis of 48 h differentially expressed genes with signal transduction annotation (from Table 2)



Gene expression level 48 h after 8 Gy is indicated by node color (red = degree of over expression, green = degree of under expression relative to unirradiated controls). Nodes are arranged according to the cellular compartment where the encoded proteins are active. The major pathways implicated in the radiation response at 48 hours are the MAPK pathways, ERK1/2 and Jnk, the Akt pathway, and the NFκB pathway.

Methods

The set of genes with the "signal transduction" gene ontology classification from the PANTHER analysis was imported into Ingenuity Pathway Analysis (IPA) (Ingenuity$^{®}$ Systems, www.ingenuity.com) to analyze network interactions and potential signaling pathways. We used the core analysis function of IPA to identify signal pathway hubs interacting with the largest number of these genes, and then used the grow, connect, and explore functions to construct a single network around these hubs using the information in the Ingenuity Pathway Knowledge Base.