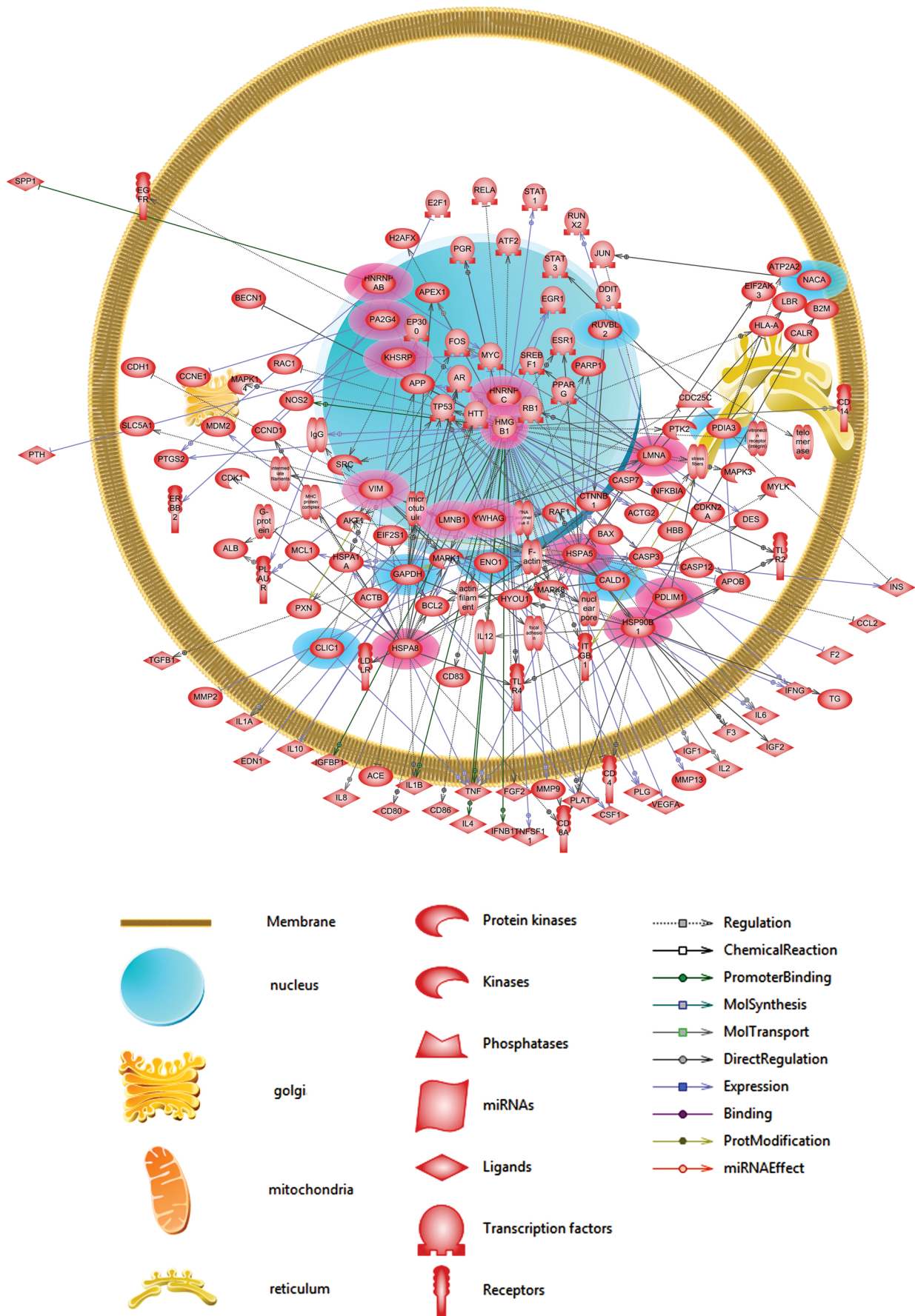


Supplemental figure 1A



Supplemental figure 1B

Supplemental Figure 1. Interaction maps generated by the Pathway Studio analysis of differentially expressed proteins. The molecular interaction maps were constructed using Common Regulator (A) and Common Target (B) methods. The input proteins identified in the 2D-gel proteomic study are highlighted in pink (upregulated) or blue (downregulated). As indicated in the map legend, the shape of the protein indicates its functional class, and the color of the lines connecting two proteins indicates the type of regulation.