Prenatal retinoic acid exposure reveals candidate genes for craniofacial disorders

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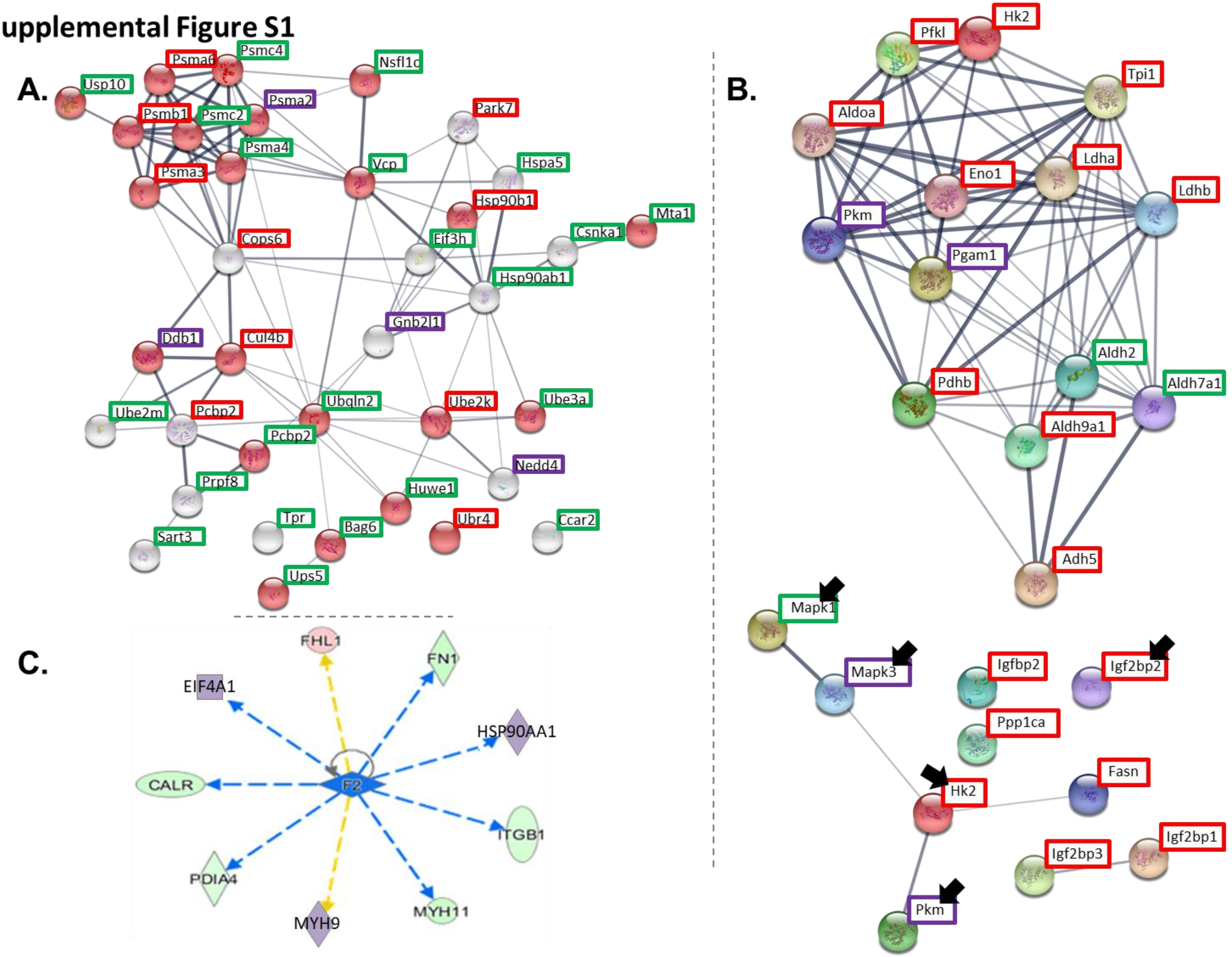
Supplemental Figure S1



Supplemental Figure S1

A. STRING® network of the 36 proteins involved in ubiquitination system, following the analysis of all dysregulated proteins (1 and 2 days of treatment). Among them, proteins involved in ubiquitin-dependent protein catabolic process are colored in red.

B. STRING® network of the 14 proteins involved in Glycolysis and Glycogenogenesis by STING® Software (up panel). All dysregulated proteins (1 and 2 days of treatment) were analyzed. Glycolysis/Glycogenesis is one of the major Kegg pathways relative to metabolic processes in our samples.
STRING® network of the 10 proteins involved in Insulin signaling pathway (down panel). Arrows highlighted proteins also linked to type II diabetes. All dysregulated proteins (1 and 2 days of treatment) were analyzed.

C. Network of F2/ Prothrombin, considered by IPA® analysis as an inhibited Upstream regulator following both 1 and 2 days of *in vivo* ATRA-treatment.

Proteins are up-regulated are framed in red, down-regulated in green following 1 and/or 2 days of ATRA-treatment, in purple, proteins are differentially regulated between 1 and 2 days of *in vivo* treatment.