

Suppl. Figure Legend

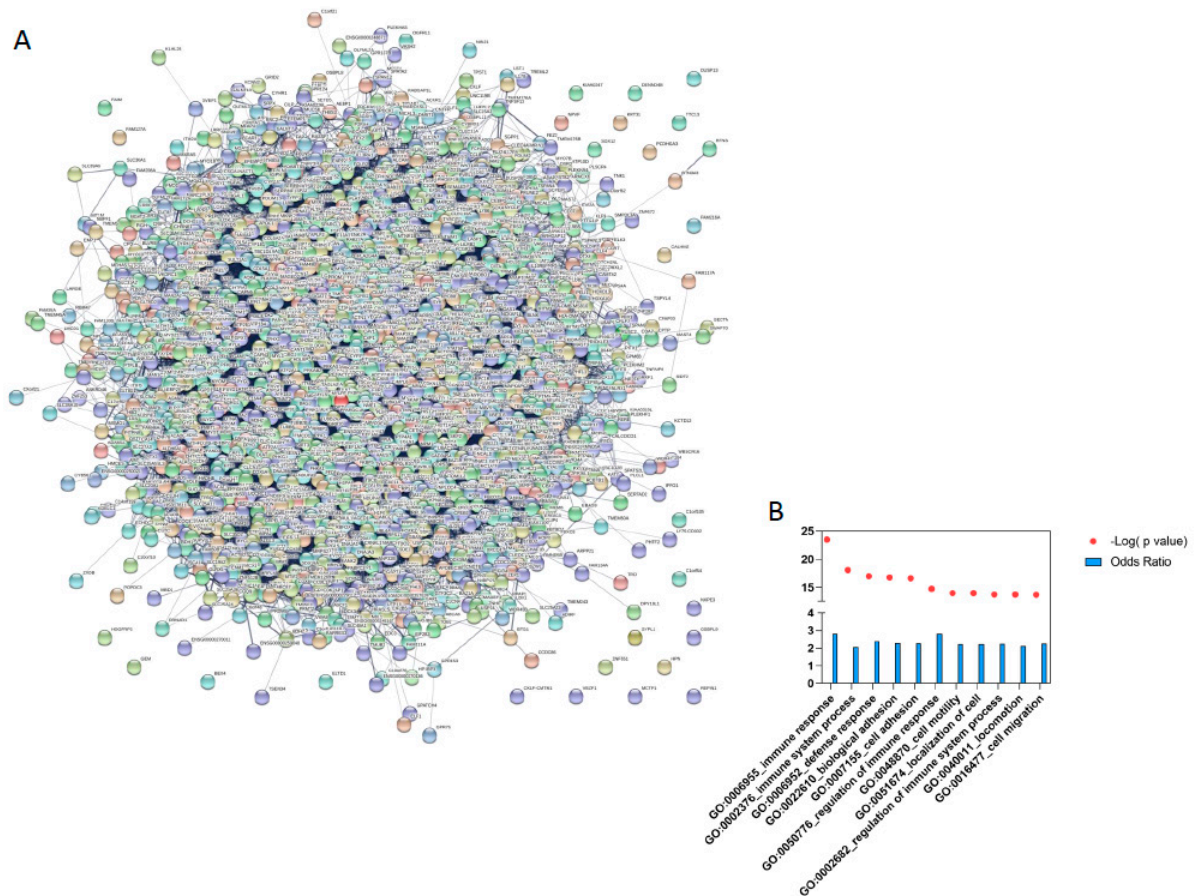


Figure 1. Network of the most significant genes from the meta-analysis **(A)** Gene network of the 2000 top genes altered in the Meta-analysis is plotted using STRING. The edges connecting the nodes represent the interactions between genes, in terms of co-expression (black), text mining (light green), protein homology (cyan), association in curated database (light blue), and high-throughput experiments (purple). Empty nodes represent proteins of uncharacterized 3D structure, while filled nodes represent proteins with known or predicted tertiary structure. Gene Enrichment Biological Process of the Meta-Analysis **(B)** Enrichment analysis is performed with Imago webtool. Red dots represent the significance of the annotations as Log (p-value), while blue histograms show the Odds Ratio for each category tested. It is shown a significant up-regulation of the immune response (p-value 3.2×10^{-24}) and of the immune system (p-value 8.2×10^{-19}).