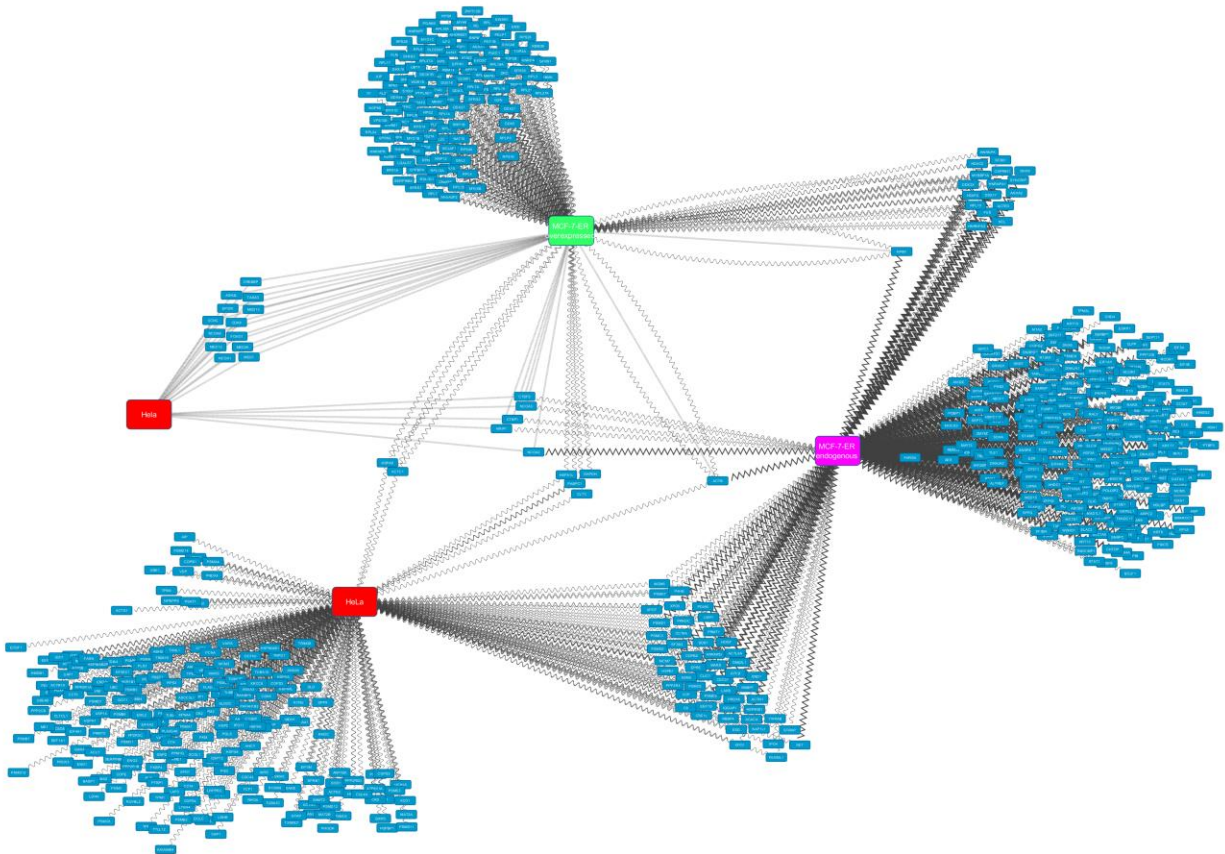
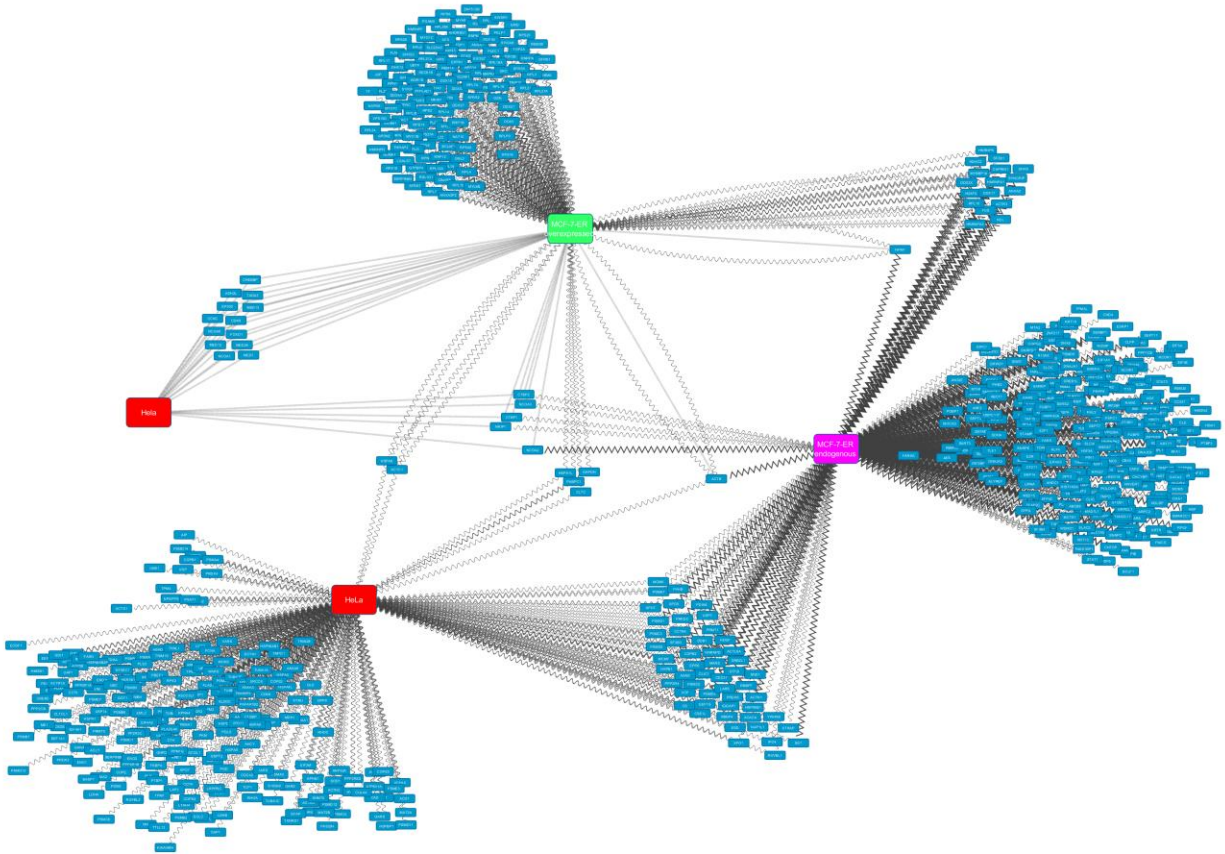


A meta-analysis to evaluate the cellular processes regulated by the interactome of endogenous and over-expressed estrogen receptor alpha

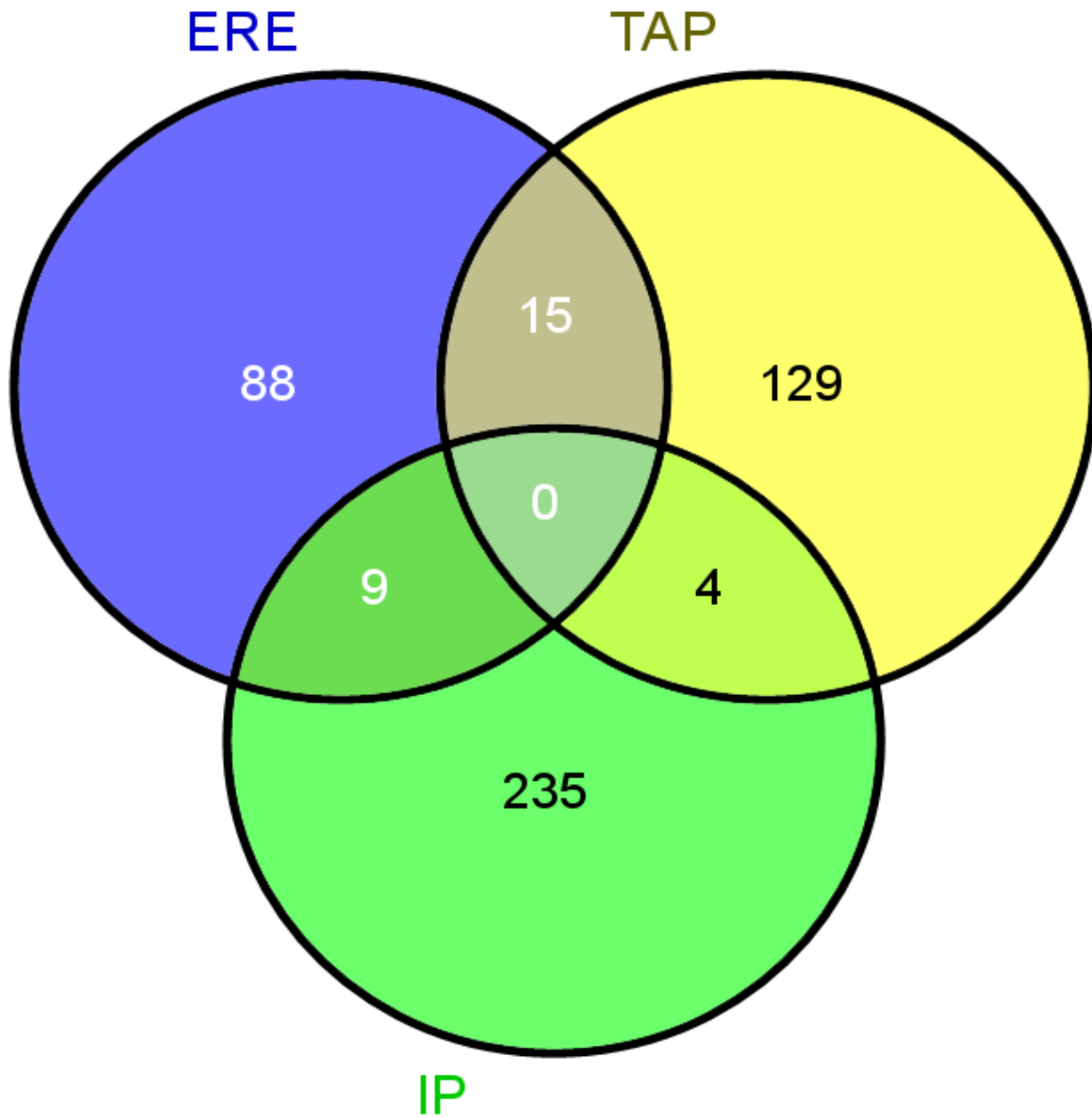
Supplementary Material



Supplementary Figure 1: A network visualizing the correlation between the ER α interacting proteins purified by three different methodologies: ERE-repetition oligonucleotides (ERE); TAP-ER α (TAP) or immunoprecipitation (IP) and identified using MS approaches. Backward slash (gel-free-based approach), zig-zag (gel-based approach), sine wave (gel-free approach). The network was constructed using the Cytoscape platform. $p < 0.05$



Supplementary Figure 2: A network visualizing the correlation between the ER α (over-expressed and/or endogenous) interacting proteins in MCF-7 and HeLa cell lines using MS approaches. Backward slash (gel-free-based approach), zig-zag (gel-based approach), sine wave (gel-free approach). The network was constructed using the Cytoscape platform. $p < 0.05$



Supplementary Figure 3: Venn diagram showing the unique and shared identifications using three different methodologies to purify ER α in MCF-7 cells: ERE-repetition oligonucleotides (ERE); TAP-ER α (TAP) or immunoprecipitation (IP).