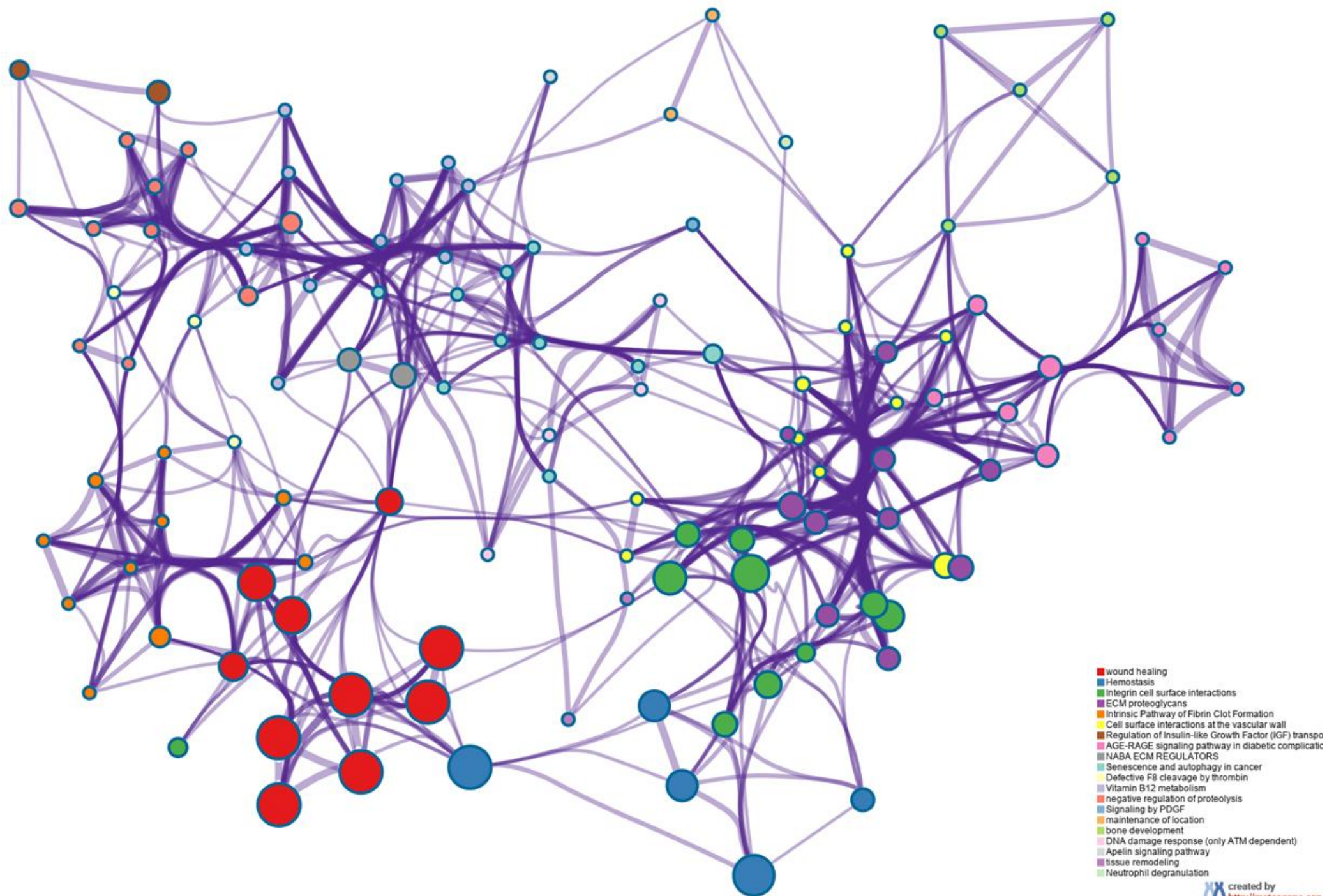
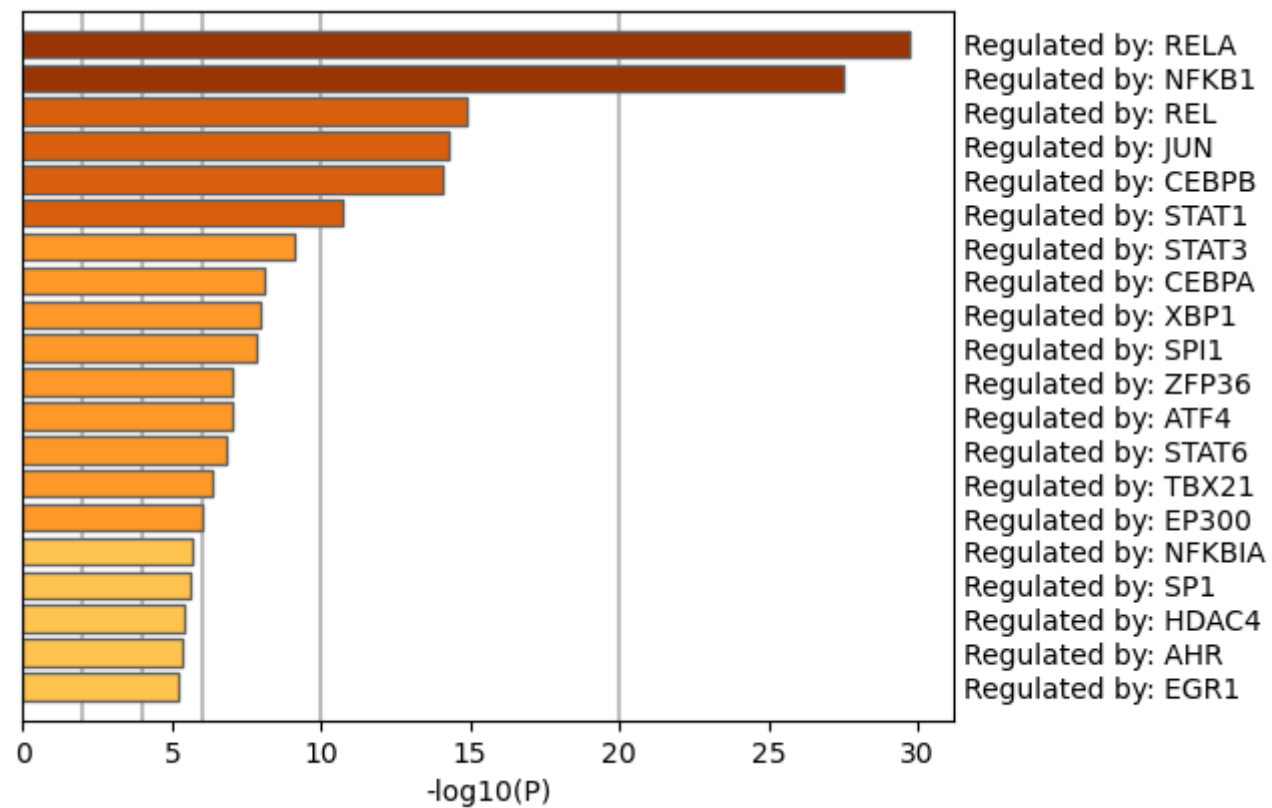


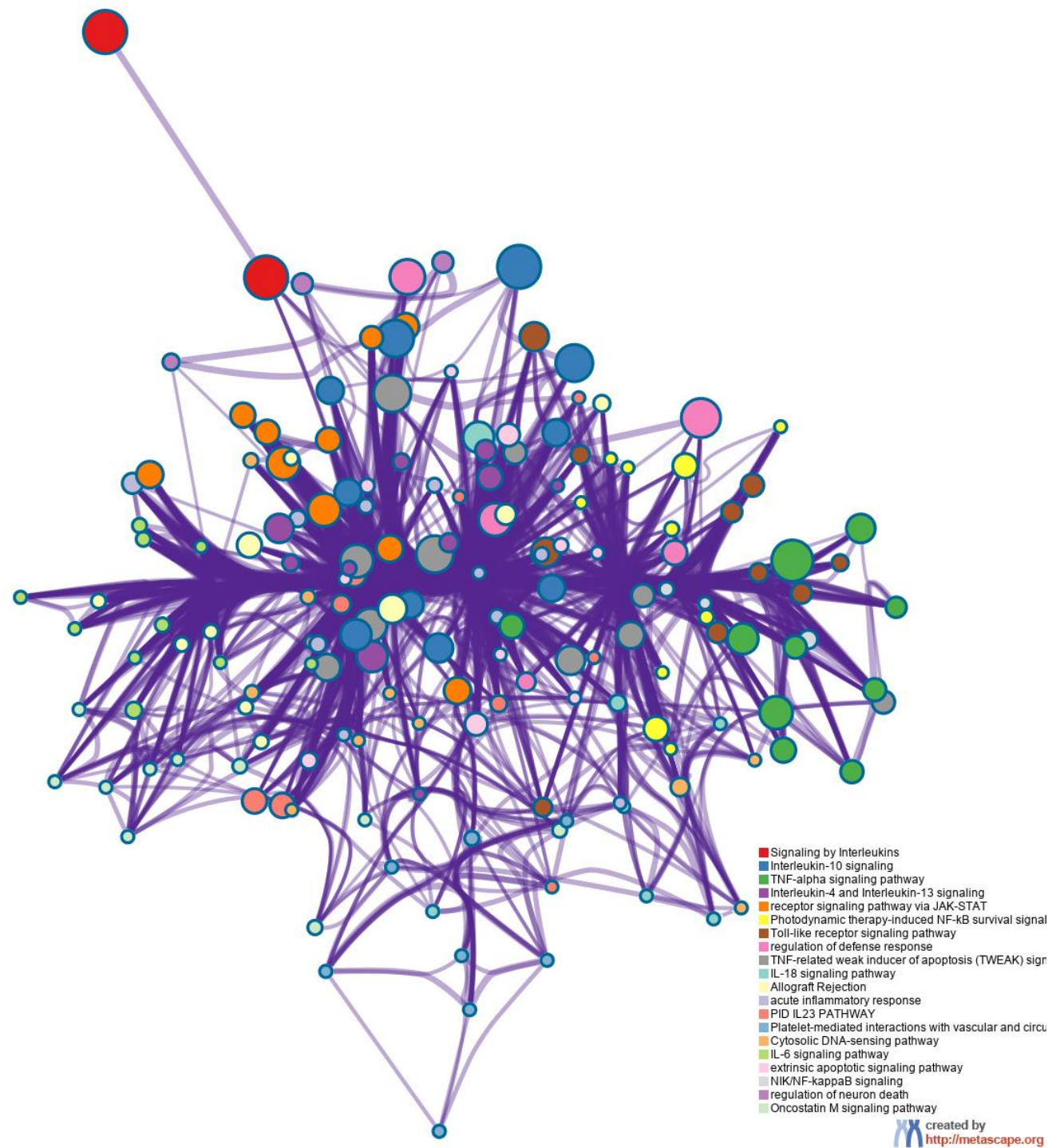
ESF1 Figure S1. Heatmap of the GO_TTRUST transcriptional factors that were enriched in the immune cluster 1 (using Metascape) showing that regulated by SP1 and NFKB1 were the top transcription factor targets.



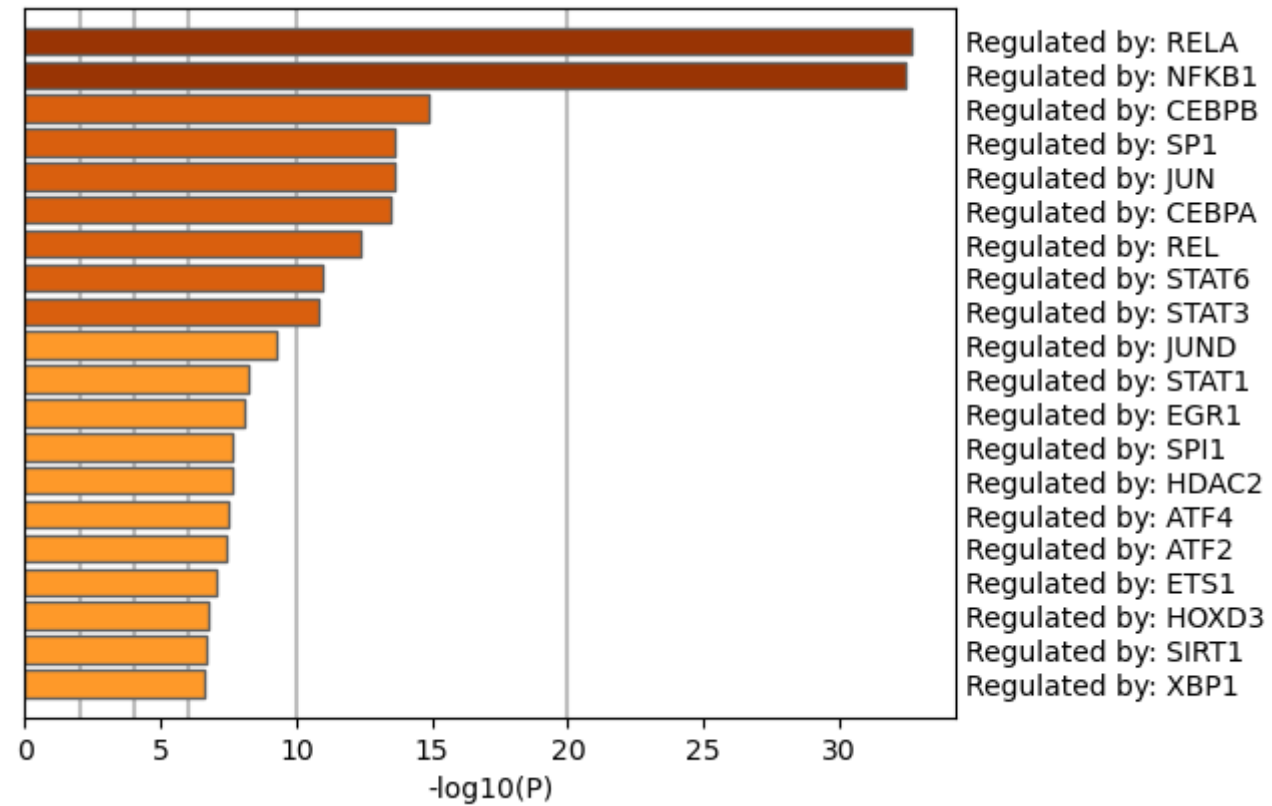
ESF1 Figure S2. Enriched ontology term clusters in the hemostasis subnetwork of death due to ischemic stroke. Terms are represented by a circle node, with the colors representing cluster identity and their size reflecting the number of input genes. One term is used to describe the clusters (colored labels). The thickness of the (bundled) edges linking the terms reflects the similarity score (threshold is $> 0,3$). The network is constructed and visualized using MetaScape and Cytoscape (v3.1.2).



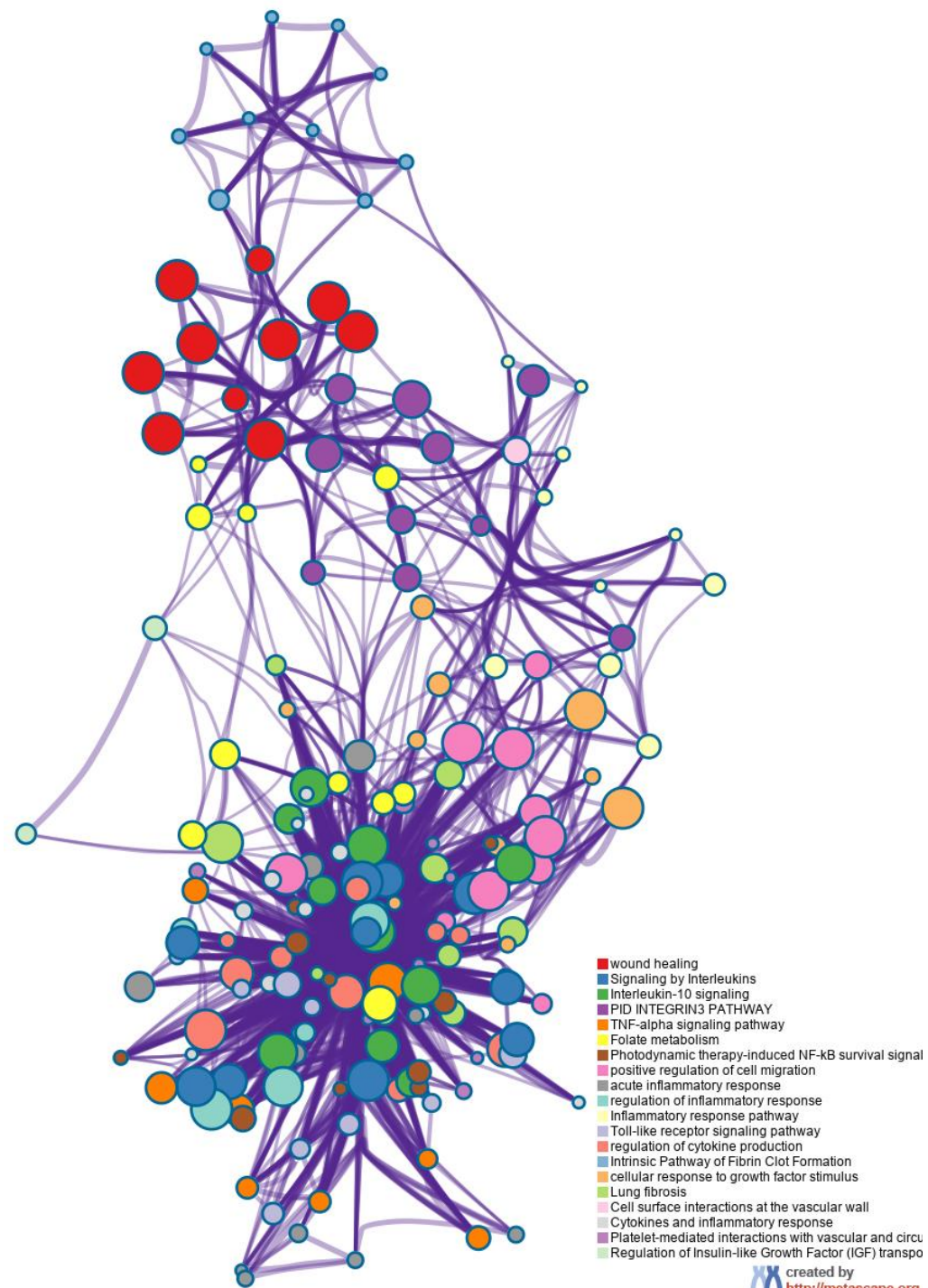
ESF1 Figure S3. Bar graph with the top-16 transcriptional factors (TTRUST) which were enriched in the hemostasis subnetwork indicating that regulated by RELA and NFkB1 were top transcription factor targets.



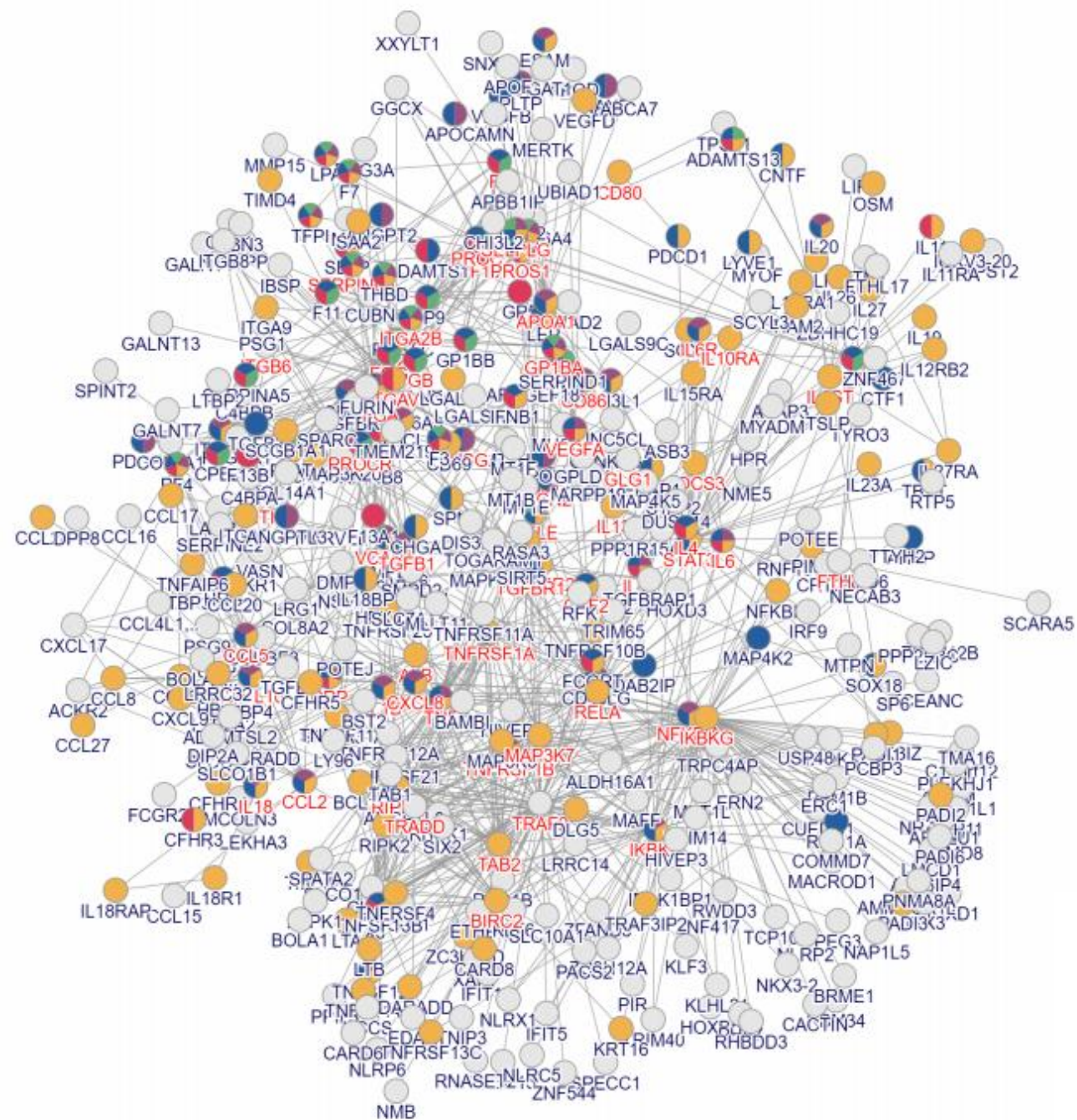
ESF1 Figure S4. Enriched ontology term clusters in the immune subnetwork of death due to ischemic stroke. Terms are represented by a circle node, with the colors representing cluster identity and their size reflecting the number of input genes. One term is used to describe the clusters (colored labels). The thickness of the (bundled) edges linking the terms reflects the similarity score (threshold is $> 0,3$). The network is constructed and visualized using MetaScape and Cytoscape (v3.1.2).



ESF1 Figure S5. Heatmap with the top TTRUST factors were enriched in all differentially expressed proteins and genes indicating that regulated by RELA and NFKB1 were the top transcription factor targets.

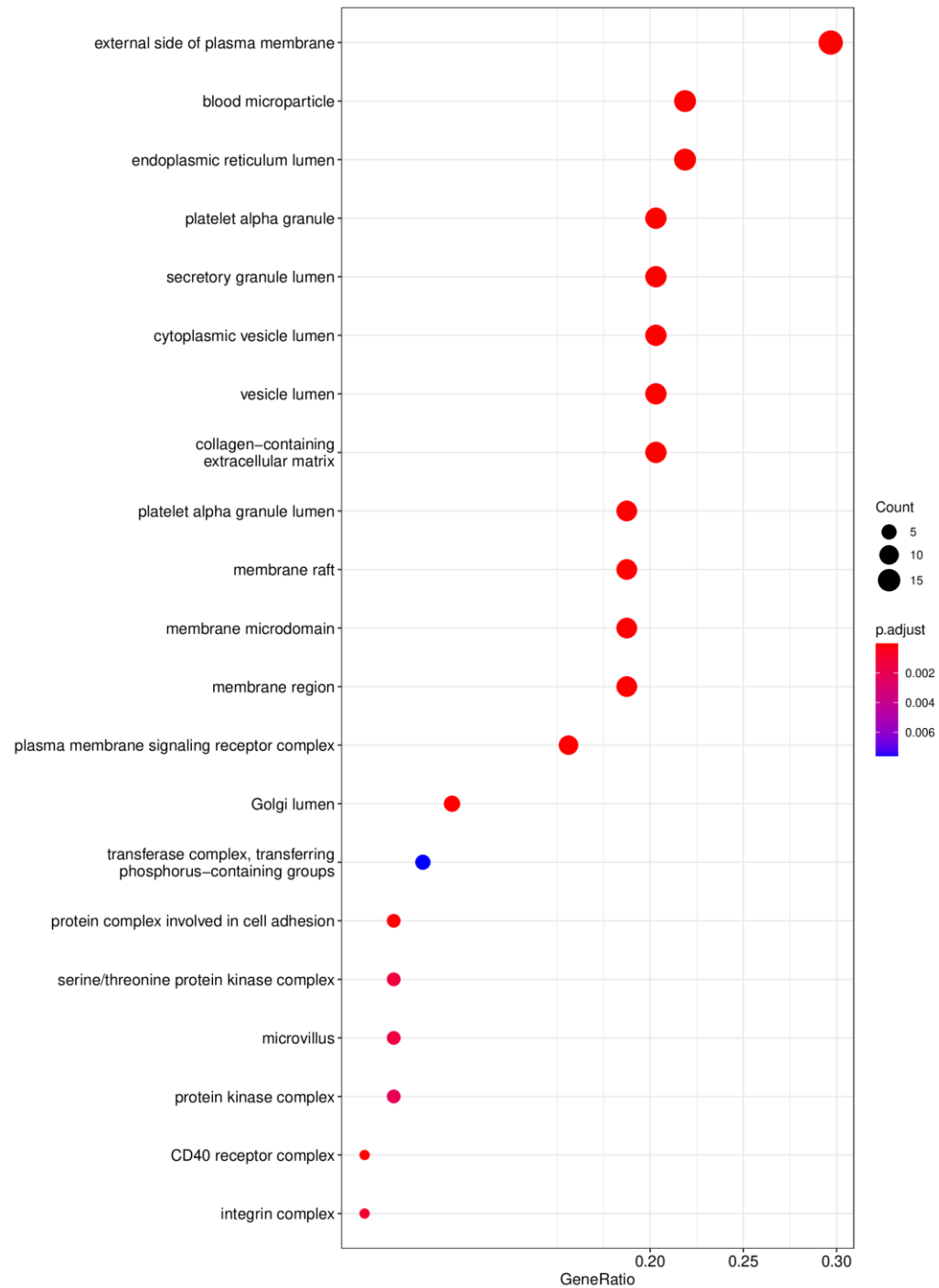


ESF1 Figure S6. Enriched ontology term clusters in the death due to ischemic stroke network based on all differentially expressed proteins and genes. Terms are represented by a circle node, with the colors representing cluster identity and their size reflecting the number of input genes. One term is used to describe the clusters (colored labels). The thickness of the (bundled) edges linking the terms reflects the similarity score (threshold is $> 0,3$). The network is constructed and visualized using MetaScape and Cytoscape (v3.1.2).

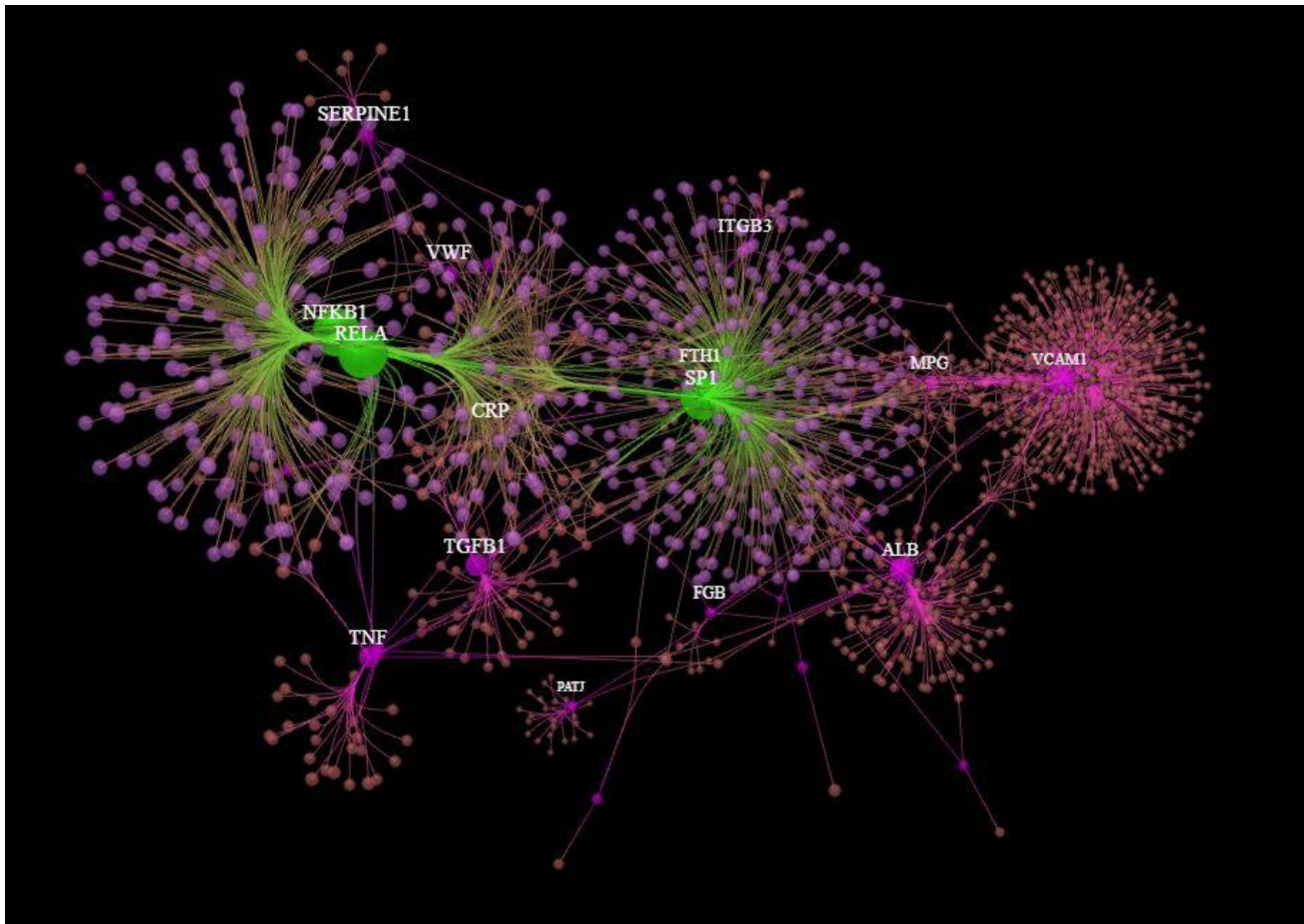


- Arteriosclerotic cardiovascular disease (DOID:2348)
- Blood coagulation disease (DOID:1247)
- Cardiovascular system disease (DOID:1287)
- Immune system disease (DOID:2914)
- Thrombosis (DOID:0060903)

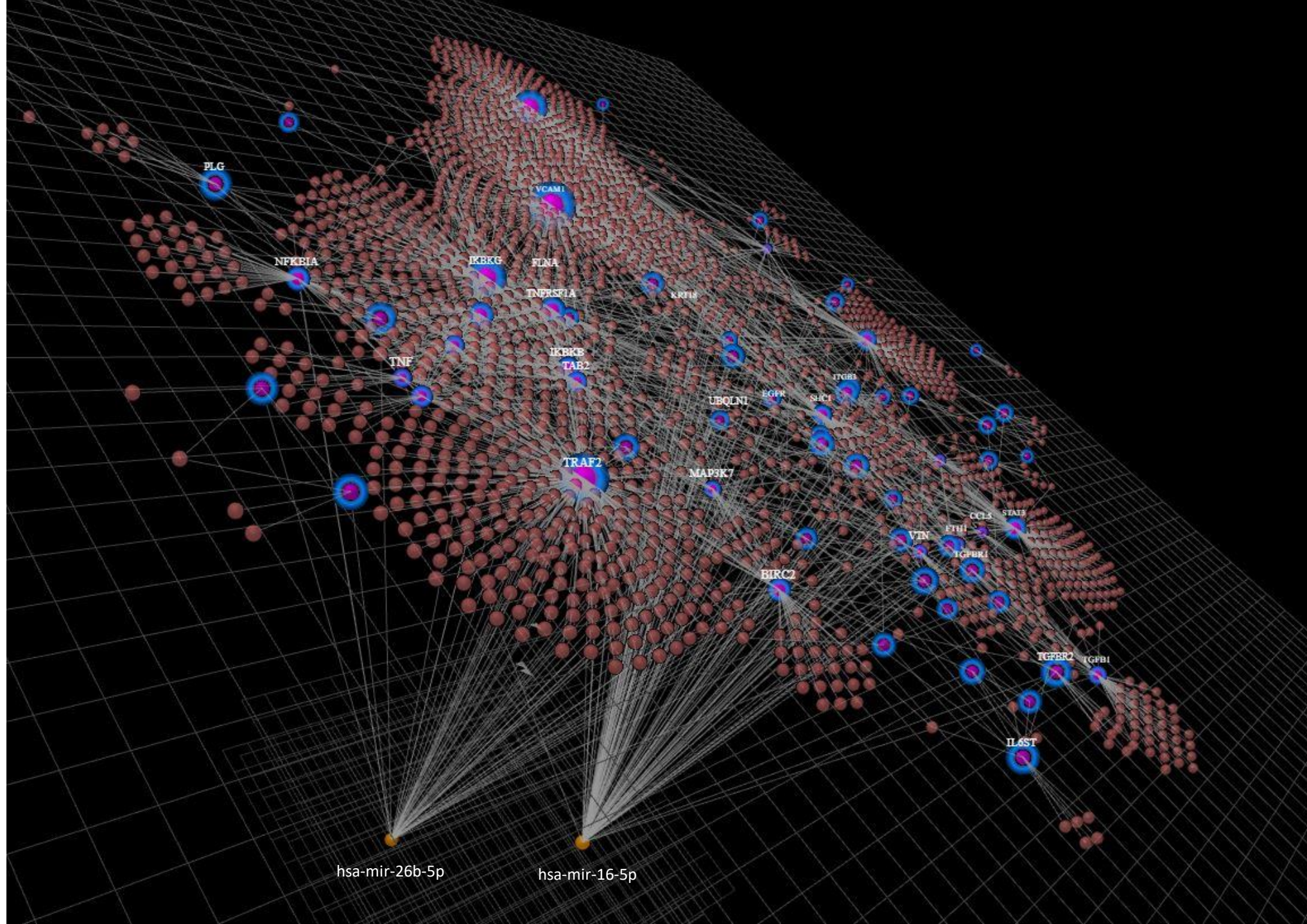
ESF1 Figure S7. An extended network constructed with inBio Discover showing the top Disease Ontology (DOID) annotations.



ESF1 Figure S8. GO functional enrichment analysis of the cellular components of all differently expressed proteins and genes using R package ClusterProfiler. The x-axis shows the gene ratio and the y-axis the annotated terms. The size of the dots is proportional to the gene number; p-values of all GO terms are colored as indicated in the figure.



ESF1 Figure S9. The targeted integration of three regulating actors, namely NFkB, RELA and SP1 (shown in green colors) in the network of death due to ischemic stroke. This MultiOmics network (using InAct, mirNET, and TTRUST) is built using differentially expressed proteins, genes, and miRNA using OmicsNet.



ESF1 Figure S10. The targeted integration of two miRNA regulating actors, namely hsa-mir-16-5p and hsa-mir-26b-5p in the network of death due to ischemic stroke. This MultiOmics network (using InAct, mirNET, and TTRUST) is built using differentially expressed proteins, genes, and miRNA using OmicsNet.