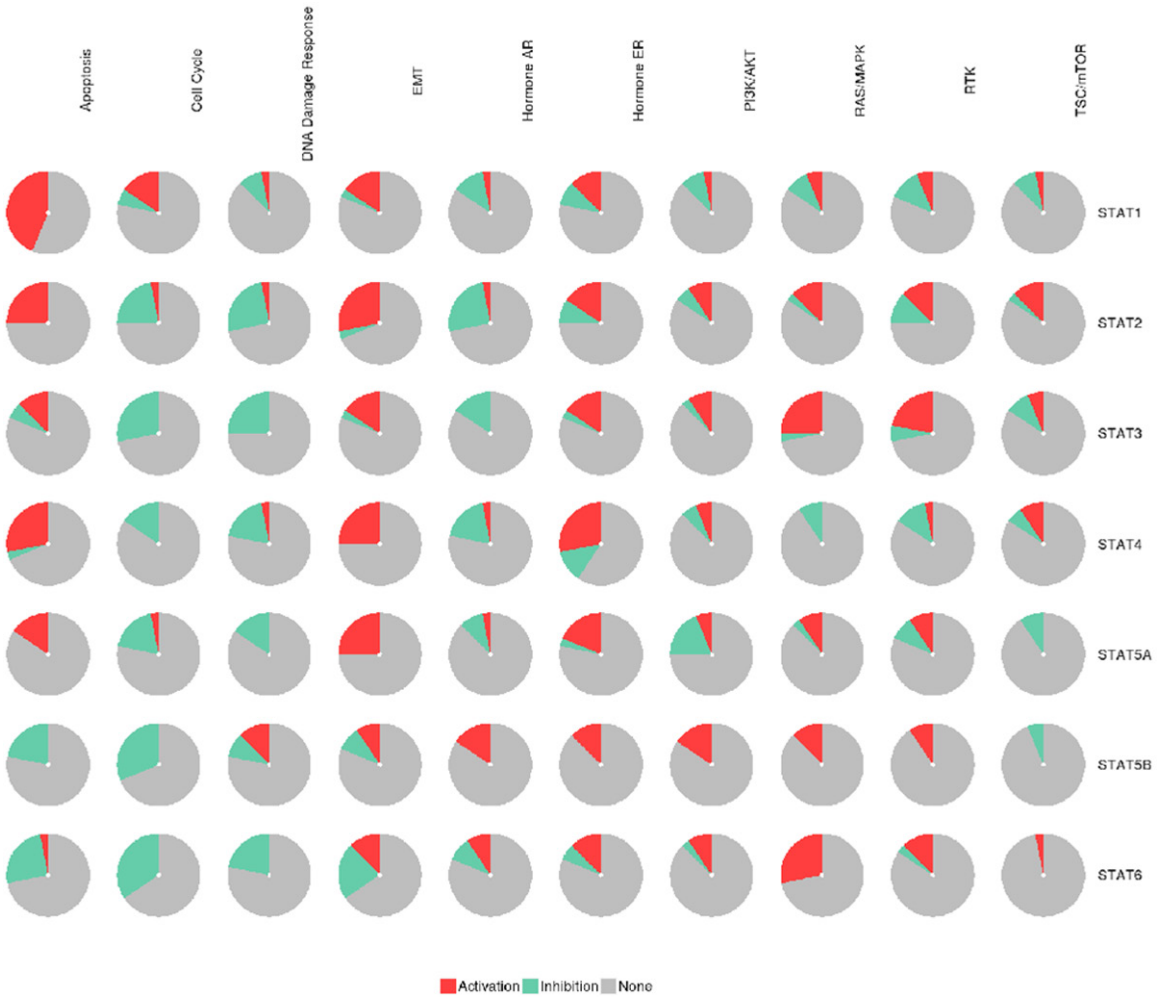
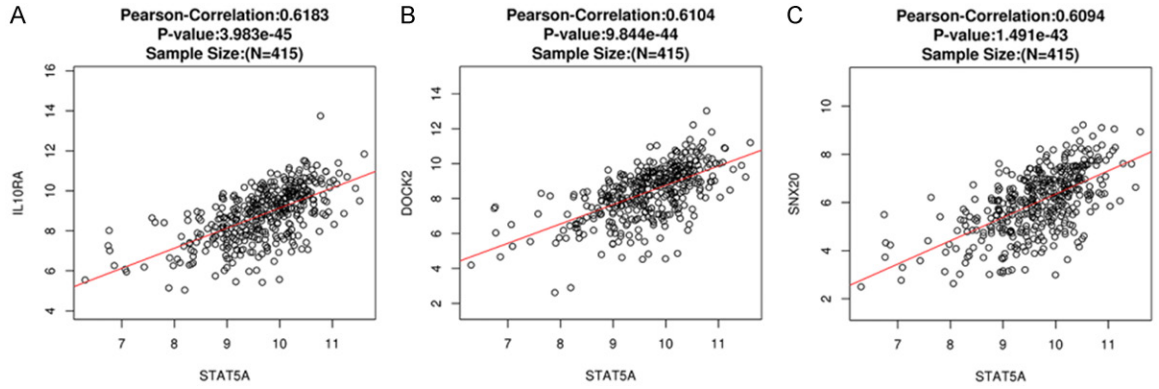
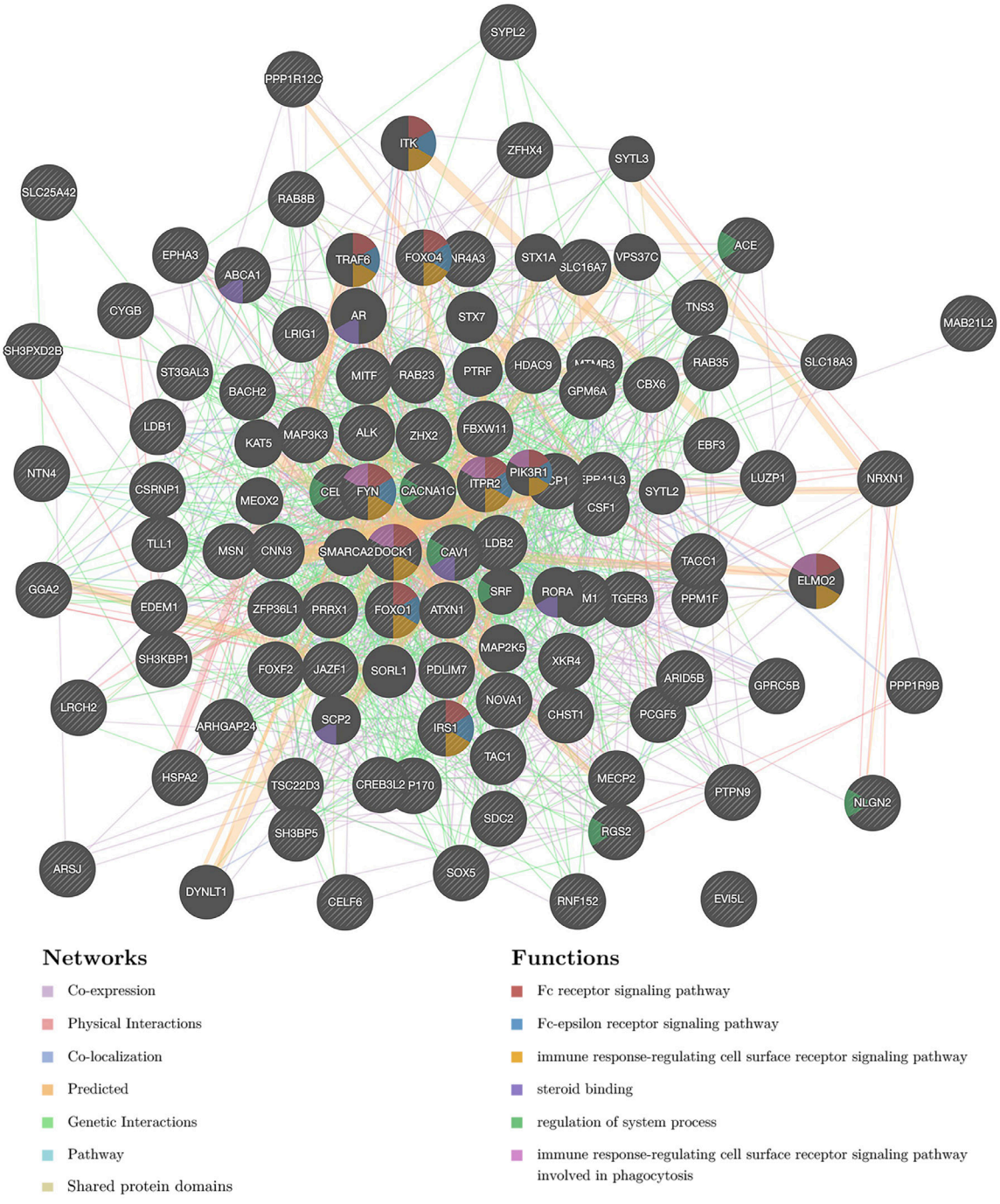


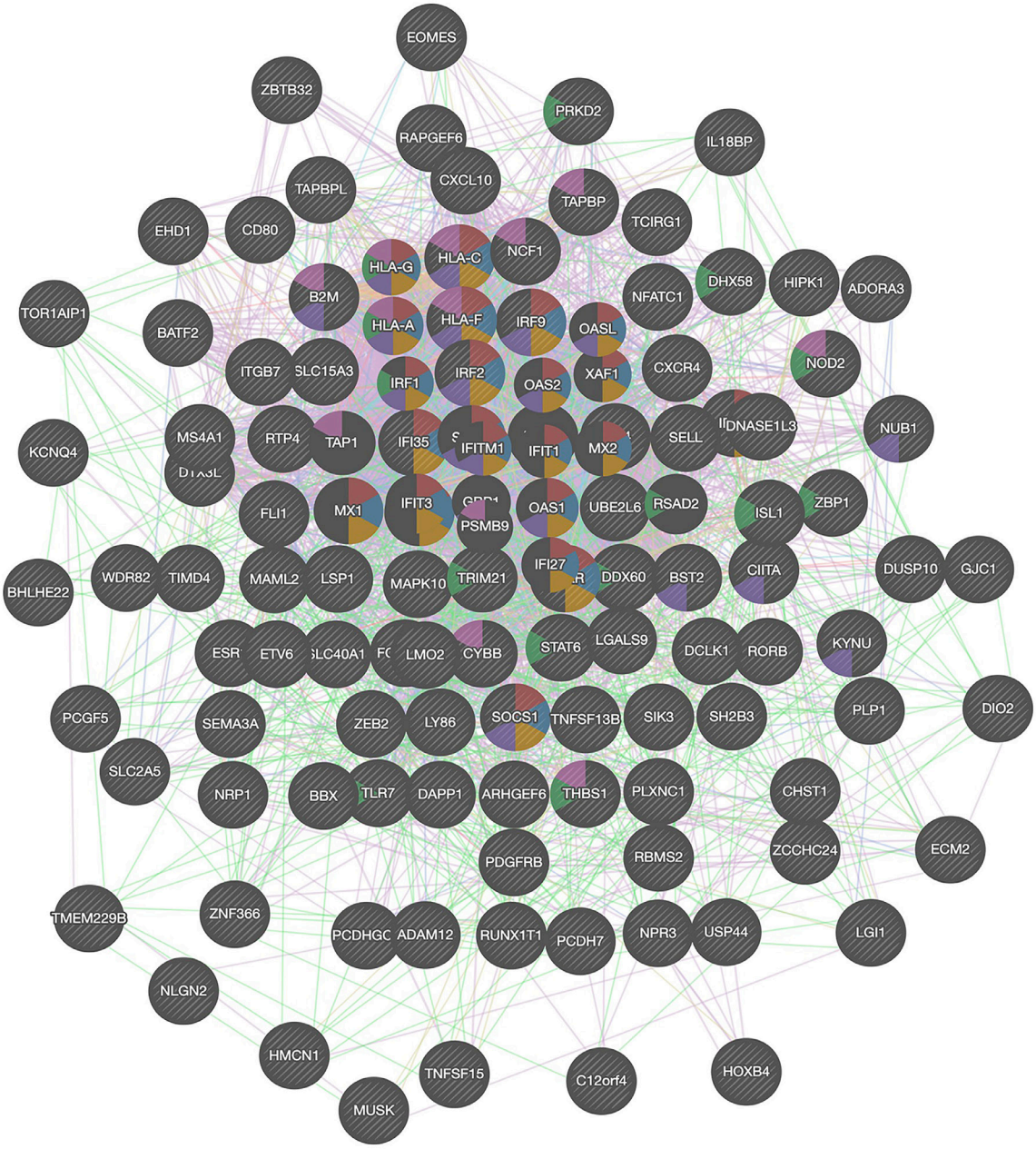
Supplementary Figure 1. The role of STAT5A in the famous cancer related pathways in STAD (GSCALite). STAT family were mainly associated with the activity of apoptosis, cell cycle, DNA damage response, EMT, Hormone ER, and RAS/MAPK pathways.



Supplementary Figure 2. The correlation between the top 3 associated genes and STAT5A in STAD (LinkedOmics). The scatter plot shows Pearson correlation of STAT5A expression with expression of IL10RA (A), DOCK2 (B), and SNX20 (C).



Supplementary Figure 3. PPI network of miR-96-target networks (GeneMANIA). PPI network and functional analysis indicating the gene set that was enriched in the target networks of miR-96. Different colors of the network edge indicate the bioinformatics methods applied: co-expression, website prediction, co-localization, shared protein domains, physical interaction, pathway and genetic interactions. The different colors for the network nodes indicate the biological functions of the set of enrichment genes.



Supplementary Figure 4. PPI network of transcription factor IRF-target networks (GeneMANIA). PPI network and functional analysis indicating the gene set that was enriched in the target networks of transcription factor IRF. Different colors of the network edge indicate the bioinformatics methods applied: co-expression, website prediction, co-localization, shared protein domains, physical interaction, pathway and genetic interactions. The different colors for the network nodes indicate the biological functions of the set of enrichment genes.