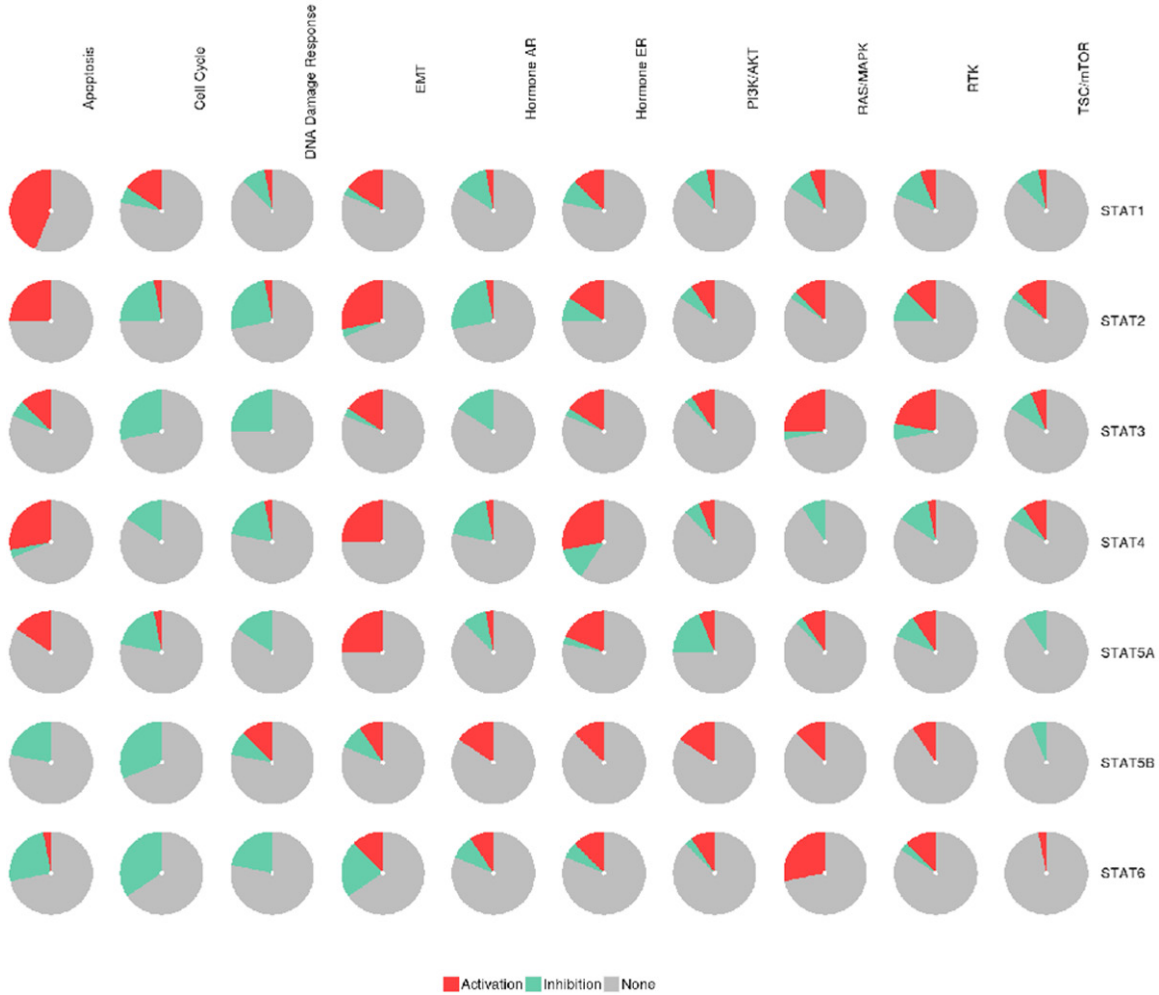
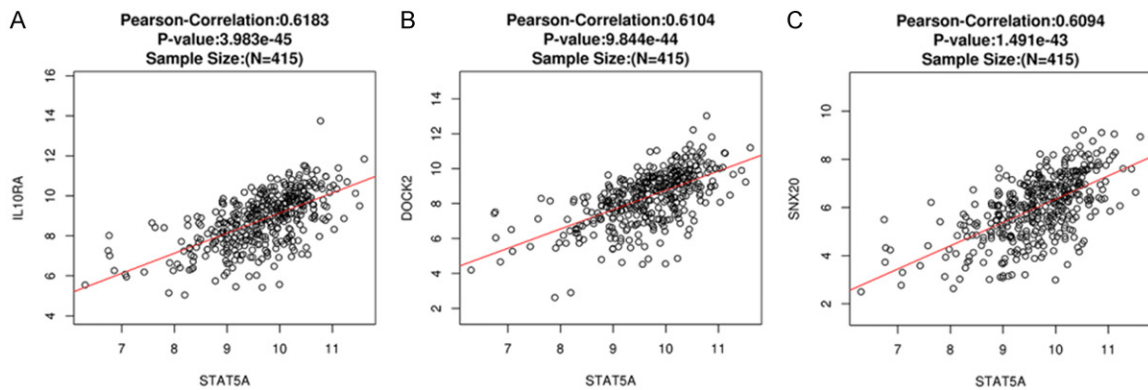


STAT family as biomarkers in stomach adenocarcinoma

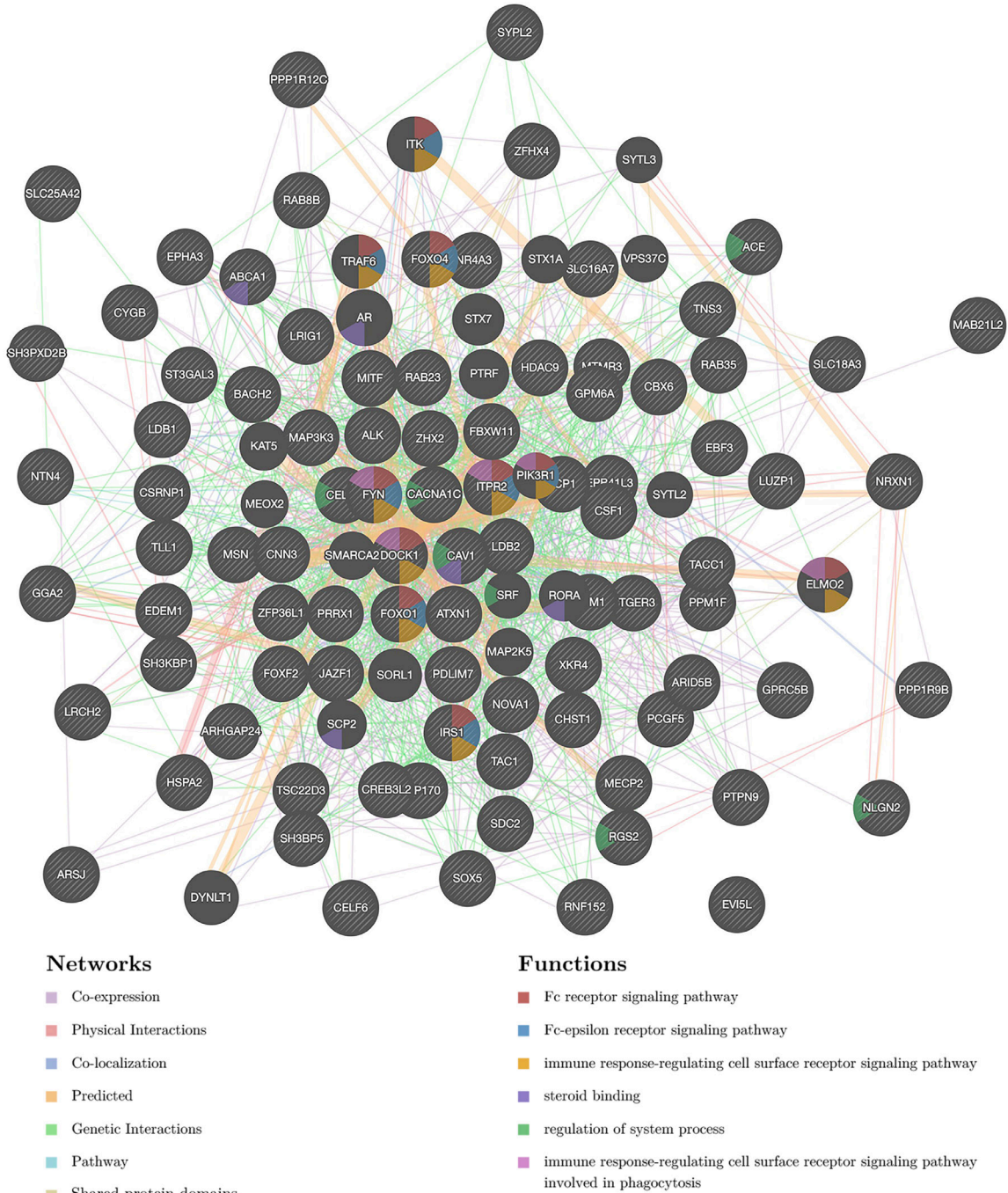


Supplementary Figure 1. The role of STAT5A in the famous cancer related pathways in STAD (GSCALite). STAT family were mainly associated with the activity of apoptosis, cell cycle, DNA damage response, EMT, Hormone ER, and RAS/MAPK pathways.



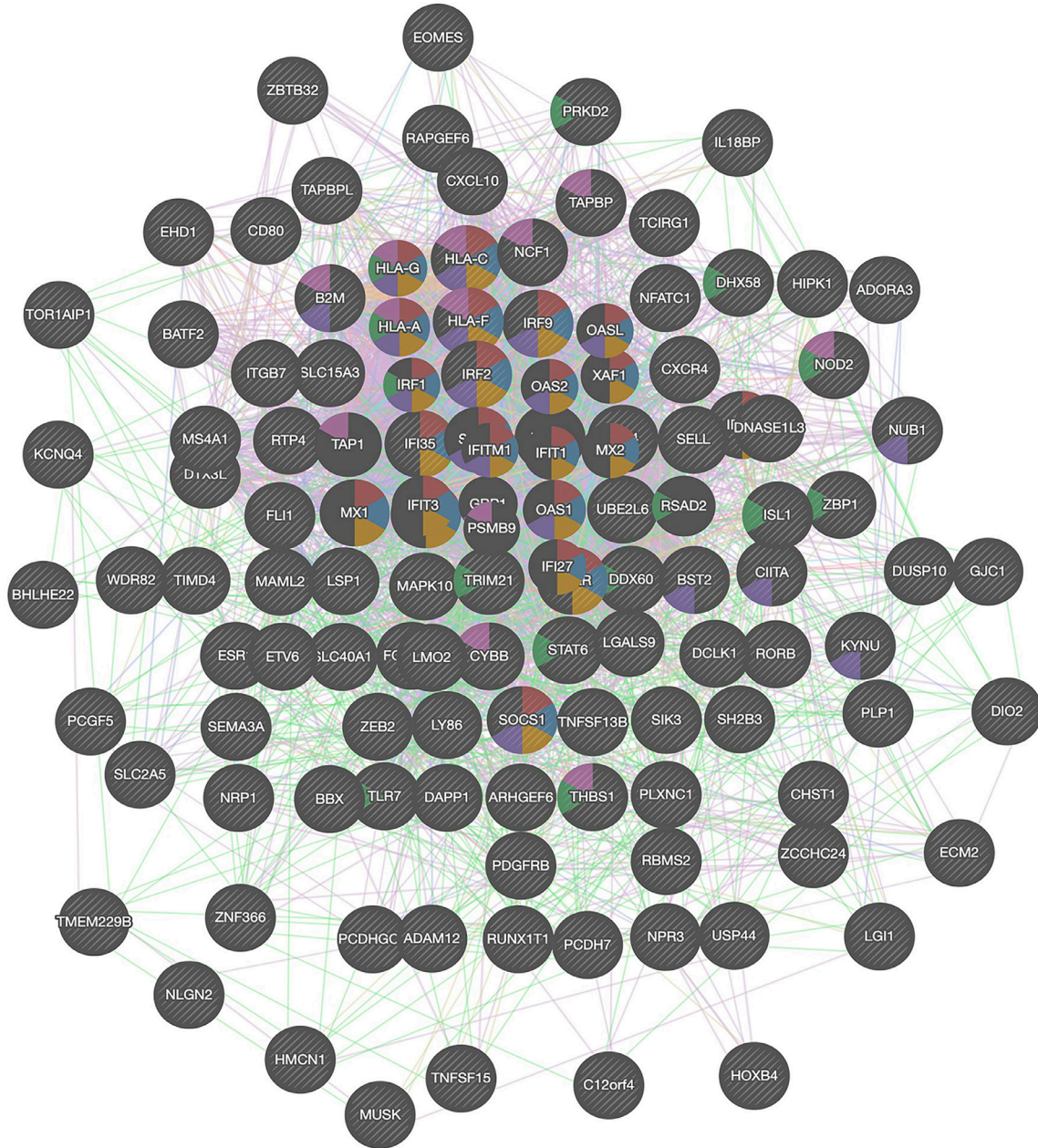
Supplementary Figure 2. The correlation between the top 3 associated genes and STAT5A in STAD (LinkedOmics). The scatter plot shows Pearson correlation of STAT5A expression with expression of IL10RA (A), DOCK2 (B), and SNX20 (C).

STAT family as biomarkers in stomach adenocarcinoma



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.

STAT family as biomarkers in stomach adenocarcinoma



Networks

- Co-expression
- Co-localization
- Physical Interactions
- Predicted
- Pathway
- Genetic Interactions
- Shared protein domains

Functions

- response to type I interferon
- cellular response to type I interferon
- type I interferon signaling pathway
- response to interferon-gamma
- positive regulation of cytokine production
- antigen processing and presentation

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.