

TP53 Target Expression Modulation Analysis (TP53-TEMA): a webtool to analyze microarray and RNA-seq data for TP53 target expression patterns

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Two of the main functions of the TP53/P53 tumor suppressor transcription factor (TF) are cell cycle arrest and induction of apoptosis. P53 directly and/or indirectly regulates the expression of many genes that are required for cell cycle progression and checkpoint control. For example, one of these indirect transcriptional mechanisms include the employment of a protein complex called DREAM that acts as a transcriptional repressor. Even though many genome-wide studies have been carried out, we could not find any webtool in literature, designed to compare or contrast multiple P53 suppressed/activated datasets with each other and together with the user's data by looking at the P53 target complexes. We developed TP53-TEMA webtool to explore RNAseq or microarray experiments performed by modulating wildtype or mutant TP53 expression levels in cancer cells to help the user visualize and analyze public or custom datasets. We also employed the pipeline to identify the repressed or activated genes in our own relevant RNAseq dataset involving treatment with an siRNA against P53 or CHRNA5 alone or in combination, in MCF7 breast cancer cell line, via clustering and heatmaps. TP53-TEMA also allows the user to carry out enrichment pathway analyses on the provided dataset based on the given logFC and FDR cutoffs; and the output is provided in the form of various plots such as a barplot to show the enriched pathways, or a CNET plot that shows the associations of the genes and their biological concept as a network. TP53-TEMA can be adapted to other TFs and their targets, and help resolve potential discrepancies in TF target discovery. TP53-TEMA webtool has been developed as part of a TUBITAK funded project (Proje no. 219Z029).