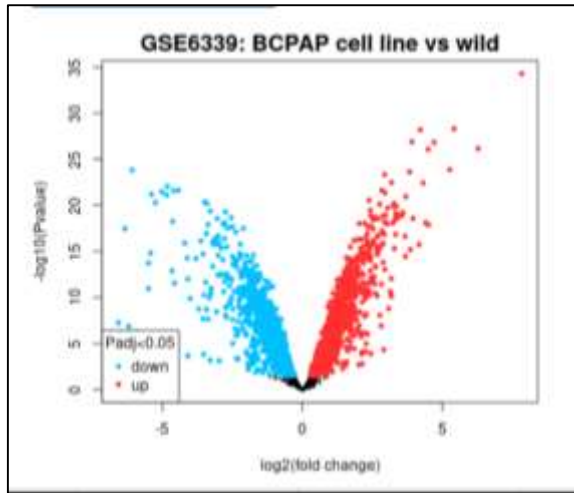
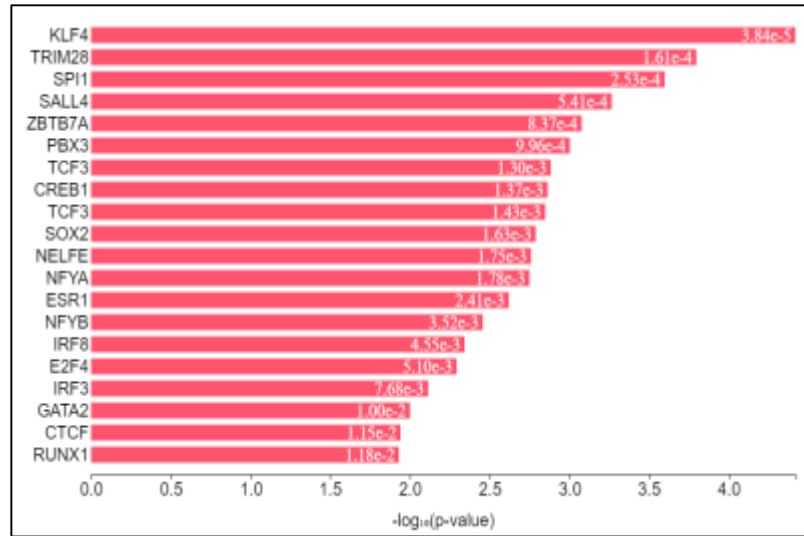


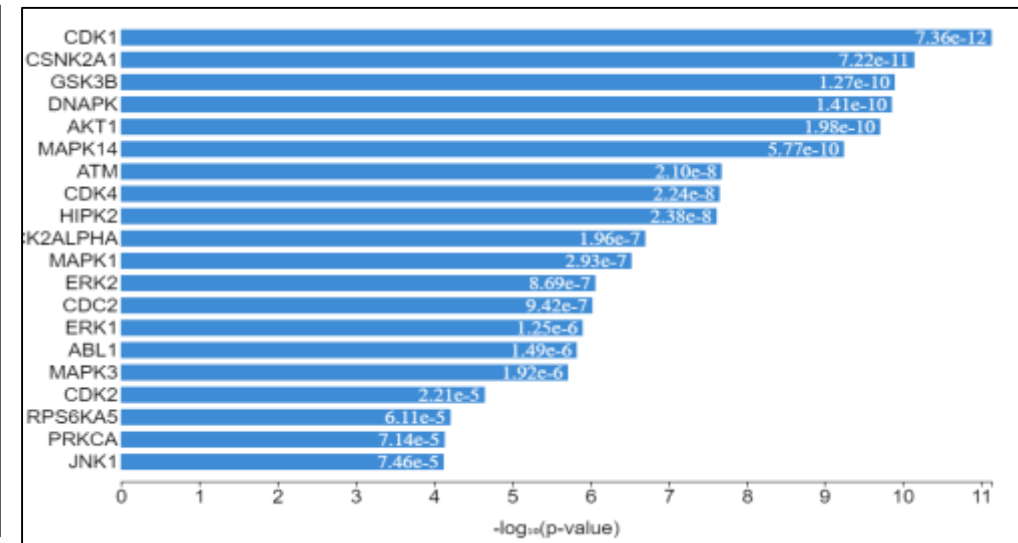
a Volcano plot of differentially expressed genes



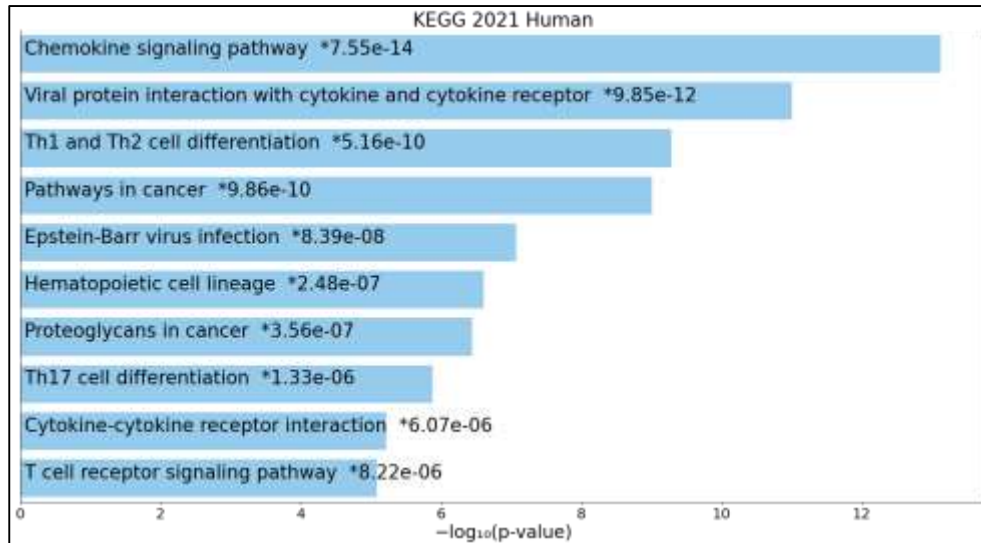
b Transcription Factor Enrichment Analysis (TFEA)



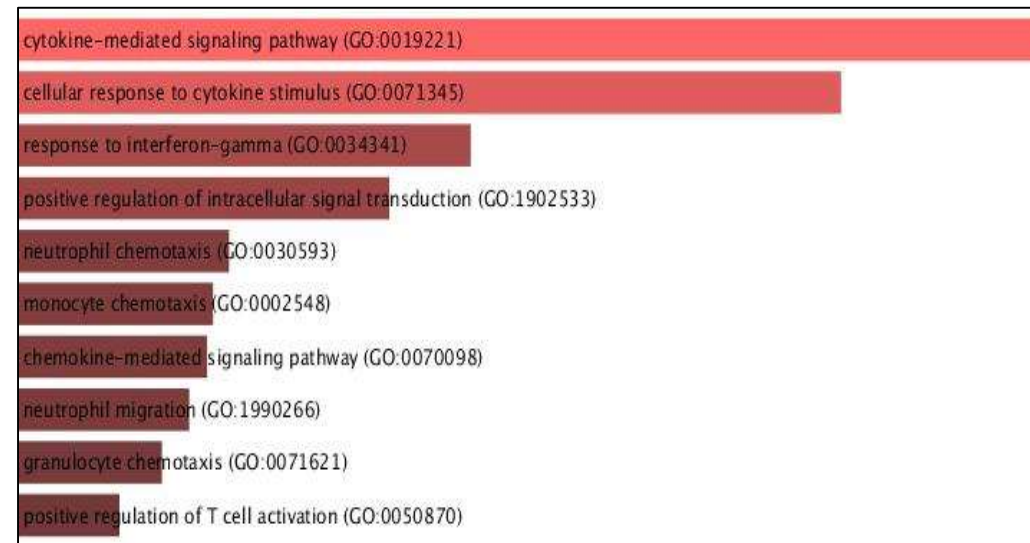
c Kinase Enrichment Analysis (KEA)



d Enrichment analysis: KEGG pathway



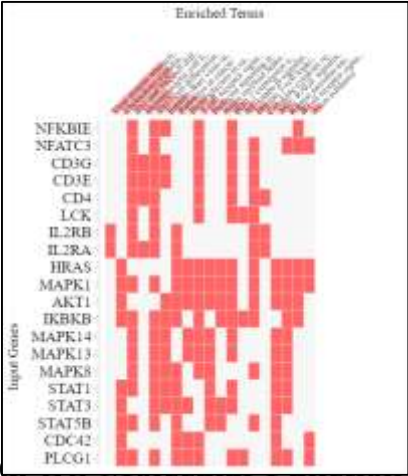
e GO Biological Process



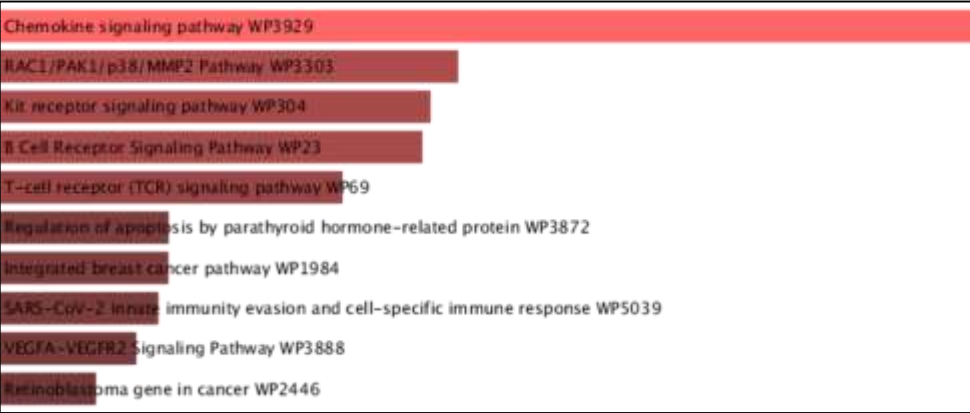
GSE6339 (BCAPAP vs Normal)

Supplementary Figure 7 (A). Gene expression data analysis of GSE6339 GEO dataset a) Volcano plot of differentially expressed genes, b) Transcription factor enrichment analysis (through X2k analysis from iLINCS database c) Kinase enrichment analysis, d) Enrichment analysis of DEGs: KEGG pathway, e) GO Biological Process

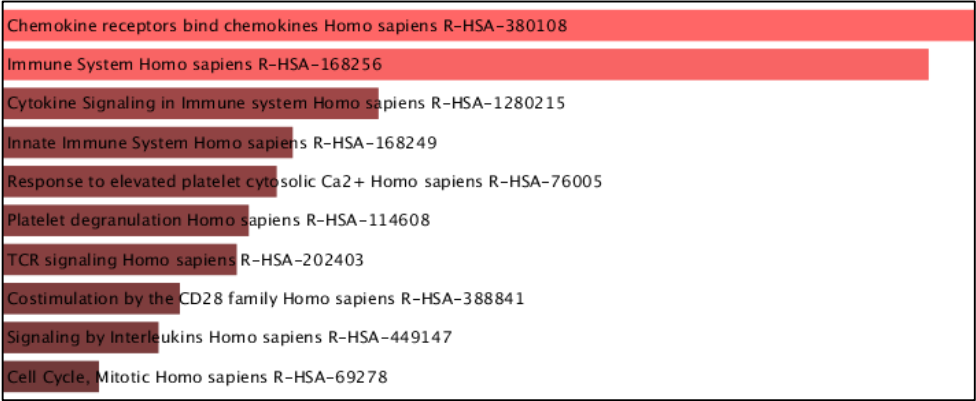
a. Clustergram



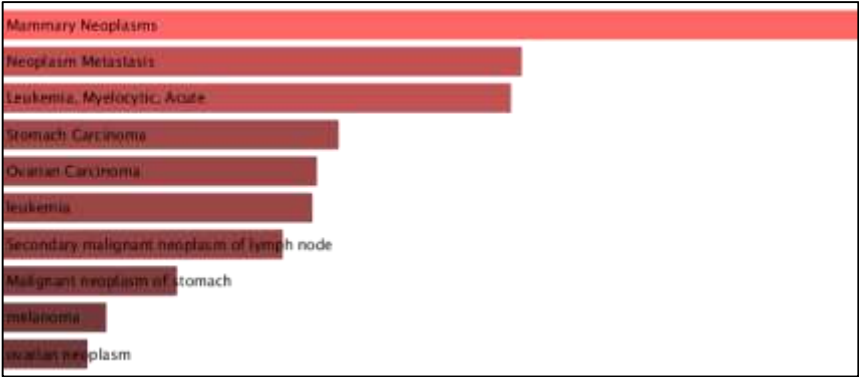
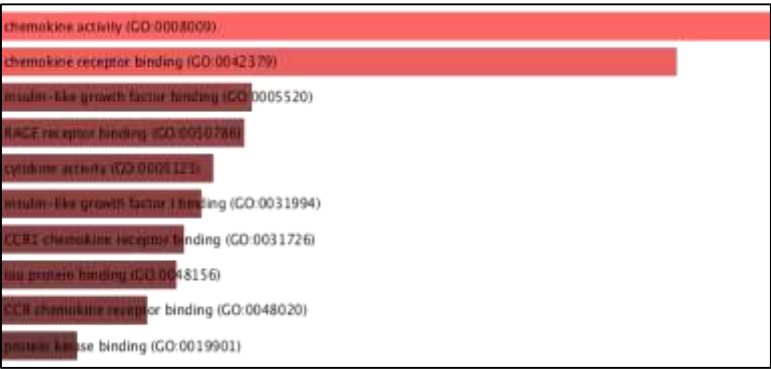
b. WIKI pathways



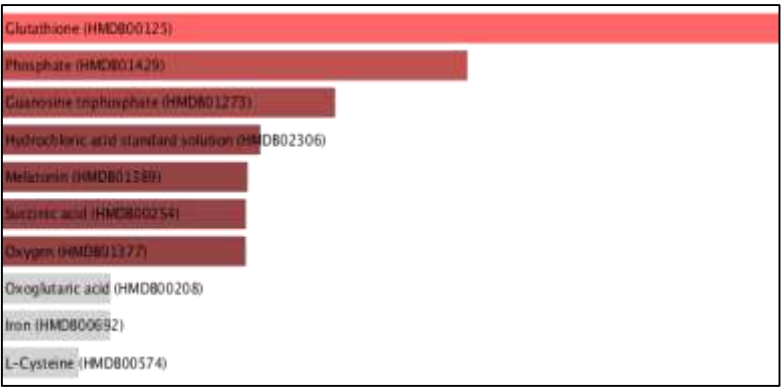
c. REACTOME pathways



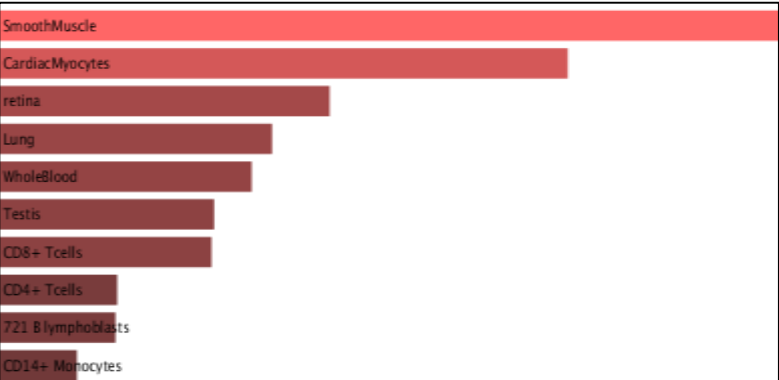
e. DisGeNET



f. HMDB



g. Cell type- Human gene Atlas



Supplementary Figure 7 (B). Transcriptomics analysis of GSE6339 dataset : Enrichr analysis a) Clustergram of significant pathways, b) WIKI pathways, c) Reactome pathways, d) Gene Ontology (GO) Molecular Function, e) diseases (DisGeNET), Metabolite (HMDB databases) and Cell type (Human gene Atlas)