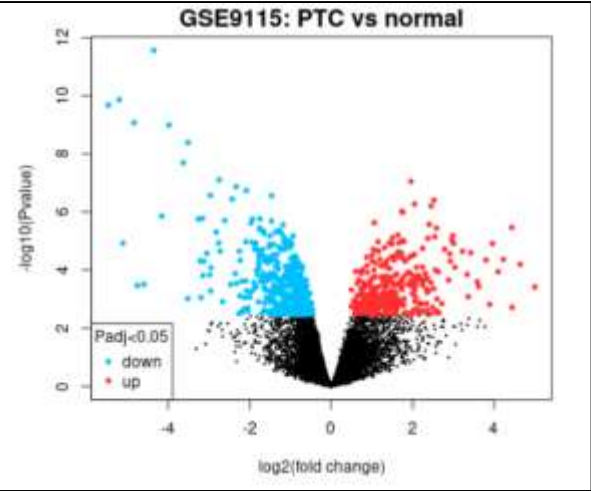
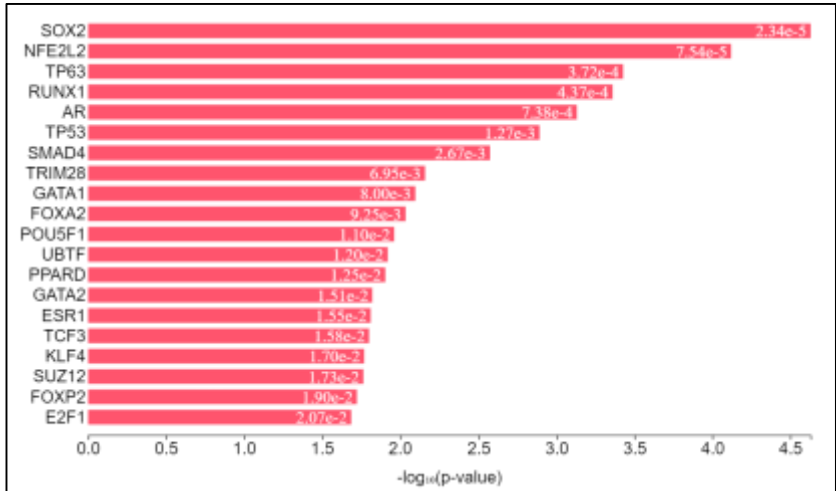


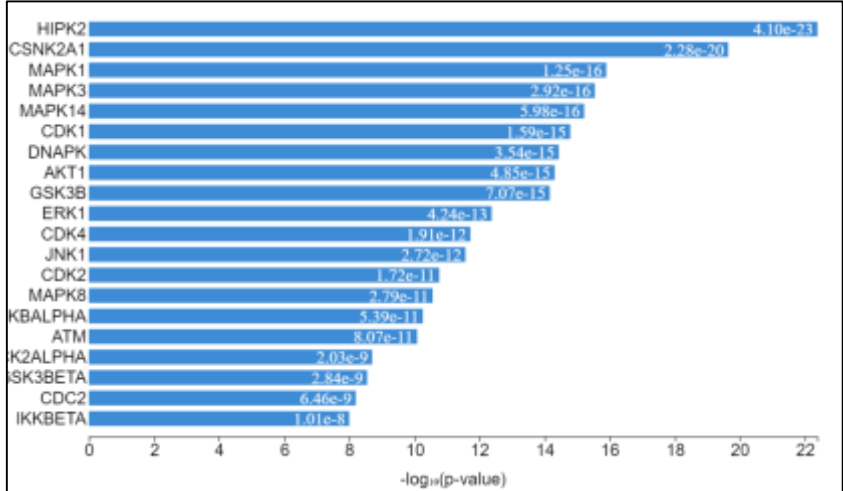
a Volcano plot of differentially expressed genes



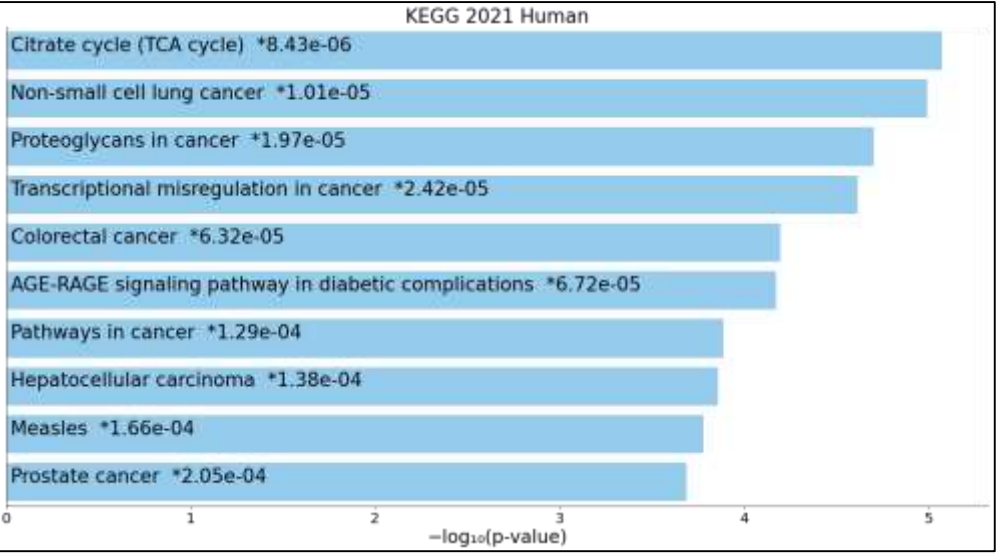
b Transcription Factor Enrichment Analysis (TFEA)



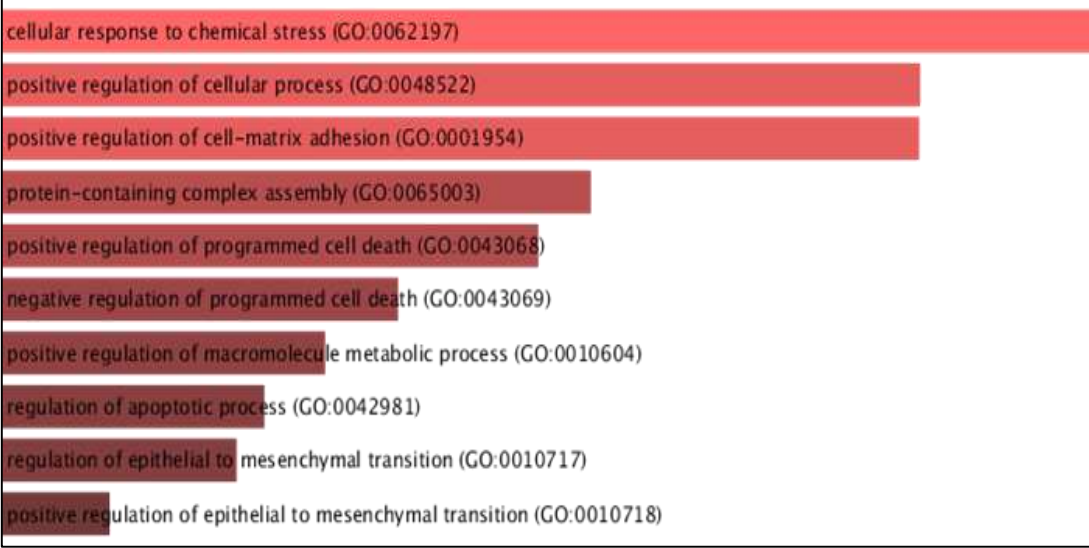
c Kinase Enrichment Analysis (KEA)



d Enrichment analysis: KEGG pathway



e GO Biological Process



GSE9115

Supplementary Figure 5 (A). Gene expression data analysis of GSE9115 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) Gene set enrichment analysis (GESA) of differentially expressed genes by WebGestalt

Biological Pathway	Number of Publications (WP)
TCA Cycle (aka Krebs or citric acid cycle)	78
BMP2-WNT4-FOXO1 pathway in primary endometrial stromal cell differentiation	3876
Non-small cell lung cancer	4255
The influence of laminopathies on Wnt signaling	4844
DNA damage response (only ATM dependent)	710
Chromosomal and microsatellite instability in colorectal cancer	4216
miRNA regulation of prostate cancer signaling pathways	3981
Endoderm differentiation	2853
VEGFA-VEGFR2 Signaling Pathway	3888
Nuclear Receptors Meta-Pathway	2882

Citric acid cycle (TCA cycle) Homo sapiens R-HSA-71403
Repression of WNT target genes Homo sapiens R-HSA-4641265
Formation of the beta-catenin/TCF transactivating complex Homo sapiens R-HSA-201722
Pyruvate metabolism and Citric Acid (TCA) cycle Homo sapiens R-HSA-71406
LICAM interactions Homo sapiens R-HSA-373760
Transcriptional regulation of pluripotent stem cells Homo sapiens R-HSA-452723
trans-CotG Network Vesicle Budding Homo sapiens R-HSA-199992
Clathrin derived vesicle budding Homo sapiens R-HSA-421837
Cellular responses to stress Homo sapiens R-HSA-2262752
Developmental Biology Homo sapiens R-HSA-1266738

GO Term	GO ID
actin binding	GO:0003779
ubiquitin-protein ligase binding	GO:0031625
protein kinase A catalytic subunit binding	GO:0034236
ADP transmembrane transporter activity	GO:0015217
ubiquitin-like protein ligase binding	GO:0044386
acyl-CoA dehydrogenase activity	GO:0003995
ATP transmembrane transporter activity	GO:0005347
MAP kinase tyrosine/serine/threonine phosphatase activity	GO:0017017
protein tyrosine/threonine phosphatase activity	GO:0008330
G-protein-coupled receptor protein tyrosine kinase activity	GO:0004714

Cancer Type	Approximate Percentage
Mammary Neoplasms	28%
Malignant neoplasm of breast	26%
Renal Cell Carcinoma	24%
Breast Carcinoma	22%
Neoplasm Metastasis	18%
Precursor Cell Lymphoblastic Leukemia Lymphoma	12%
Adenoma	10%
Thyroid Neoplasm	8%
Adenocarcinoma	5%
Stomach Neoplasms	3%

Metabolite (ID)	Count
Succinic acid (HMD800254)	10
FAD (HMD801248)	9
Cyclic AMP (HMD800058)	7
Sulfate (HMD800598)	5
Pyruvic acid (HMD802061)	4
QH2 (HMD001394)	3
Serotonin (HMD800588)	2
Coenzyme Q (HMD806709)	2
3,4-Dihydroxybenzaldehyde (HMD806242)	1
Ubiquinone Q1 (HMD802012)	1

Tissue	Number of Genes
Thyroid	1000
Colorectal adenocarcinoma	~450
Bronchial Epithelial Cells	~420
Prefrontal Cortex	~380
Heart	~280
colon	~220
Cardiac Myocytes	~120
Uterus	~100
Lung	~90
Smooth Muscle	~80

Supplementary figure 5 (B). Transcriptomics analysis of GSE9115 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)