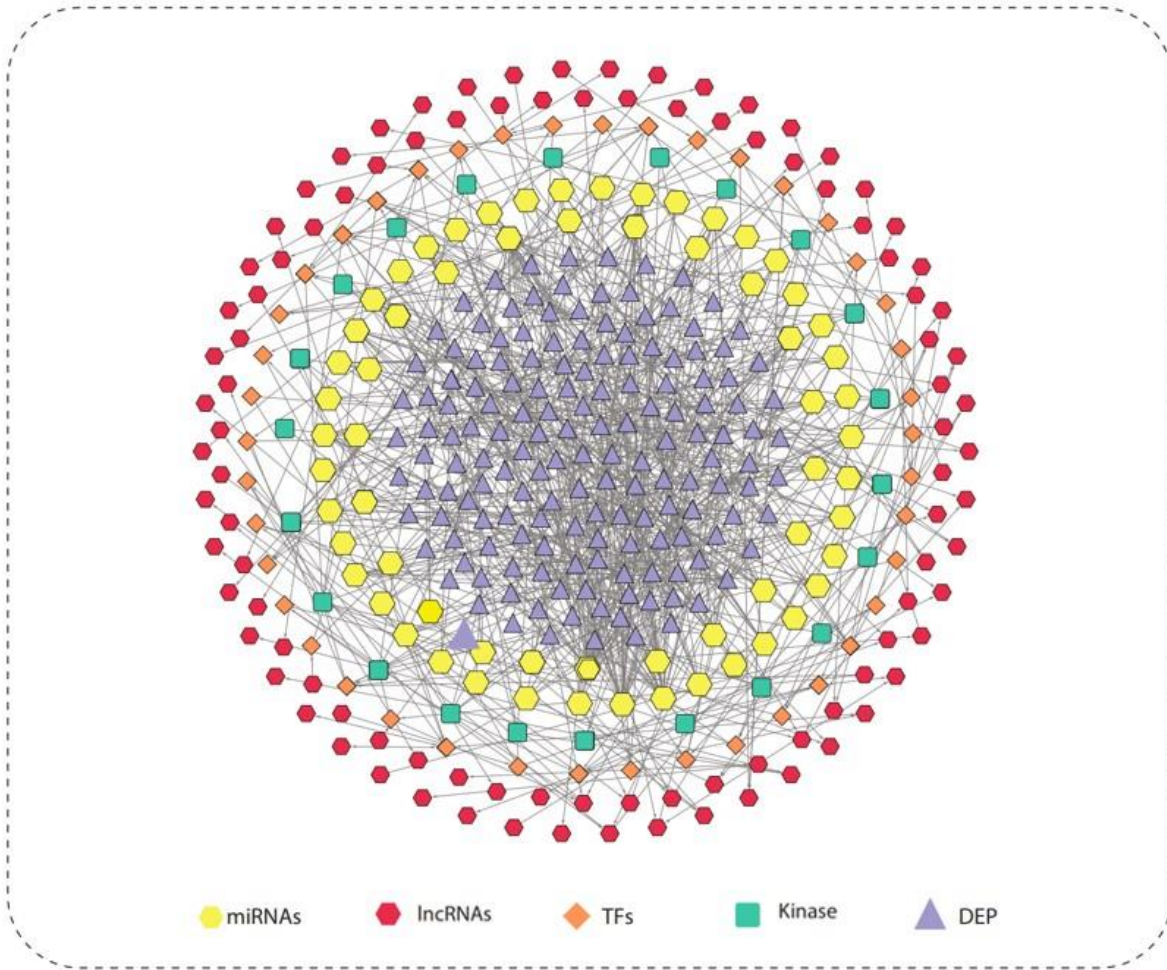


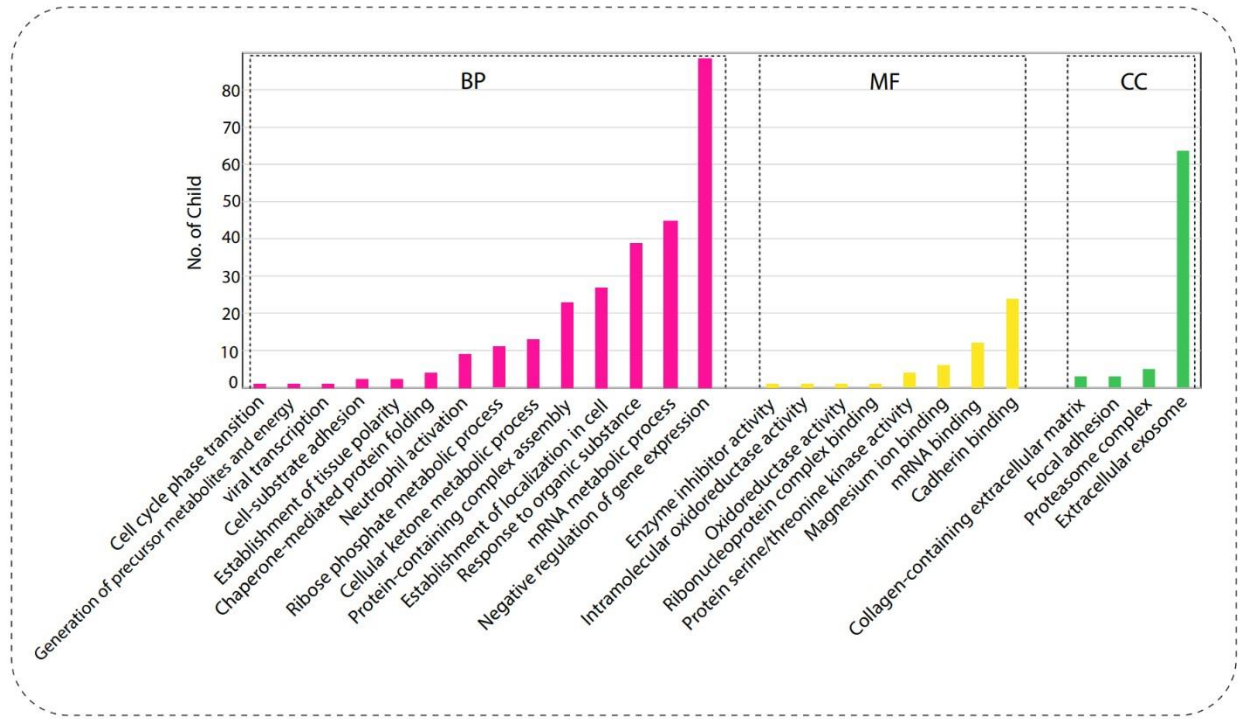
**Supplement 1.** Dataset quality assessment. **A.** Principal component analysis (PCA) was applied to assess the sample quality of the used dataset. The non-tumor tissues are represented by green circles, whereas tumors are represented by pink squares. **B.** Heatmap visualized the protein expression patterns of samples (non-tumor and tumor) in dataset. Proteins with decreased expression are shown in green color, whereas proteins with increasing expression represented in pink. The histogram displays the number of proteins with significant expression changes.



**Supplement 2.** Regulatory network construction. A multilayer complex network was developed to find differentially expressed proteins, transcription factors, kinases, miRNAs, and lncRNAs that might be used as breast cancer biomarkers.

**Supplement 3.** Central hub molecules: Top 10 molecules with considering topological parameters such as degree, betweenness and closeness were chosen in each layer.

<b>Hub-lncRNAs</b>	<b>Hub-miRNAs</b>	<b>Hub-DEPs</b>	<b>Hub-KEAs</b>	<b>Hub-ChEAs</b>
WWTR1-AS1	hsa-miR-16-5p	PON1	MAPK14	HNF4A
PLCG1-AS1	hsa-miR-92a-3p	LAMC1	CSNK2A1	FLI1
ERCC8-AS1	hsa-miR-615-3p	APOA1	RPS6KA3	RUNX1
WASHC5-AS1	hsa-miR-484	COL1A2	GSK3B	MITF
IGBP1-AS2	hsa-miR-193b-3p	COL4A1	MAPK1	SPI1
TMED2-DT	hsa-let-7b-5p	CAV1	CDK2	E2F4
C4A-AS1	hsa-miR-26b-5p	COL4A2	MAPK3	GABP
LINC02067	hsa-miR-1-3p	TNS1	CDK1	FOXP1
EML4-AS1	hsa-miR-124-3p	NID1	PRKACA	VDR
BZW1-AS1	hsa-miR-155-5p	HBA1	MAPK8	XRN2



**Supplement 4.** Functional enrichment analysis. Top GO enrichment analysis was performed based on common DEPs and predicted regulatory elements that categorized in biological process (BP), Molecular function (MF), Cellular component (CC) and represented with pink, yellow, green color respectively.