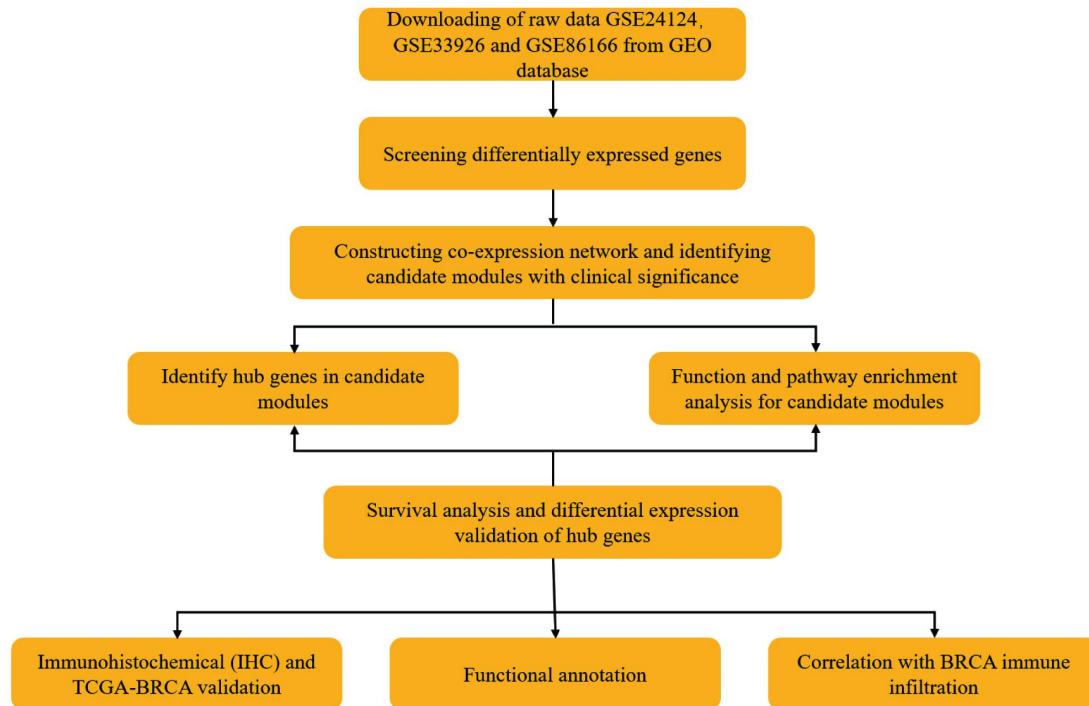
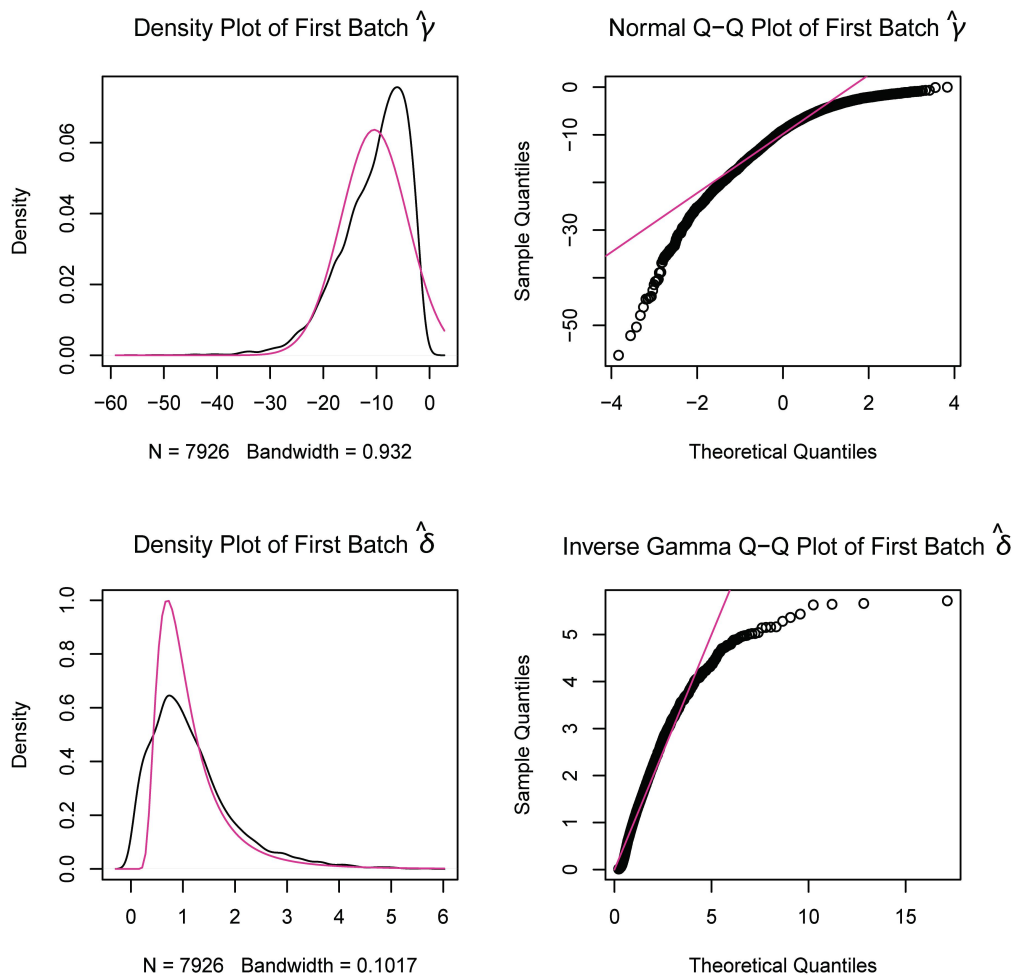


## Supplementary Figure 1



**Supplementary Figure 1.** Flowchart of the analysis procedure showing data preparation, processing, analysis, and validation.

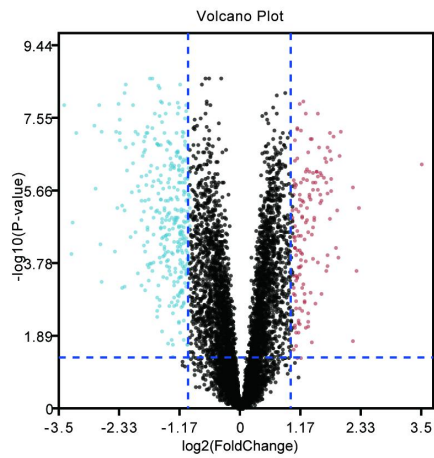
**Supplementary Figure 2**



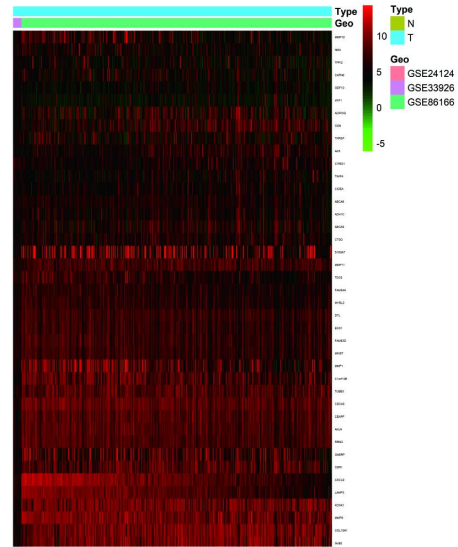
**Supplementary Figure 2.** Batch normalization of GSE24124, GSE33926, and GSE86166 datasets.

### Supplementary Figure 3

A

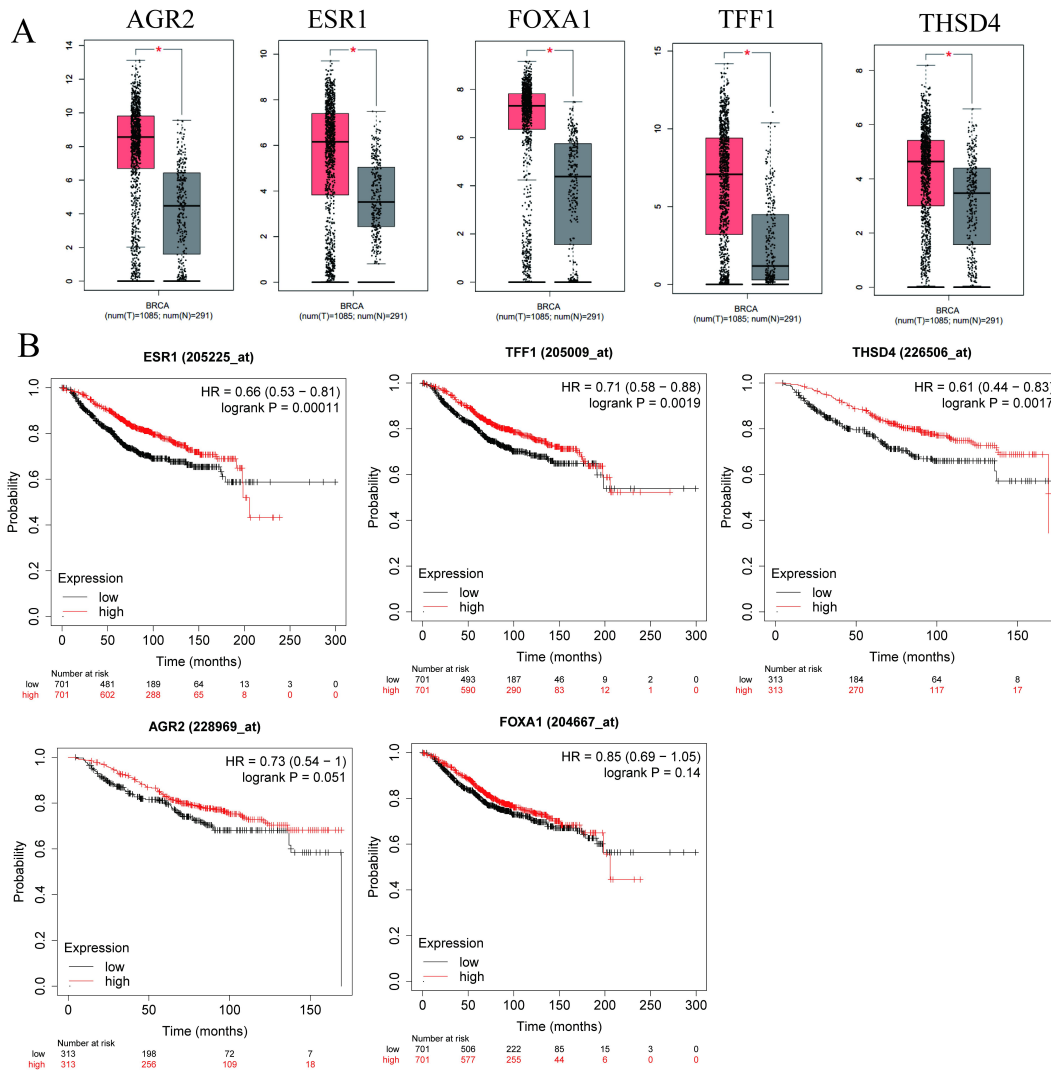


B



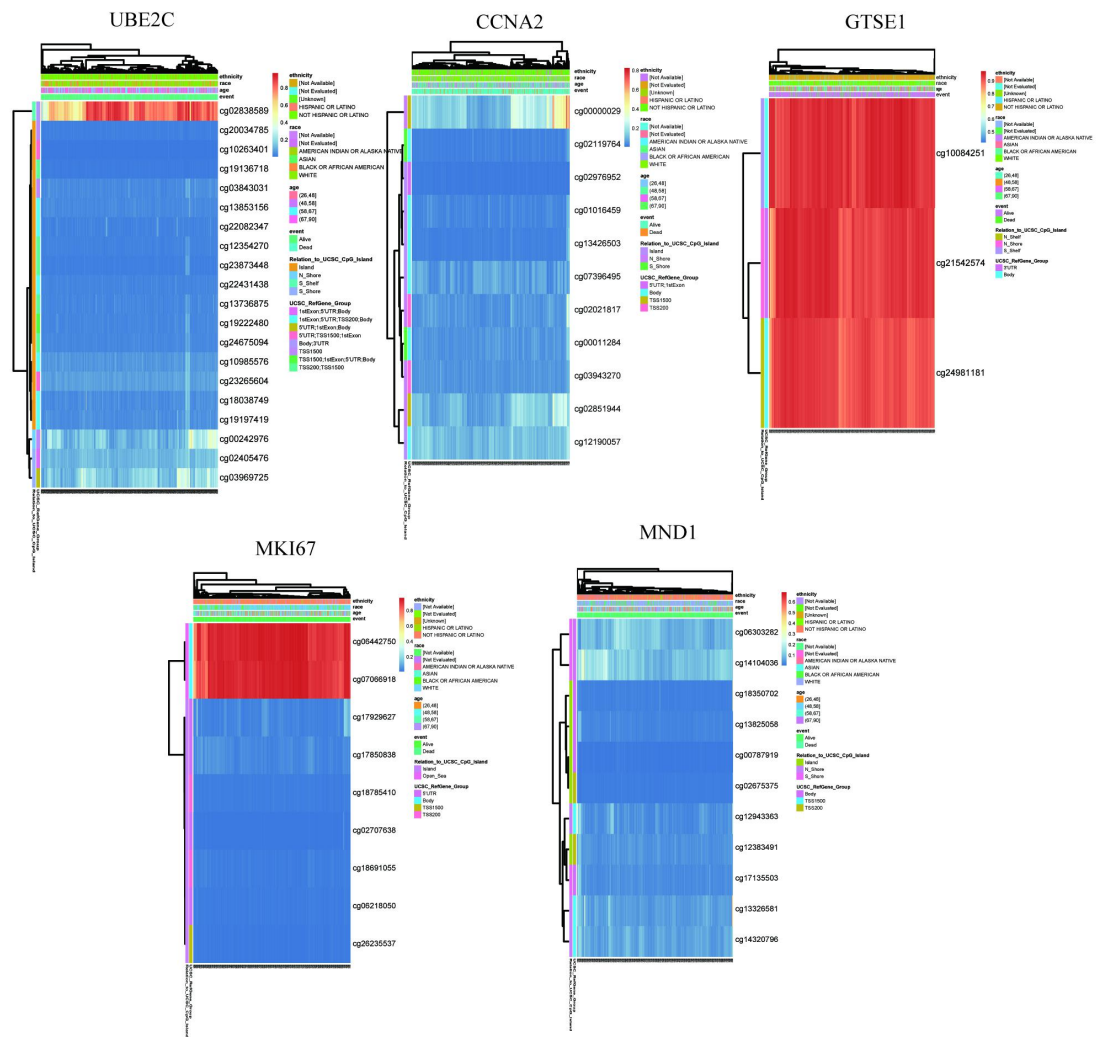
**Supplementary Figure 3.** Identification of mRNAs differentially expressed between normal tissue and tumor tissue in the GSE24124, GSE33926, and GSE86166 datasets. (A) Volcano plot showing the fold-change and statistical significance ( $-\log_{10}$  p-values) of mRNA expression between normal and tumor tissues. The blue and red dots represent the significantly downregulated and upregulated genes, respectively. The black dots represent genes that are not differentially expressed. (B) Heat map depicting relative expression level of top 50 significantly modulated mRNAs in normal and tumor tissues.

## Supplementary Figure 4



**Supplementary Figure 4.** Survival analysis and differential expression of hub genes in brown modules. (A) Differential expression of hub genes analyzed using the GEPIA database. Box plots show mRNA expression of hub genes in breast cancer (red plot) and the corresponding normal tissues (gray plot). “\*” represents  $P < 0.05$ . (B) Overall survival analysis of the hub genes in breast cancer (Kaplan–Meier plot).

## Supplementary Figure 5



**Supplementary Figure 5.** The heat maps of DNA methylation clustered expression level of five hub genes in blue modules.