**Supplementary Materials:**

**Supplementary Fig. S1.** The 20 most significant up-regulated genes and down-regulated genes according to adjusted P values based on RRA analysis. Each row in the figure represents one gene and each column is one dataset. Red shows up-regulation and green signifies down-regulation. The numbers in the heatmap squares indicates fold changes (breast cancer. Vs. Normal breast tissue) in each dataset that conducted in the “limma” R package.

**Supplementary Fig. S2.** The most signifificant module (module1) based on the protein–protein interaction (PPI) network analysis of 512 robust DEGs.

**Supplementary Fig. S3.** EZH2 are significantly upregulated in BC compared with normal breast tissues in GEPIA database.

**Supplementary Fig. S4.** Expression levels of EZH2 is significantly associated with the OS of patients in BC.

**Supplementary Fig. S5.** cell proliferation related gene-sets were significantly enriched in the high-expression group of EZH2.

**Supplementary Fig. S6.** Validation of the mRNA expression levels of CENPL, ISG20L2, MRPL3 and LSM4 between BC and normal breast tissues based on the TCGA\_BRCA and match TCGA normal and GTEx data in GEPIA database.

**Supplementary Fig. S7.** Immunohistochemistry staining of expression status of four hub genes in breast lobular carcinoma tissues and normal tissues using the Human Protein Atlas (HPA) database. **a** shows CENPL expression with HPA044520 antibody; **b** shows ISG20L2 expression with HPA028005 antibody; **c** shows LSM4 expression with HPA040932 antibody; **d** shows MRPL3 expression with HPA043665 antibody.

**Supplementary Fig. S8.** Clustering heatmaps of differentially expressed pathways derived from GSVA of each hub genes in the METABRIC dataset. **a** CENPL; **b** ISG20L2; **c** LSM4 and **d** MRPL3.

**Supplementary Fig. S9.** Correlation analysis of the mRNA expression levels of CENPL, ISG20L2, LSM4, and MRPL3 with EZH2 expression level in BC based on GEPIA database.

**Supplementary Table S1.** A total of 512 robust DEGs were identified, containing 202 up-regulated genes and 310 down-regulated genes based on RRA.

**Supplementary Table S2**. 512 robust DEGs were significantly enriched in 720 GO terms.

**Supplementary Table S3**. 512 robust DEGs were significantly enriched in 9 KEGG pathways.