

Supplementary Figure 2. (A) Scatter plot shows the signed -log10 p-value of genes (identified by the KIPA) in TMT-based proteomics and RNA-seq of the CPTAC-TNBC study. p-values were determined by Wilcoxon rank-sum tests comparing the protein (x-axis) and mRNA (y-axis) levels for pCR samples to non-pCR samples. Differential genes from the KIPA (p < 0.05) were highlighted in red (higher in pCR) or blue (higher in non-pCR). (B) Citation number of each signature protein in the field of "chemotherapy" and "breast cancer" was obtained using R package RISmed. (C) Matrix shows the correlation between the mRNA levels and protein levels of seven PBP signature genes in the CPTAC-TNBC dataset. The number is the correlation coefficient of each spearman correlation. Blue and red represent positive and negative correlation respectively.