

Supplementary Figure 1. (A) Venn diagram shows the overlapping number of proteins across KIPA, RNA-seq and TMT-based proteomics. (B) Volcano plot shows results from differential analysis of human kinases between pCR and non-pCR samples with the KIPA. X-axis is the log10 fold change between median value of pCR and non-pCR samples for each kinase. Y-axis is the -log10 p-value from Wilcoxon rank-sum tests comparing kinase levels in pCR samples to non-pCR samples. Pink points indicate significant (0.01 < p < 0.05) proteins.