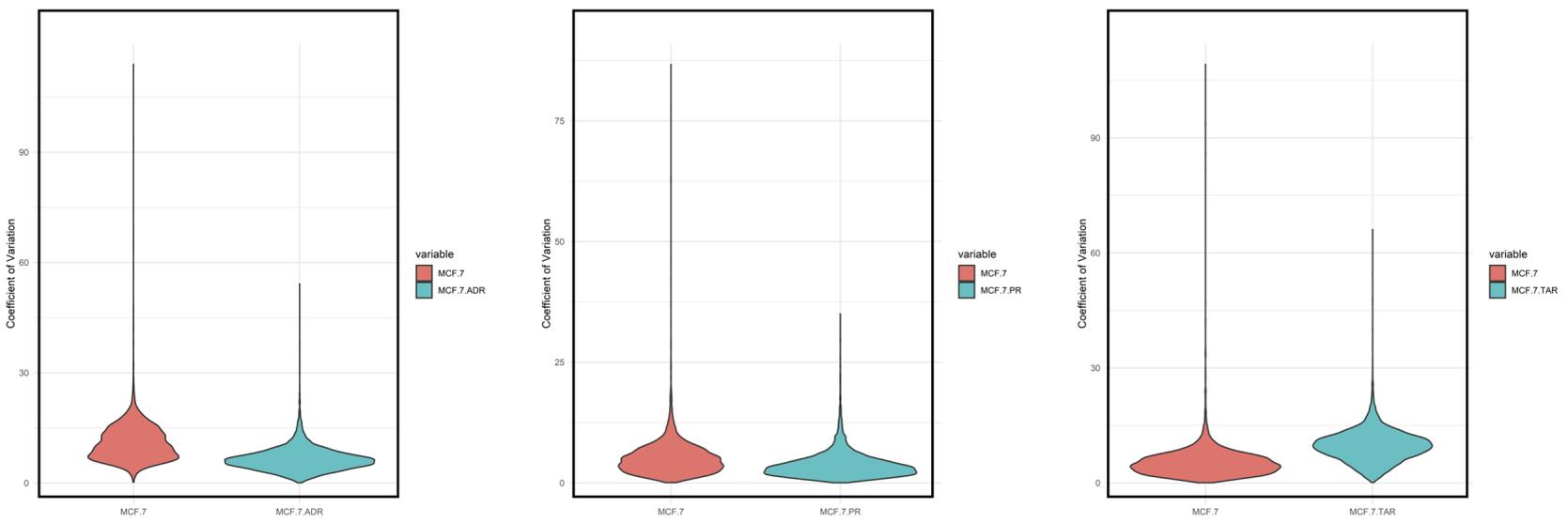


Figure S1. Distribution of number of unique peptides per protein identification in TMT 6-plex and TMT 10-plex experiments

(a)



(b)

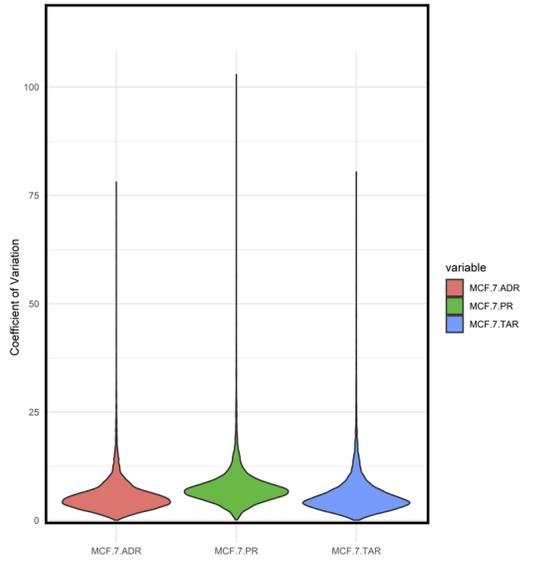
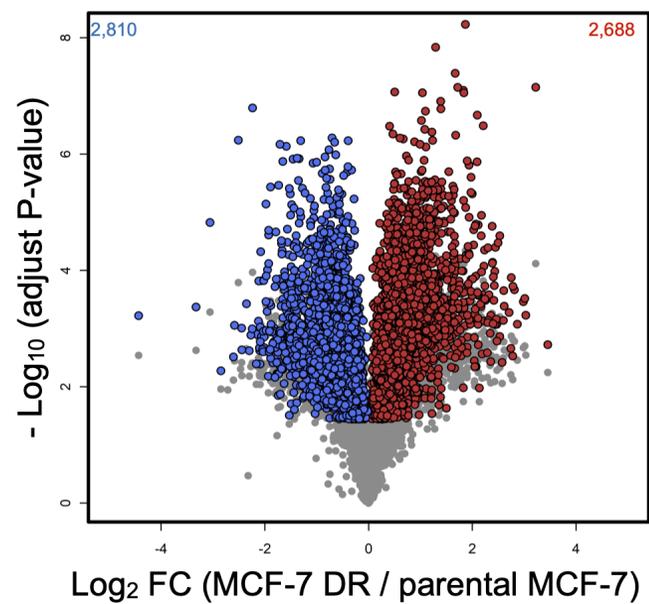
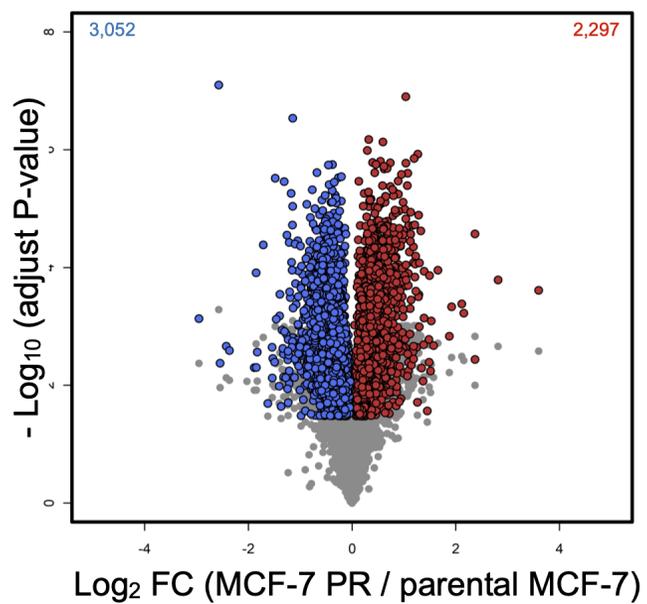


Figure S2. Violin plots of CV (coefficient of variance) between biological replications in each experimental sets. CV value calculate from the biological replicates of TMT 6-plex labels (a) and TMT 10-plex label (b) data

(a)



(b)



(c)

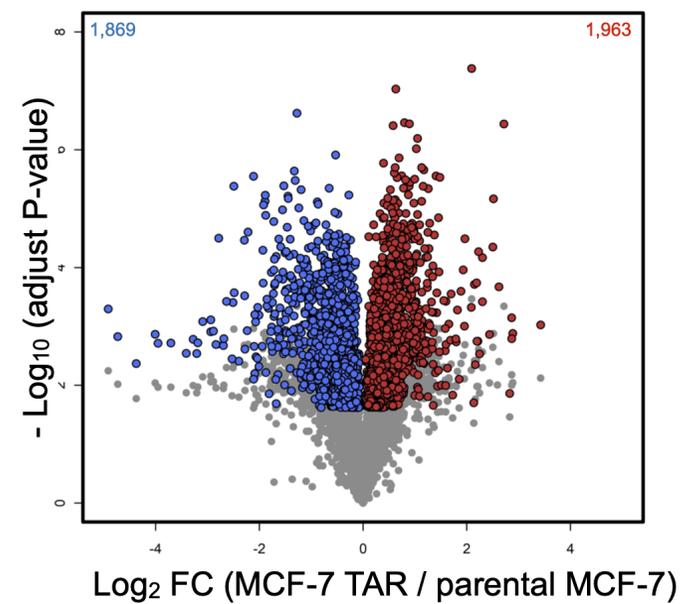


Figure S3. Volcano plots of significantly altered proteins between parental MCF-7 and drug-resistant cells in each TMT 6-plex experiments. The red and blue spots indicate significantly over-expressed proteins in drug-resistant MCF-7 cells (red) or parental MCF-7 (blue).

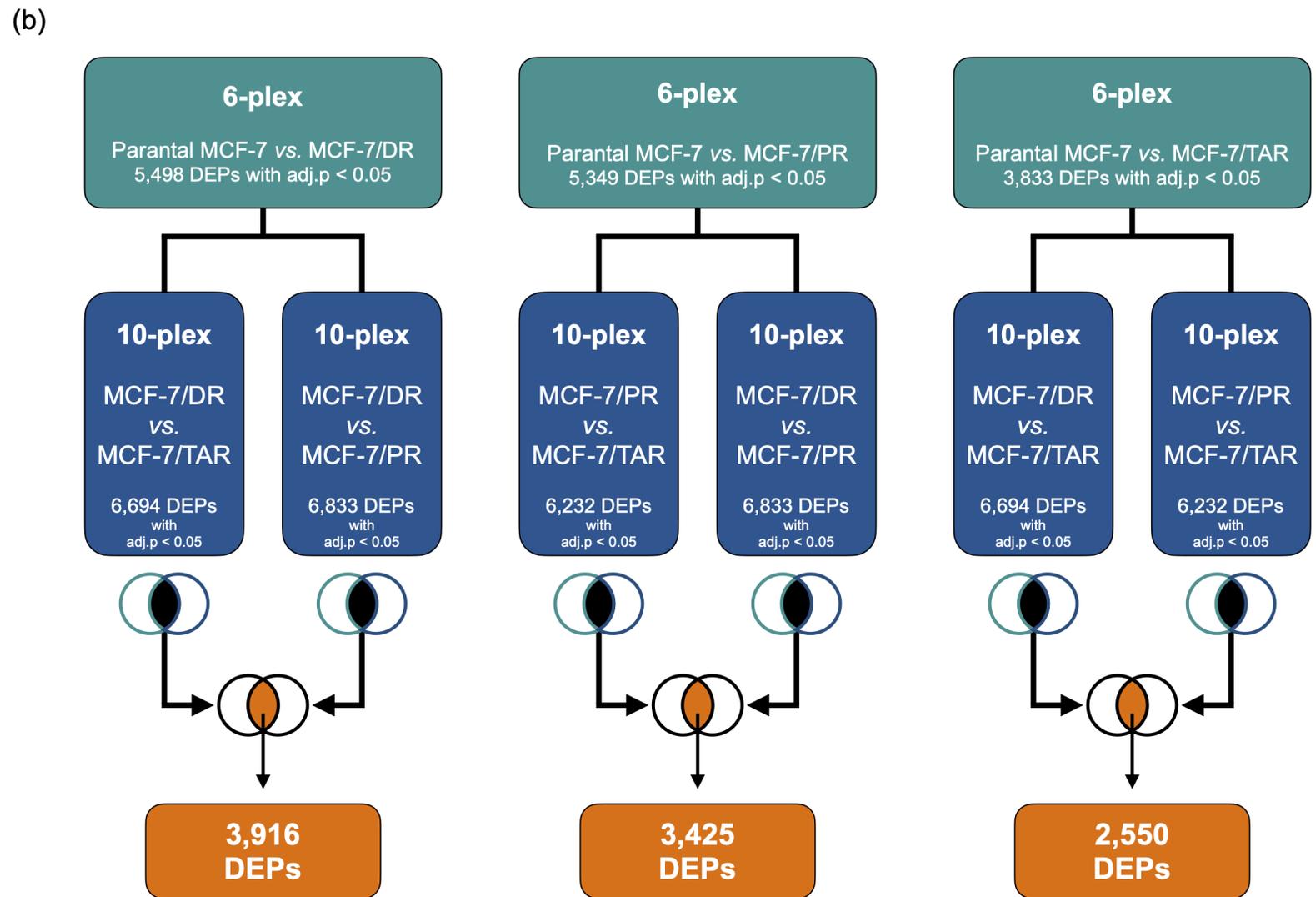
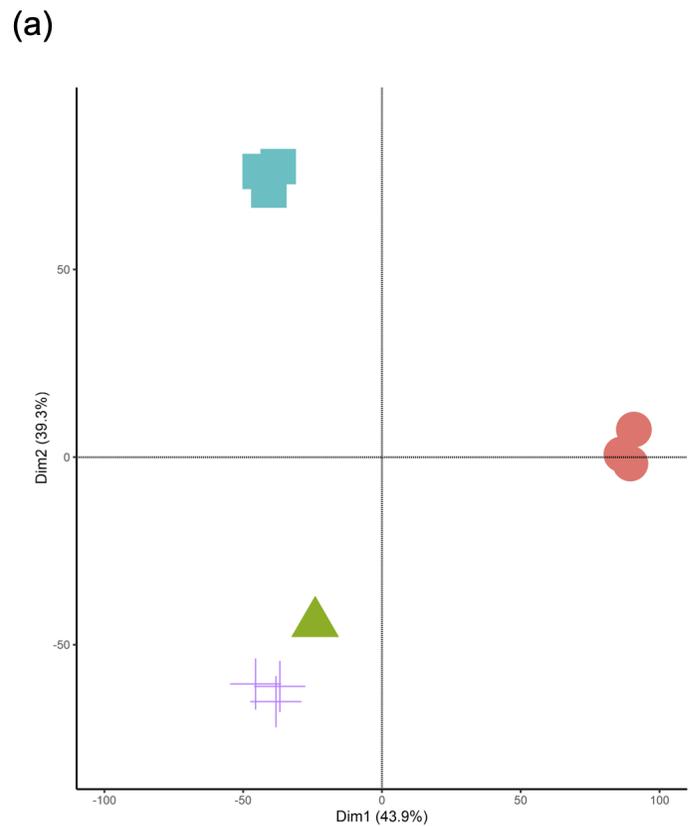
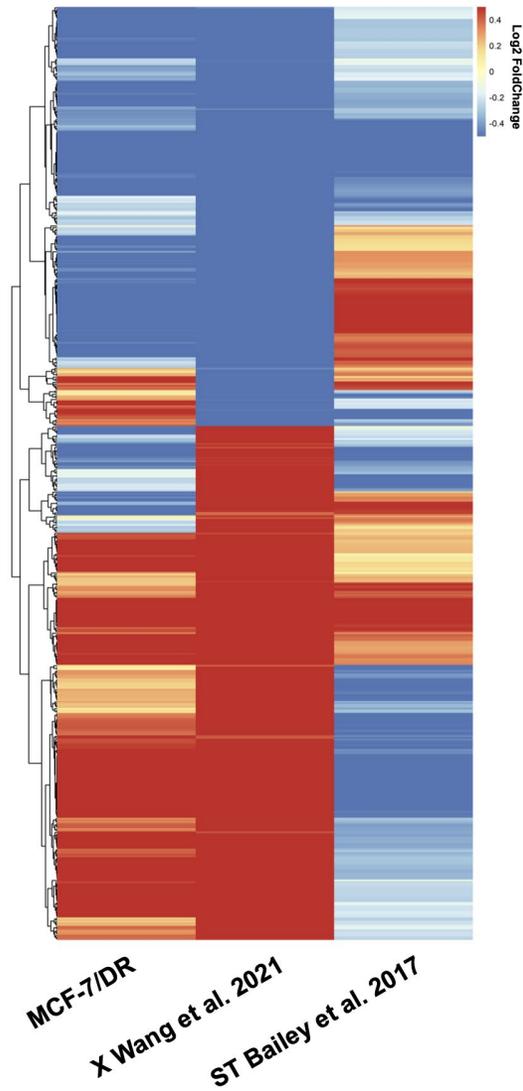
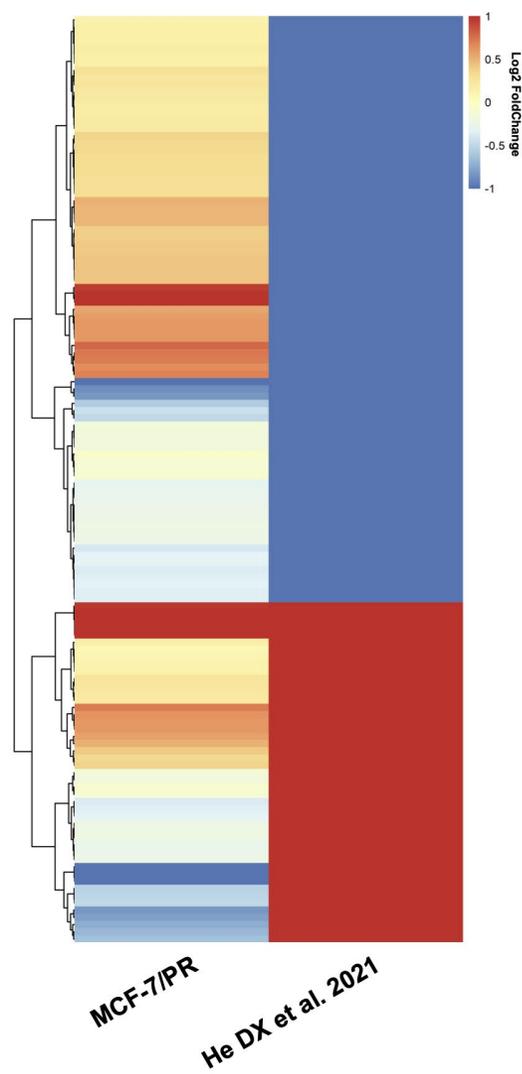


Figure S4. Direct comparison analysis between three drugs and combined analysis using TMT 6-plex and 10-plex data. (a) Principle component analysis of proteins quantified in TMT 10-plex experiment. (b) Schematic diagram of combining process of DEPs between 6-plex and 10-plex data.

(a)



(b)



(c)

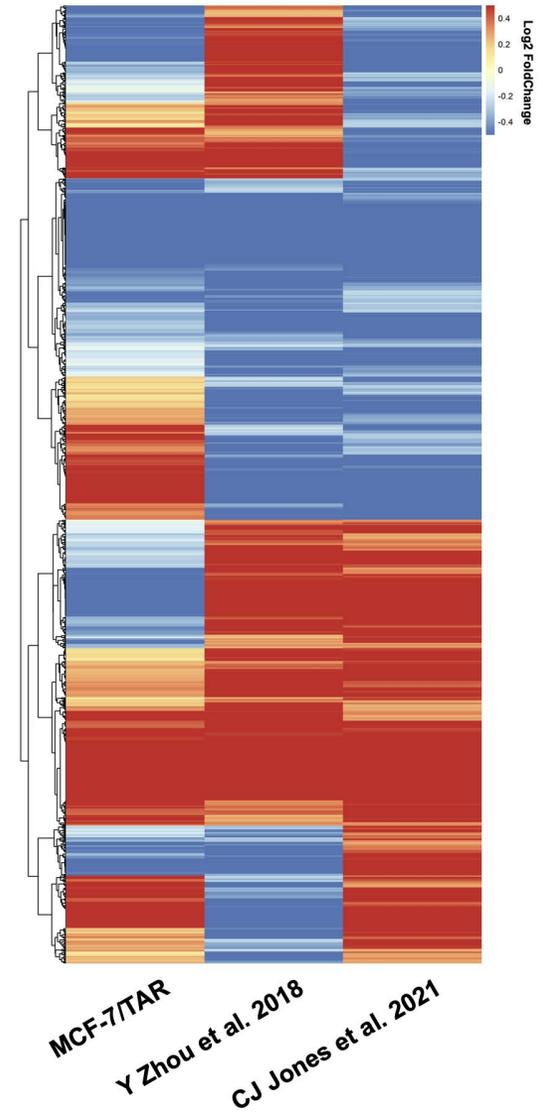


Figure S5. Heatmap showed relative expression levels between MCF-7 and drug-resistant cells in each experimental sets with log₂ fold change. (a) Expression patterns of 543 genes have been detected in three datasets of doxorubicin resistant cells. (b) Relative expression levels of 979 genes related to MCF-7/PR were identified from DEPs and DEGs. (c) The 1,058 genes were overlapped in both proteome and transcriptome. The expression levels were indicated with relative expression Levels by log₂(fold-change).

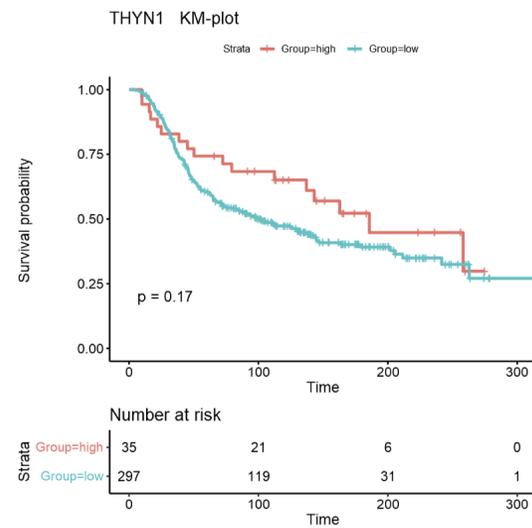
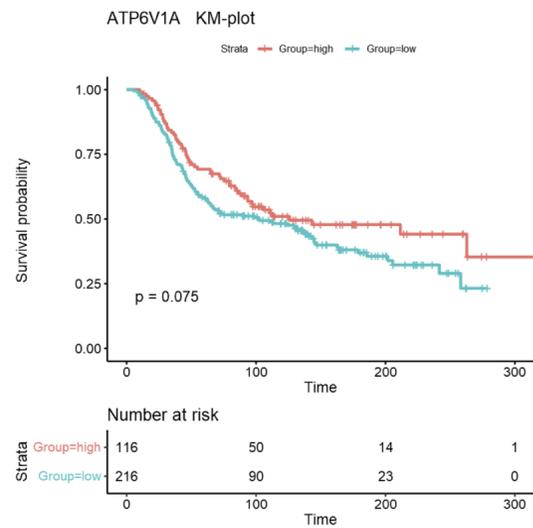
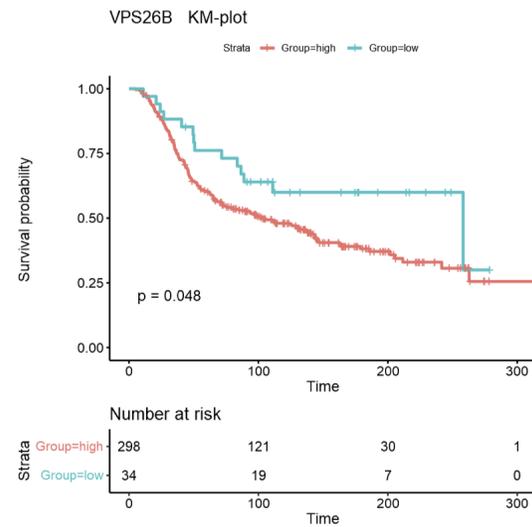
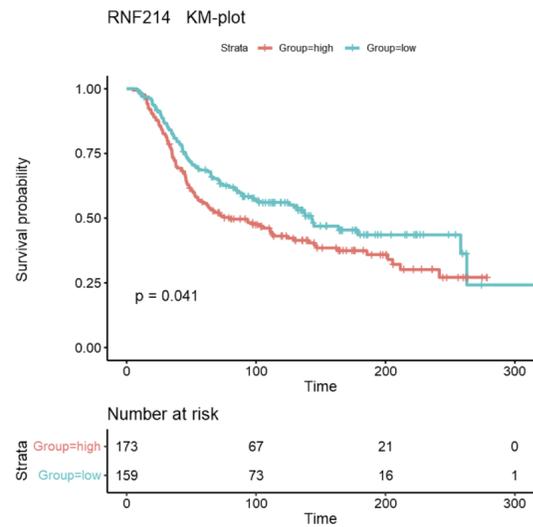


Figure S6. Overall survival plot with Kaplan-Meier model with highly significant genes of figure 6a under Metabric chemotherapy patients data

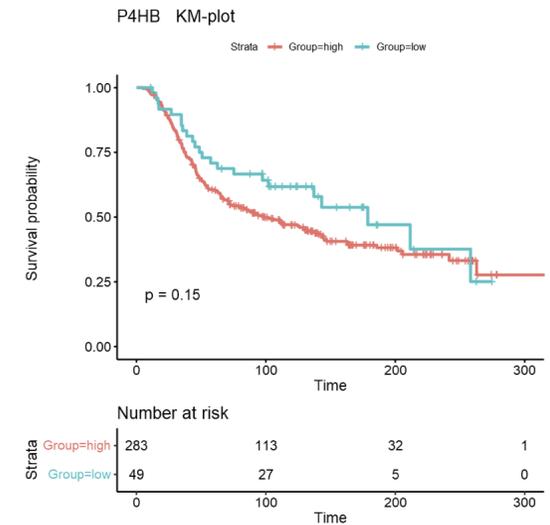
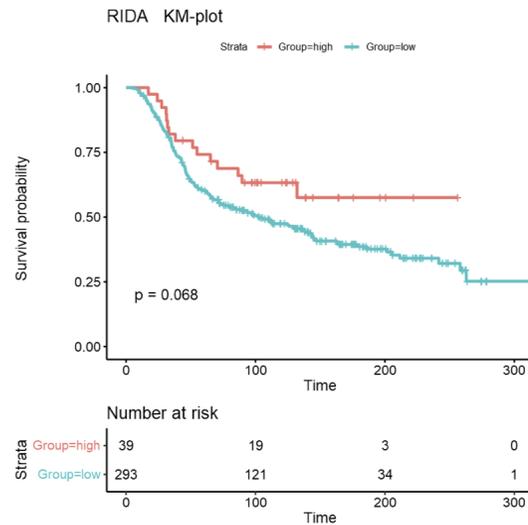
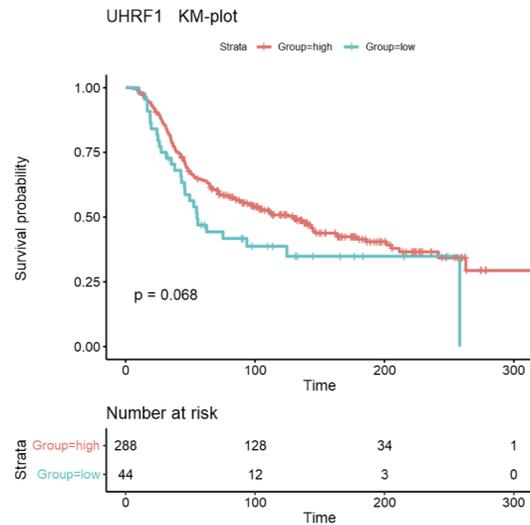
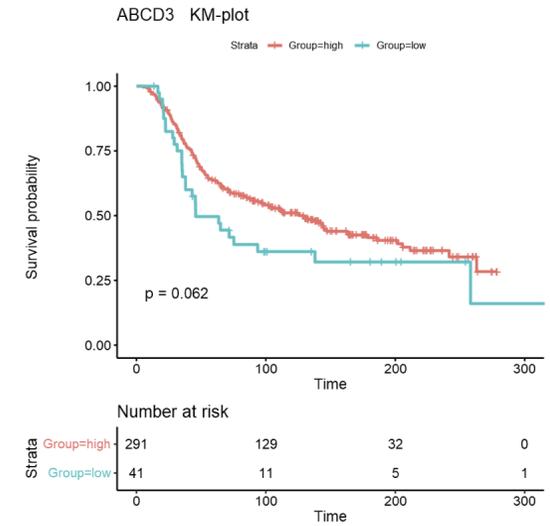
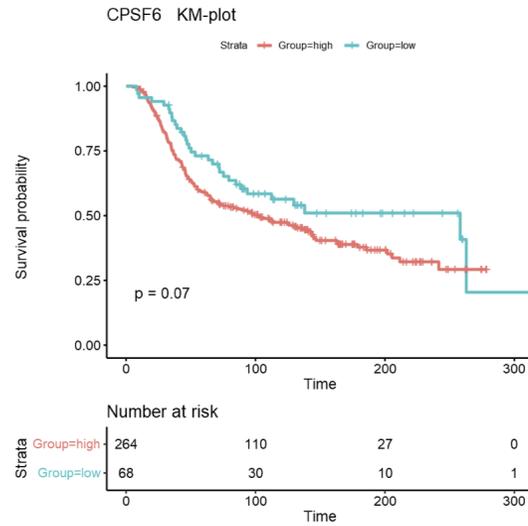
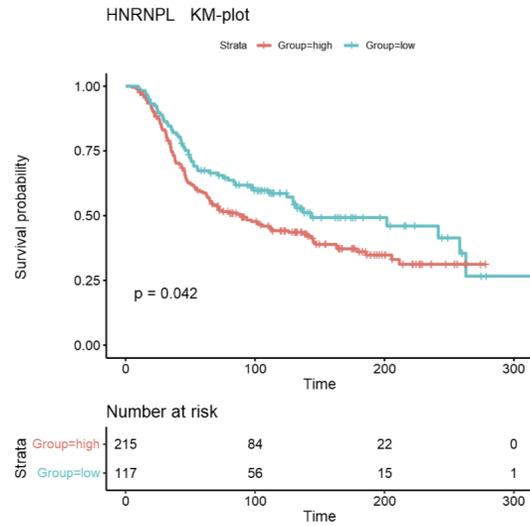


Figure S7. Overall survival plot with Kaplan-Meier model with highly significant genes of figure 6b under Metabrc chemotherapy patients data

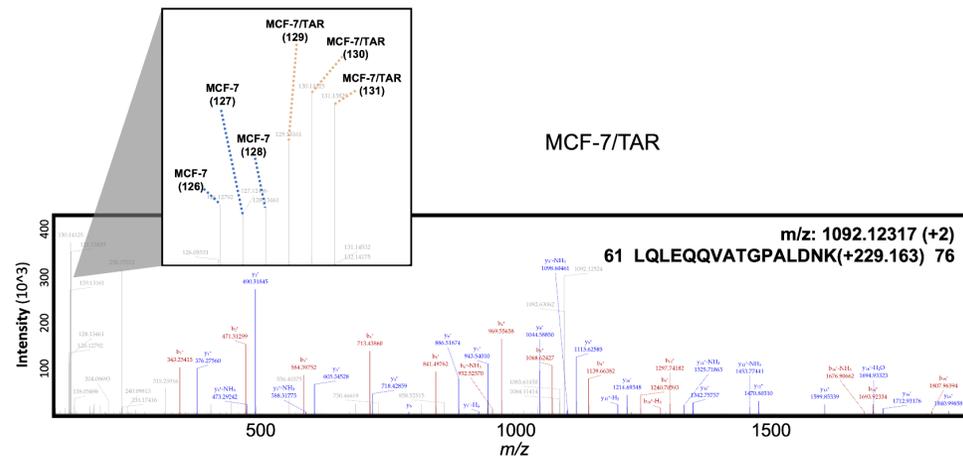
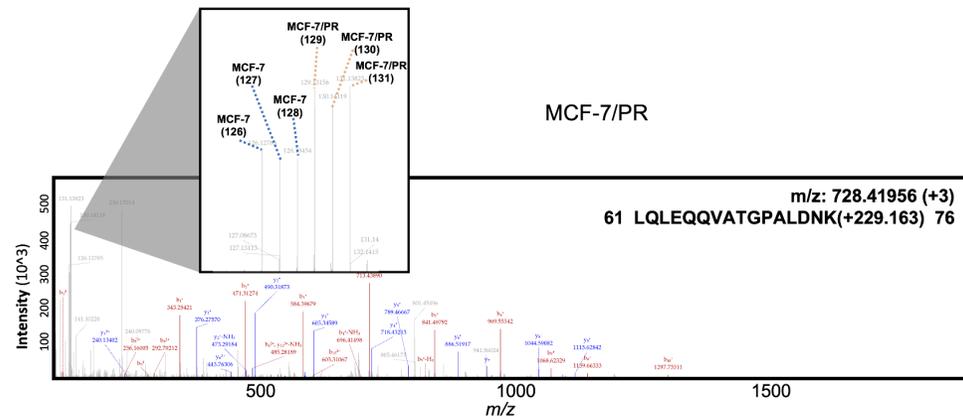
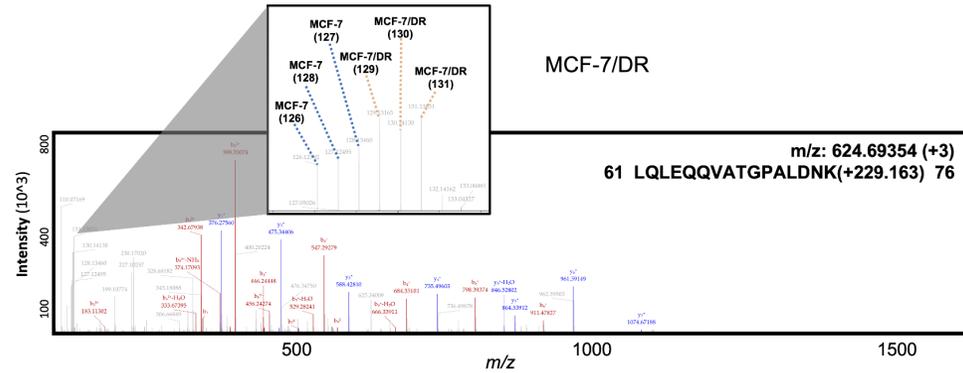


Figure S8. Representative MS/MS spectrum of LQLEQQVATGPALDNK peptide in PLXNB2

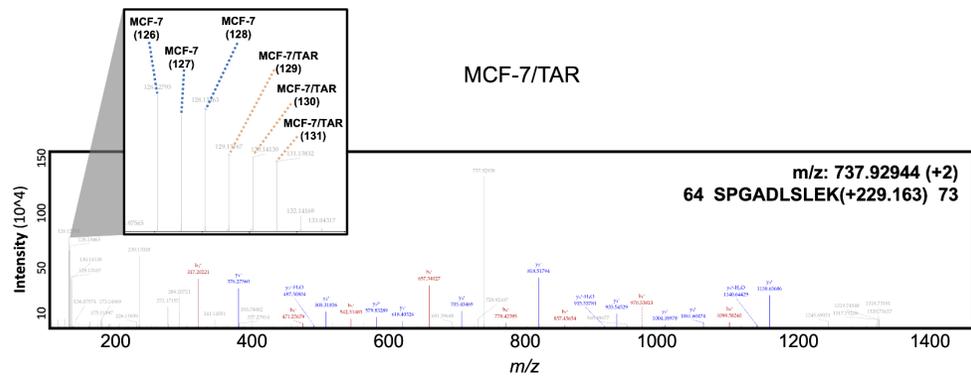
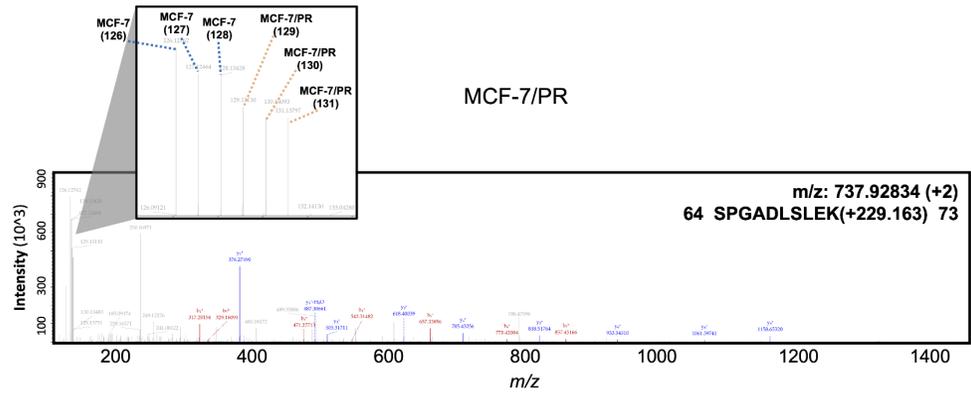
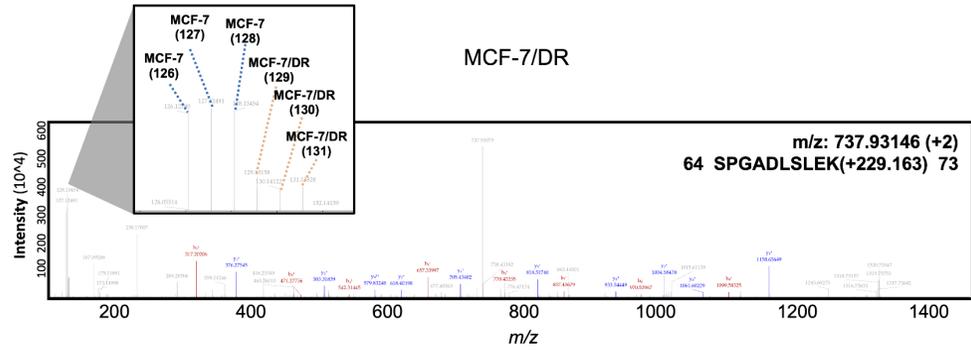


Figure S9. Representative MS/MS spectrum of SPGADLSLEK peptide in ACOX3

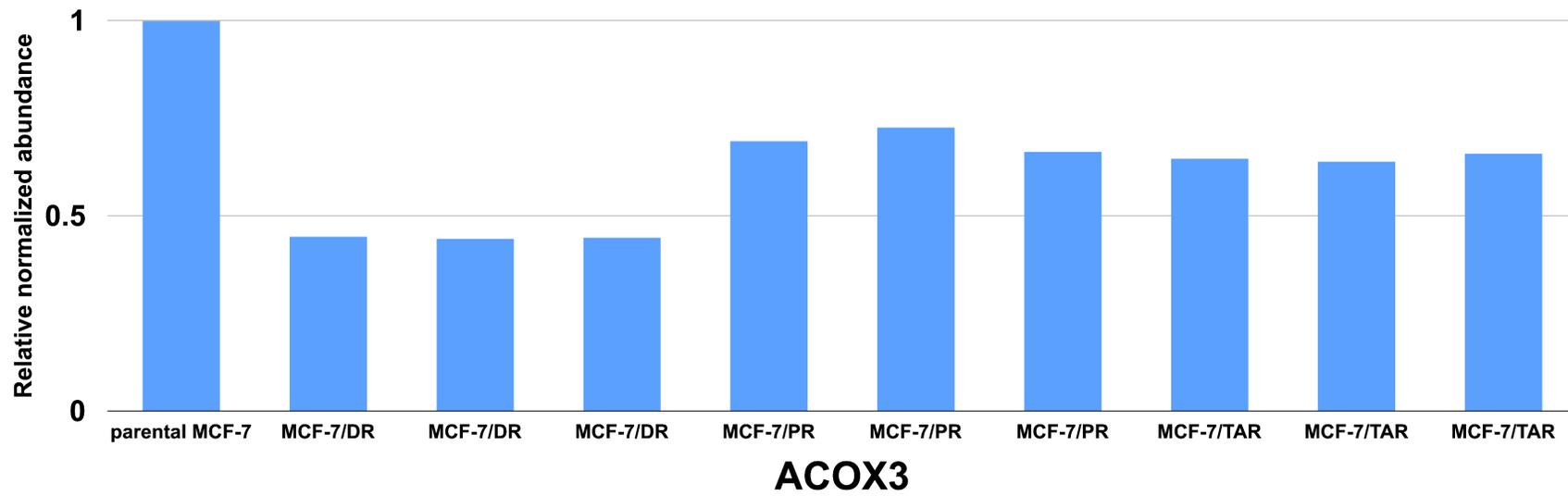
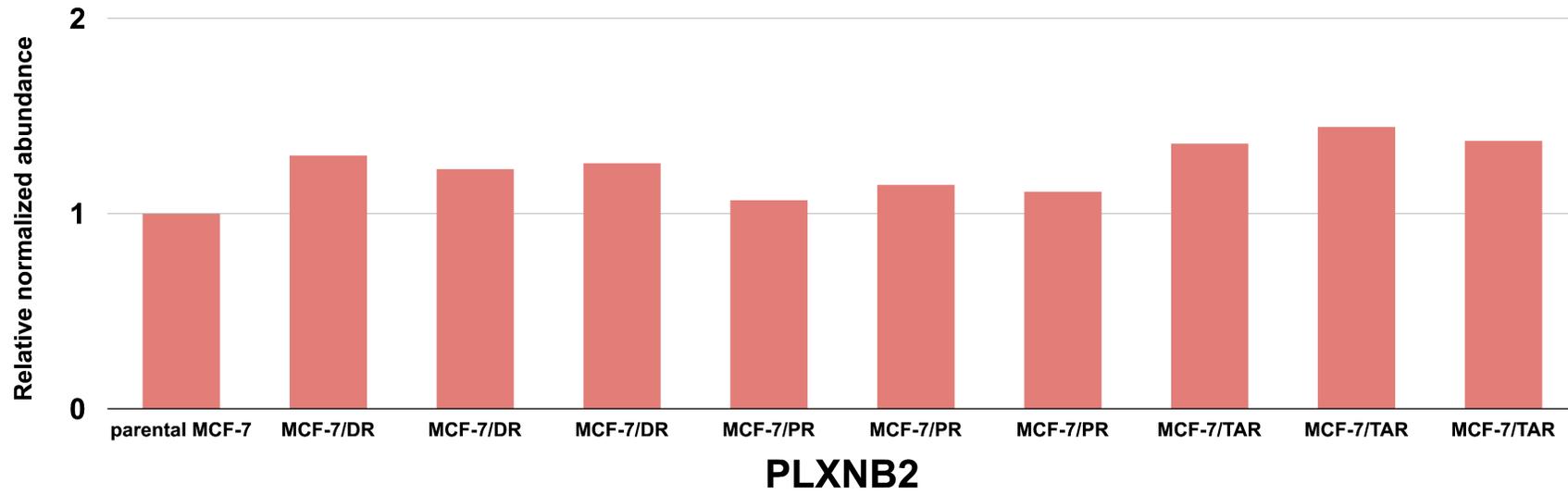


Figure S10. Expression patterns of PLXNB2 and ACOX3 in TMT 10-plex data