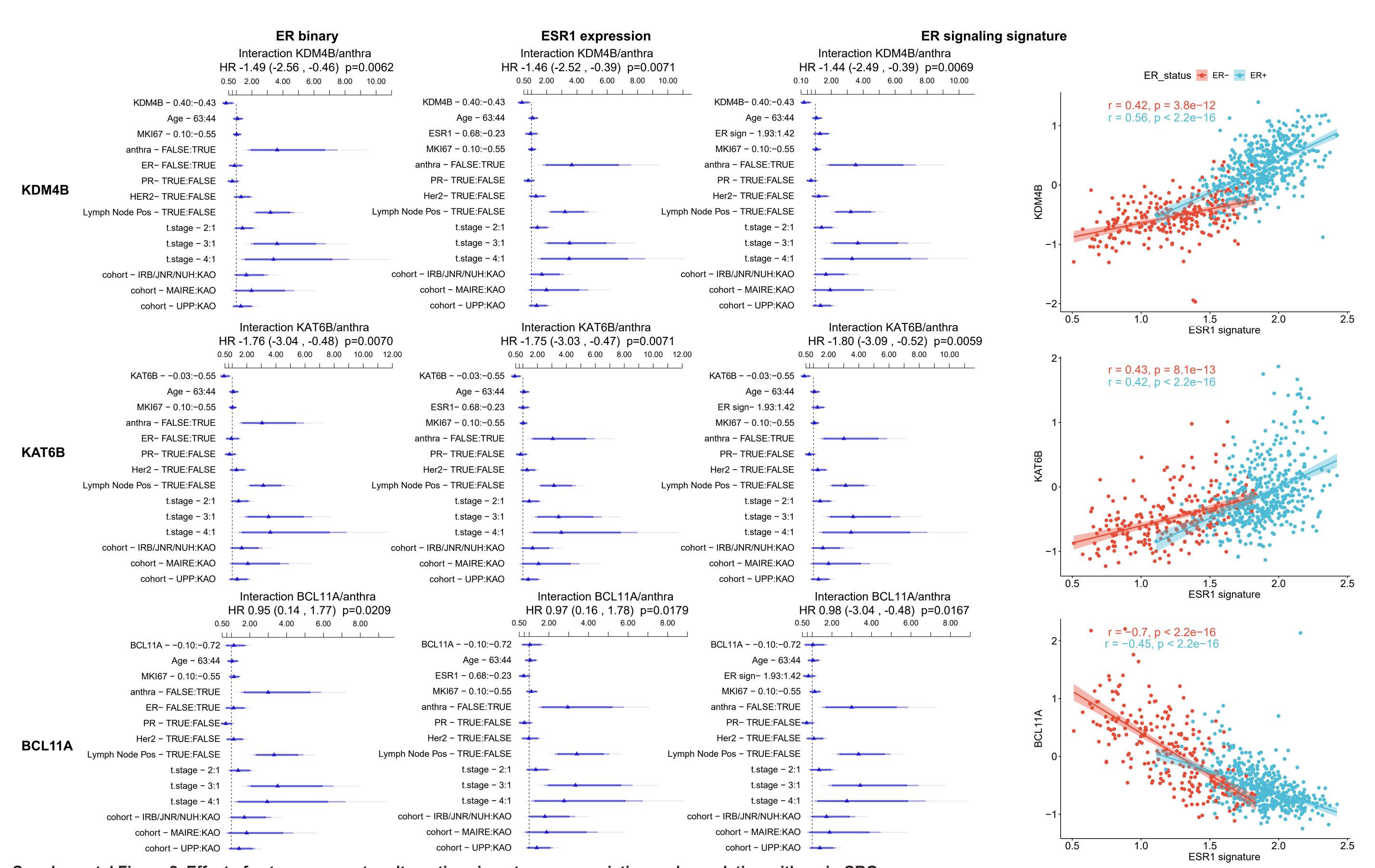


Supplementary Figure 1. Gene Set Enrichment Analysis (GSEA) enrichment of 12 CRGs from Viper and clinical analysis with different drug response dataset and chemotherapies.

Datasets include Heiser, GDSC1000, CCLE, gSCI, CTRPv2 and FIMM. Only chemotherapies relevant for breast cancer treatment have been included. P-values obtained from GSEA enrichment are based on random permutations.

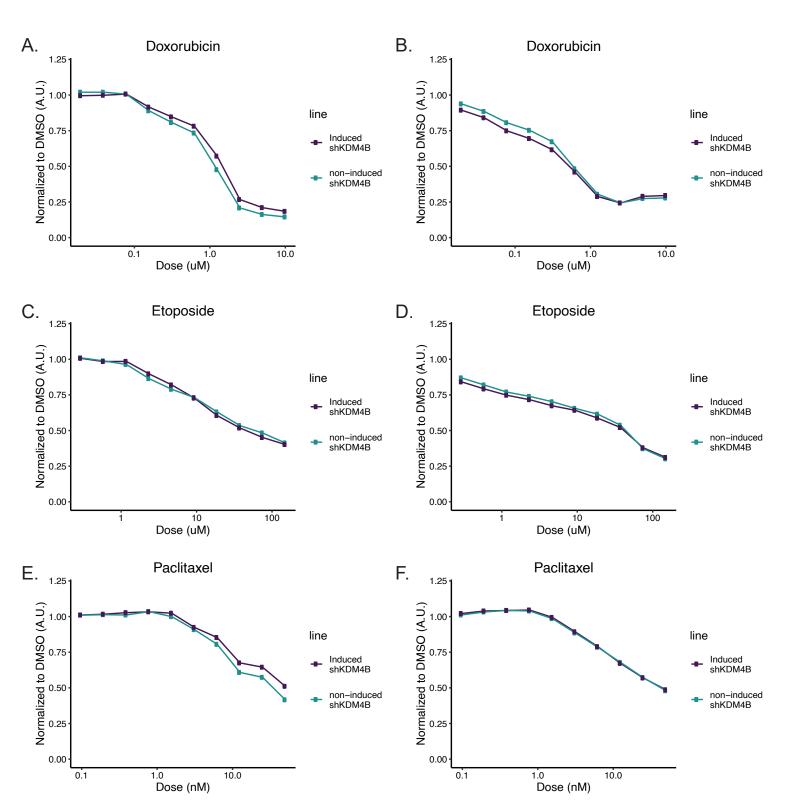


Supplemental Figure 2. Effect of estrogen receptor alternatives in outcome association and correlation with main CRGs.

Comparison of the effect of estrogen receptor (as a binary value, ESR1 expression value and estrogen receptor signaling (ESR1) signature from genefu ) in the Cox Proportional Hazard models of

KDM4B, KAT6B and BCL11A in the anthracycline vs non anthracycline metacohort (N=760 independent individuals). Scatter plots show the correlation between the ESR1 signaling signature and the CRGs stratified by ER status in the anthracycline vs non anthracycline metacohort (N=760 independent individuals). While ER status is correlated with KDM4B, KAT6B and BCL11A (Pearson correlation r = 0.75, 0.37, -0.57), the use of different ER measures to adjust the model does not affect the interaction association between the gene and the outcome. The forest plots show the log-2 hazard ratios (boxes) and error bars represent 95% confidence intervals.

HCC1806 Cal51



Supplemental Figure 3: Anthracycline Response to shKDM4B in TNBC cell lines. Left Panels: HCC1806; Right Panels: Cal51.

Panel A & B: Doxorubicin dose response curve for KDM4B induced shRNAs (shRNA 1) and non-induced cells normalized to DMSO vehicle. Panel C & D: Etoposide dose response curve for KDM4B induced shRNAs (shRNA 1) cells and non-induced cells normalized to DMSO vehicle. Panel E & F: Paclitaxel dose response curve for KDM4B induced shRNAs (shRNA 1) cells and non-induced cells normalized to DMSO vehicle. n=2 independent experiments for all panels. Center points equal mean value.