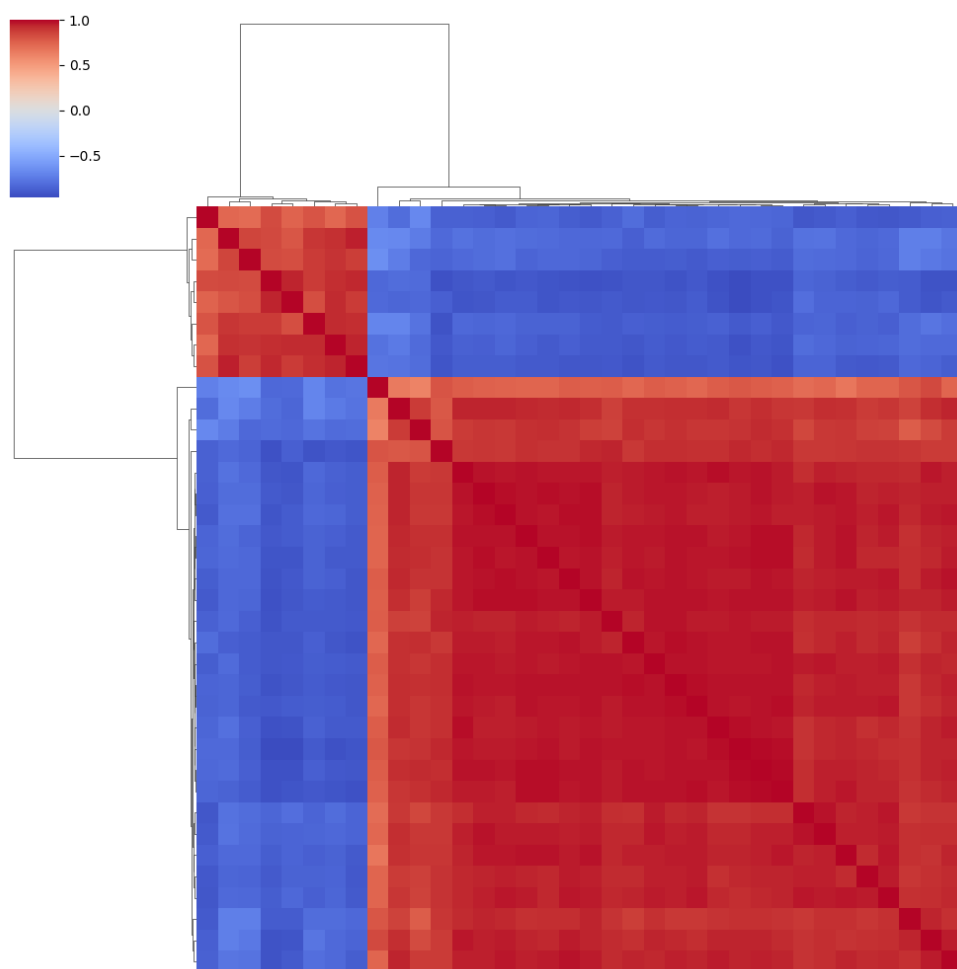
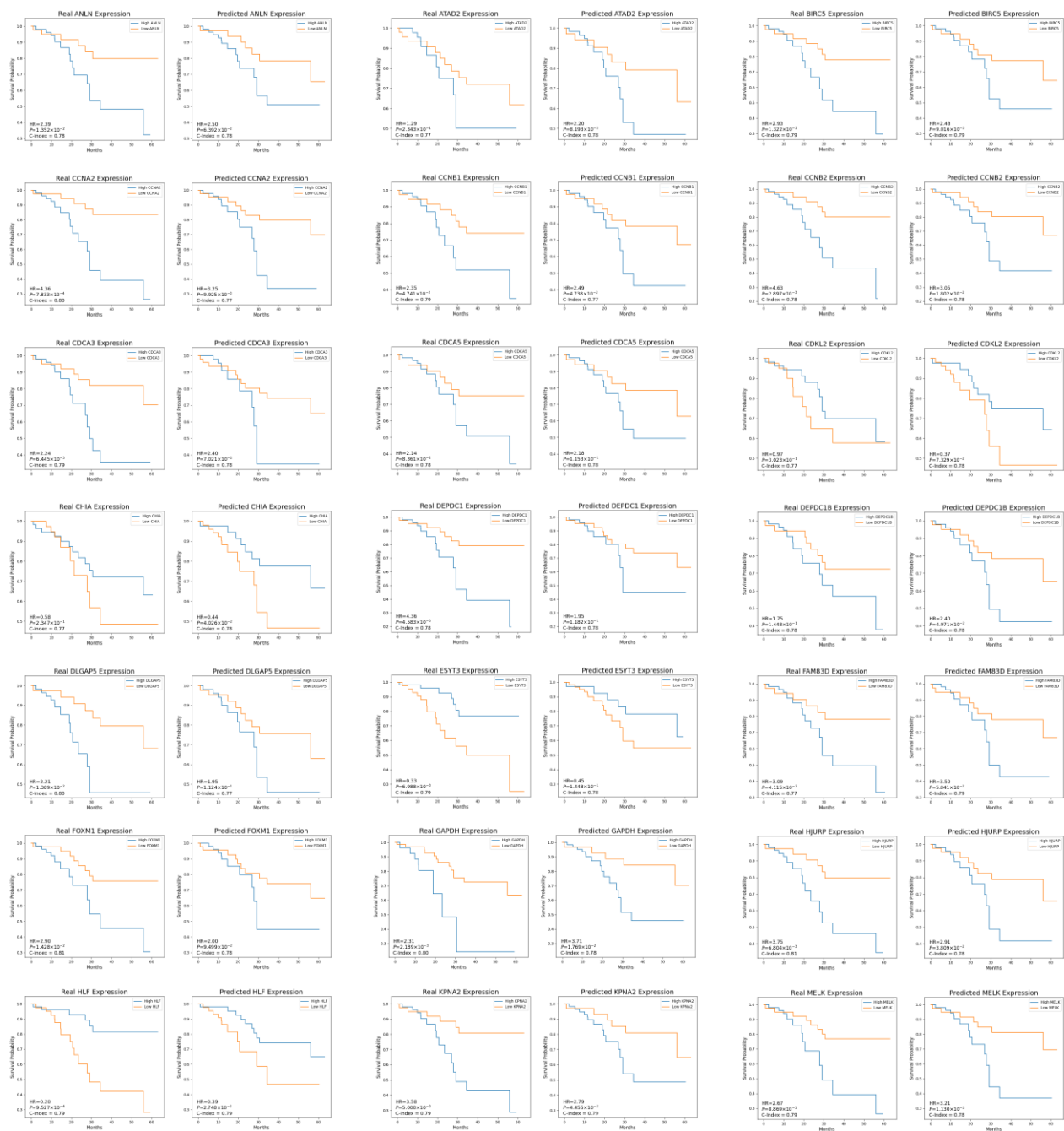


Suppl. Fig. 1: Study design flow chart.

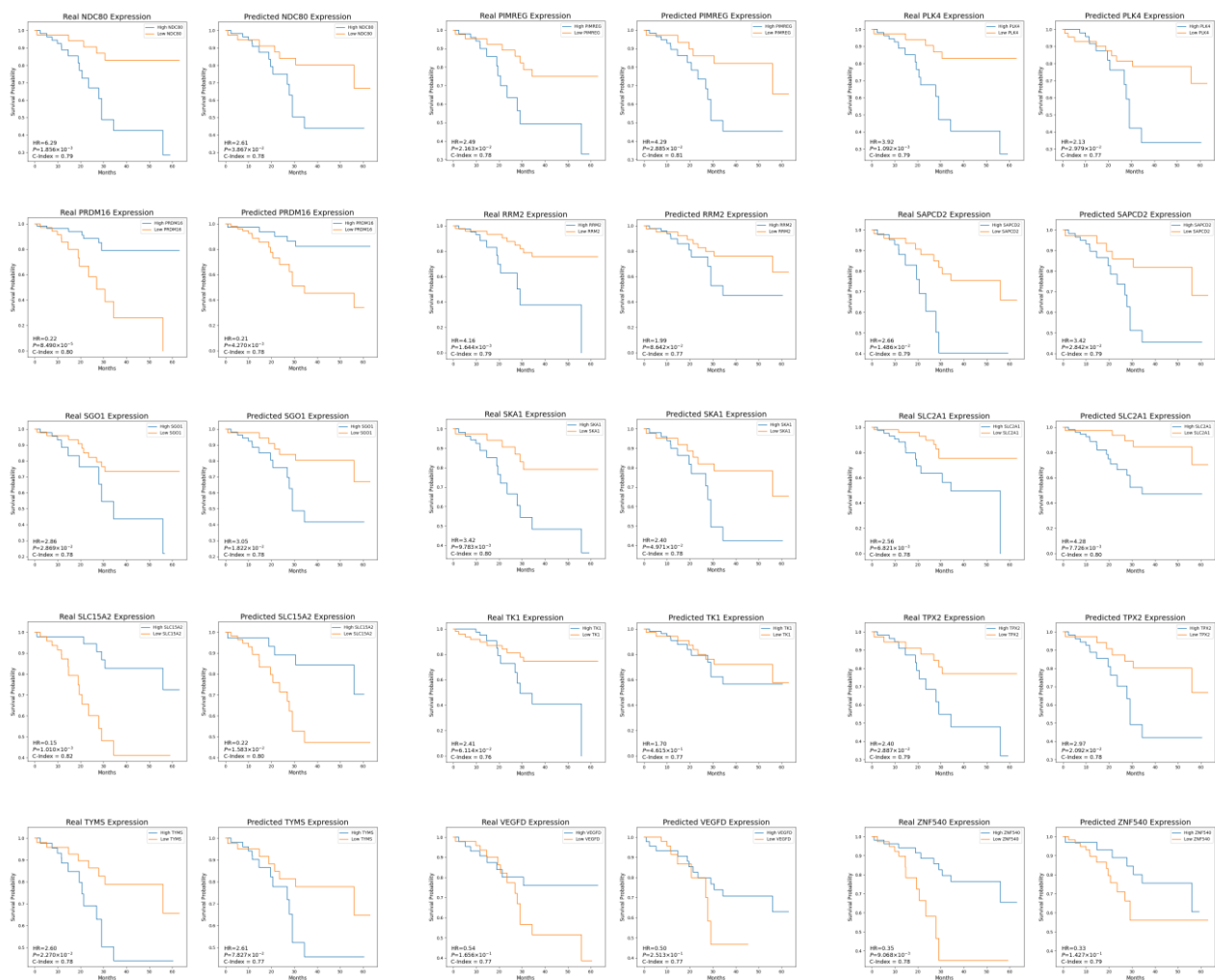


Suppl. Fig. 2: Clustergram of the predicted expression of the 36 genes that were found to have predicted expression that was prognostic of OS.



Suppl. Fig. 3:

Kaplan-Meier plots of risk groups as determined using KMeans clustering with k set to 2 for real and predicted gene expression. Plots are shown for each of the 36 genes for which gene expression predicted from WSIs in the CPTAC-LUAD dataset was found to be prognostic of overall survival. Hazard ratios (HR) were determined by setting risk group as a covariate in Cox regression adjusting for age, stage, and sex. Corresponding concordance indices (C-index) are also shown along with log-rank P -values.



Suppl. Fig. 3 contd.