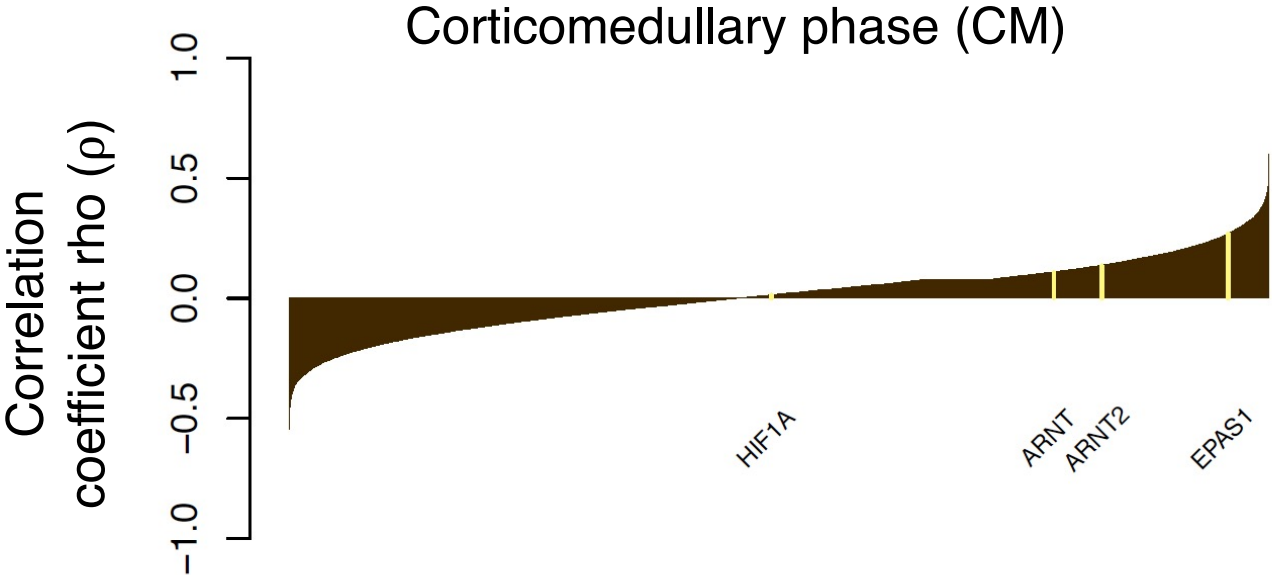


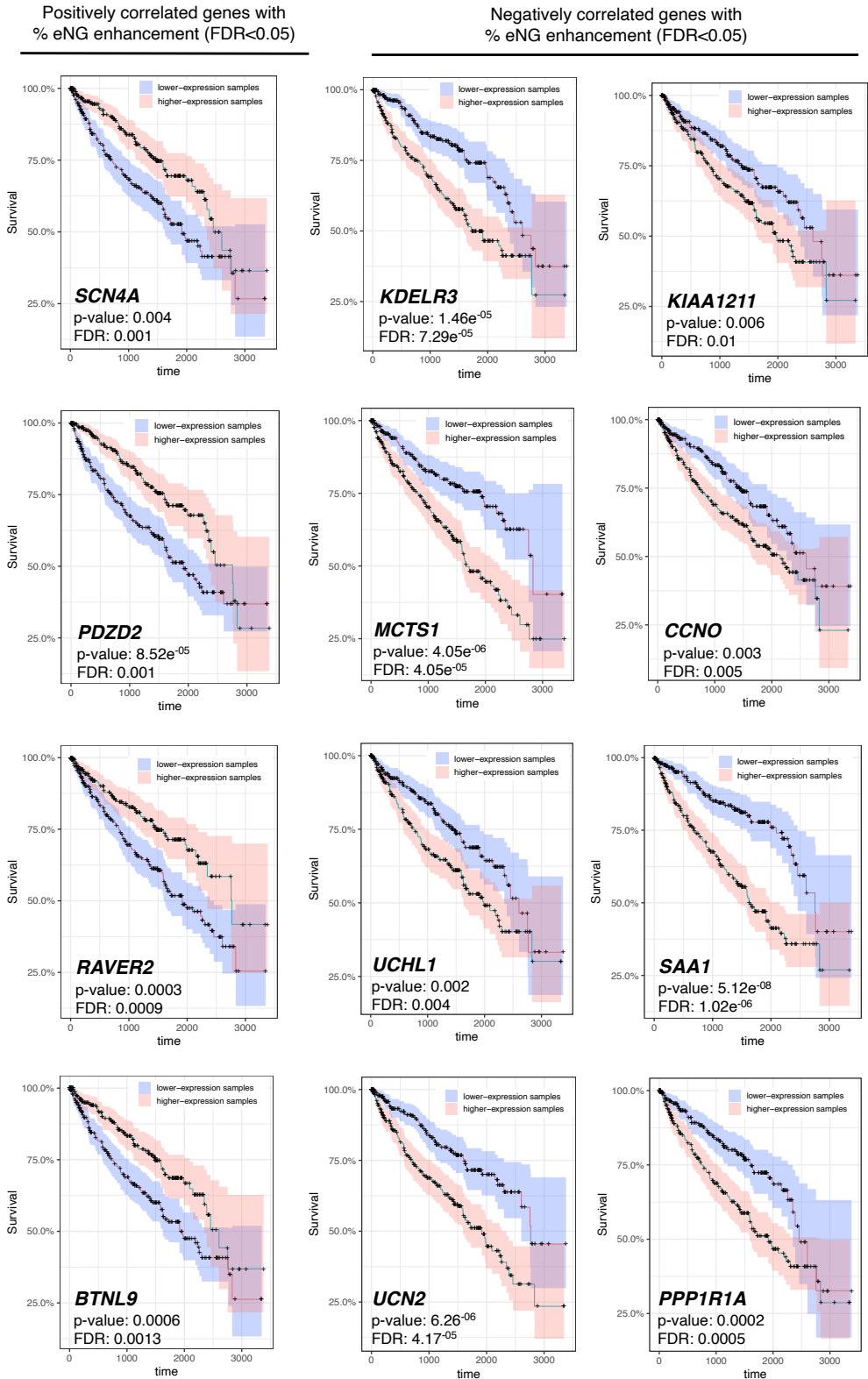
Supplementary Figure S1

Contrast enhancement (% Enhancement) at CM phase compared to RNA expression of all genes. Waterfall plot of correlation coefficient values for all genes.



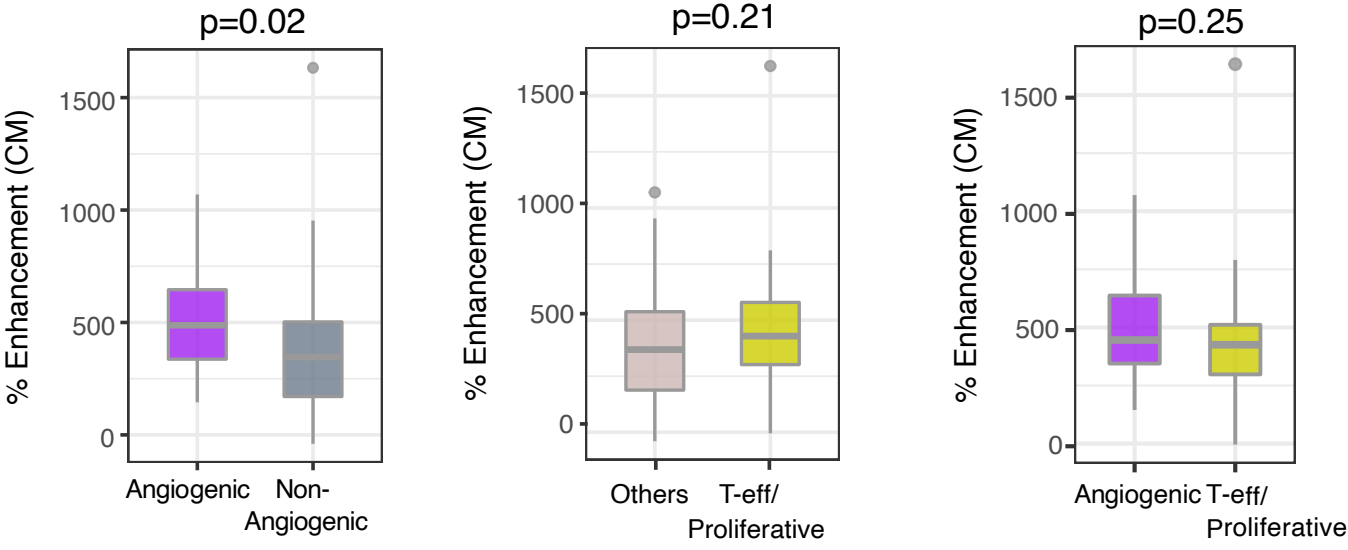
Supplementary Figure S2

Gene expression based survival analysis of TCGA-KIRC cohort



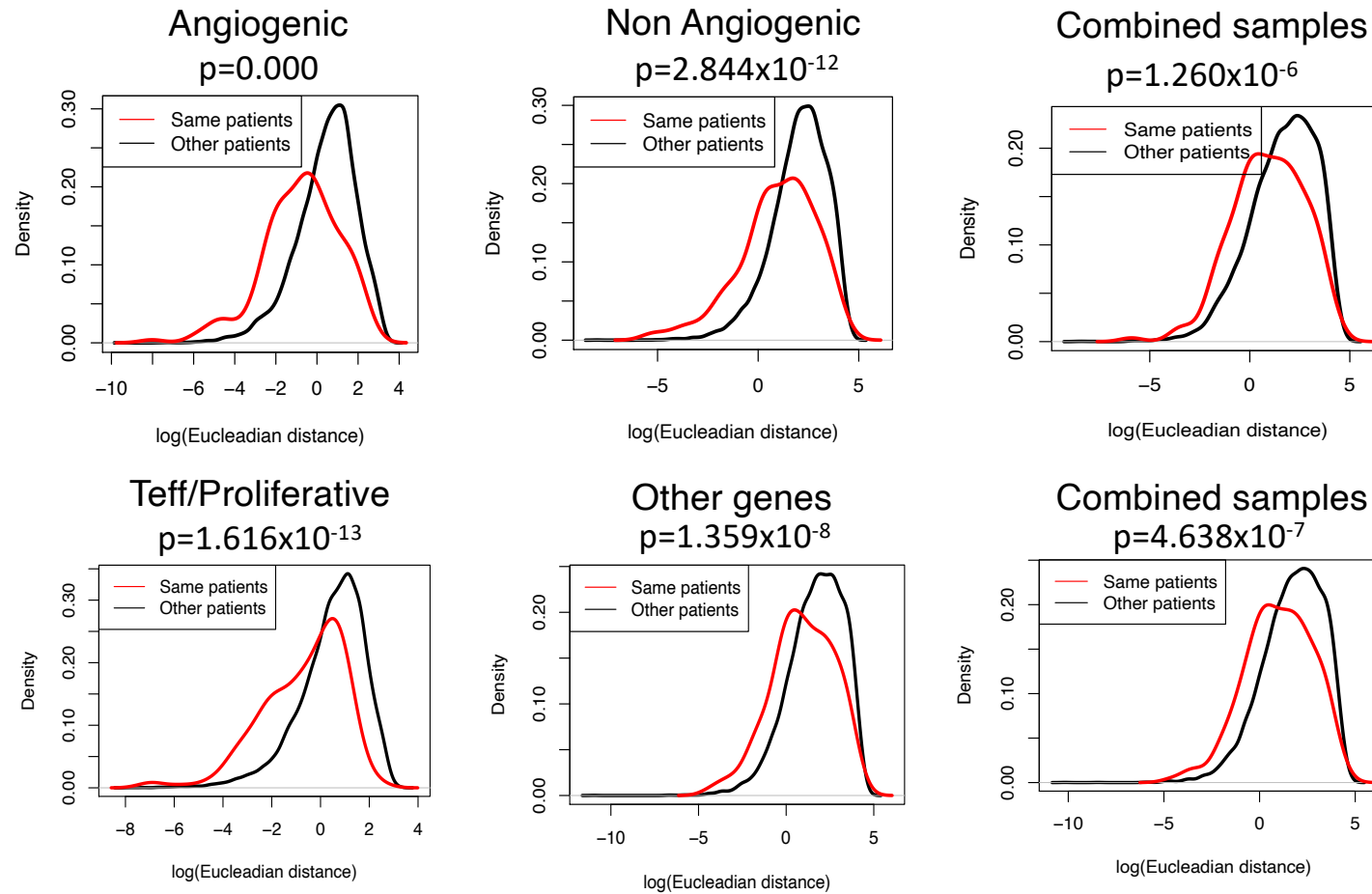
Gene expression based survival analysis of TCGA-KIRC cohort. The plots represent survival analysis for TCGA-KIRC patient cohort as a function of gene expression levels. X-axis indicates time of survival in days. Y-axis indicates percentage of survival. Left column represents survival plots for genes positively correlated with enhancement (*SCN4A*, *PDZD2*, *RAVER2*, and *BTNL9*). The middle and right columns represent survival plots for genes negatively correlated with enhancement (*KDELR3*, *MCTS1*, *UCHL1*, *UCN2*, *KIAA1211*, *CCNO*, *SAA1*, and *PP1R1A*). The red curve indicates ccRCC tumor group with high RNA expression of the genes and the blue curve indicates ccRCC tumor group with low RNA expression of the genes. P-values and FDR are shown in the inserts of each graph.

Supplementary Figure S3



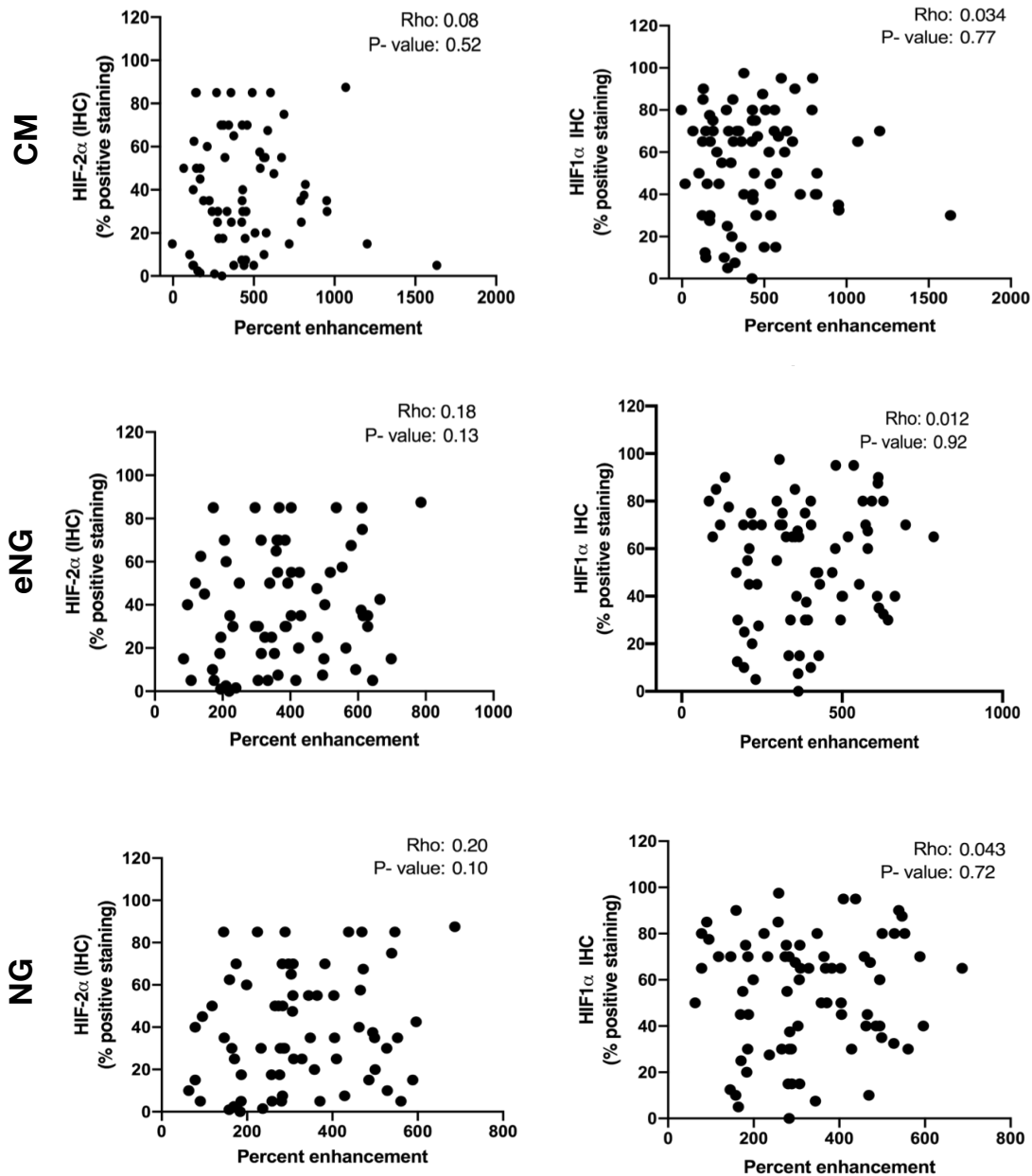
Box plot comparing % enhancement in the CM phase of the dynamic contrast enhanced MRI between angiogenic and non angiogenic sample groups (Left), between Teffector/Proliferative and other genes sample groups (Middle), and between exclusively angiogenic and Teffector/Proliferative sample groups (Right). All P-values are indicated in the plots.

Supplementary Figure S4



Euclidean distance plots for the angiogenic, non angiogenic, and combined sample groups (**Top panels**). Euclidean distance plots for Teffector/Proliferative, Other genes, and combined sample groups (**Bottom panels**). Black and red curves represent variability in gene expression between different patient tumors and variability within the same tumor respectively.

Supplementary Figure S5



Correlation analysis of protein expression levels of HIF-1 α and HIF-2 α with DCE post-contrast phases. Left column shows the Spearman ranked correlation between HIF-2 α protein expression levels, measured as percentage positive staining on immunohistochemistry (Y-axis), and the percentage enhancement on DCE phases (X-axis). CM phase (top row), eNG phase (middle row), and NG phase (bottom row). The right column shows similar Spearman ranked correlation between HIF-1 α protein expression levels and DCE percentage enhancement on DCE phases. The correlation coefficient (rho) and P-values are shown in each graph.