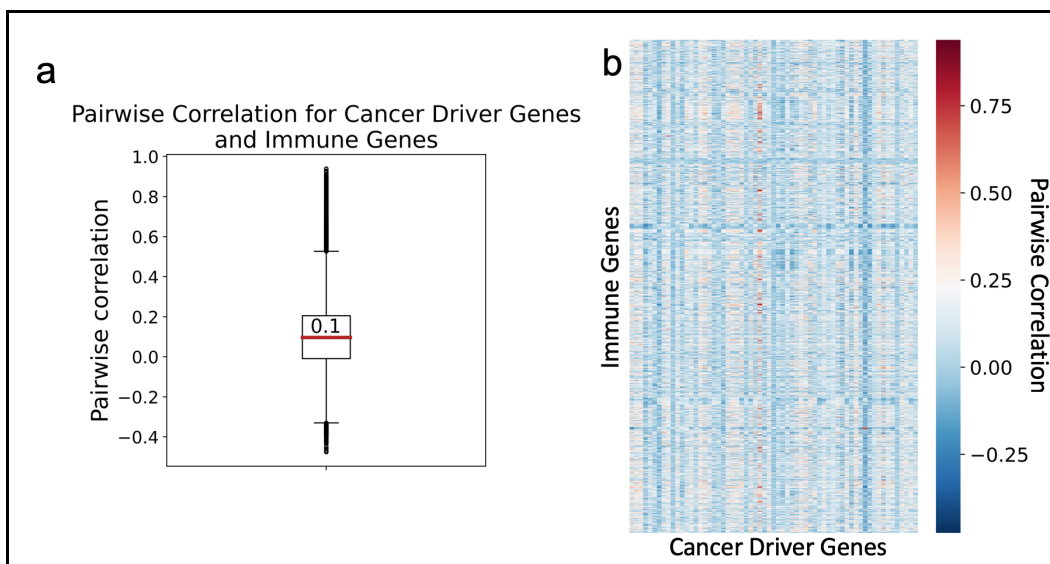
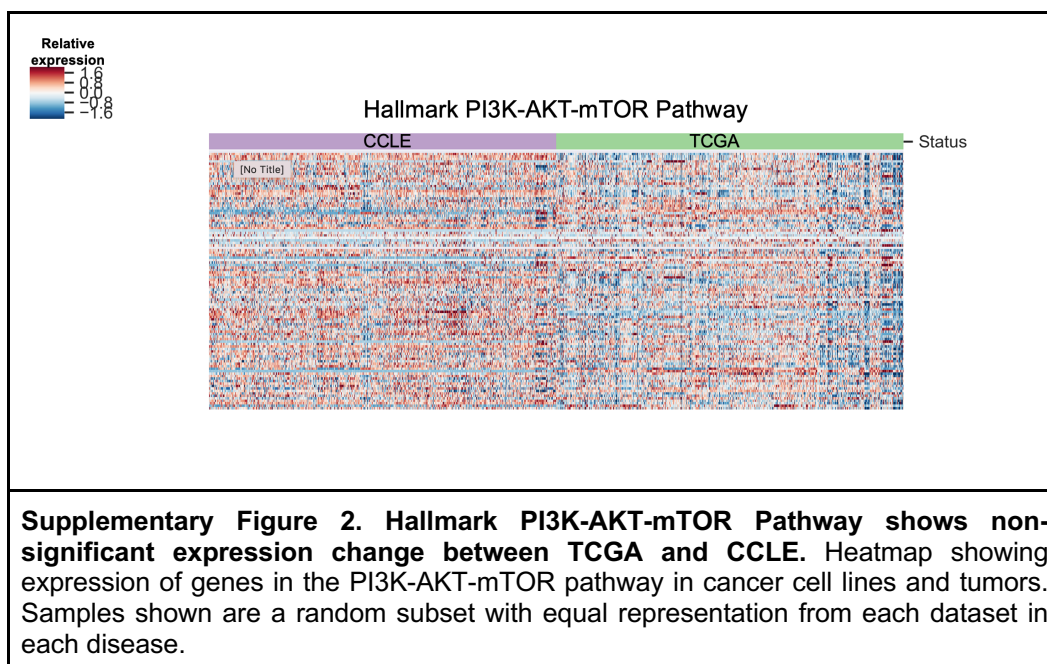


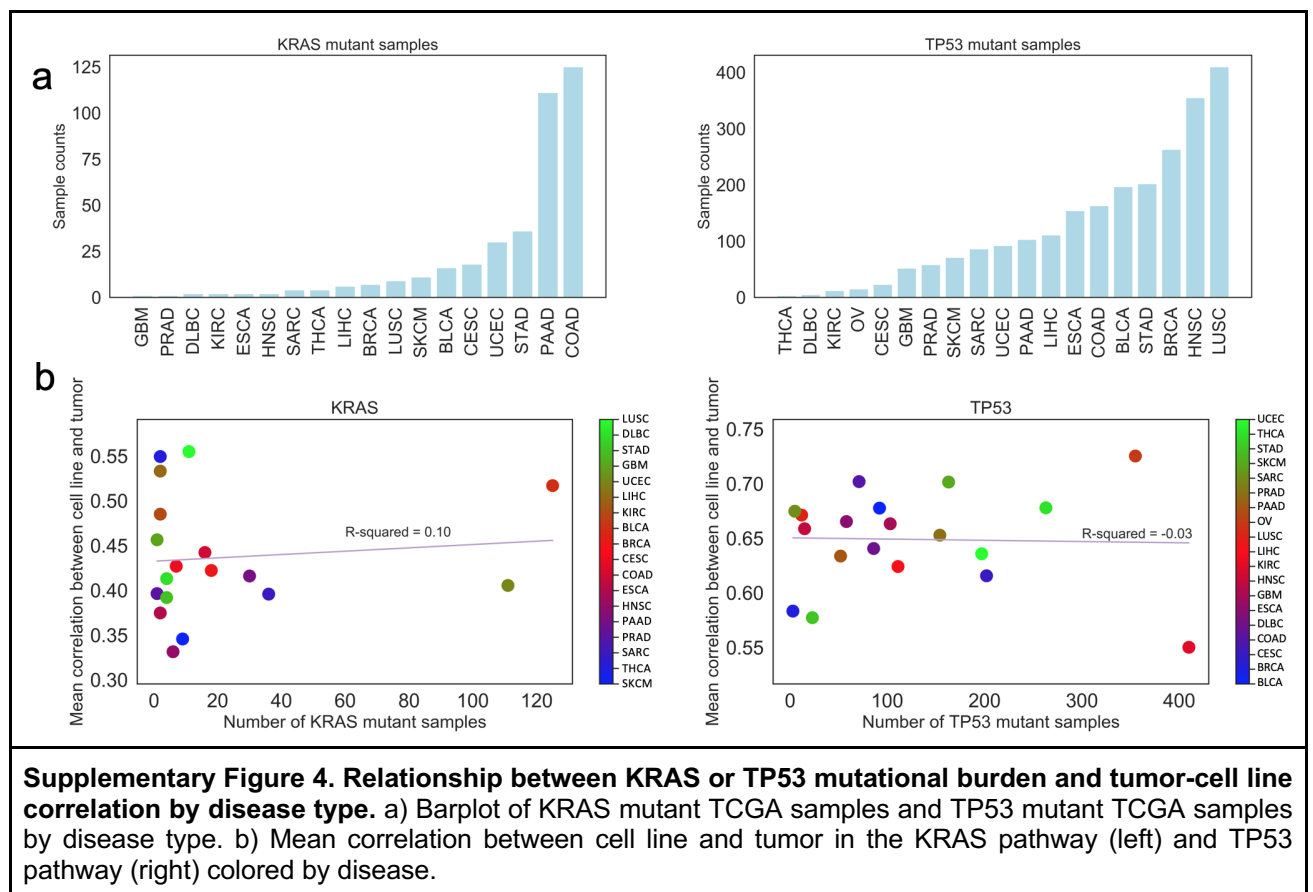
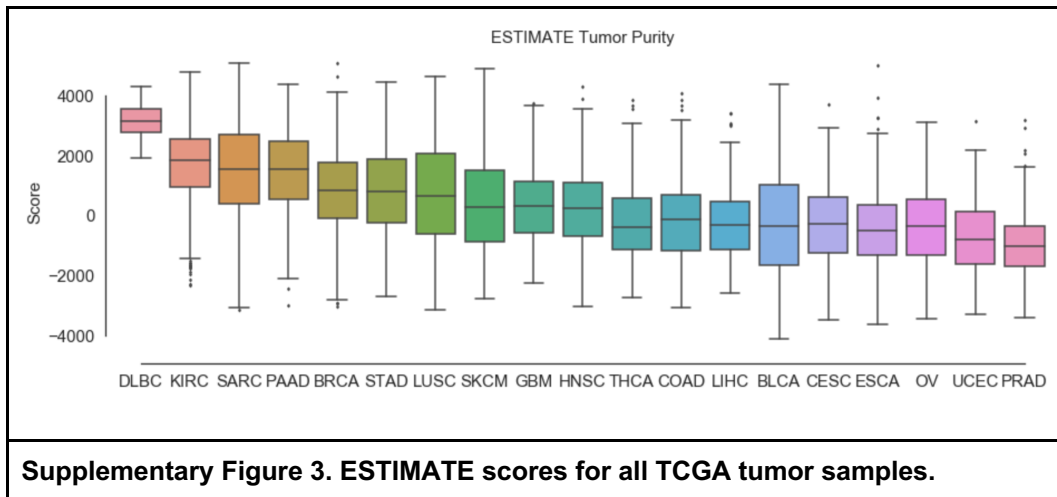
## Supplementary Figures

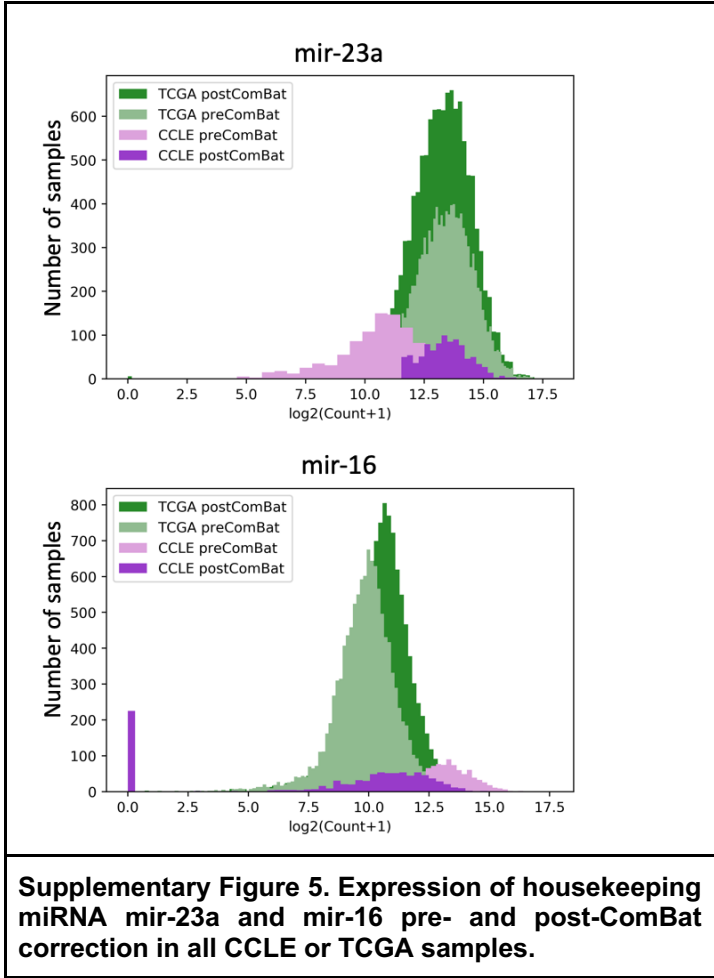


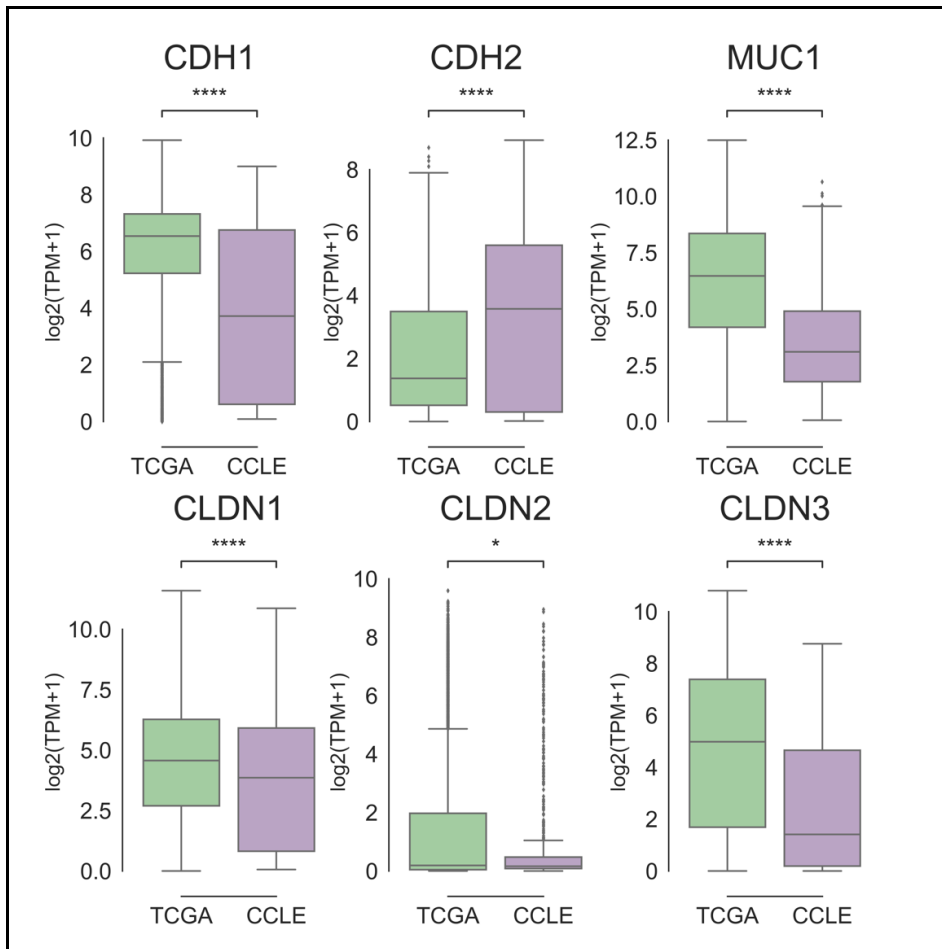
**Supplementary Figure 1. Pairwise correlation of expression of immune genes and cancer driver genes.** a) Pairwise correlation between the immune genes removed from the SVM analysis and the cancer driver genes identified by the SVM analysis (mean correlation=0.1). b) Heatmap showing pairwise correlation scores between immune genes and cancer driver genes.



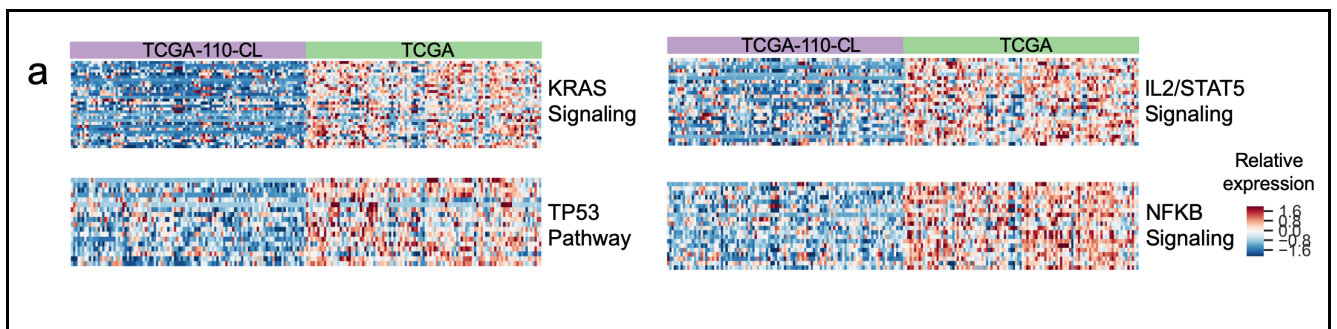
**Supplementary Figure 2. Hallmark PI3K-AKT-mTOR Pathway shows non-significant expression change between TCGA and CCLE.** Heatmap showing expression of genes in the PI3K-AKT-mTOR pathway in cancer cell lines and tumors. Samples shown are a random subset with equal representation from each dataset in each disease.





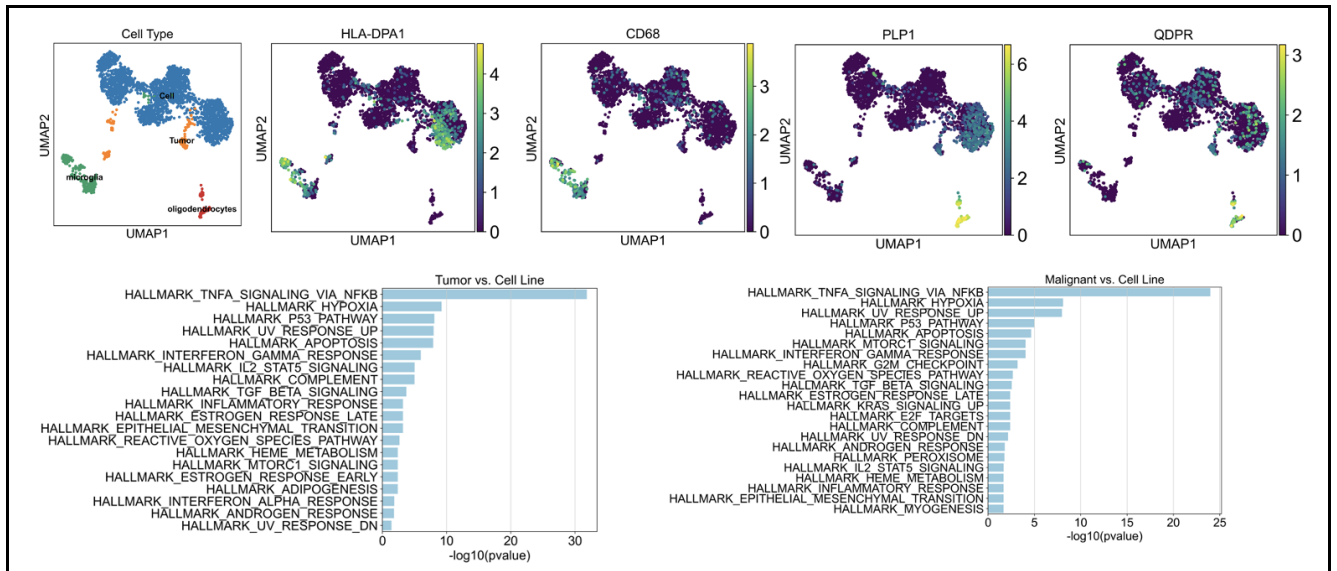


**Supplementary Figure 6. Expression of cell type markers in TCGA vs. CCLE.** Boxplots showing expression of the E-cadherin/*CDH1* (an epithelial cell marker) and N-cadherin/*CDH2*, *MUC1*, and claudins *CLDN1*, *CLDN2*, *CLDN3* (mesenchymal cell markers) in TCGA and CCLE. All samples from both datasets are shown. (Mann-Whitney significance test; \* pvalue < 0.05, \*\*\*\* pvalue < 0.0001)

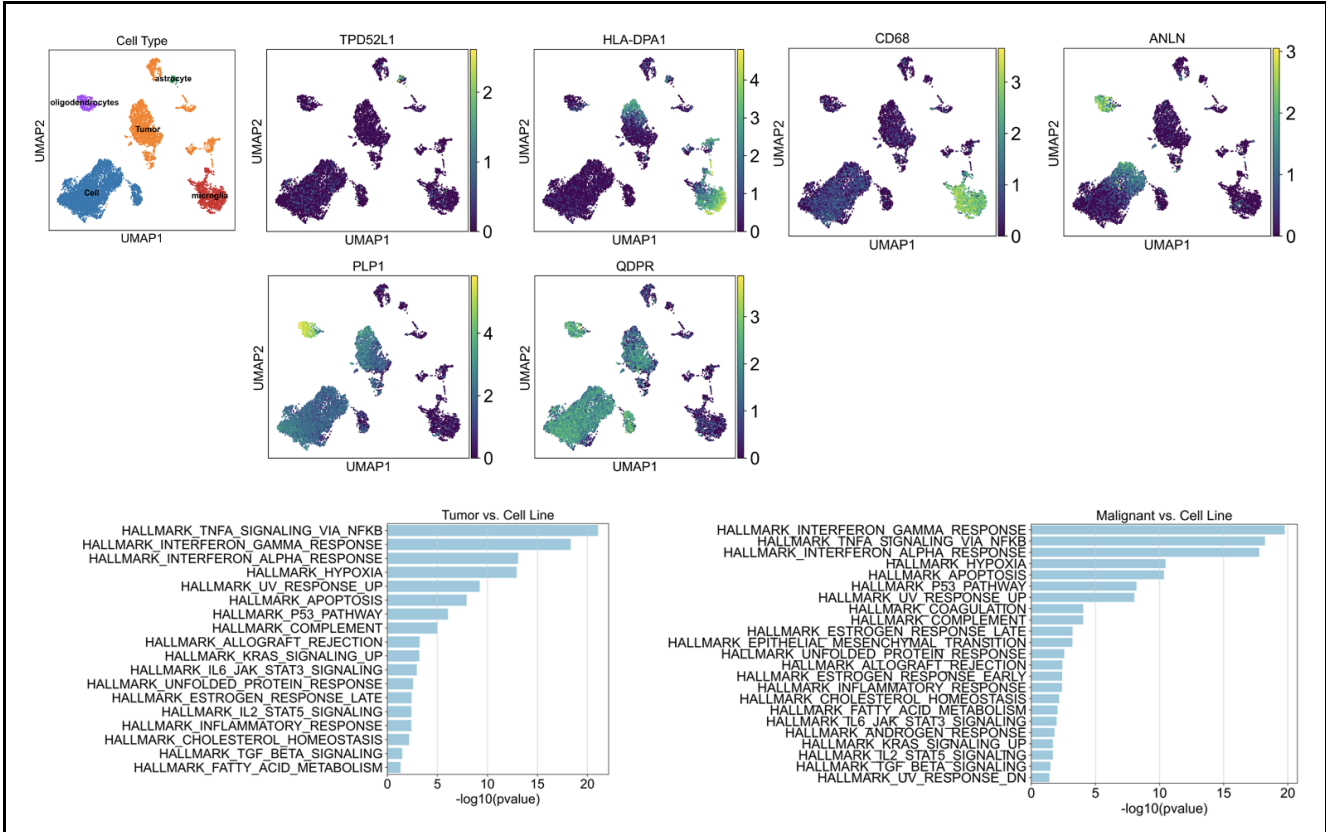


**Supplementary Figure 7. Expression of cancer driver pathways in TCGA-110-CL.** a) Heatmaps showing expression of SVM-identified genes in 4 cancer driver pathways in TCGA-110-CL cell lines as compared to TCGA samples. Samples shown are a random subset with equal representation from each dataset in each

disease.



**Supplementary Figure 8. Single cell RNA sequencing analysis of matched melanoma metastasis cancer cells and cell culture cells (UAMS Sample CI000035650).** The UMAP plots show cell type markers used to derive cell types. The bar plots show enrichment of cancer pathways in genes with differential expression between either all tumor cells and all cell line cells, or malignant tumor cells and all cell line cells (pvalue < 0.05).



**Supplementary Figure 9. Single cell RNA sequencing analysis of matched melanoma brain metastasis cancer cells and cell culture cells (UAMS Sample C1000035270).** The UMAP plots show cell type markers used to derive cell types. The bar plots show enrichment of cancer pathways in genes with differential expression between either all tumor cells and all cell line cells, or malignant tumor cells and all cell line cells (pvalue < 0.05).