

Figure S9

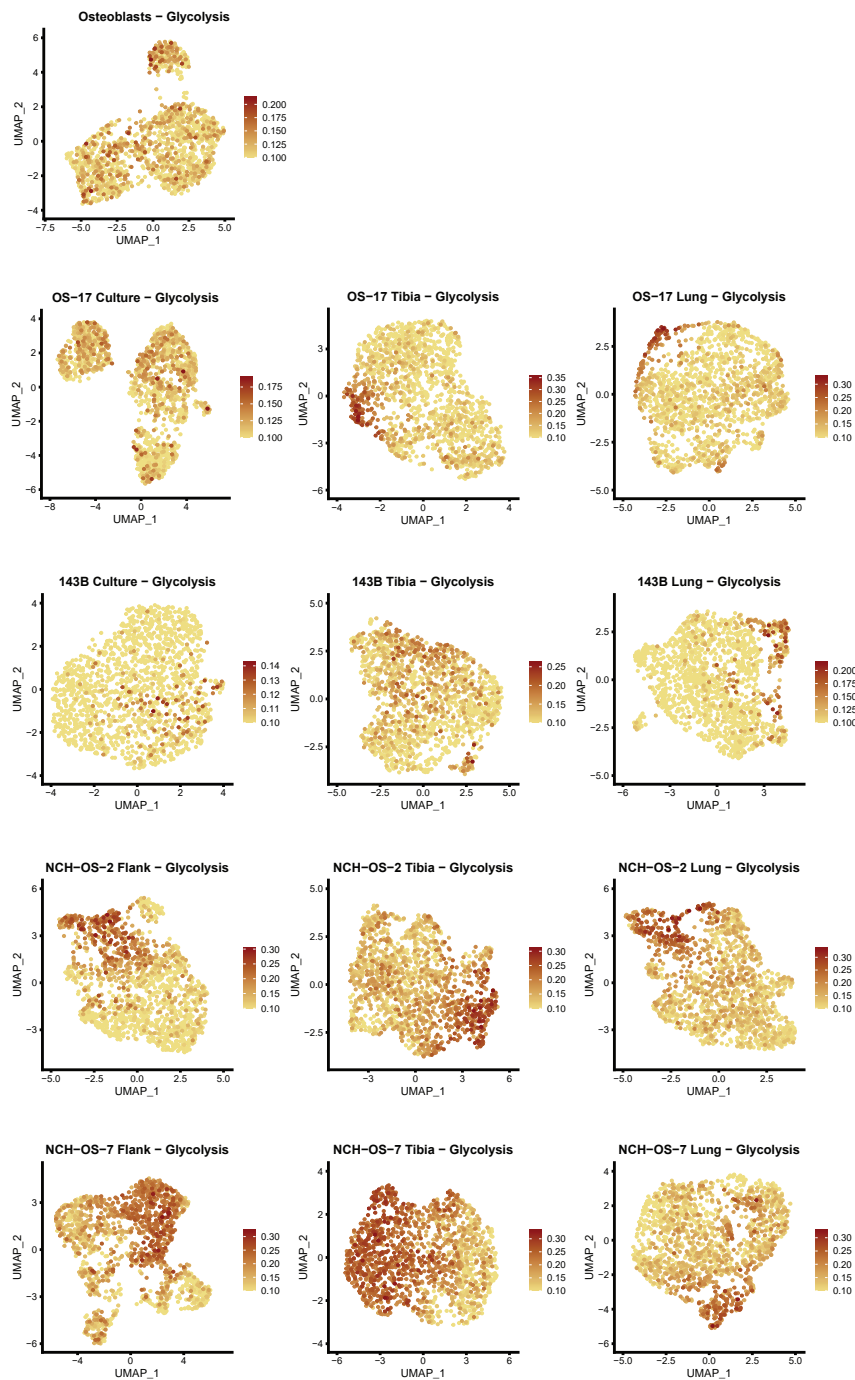


Figure S9. Heterogeneous activation of glycolysis identified across multiple cell line and PDX tumor datasets. FeaturePlots for glycolysis module score in each of the datasets. Module score for glycolysis was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_GLYCOLYSIS genes as input features for the expression program.

Figure S10

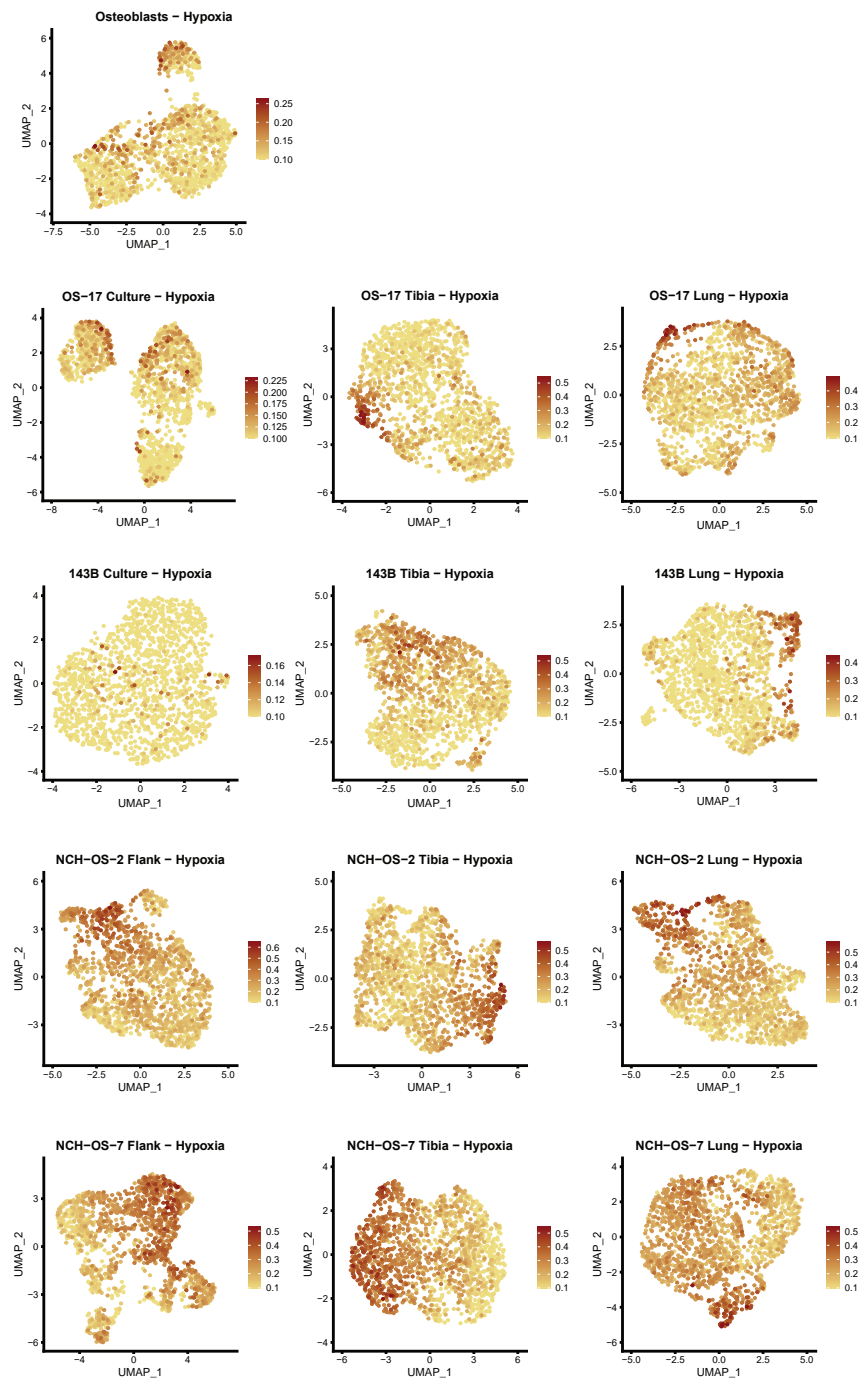


Figure S10. Heterogeneous activation of hypoxia related genes identified across multiple cell line and PDX tumor datasets. FeaturePlots for hypoxia module score in each of the datasets. Module score for hypoxia was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_HYPOXIA genes as input features for the expression program.

Figure S11

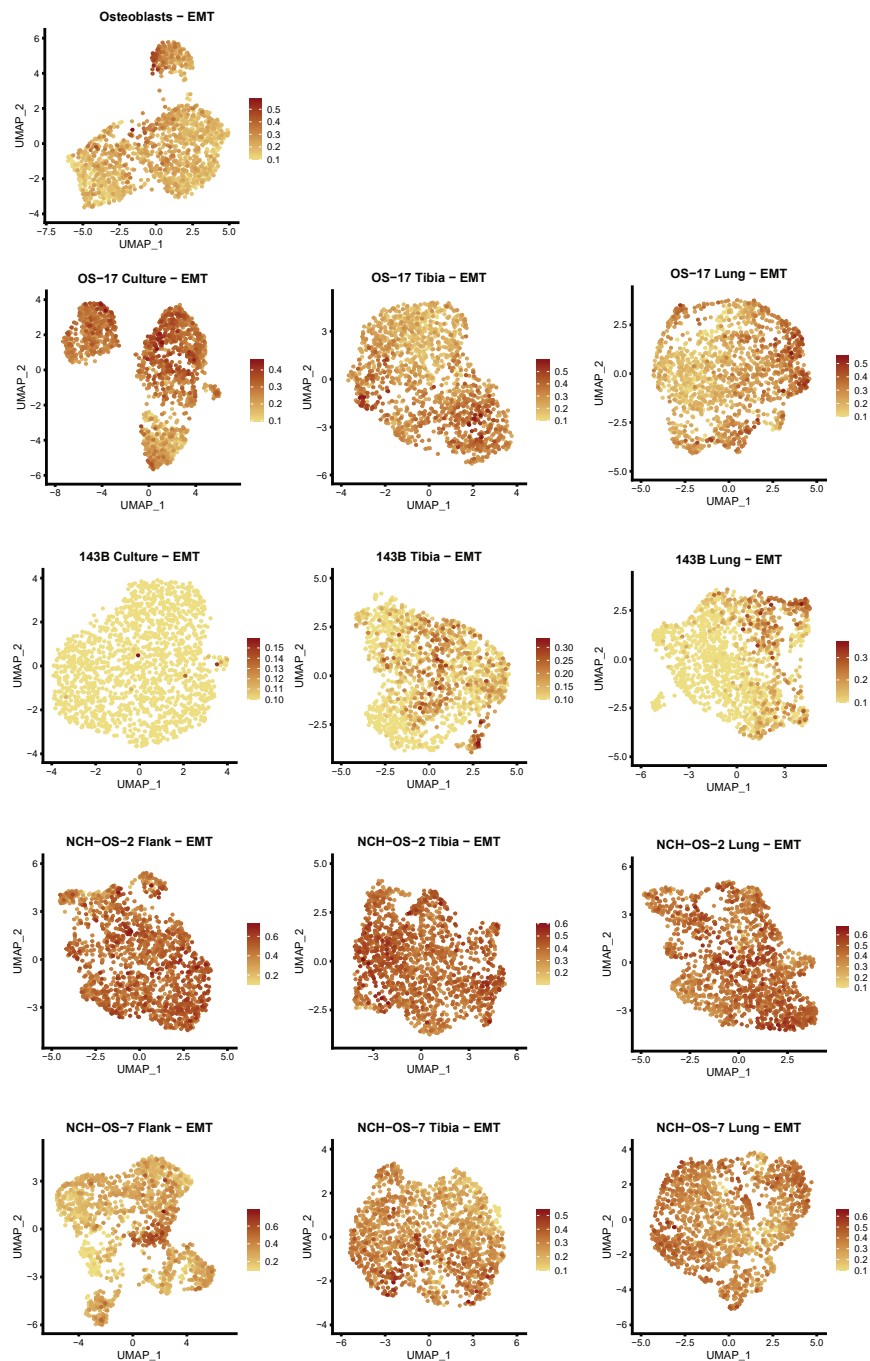


Figure S11. Heterogeneous activation of EMT identified across multiple cell line and PDX tumor datasets. FeaturePlots for EMT module score in each of the datasets. Module score for EMT was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_EMT genes as input features for the expression program.

Figure S12

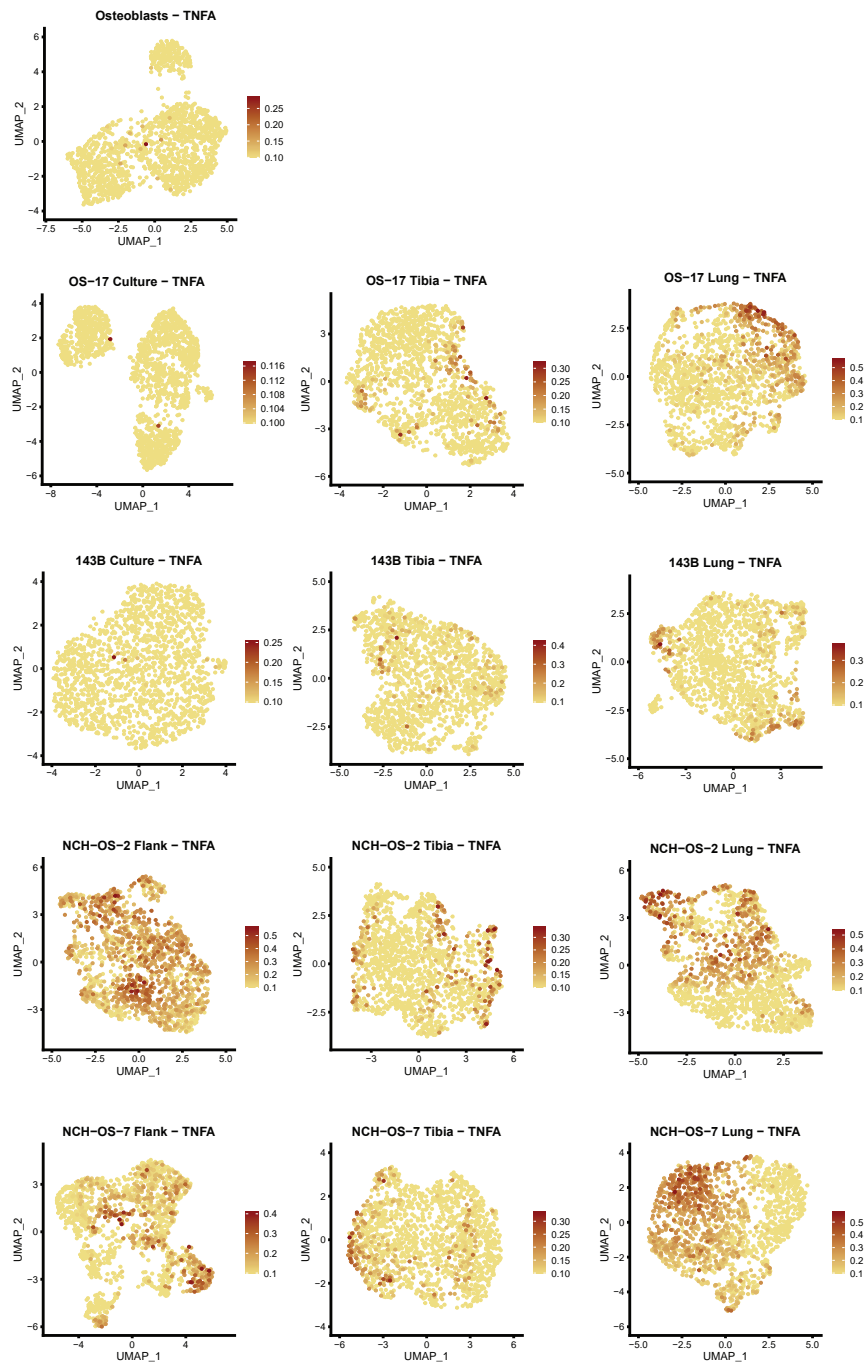


Figure S12. Heterogeneous activation of ‘TNF α signaling via NF κ B’ identified across multiple cell line and PDX tumor datasets. FeaturePlots for TNF α signaling via NF κ B module score in each of the datasets. Module score for EMT was calculated using the ‘AddModuleScore’ function in Seurat with msigdb HALL-MARK_TNFA genes as input features for the expression program.