

Figure S19

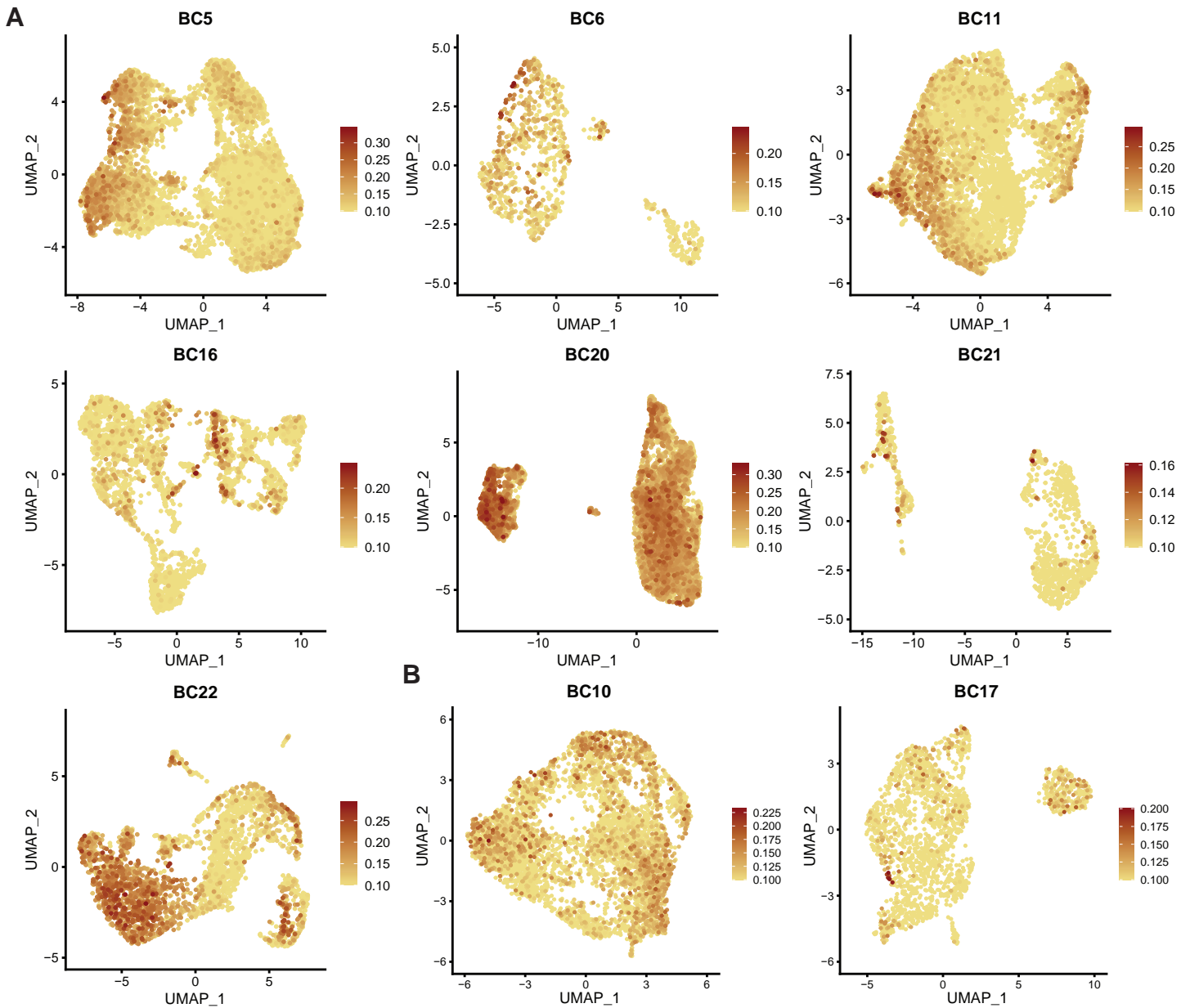


Figure S19. Heterogeneous activation of glycolysis identified across multiple patient primary and metastatic tumor datasets. A) Primary and B) metastatic patient tumor FeaturePlots showing glycolysis module score in each of the datasets. Module score for glycolysis was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_GLYCOLYSIS genes as input features for the expression program. Patient data is from GSE152048.

Figure S20

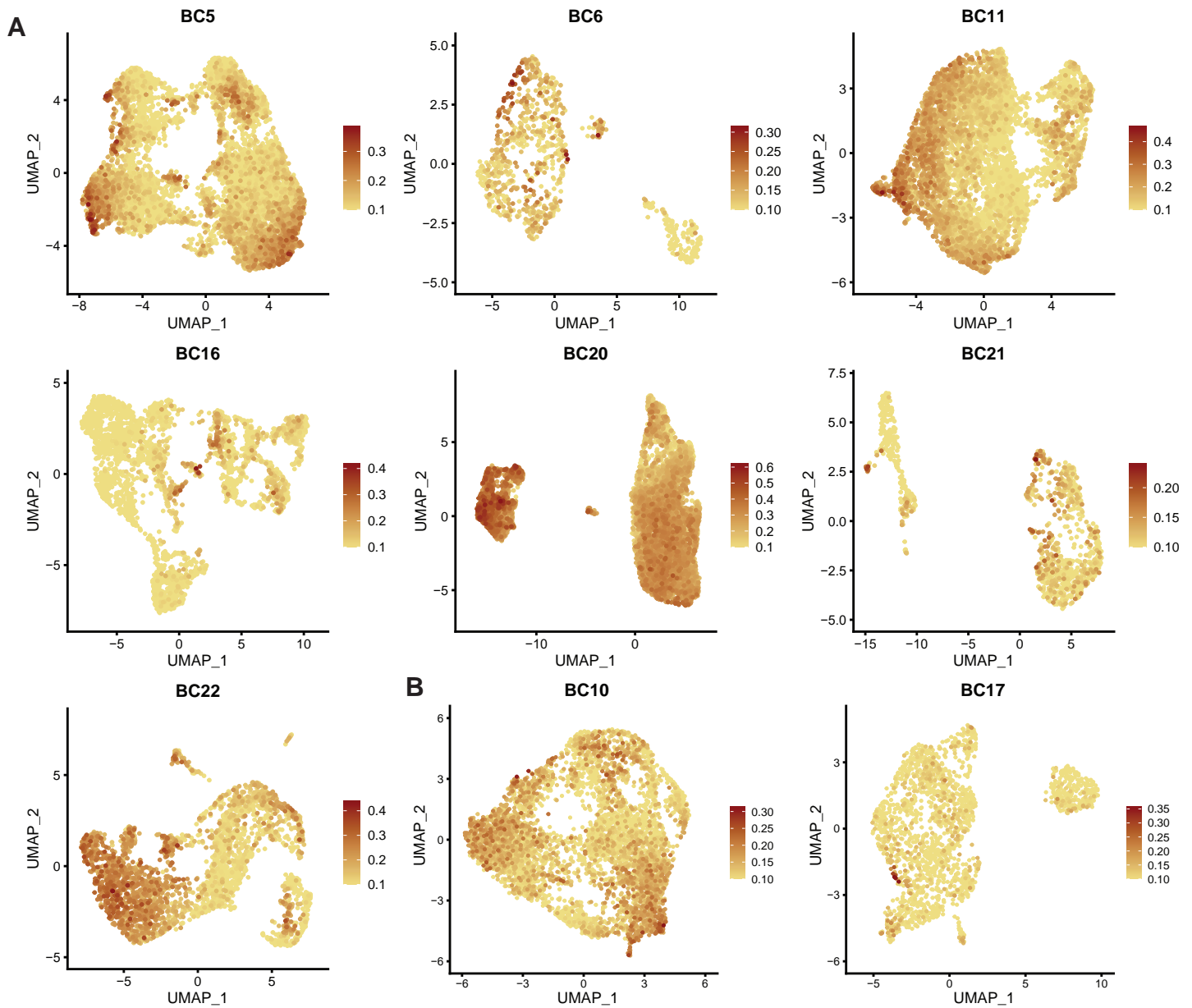


Figure S20. Heterogeneous activation of hypoxia related genes identified across multiple patient primary and metastatic tumor datasets. A) Primary and B) metastatic patient tumor FeaturePlots showing hypoxia module score in each of the datasets. Module score for hypoxia was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_HYPOXIA genes as input features for the expression program. Patient data is from GSE152048.

Figure S21

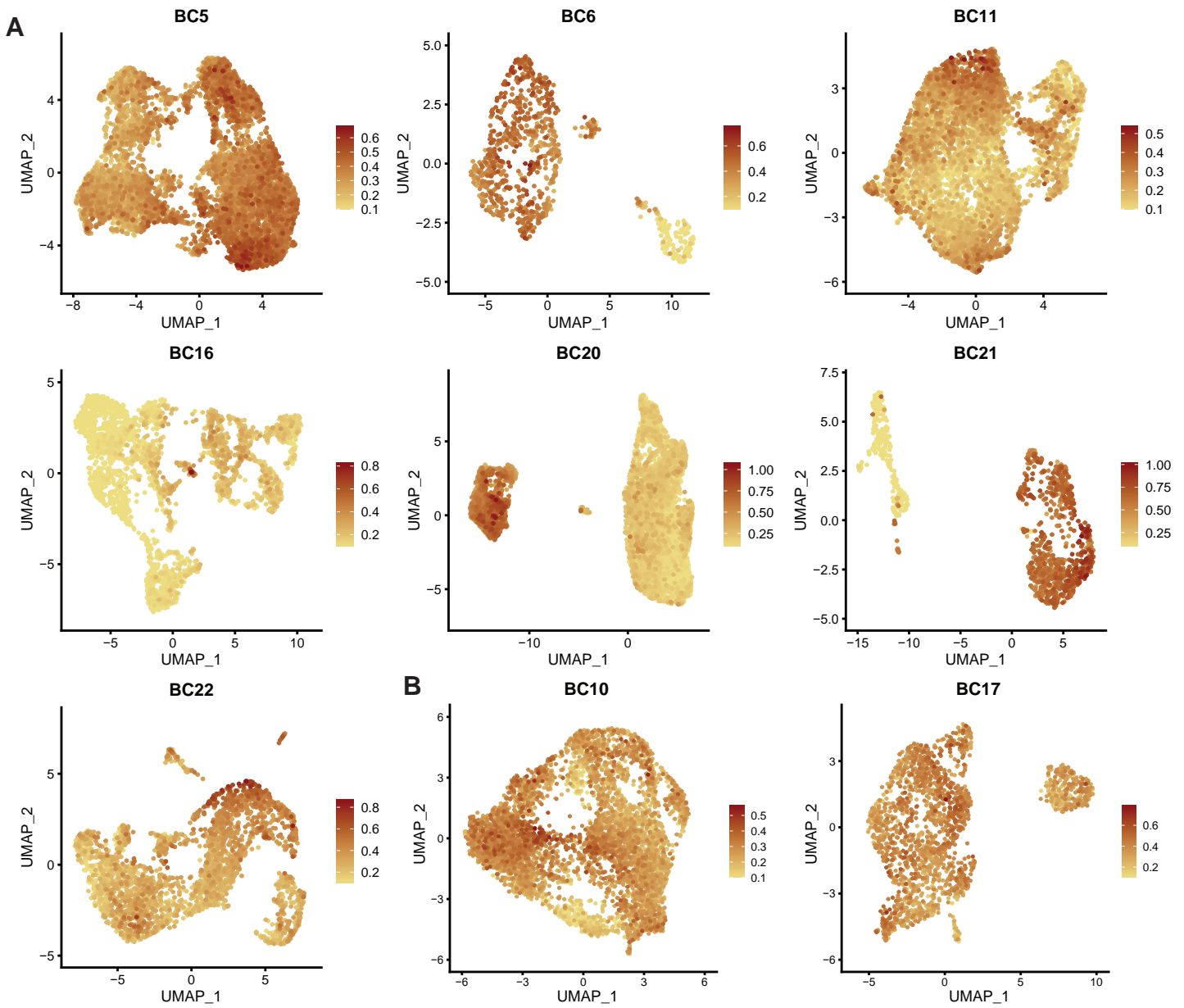


Figure S21. Heterogeneous activation of EMT related genes identified across multiple patient primary and metastatic tumor datasets. A) Primary and B) metastatic patient tumor FeaturePlots showing EMT module score in each of the datasets. Module score for EMT was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION genes as input features for the expression program. Patient data is from GSE152048.

Figure S22

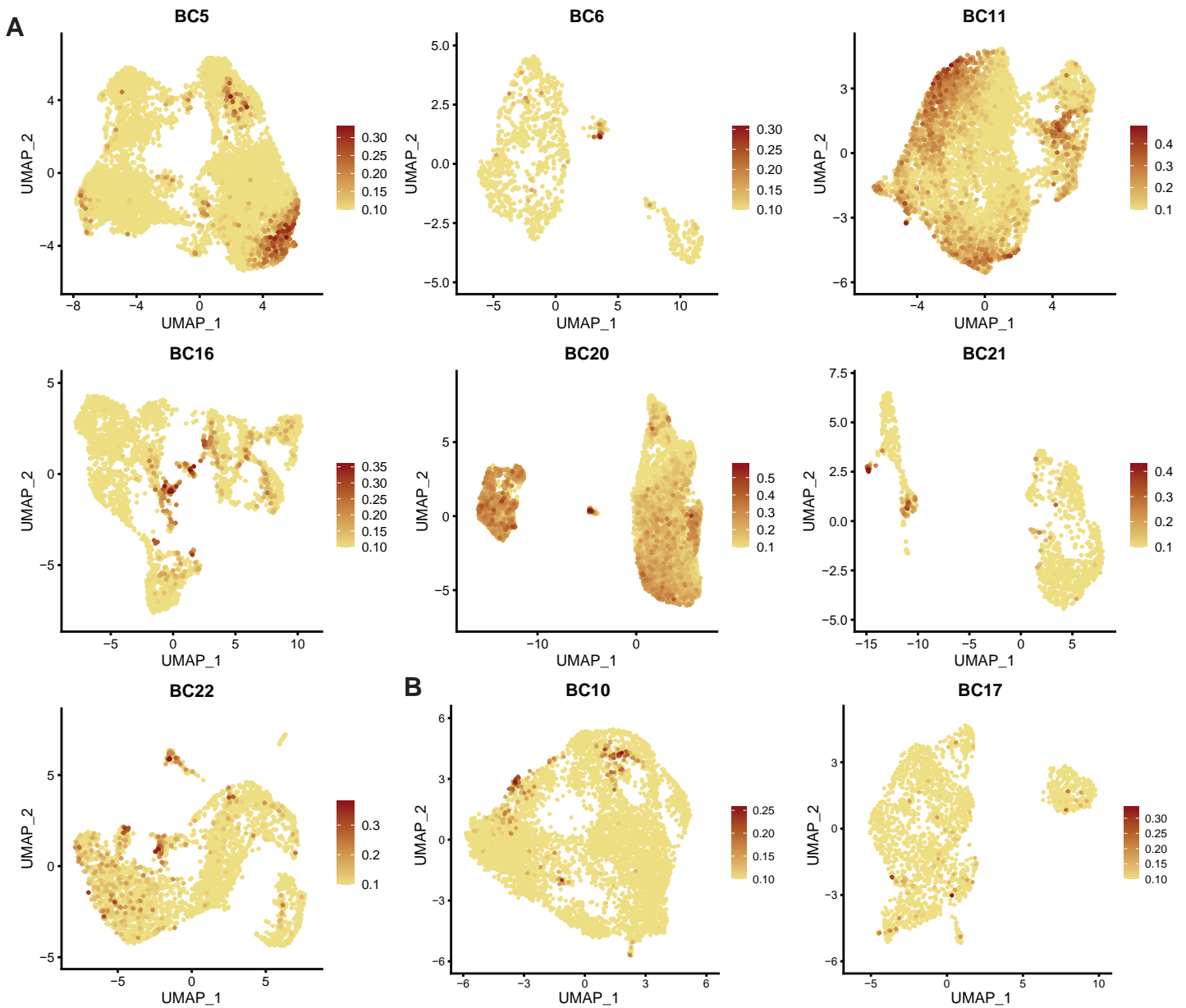


Figure S22. Heterogeneous activation of 'TNF α signaling via NF κ B' related genes identified across multiple patient primary and metastatic tumor datasets. A) Primary and B) metastatic patient tumor FeaturePlots showing TNF α signaling via NF κ B module score in each of the datasets. Module score for TNF α signaling via NF κ B was calculated using the 'AddModuleScore' function in Seurat with msigdb HALLMARK_TNF α _SIGNALING_VIA_NFKB genes as input features for the expression program. Patient data is from GSE152048.