



(A) The UMAP plot of embeddings outputted by monocyte subclusters for human and mouse lung cancer with csMAHN. (B) dot plot showing posterior probability of the mouse monocyte integrating human and mouse lung cancer monocyte subclusters using csMAHN. The size of the dots corresponds to the proportion of each original label that is assigned to each csMAHN label. (C) dot plot showing scaled gene expression levels of monocyte subclusters, human (top panel), mouse (bottom panel). (D) The UMAP plot of embeddings outputted by neutrophils subclusters for human and mouse lung cancer with csMAHN. (E) dot plot showing posterior probability of the mouse neutrophils integrating human and mouse lung cancer neutrophilss subclusters using csMAHN. (F) dot plot showing scaled gene expression levels of neutrophils subclusters, human (left panel), mouse (right panel).