



Supplementary Figure S9 | *In silico* removal and characterization of isolation of murine cells. Number of cell counts identified in each sample that maps to the human or mouse genome from NCI-H209 (**A**) and NCI-H82 cells (**B**). **C**, UMAP plot of the isolated murine cells from all samples cluster into two groups which are derived from either immune or fibroblast microenvironmental cells.