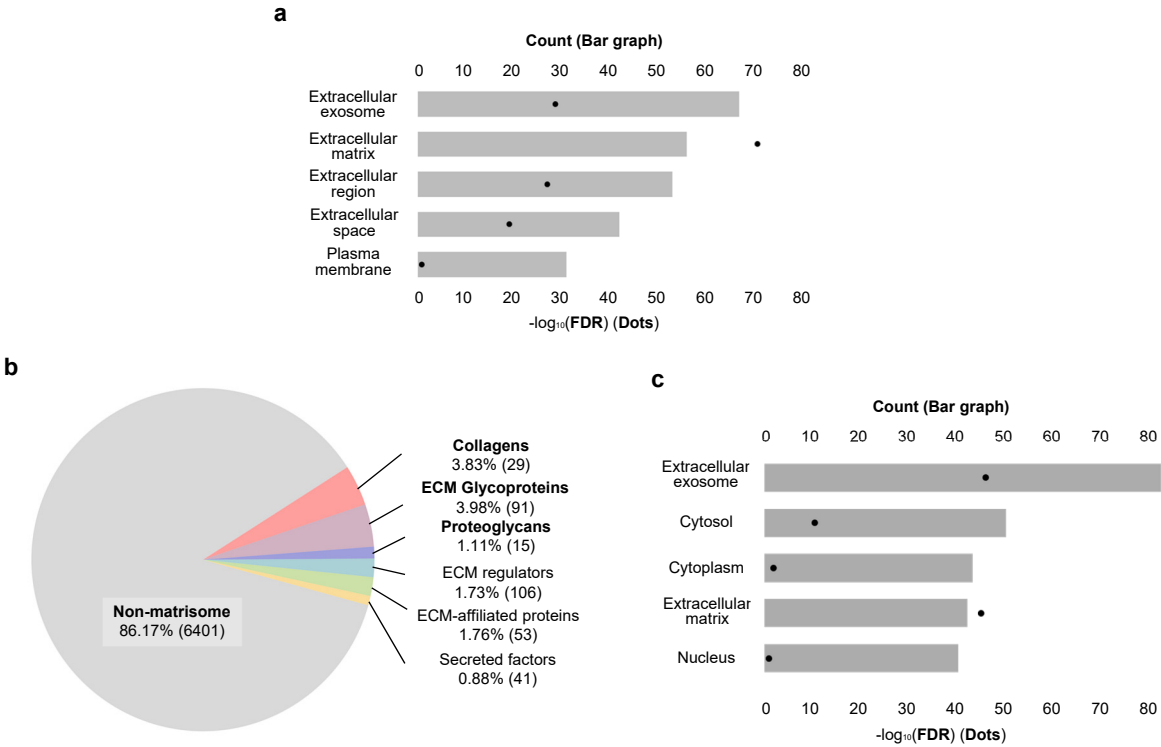
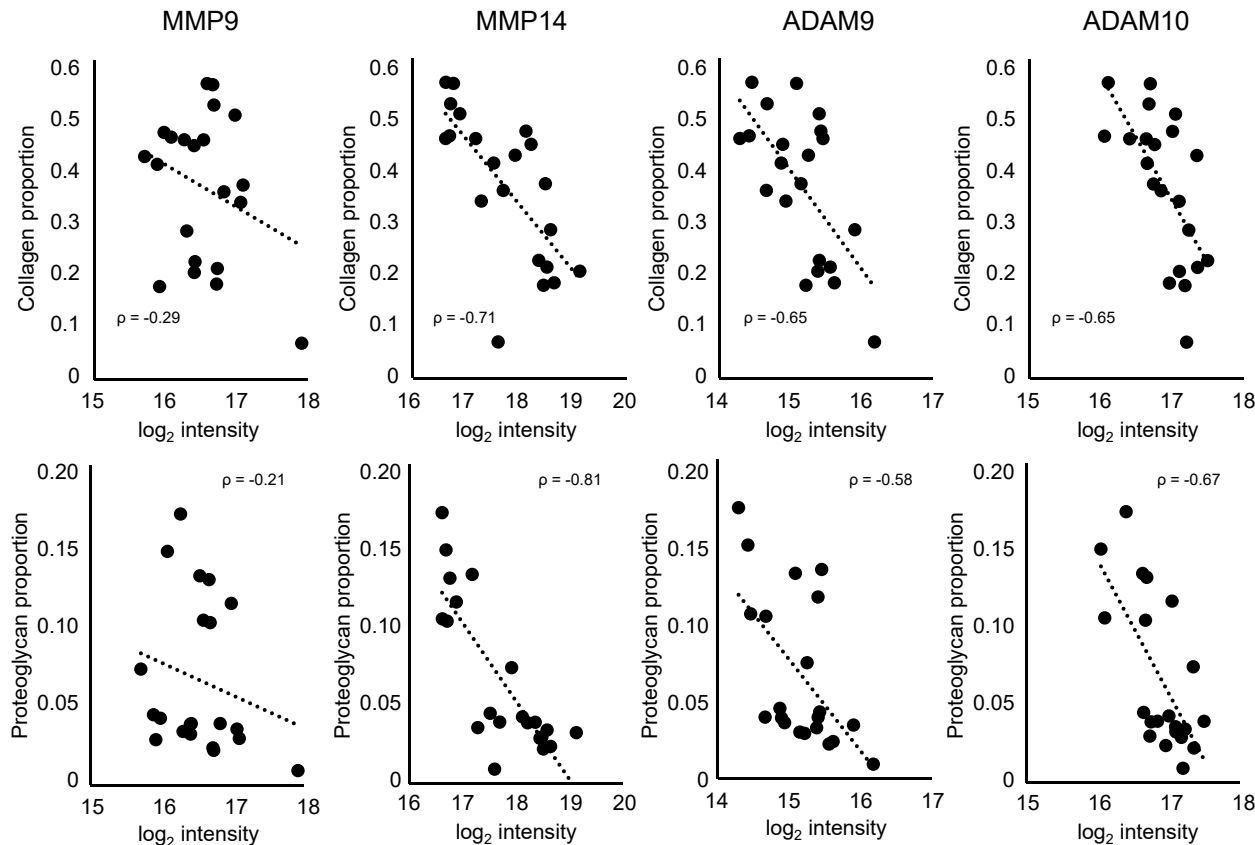


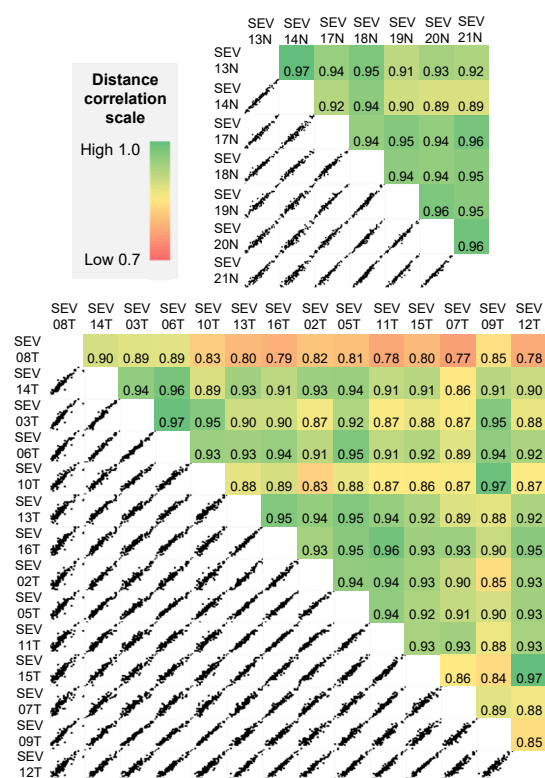
Supple. Fig. 1



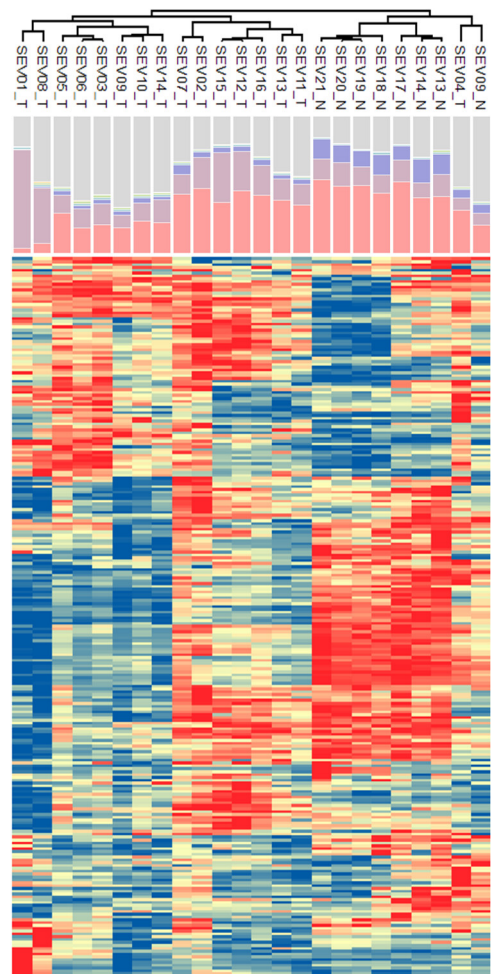
Supple. Fig. 2



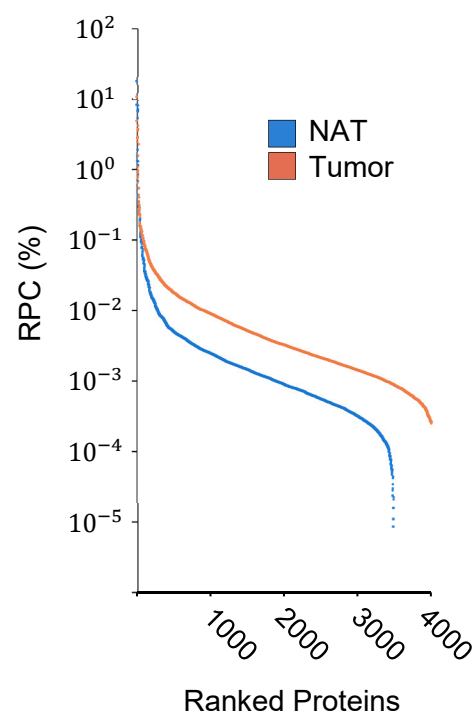
Supple. Fig. 3



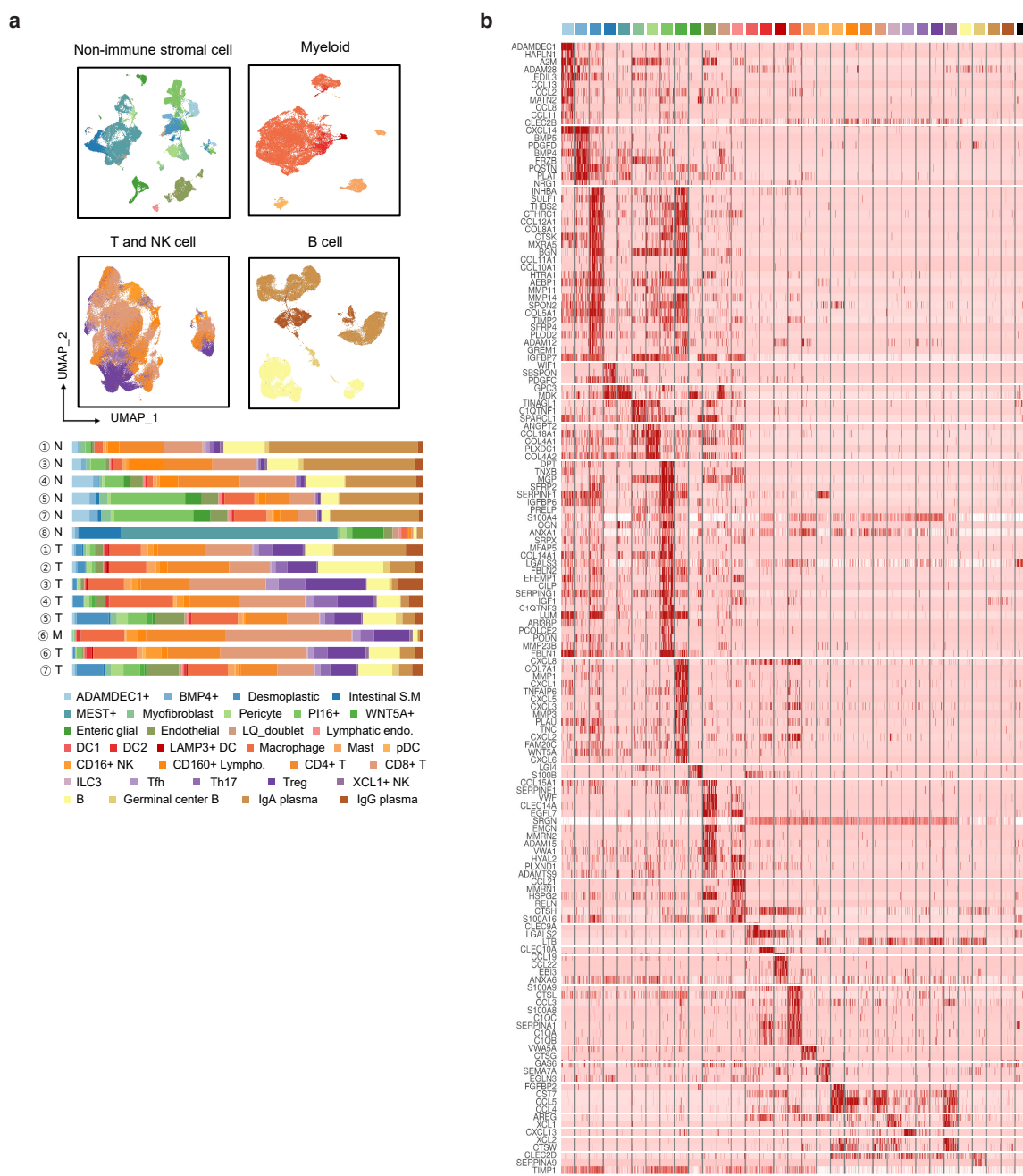
Supple. Fig. 4



Supple. Fig. 5



Supple. Fig. 6



Supplementary Figure Legends

Supple. Fig. 1 | Characterization of patient-derived tissue (pd-tissue) a) Cellular location annotation of top 100 enriched protein of reference patient derived ECM (pdECM) sample. b) Quantitative abundance of matrisome proteins in equally mixed internal reference pd-tissue sample from the publicly accessed data(1). The number of detected proteins were expressed in the parentheses. c) Cellular location annotation of top 100 enriched protein of reference pd-tissue sample.

Supple. Fig. 2 | Correlation between collagen/proteoglycan and metalloproteinases The scatter plot of collagen or proteoglycan proportion and metalloproteinases (MMP9, MMP14, ADAM9, ADAM10). $\log_2$ intensity of metalloproteinases and the proportion of collagen or proteoglycan in each sample were shown.

Supple. Fig. 3 | Matrisome profile correlation among pdECM Distance correlation coefficient values and scatter plot of protein intensities among pdECM samples.

Supple. Fig. 4 | Matrisome profiles including excluded samples Hierarchical clustered heatmap with a matrisome profile was shown. Stacked bar plot shows the RPC of each category of matrisome among pdECM samples.

Supple. Fig. 5 | Protein distribution profiles in NAT and tumor pdECM Protein distributions in normal and tumor groups. Detected proteins were ranked according to RPC.

Supple. Fig. 6 | Matrisome markers of heterogenous cell types in integrated scRNA-seq dataset a) Distribution of each cell types in each dataset. b) Matrisome markers of each cell types.

Reference

1. Vasaikar S, Huang C, Wang X, Petyuk VA, Savage SR, Wen B, *et al.* Proteogenomic analysis of human colon cancer reveals new therapeutic opportunities. *Cell* **2019**;177:1035-49. e19