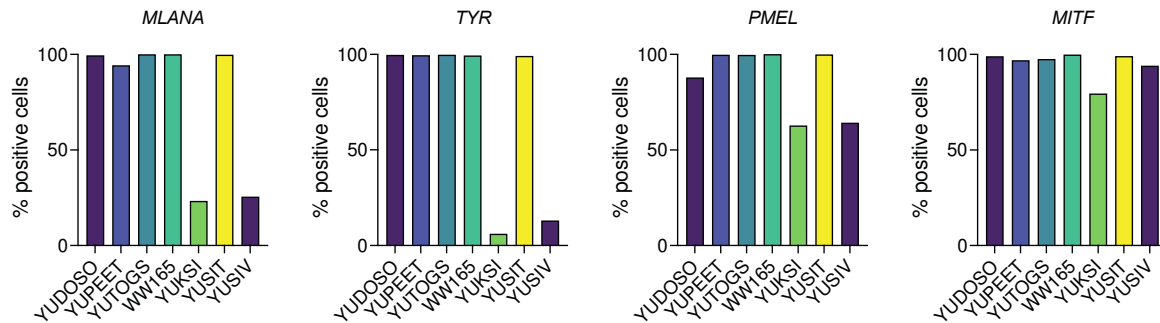
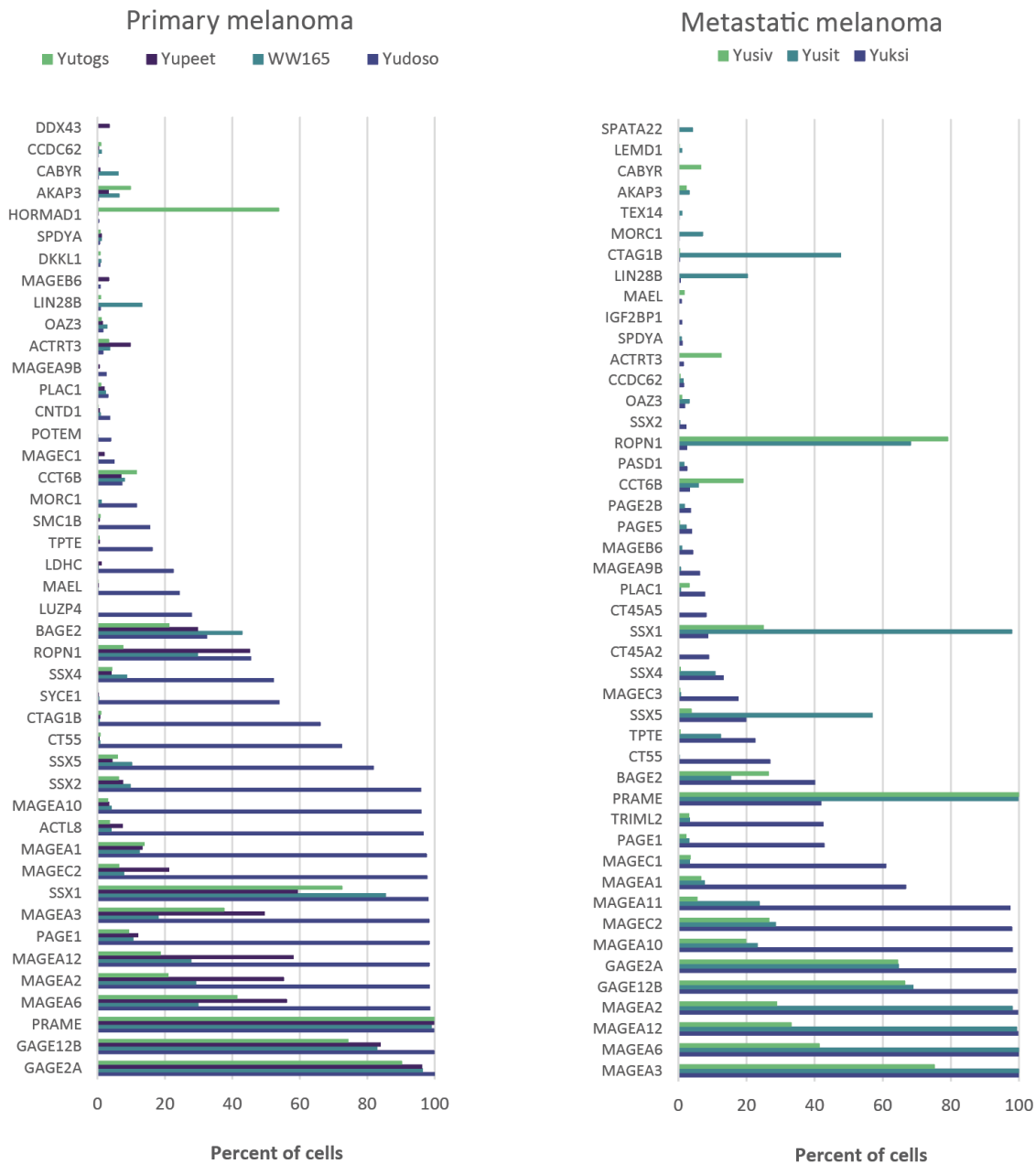


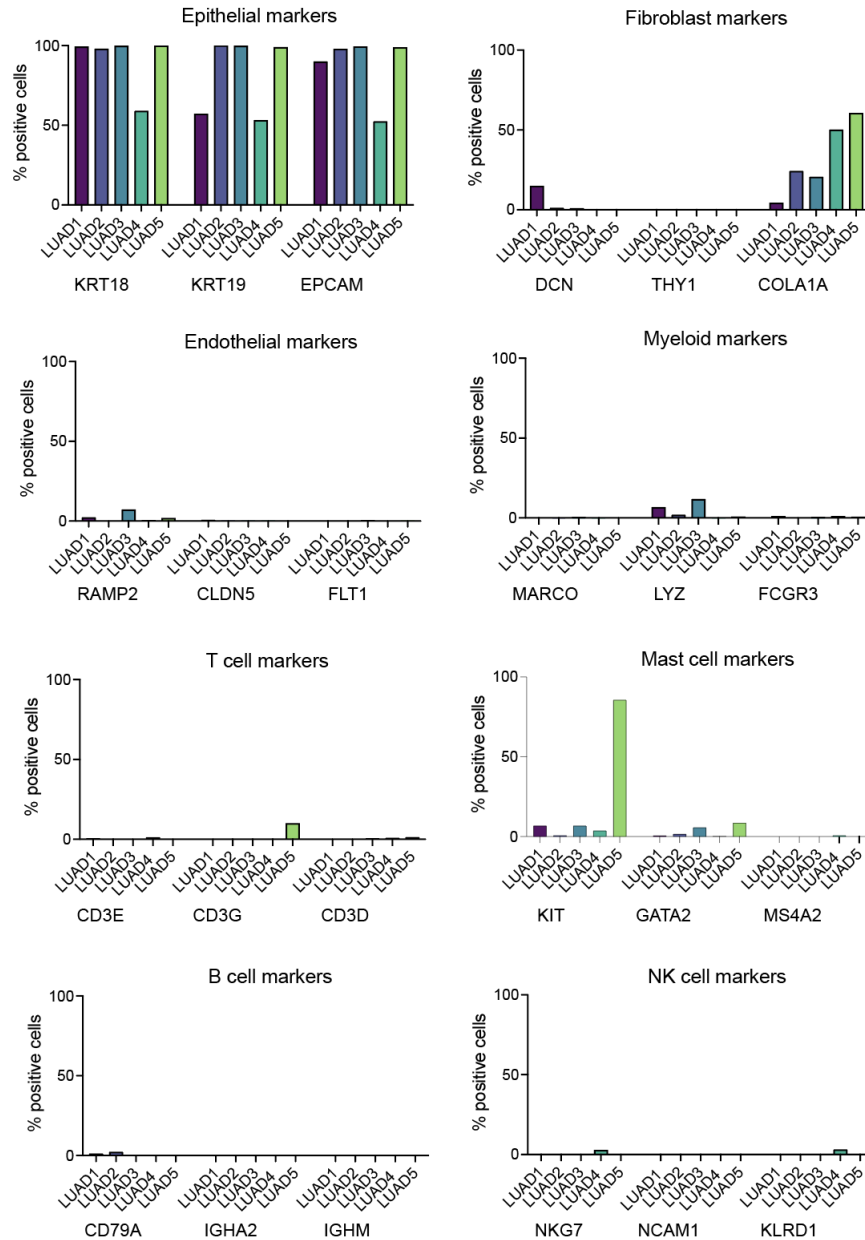
Supplementary Figure 1. Intratumoral heterogeneity in the expression of CTAs in melanoma and lung cancer. Immunostaining of selected CTA genes in melanomas and lung adenocarcinomas (LUADs) (brown). Representative images are shown. Counterstain: Hematoxylin (blue). Size bars = 100 μm.



Supplementary Figure 2. Characterization of expression of melanocytic marker genes in melanoma primary tumors (YUDOSO, YUPEET, YUTOGS, WW165) or metastases (YUKSI, YUSIV, YUSIT) using scRNAseq analysis. Plots show the frequency of cells expressing the indicated genes.

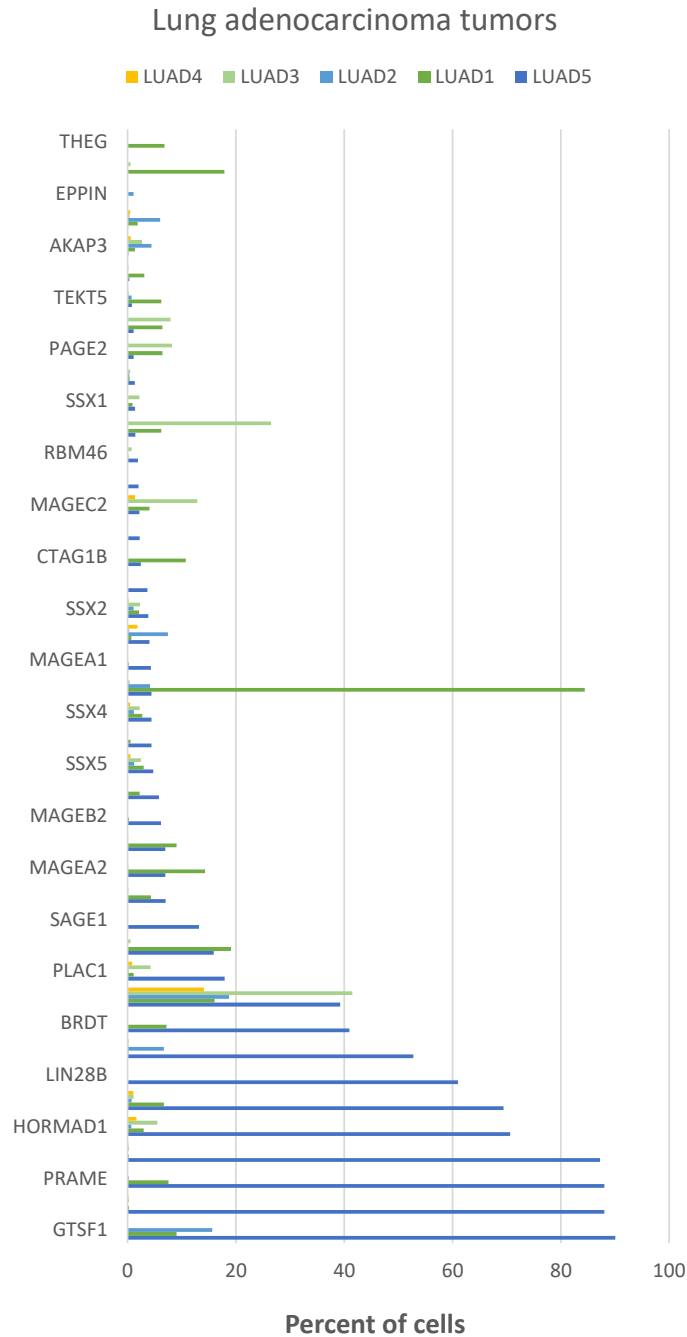


Supplementary Figure 3. Expression frequency of CTA genes among cancer cells of melanoma tumors, as determined by scRNAseq analysis. Genes expressed in at least 1% of cells in at least one tumor are shown.



Supplementary Figure 4. Characterization of the expression of genes representing different cellular subsets of the human lung in purified lung adenocarcinoma cells. Purified cancer cells from lung adenocarcinoma (LUAD) tumors were characterized for the expression of marker genes for different lung cell subsets using scRNAseq analysis. Plots show the frequency of cells expressing

the indicated genes. Marker genes were adapted from *Travaglini, K.J., et al., A molecular cell atlas of the human lung from single-cell RNA sequencing. Nature, 2020. 587(7835): p. 619-625.*



Supplementary Figure S5. Expression frequency of CTA genes among cancer cells of lung adenocarcinoma (LUAD) tumors, as determined by scRNAseq analysis. Genes expressed in at least 1% of cells in at least one tumor are shown