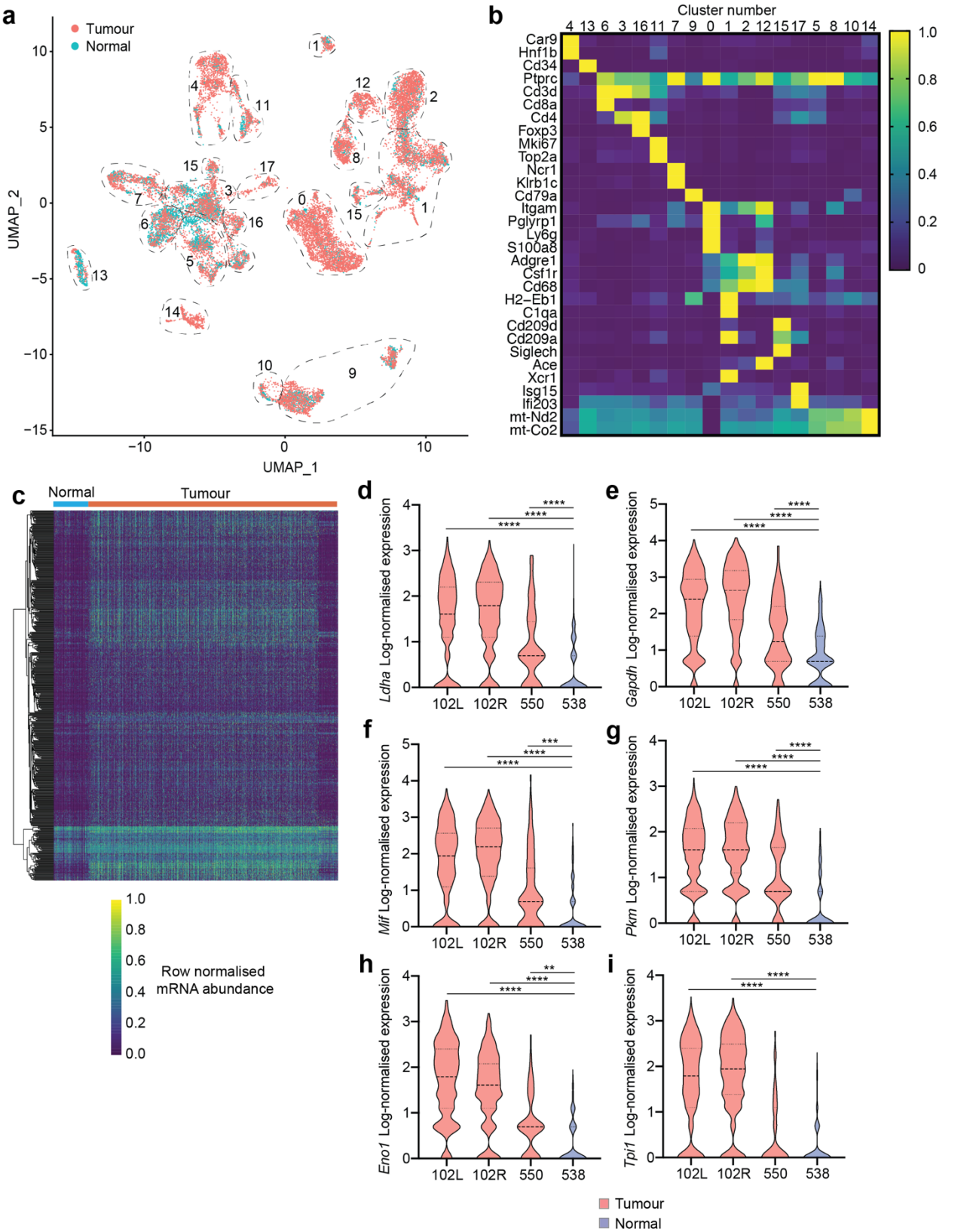
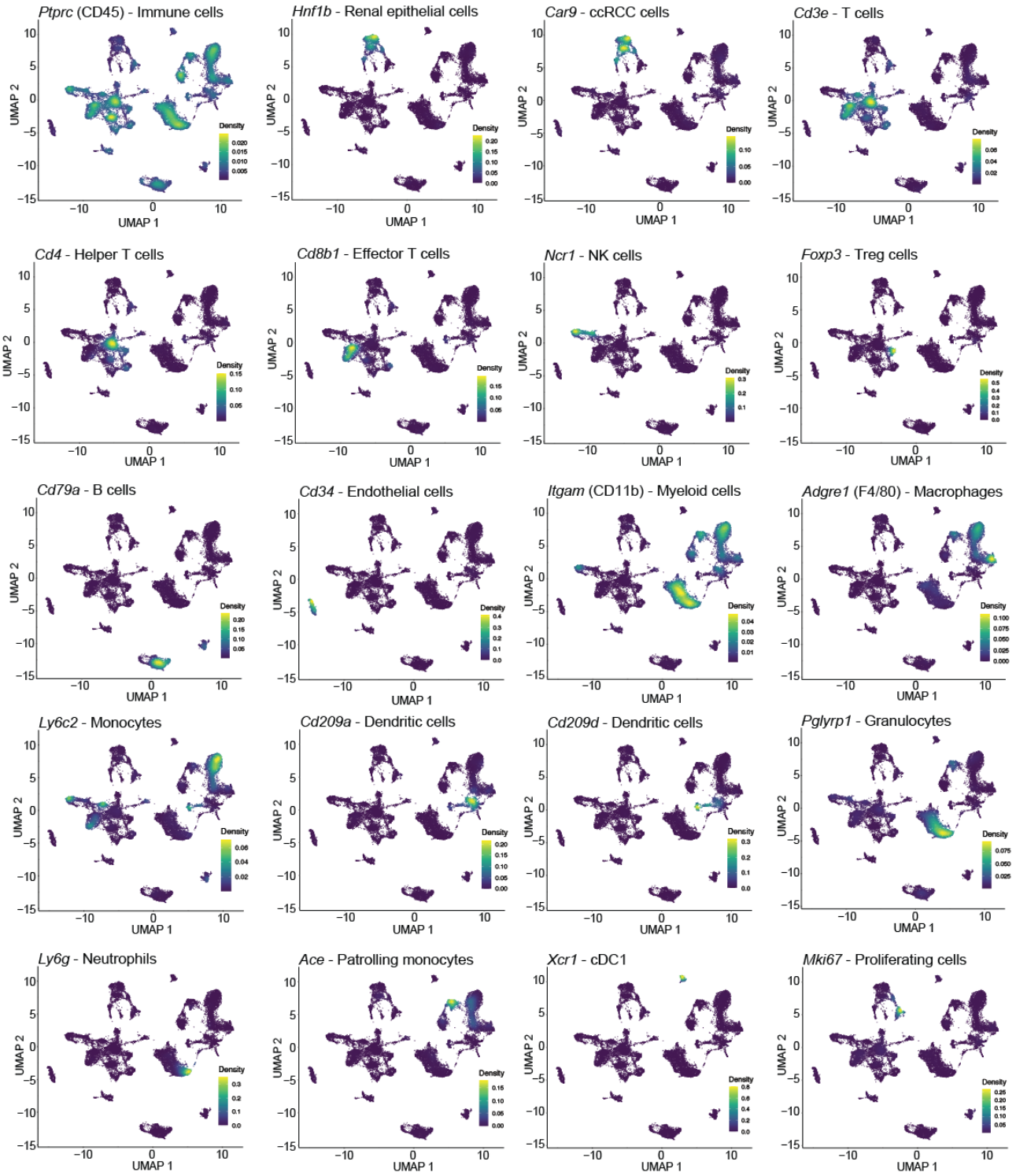
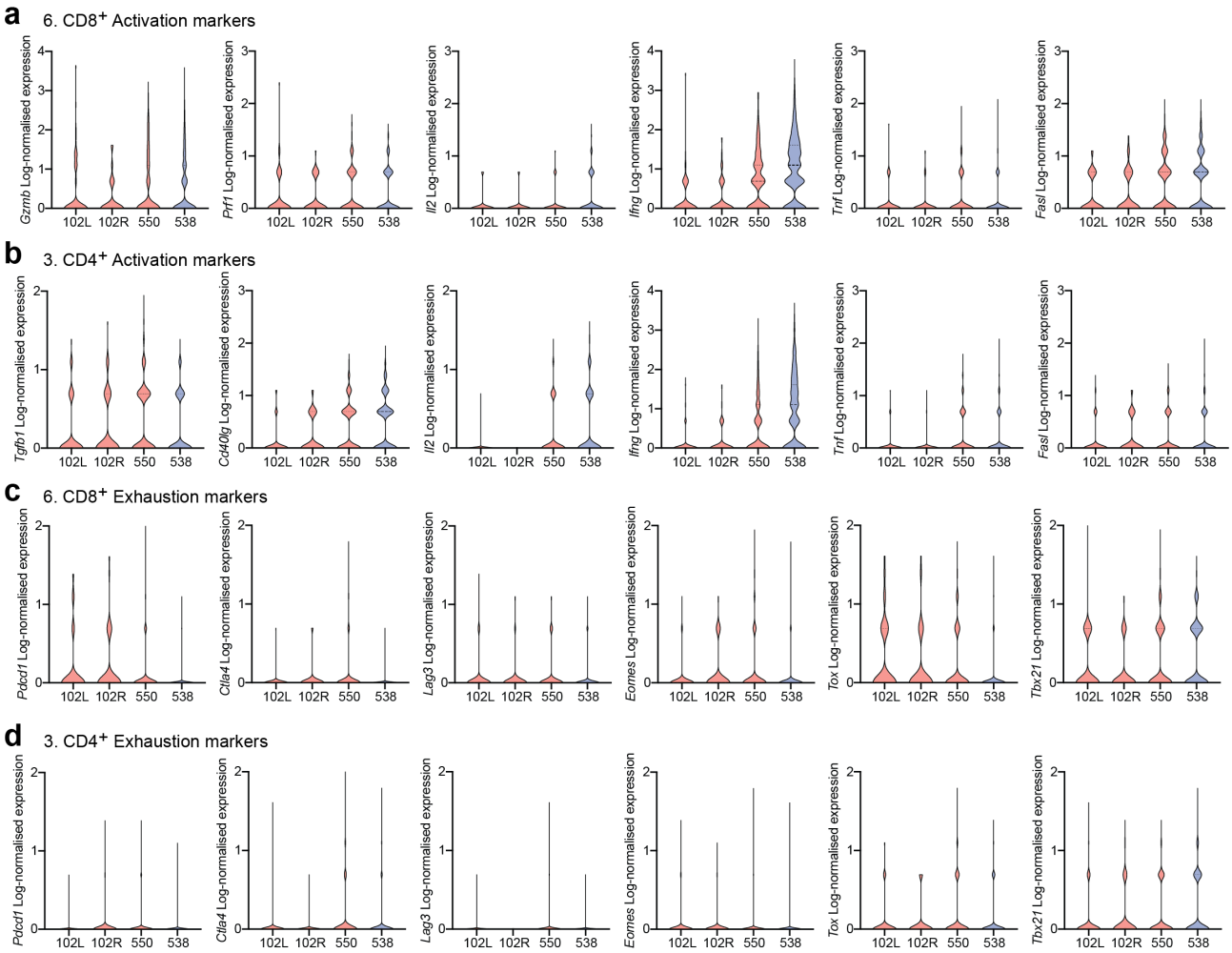


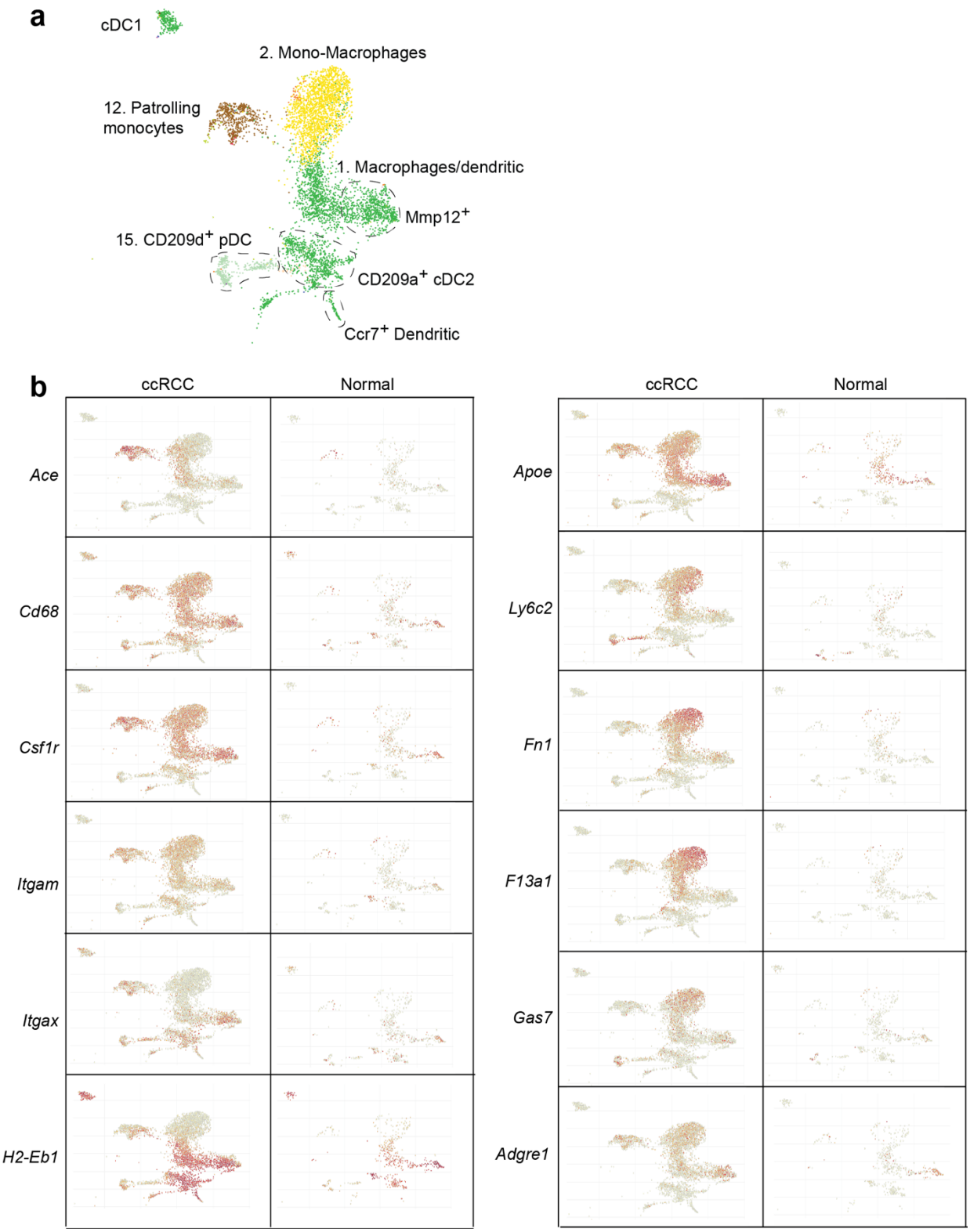
Supplementary Fig. 1: a. UMAP plot depicting cellular distributions from one normal kidney and three ccRCC tumours. **b.** Gene expression heatmap of selected genes that are specific to individual cellular lineages. **c.** Heatmap of differentially expressed genes between normal and tumour cells from cluster 4. **d-i.** Violin plots of the expression of selected HIF-α target genes in cluster 4 (epithelial cells and ccRCC cells) from scRNA-seq of mouse normal kidney and VpR ccRCC. *P* values were calculated using Kruskal-Wallace non-parametric one-way ANOVA with Dunn's multiple comparisons test.



Supplementary Fig. 2: Expression of indicated genes that are specific to the indicated cell types in UMAP plots of scRNA-seq of normal kidney and VpR ccRCC tumours.



Supplementary Fig. 3: a-d. Violin plots of the expression of selected genes that reflect CD8$^+$ T cell activation (**a.**), CD4$^+$ T cell activation (**b.**) or T cell exhaustion (**c,d.**) in the CD8$^+$ T cell cluster 6 (**a,c.**) or the CD4$^+$ T cell cluster 3 (**b,d.**) from scRNA-seq of mouse normal kidney and VpR ccRCC. Kruskal-Wallace non-parametric one-way ANOVA revealed that there were no statistically significant differences in gene expression between normal and tumour samples.



Supplementary Fig. 4: a. UMAP plot of monocyte, macrophage and dendritic cell cluster. **b.** Expression of indicated genes projected onto UMAP plots of scRNA-seq of normal kidney and VpR ccRCC tumours. Red colour indicates increased gene expression.