

snRNA-seq Pilot Data

Functions & Colors

```
In [1]: source('jupyterFunctions.R')
```

```
In [2]: ra_colors <- readRDS('../data/misc/RA_colors.rds')
covid_colors <- readRDS('../data/misc/COVID19_colors.rds')
```

```
In [3]: iLISI_low_color <- '#ffd66a'
iLISI_high_color <- '#9d7b00'
cLISI_low_color <- '#028989'
cLISI_high_color <- '#5afdfd'
```

```
In [59]: save_dir <- NA #'../output/' #or NA if don't want to save
file_extension <- '.pdf'
```

Dataset 1

```
In [5]: data_dir <- '../data/dataset1/'
dataset_str <- 'dataset1'
dataset_str_long <- 'Dataset 1'
CT_str <- 'RA Cell Type'
sample_str <- '(n=12 samples)'

meta <- readRDS(paste(sep=' ',data_dir,dataset_str,'_metadata.rds'))
#Since we are using the original annotations, we don't need gene-level plots
```

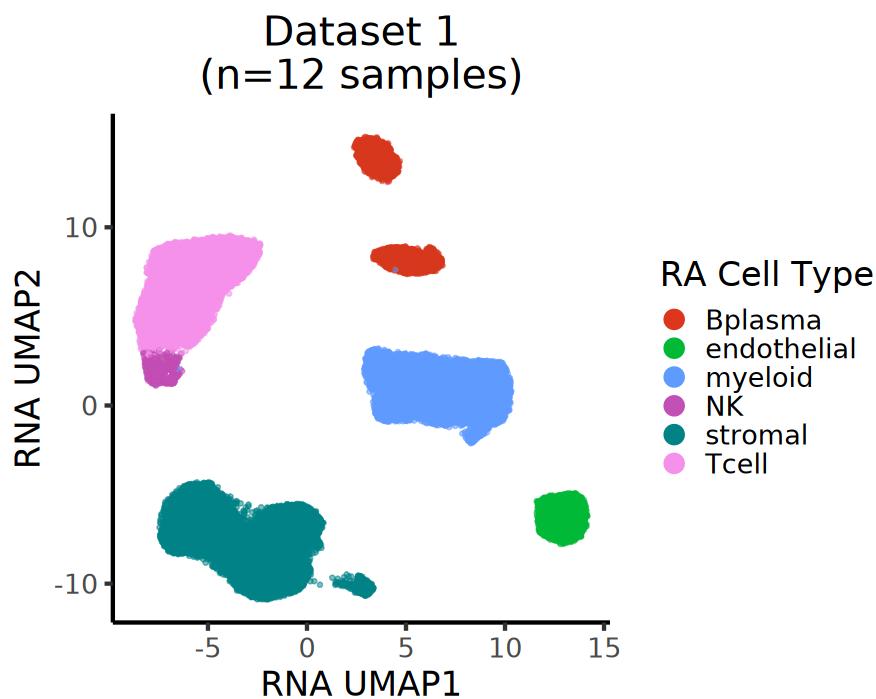
```
In [6]: options(repr.plot.height=6,repr.plot.width=7.5)
g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=RNA_cell_type)) +
    rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
    theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
    scale_color_manual(values=ra_colors) +
    ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
```

```

        labs(color=CT_str,x='RNA UMAP1',y='RNA UMAP2') +
        guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_cellState',file_extension),
         plot=g,units='in',height=6,width=7.5,dpi=300)
}

```



In [7]:

```

options(repr.plot.height=6,repr.plot.width=7)

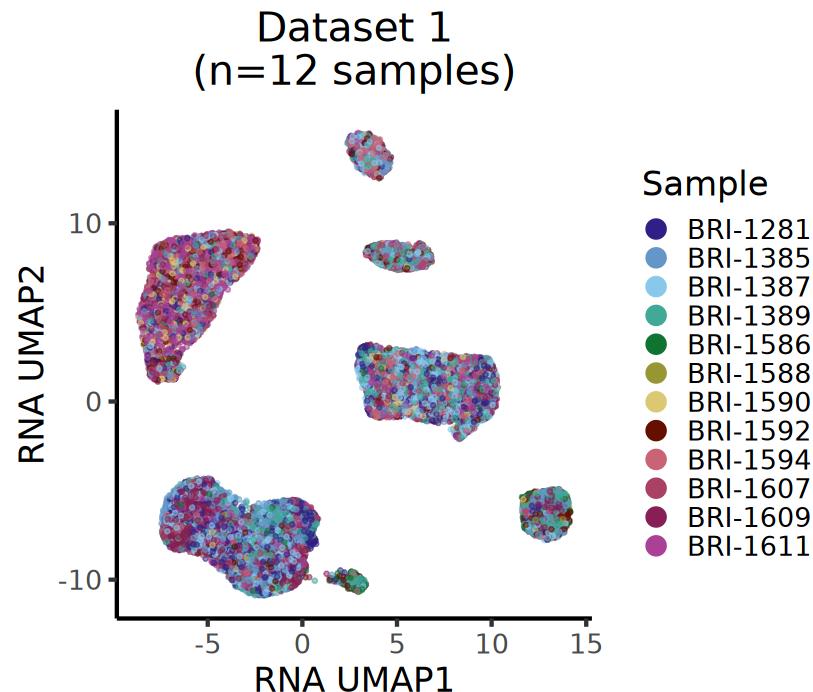
set.seed(0)
g <- ggplot(meta[sample(nrow(meta),nrow(meta)),],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=sample)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_manual(values=ra_colors) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color='Sample',x='RNA UMAP1',y='RNA UMAP2') +
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

```

```

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_sample', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}

```



```

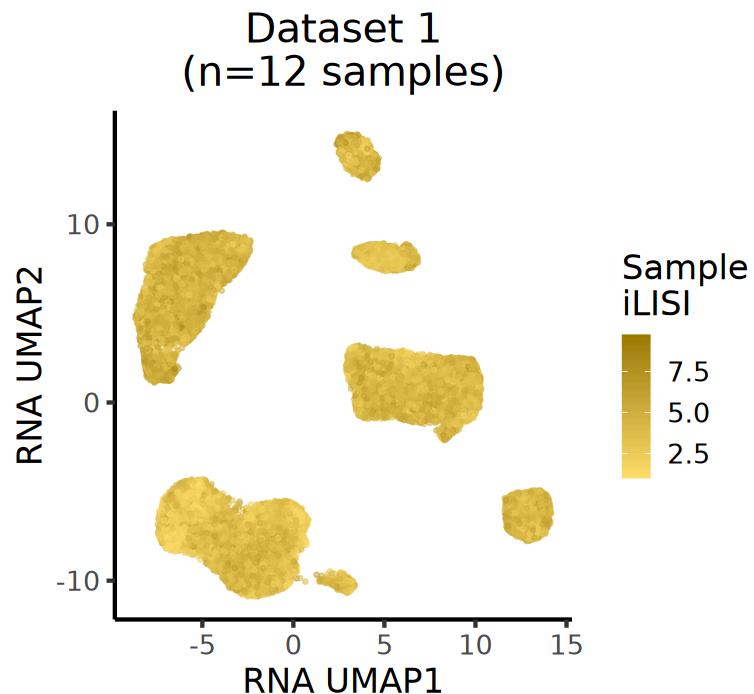
In [8]: options(repr.plot.height=6, repr.plot.width=6.5)

set.seed(0)
g <- ggplot(meta[sample(nrow(meta), nrow(meta)), ], aes(x=RNA_UMAP1, y=RNA_UMAP2, color=lisi_sample)) +
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=iLISI_low_color, high=iLISI_high_color, limits=c(1,NA)) +
  ggtitle(paste(sep='\n', dataset_str_long, sample_str)) +
  labs(color='Sample\niLISI', x='RNA UMAP1', y='RNA UMAP2')
print(g)

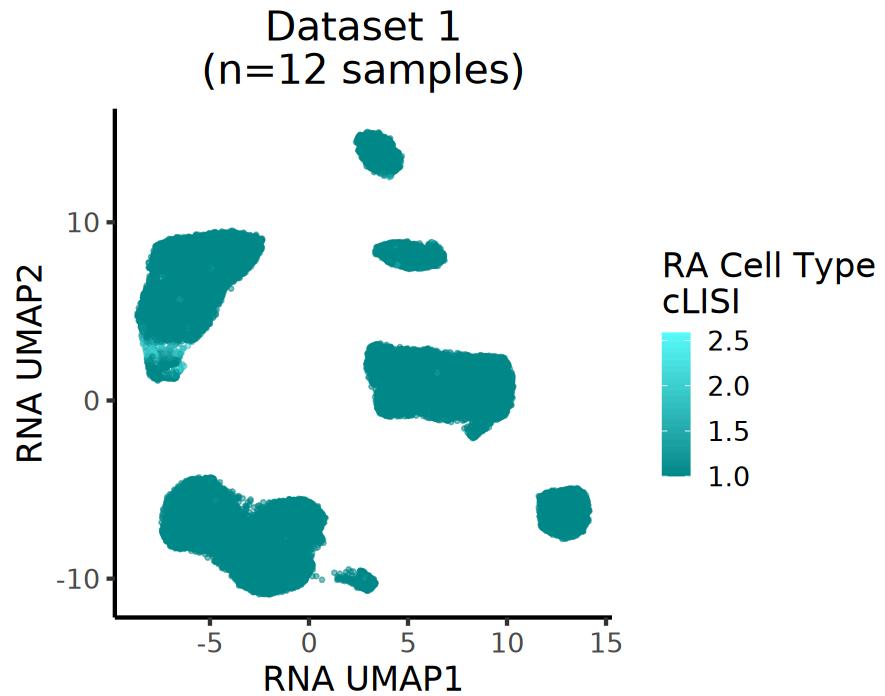
if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_lisiSample', file_extension),

```

```
    plot=g,units='in',height=6,width=6.5,dpi=300)  
}
```



```
In [9]: options(repr.plot.height=6,repr.plot.width=7.5)  
  
g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_cell_type)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_gradient(low=cLISI_low_color,high=cLISI_high_color,limits=c(1,NA)) +  
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +  
  labs(color=paste(sep='\n',CT_str,'cLISI'),x='RNA UMAP1',y='RNA UMAP2')  
print(g)  
  
if(!is.na(save_dir)){  
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiCellType',file_extension),  
         plot=g,units='in',height=6,width=7.5,dpi=300)  
}
```



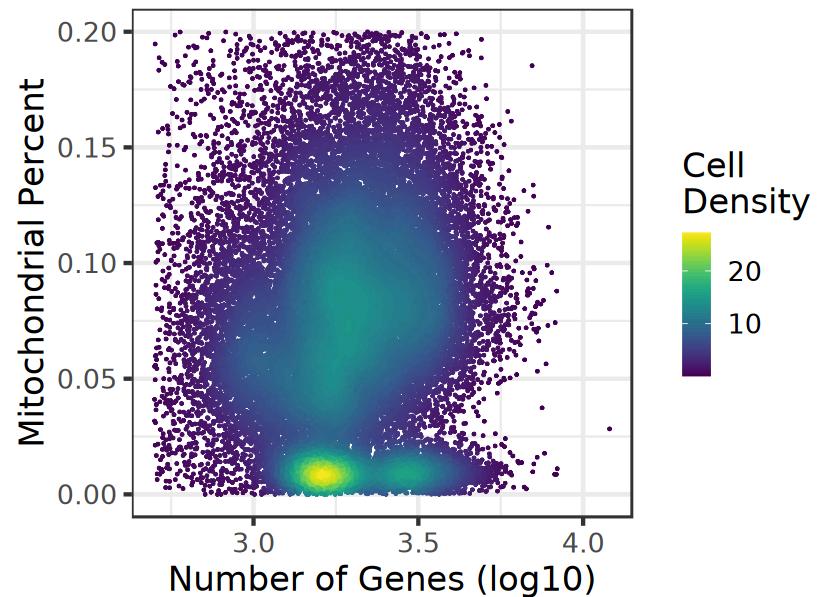
```
In [10]: options(repr.plot.height=6,repr.plot.width=7)

toPlot <- data.frame('log10_nGene'=log10(meta$nGene),'MTperc'=meta$MTperc)
toPlot$density <- get_2D_density(toPlot$log10_nGene,toPlot$MTperc,n=1000)

g <- ggplot(toPlot,aes(x=log10_nGene,y=MTperc,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Genes (log10)',y='Mitochondrial Percent',color='Cell\nDensity',
       title=paste(sep='\n',dataset_str_long,'snRNA-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_RNA_QC',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 1 snRNA-seq QC metrics



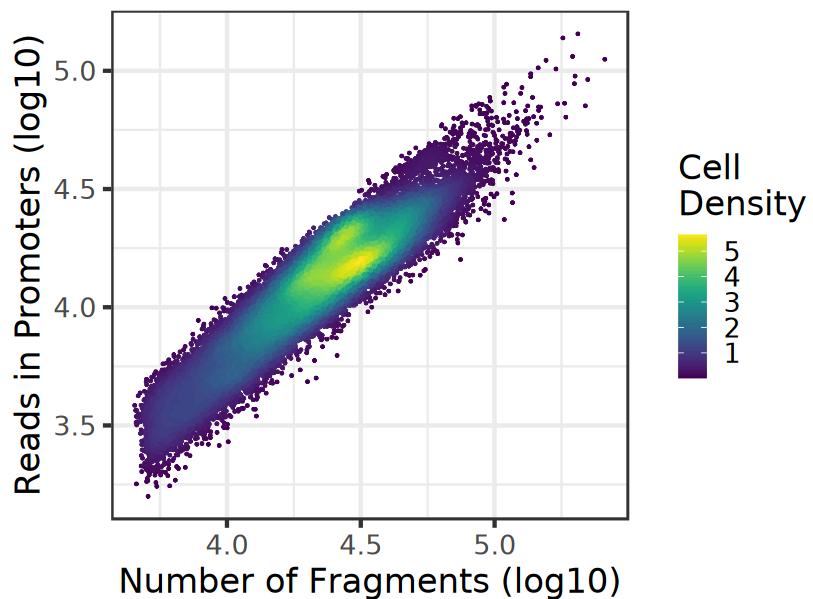
```
In [11]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nFrag'=log10(meta$nFrags), 'log10_Prom'=log10(meta$ReadsInPromoter))
toPlot$density <- get_2D_density(toPlot$log10_nFrag,toPlot$log10_Prom,n=1000)

g <- ggplot(toPlot,aes(x=log10_nFrag,y=log10_Prom,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Fragments (log10)',y='Reads in Promoters (log10)',
       color='Cell\nDensity',title= paste(sep='\n',dataset_str_long,'snATAC-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ', save_dir, dataset_str, '_ATAC_QC', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}
```

Dataset 1 snATAC-seq QC metrics



Dataset 2

```
In [12]: data_dir <- '../data/dataset2/'  
dataset_str <- 'dataset2'  
dataset_str_long <- 'Dataset 2'  
CT_str <- 'RA T Cell State'  
ori_CT_str <- 'RA T Cell Chromatin Class'  
sample_str <- '(n=12 samples)'  
  
meta <- readRDS(paste(sep=' ',data_dir,dataset_str,'_metadata.rds'))  
gxc_norm <- readRDS(paste(sep=' ',data_dir,dataset_str,'_gxc_norm.rds'))  
gxCT_norm <- readRDS(paste(sep=' ',data_dir,dataset_str,'_gxCT_norm.rds'))  
chosenGenes <- readRDS(paste(sep=' ',data_dir,dataset_str,'_chosenGenes.rds'))
```

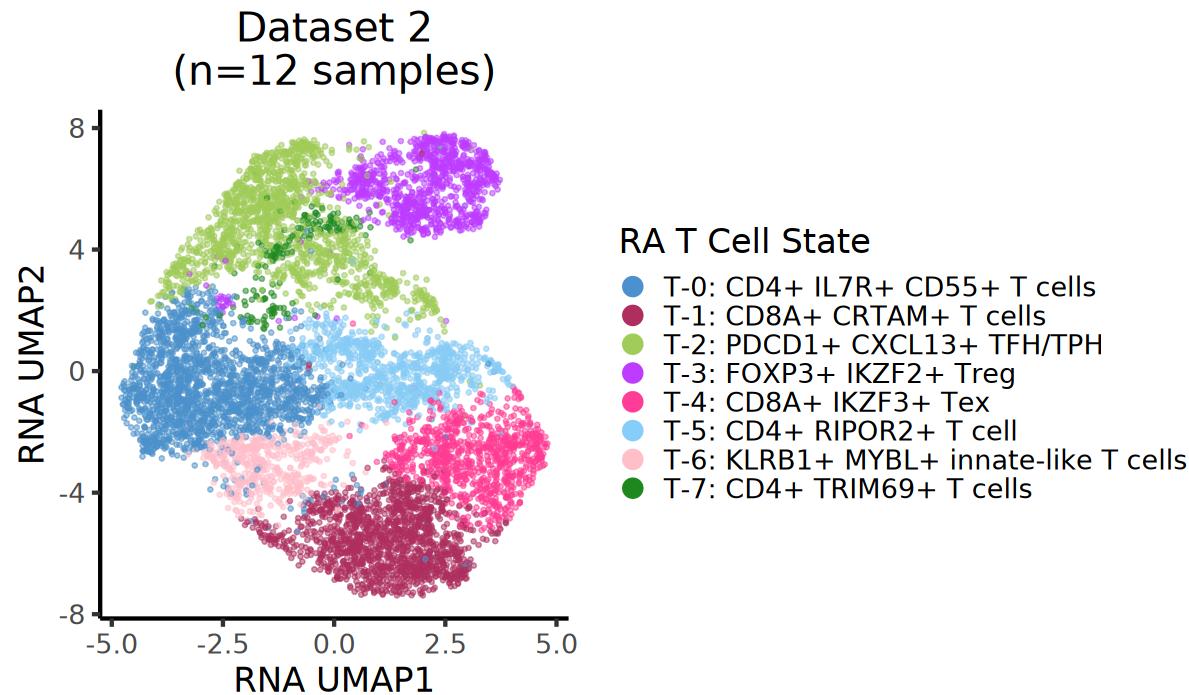
```
In [13]: options(repr.plot.height=6,repr.plot.width=10)  
g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=RNA_state_name)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
```

```

    scale_color_manual(values=ra_colors) +
    ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
    labs(color=CT_str,x='RNA UMAP1',y='RNA UMAP2') +
    guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_cellState',file_extension),
         plot=g,units='in',height=6,width=10,dpi=300)
}

```



In [14]: `state_order <- paste(sep=' ', 'T-', c(1,4,6,0,5,7,2,3))`

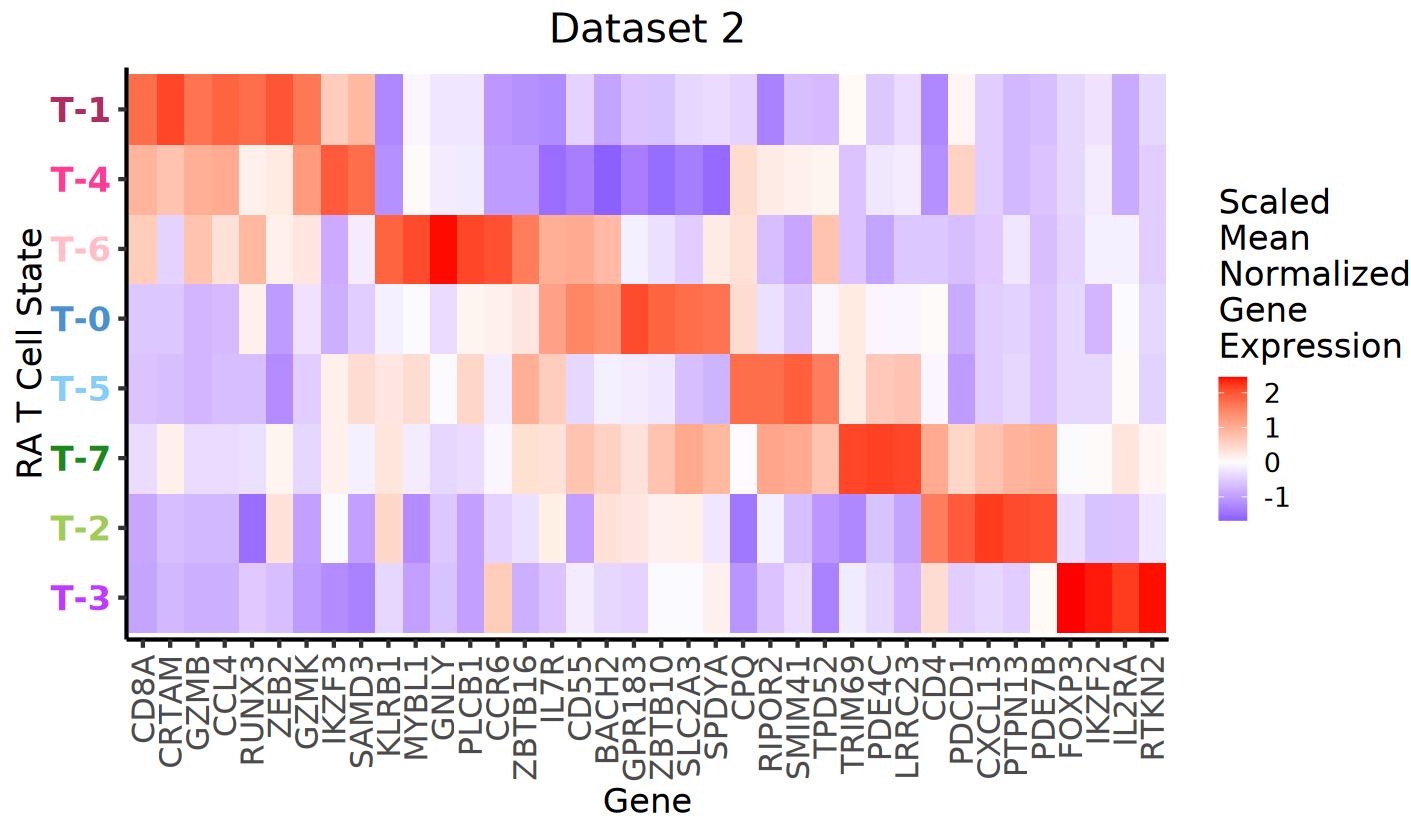
In [15]: `options(repr.plot.height=7,repr.plot.width=12)
g <- pseudobulk_scaled_heatmap(scaleGene_forHeatmap(chosenGenes,state_order,gxCT_norm),
 'Gene',CT_str,
 'Scaled\nMean\nNormalized\nGene\nExpression',
 plotTit=dataset_str_long,
 clustColors=ra_colors)
g <- g + theme(axis.text.x = element_text(size=19))`

```

print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_markerGeneExp', file_extension),
         plot=g, units='in', height=7, width=12, dpi=300)
}

```



```

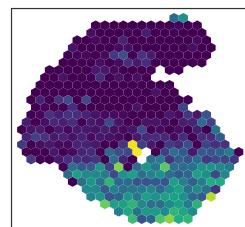
In [16]: genes_forUMAPs <- c('CD8A', 'CRTAM', 'IKZF3', 'KLRB1',
                           'CD4', 'IL7R', 'PDCD1', 'CXCL13', 'FOXP3', 'IKZF2', 'RIPOR2', 'TRIM69')
if(!all(genes_forUMAPs %in% chosenGenes)) stop('Genes for UMAP not in chosen genes')

options(repr.plot.height=8, repr.plot.width=10)
g <- plot_markerPeaks_norm_hex_v2(meta, gxc_norm[, rownames(meta)], 'RNA_UMAP1', 'RNA_UMAP2',
                                     plot_genes=genes_forUMAPs, plotCol=4,
                                     titleSize=16, hex_bins=23, cutCap=0)
grid.draw(g)

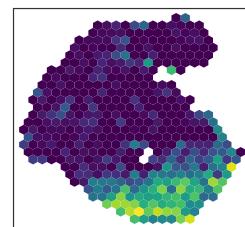
```

```
if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_markerGeneExp'), file_ex-
```

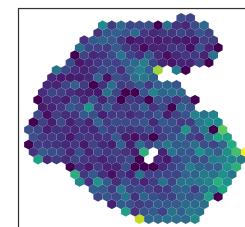
CD8A



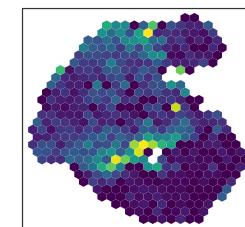
CRTAM



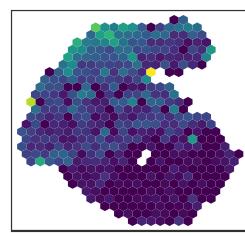
IKZF3



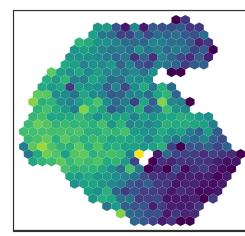
KLRB1



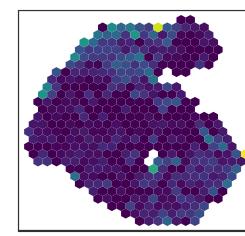
CD4



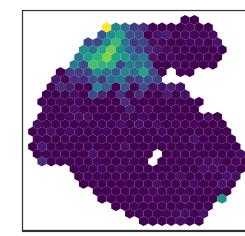
IL7R



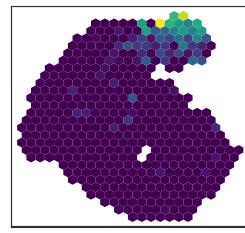
PDCD1



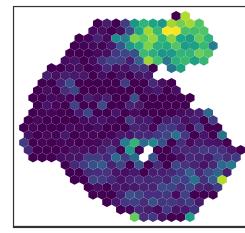
CXCL13



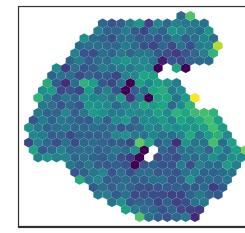
FOXP3



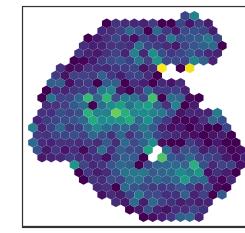
IKZF2



RIPOR2



TRIM69



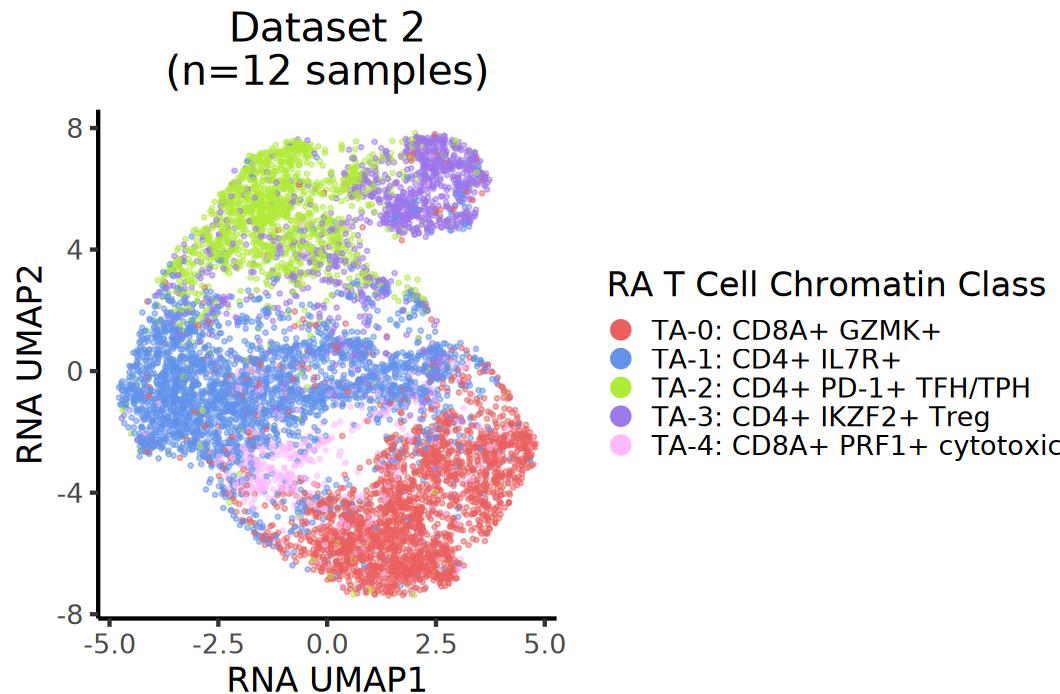
In [17]:

```
options(repr.plot.height=6,repr.plot.width=9)
g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=ATAC_class_name)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_manual(values=ra_colors) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color=ori_CT_str,x='RNA UMAP1',y='RNA UMAP2') +
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)
```

```

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_oriCT', file_extension),
         plot=g, units='in', height=6, width=9, dpi=300)
}

```



```

In [18]: fisher_df <- calc_OR(meta, 'RNA_state_abbr', 'ATAC_class_abbr')

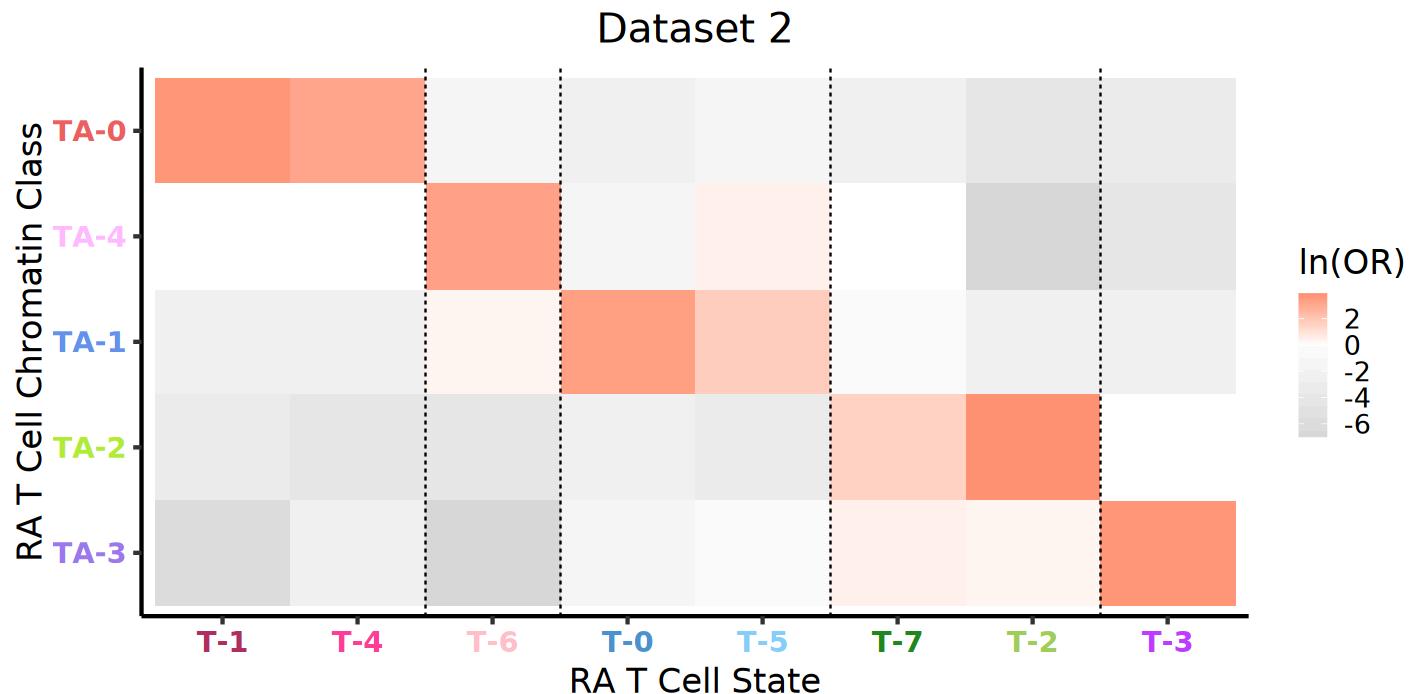
g <- plot_OR(fisher_df, 'RNA_state_abbr', 'ATAC_class_abbr',
              CT_str, ori_CT_str,
              state_order, c('TA-0', 'TA-4', 'TA-1', 'TA-2', 'TA-3'),
              clustColors=ra_colors)
g <- g + geom_vline(xintercept=c(2.5,3.5,5.5,7.5), linetype='dashed') +
  ggtitle(dataset_str_long) + theme(plot.title = element_text(hjust = 0.5))

options(repr.plot.height=6, repr.plot.width=12)
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_oriCTlnOR', file_extension),
         plot=g, units='in', height=6, width=9, dpi=300)
}

```

```
    plot=g,units='in',height=6,width=12,dpi=300)
}
```

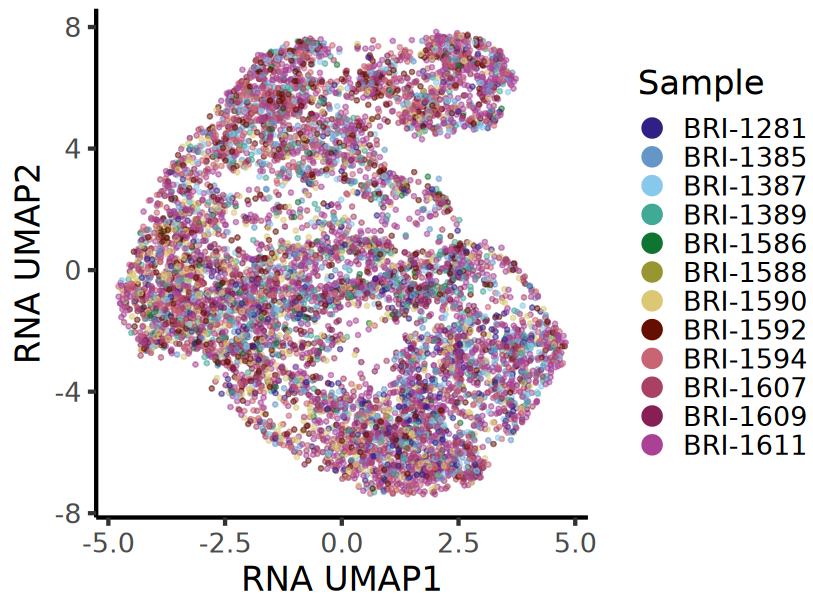


```
In [19]: options(repr.plot.height=6,repr.plot.width=7)

set.seed(0)
g <- ggplot(meta[sample(nrow(meta),nrow(meta)),],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=sample)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_manual(values=ra_colors) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color='Sample',x='RNA UMAP1',y='RNA UMAP2') +
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_sample',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

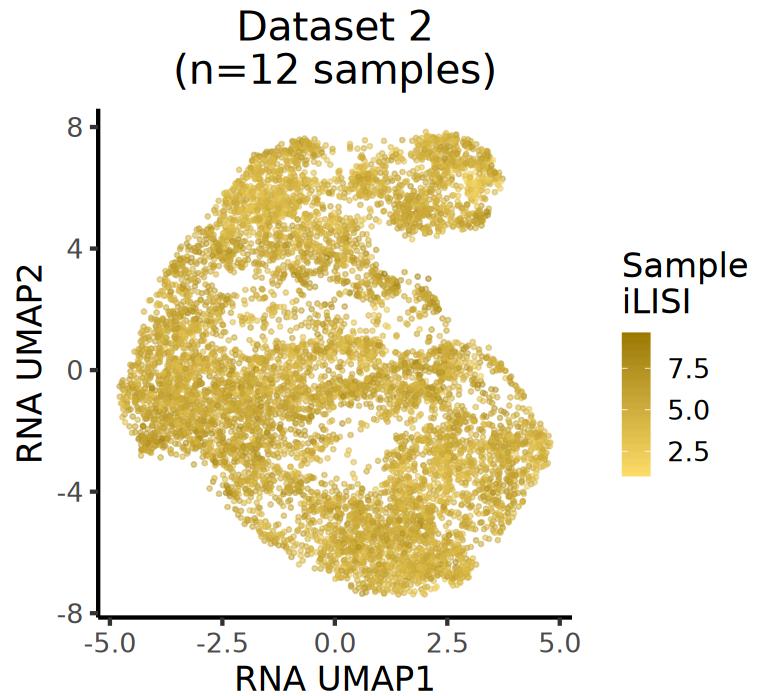
Dataset 2
(n=12 samples)



```
In [20]: options(repr.plot.height=6,repr.plot.width=6.5)

set.seed(0)
g <- ggplot(meta[nrow(meta),nrow(meta)], aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_sample)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=iLISI_low_color,high=iLISI_high_color,limits=c(1,NA)) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color='Sample\niLISI',x='RNA UMAP1',y='RNA UMAP2')
print(g)

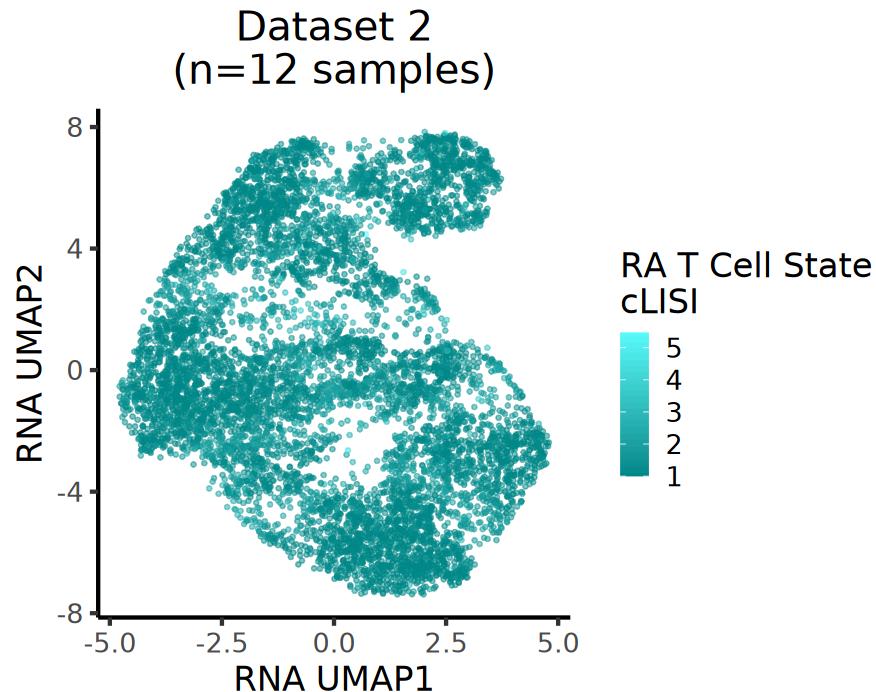
if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiSample',file_extension),
         plot=g,units='in',height=6,width=6.5,dpi=300)
}
```



```
In [21]: options(repr.plot.height=6,repr.plot.width=7.5)

g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_cell_state)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=cLISI_low_color,high=cLISI_high_color,limits=c(1,NA)) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color=paste(sep='\n',CT_str,'cLISI'),x='RNA UMAP1',y='RNA UMAP2')
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiCellType',file_extension),
         plot=g,units='in',height=6,width=7.5,dpi=300)
}
```



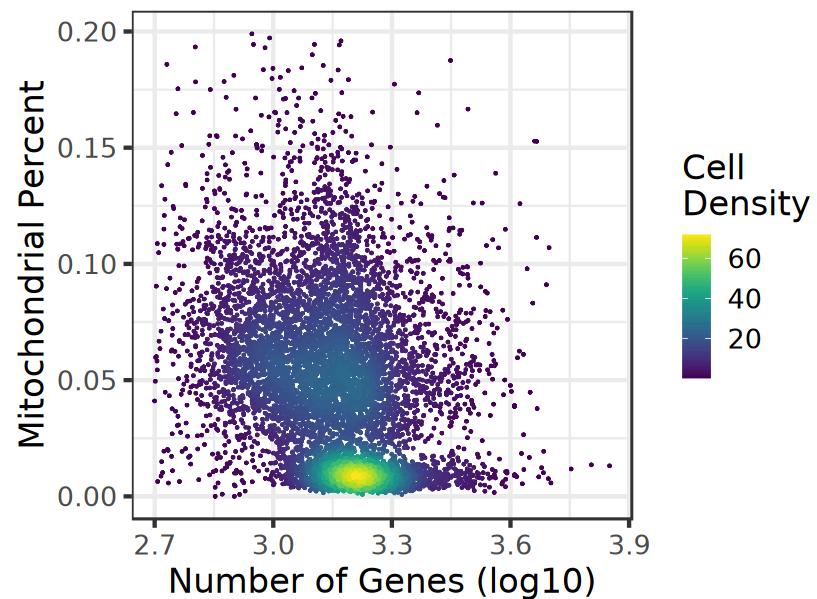
```
In [22]: options(repr.plot.height=6,repr.plot.width=7)

toPlot <- data.frame('log10_nGene'=log10(meta$nGene),'MTperc'=meta$MTperc)
toPlot$density <- get_2D_density(toPlot$log10_nGene,toPlot$MTperc,n=1000)

g <- ggplot(toPlot,aes(x=log10_nGene,y=MTperc,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Genes (log10)',y='Mitochondrial Percent',color='Cell\nDensity',
       title=paste(sep='\n',dataset_str_long,'snRNA-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_RNA_QC',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 2 snRNA-seq QC metrics

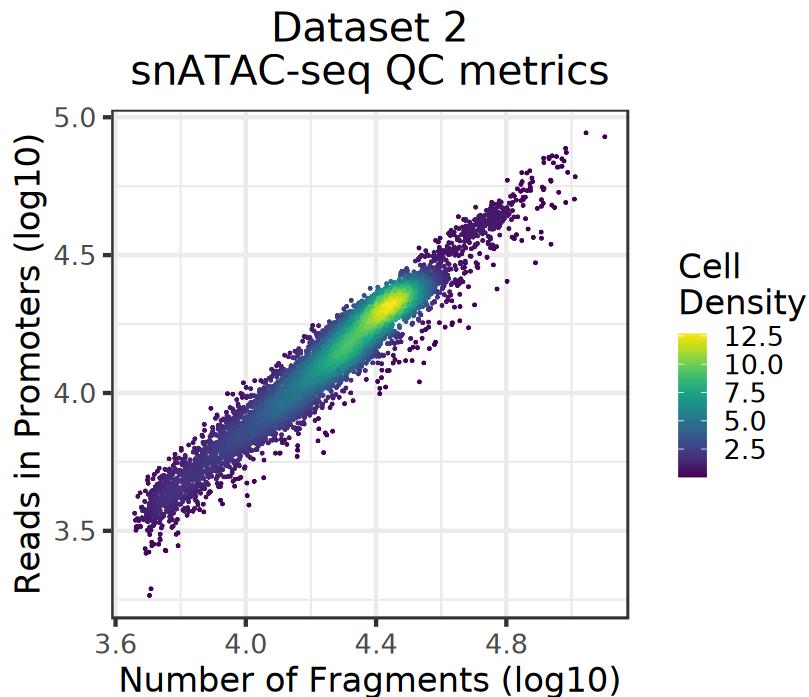


```
In [23]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nFrag'=log10(meta$nFrags), 'log10_Prom'=log10(meta$ReadsInPromoter))
toPlot$density <- get_2D_density(toPlot$log10_nFrag,toPlot$log10_Prom,n=1000)

g <- ggplot(toPlot,aes(x=log10_nFrag,y=log10_Prom,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Fragments (log10)',y='Reads in Promoters (log10)',
       color='Cell\nDensity',title= paste(sep='\n',dataset_str_long,'snATAC-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ', save_dir, dataset_str, '_ATAC_QC', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}
```



Dataset 3

```
In [24]: data_dir <- '../data/dataset3/'  
dataset_str <- 'dataset3'  
dataset_str_long <- 'Dataset 3'  
CT_str <- 'RA FACS\nT Cell Substate'  
sample_str <- '(n=2 runs)'  
  
meta <- readRDS(paste(sep=' ',data_dir,dataset_str,'_metadata.rds'))  
#Since we are using the original annotations, we don't need gene-level plots
```

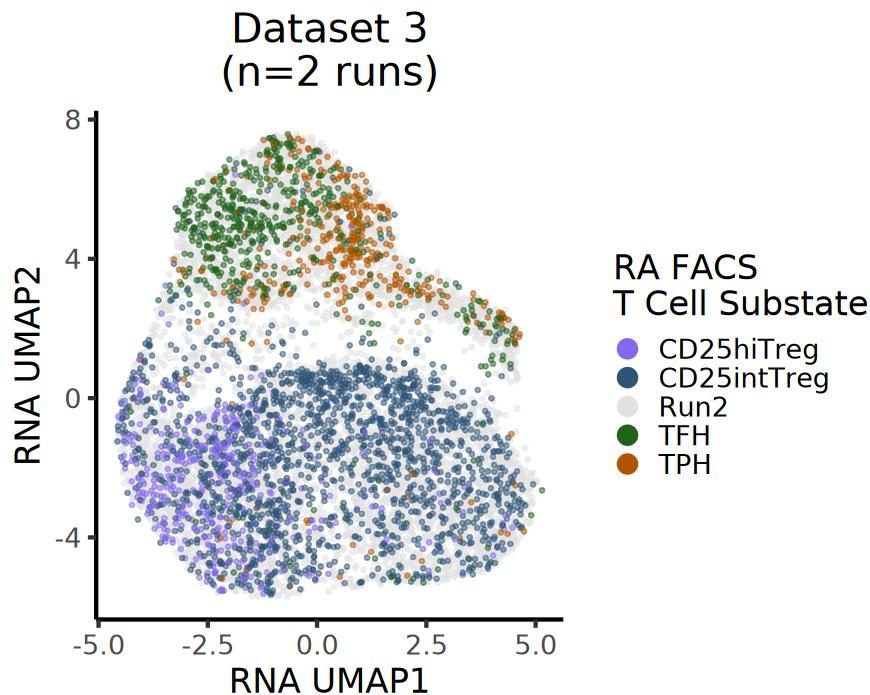
```
In [25]: options(repr.plot.height=6,repr.plot.width=7.5)  
g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=snHT0_name)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_manual(values=ra_colors) +  
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +  
  labs(color=CT_str,x='RNA UMAP1',y='RNA UMAP2') +
```

```

        guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_cellState',file_extension),
         plot=g,units='in',height=6,width=7.5,dpi=300)
}

```



```

In [26]: options(repr.plot.height=6,repr.plot.width=7)

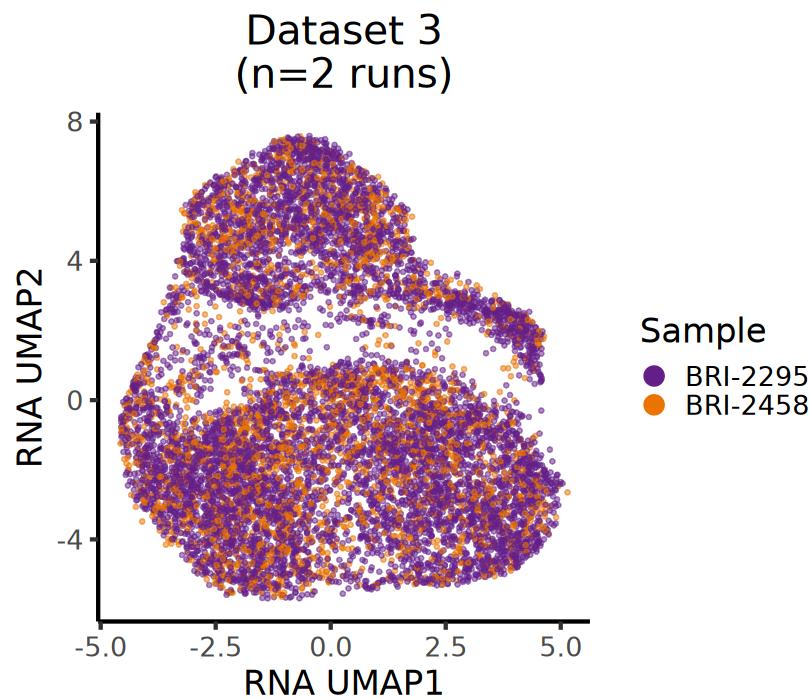
set.seed(0)
g <- ggplot(meta[sample(nrow(meta),nrow(meta)),],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=sample)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_manual(values=ra_colors) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color='Sample',x='RNA UMAP1',y='RNA UMAP2') +
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

```

```

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_sample', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}

```



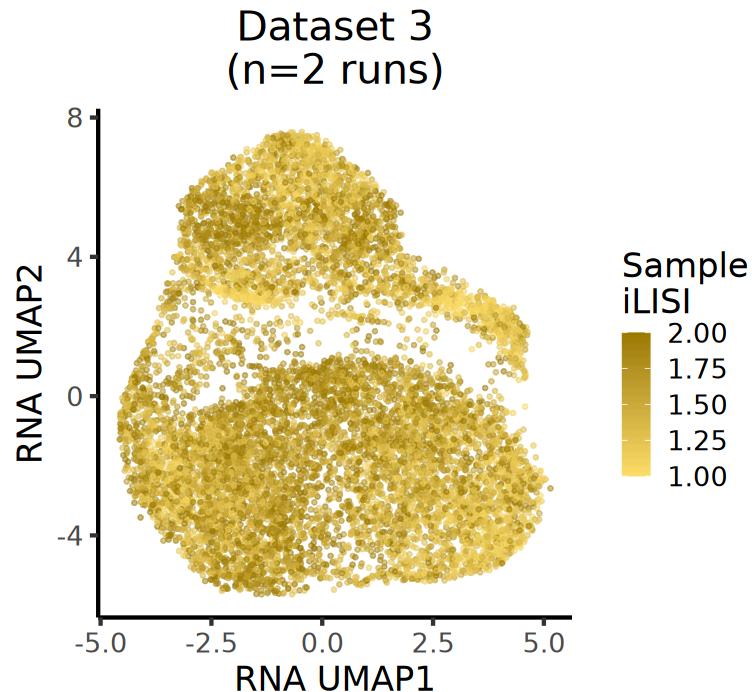
```

In [27]: options(repr.plot.height=6, repr.plot.width=6.5)

set.seed(0)
g <- ggplot(meta[sample(nrow(meta), nrow(meta)), ], aes(x=RNA_UMAP1, y=RNA_UMAP2, color=lisi_sample)) +
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=iLISI_low_color, high=iLISI_high_color, limits=c(1,NA)) +
  ggtitle(paste(sep='\n', dataset_str_long, sample_str)) +
  labs(color='Sample\niLISI', x='RNA UMAP1', y='RNA UMAP2')
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_lisiSample', file_extension),
         plot=g, units='in', height=6, width=6.5, dpi=300)
}

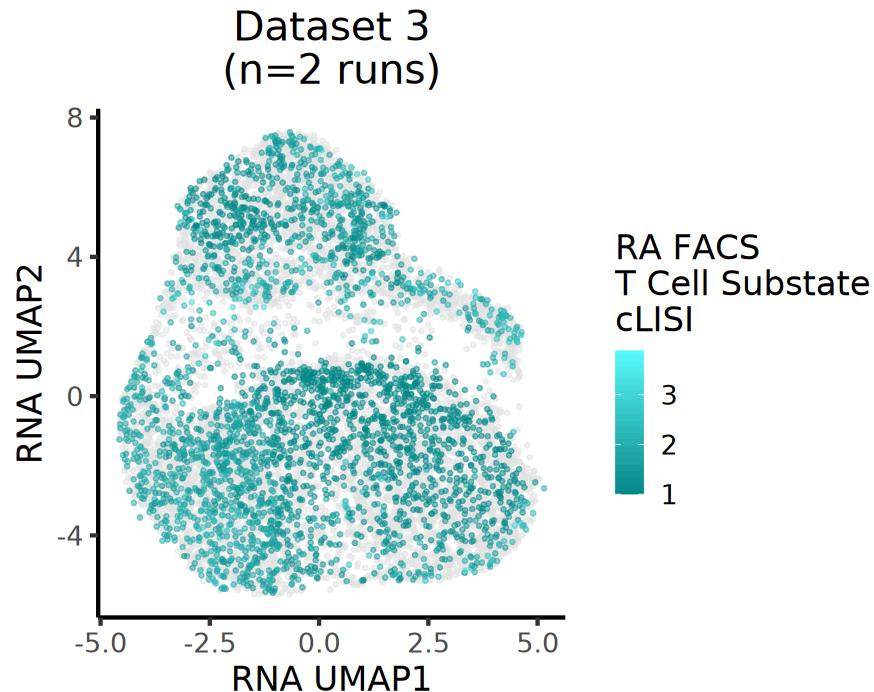
```



```
In [28]: options(repr.plot.height=6,repr.plot.width=7.5)

g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_snHT0_name)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=cLISI_low_color,high=cLISI_high_color,na.value = "grey90",limits=c(1,NA))
  gtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color= paste(sep='\n',CT_str,'cLISI'),x='RNA UMAP1',y='RNA UMAP2')
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiCellType',file_extension),
         plot=g,units='in',height=6,width=7.5,dpi=300)
}
```



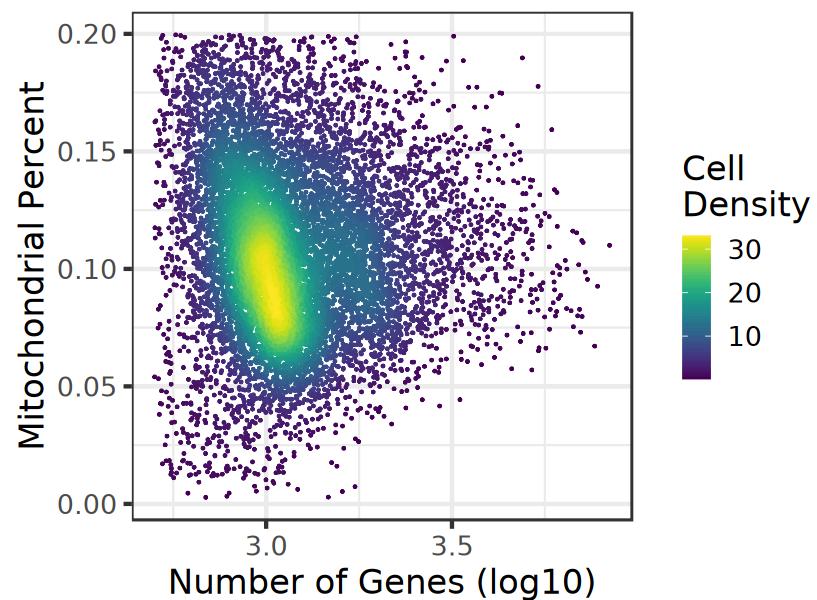
```
In [29]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nGene'=log10(meta$nGene), 'MTperc'=meta$MTperc)
toPlot$density <- get_2D_density(toPlot$log10_nGene,toPlot$MTperc,n=1000)

g <- ggplot(toPlot,aes(x=log10_nGene,y=MTperc,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Genes (log10)',y='Mitochondrial Percent',color='Cell\nDensity',
       title=paste(sep='\n',dataset_str_long,'snRNA-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_RNA_QC',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 3 snRNA-seq QC metrics



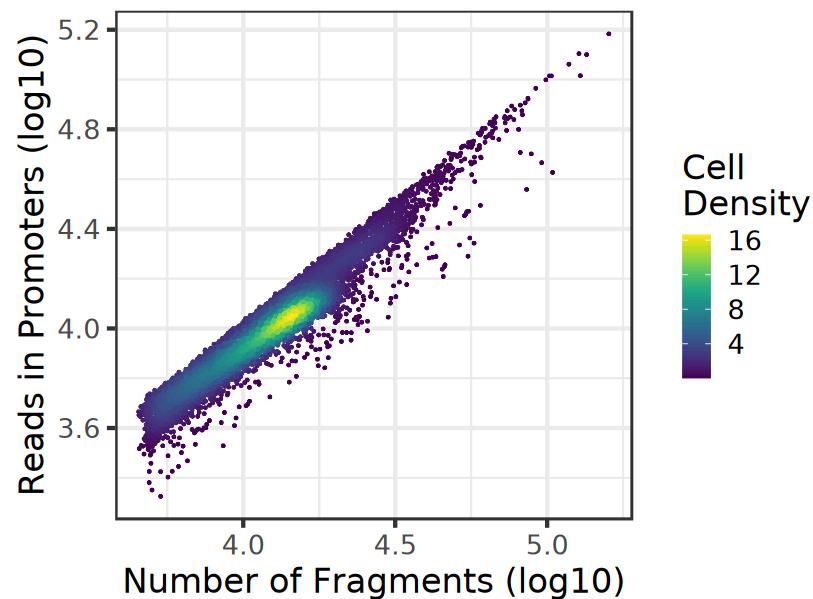
```
In [30]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nFrag'=log10(meta$nFrags), 'log10_Prom'=log10(meta$ReadsInPromoter))
toPlot$density <- get_2D_density(toPlot$log10_nFrag,toPlot$log10_Prom,n=1000)

g <- ggplot(toPlot,aes(x=log10_nFrag,y=log10_Prom,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Fragments (log10)',y='Reads in Promoters (log10)',
       color='Cell\nDensity',title= paste(sep='\n',dataset_str_long,'snATAC-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ', save_dir, dataset_str, '_ATAC_QC', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}
```

Dataset 3 snATAC-seq QC metrics



Dataset 4

```
In [31]: data_dir <- '../data/dataset4/'  
dataset_str <- 'dataset4'  
dataset_str_long <- 'Dataset 4'  
CT_str <- 'Re-annotated\nPBMC/HSPC\nCell Type'  
ori_CT_str <- 'PBMC/HSPC\nCell Type'  
sample_str <- '(n=30 samples)'  
  
meta <- readRDS(paste(sep=' ', data_dir, dataset_str, '_metadata.rds'))  
gxc_norm <- readRDS(paste(sep=' ', data_dir, dataset_str, '_gxc_norm.rds'))  
gxCT_norm <- readRDS(paste(sep=' ', data_dir, dataset_str, '_gxCT_norm.rds'))  
chosenGenes <- readRDS(paste(sep=' ', data_dir, dataset_str, '_chosenGenes.rds'))
```

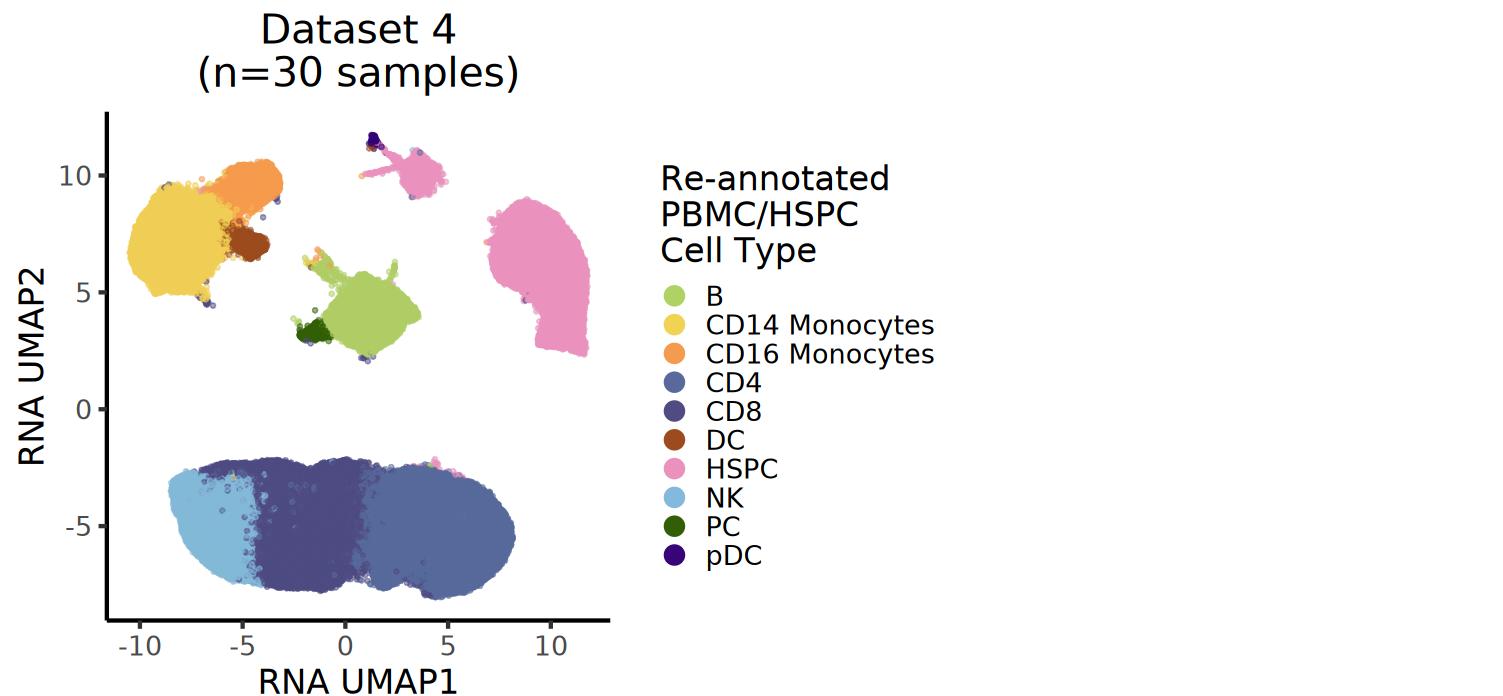
```
In [32]: options(repr.plot.height=6, repr.plot.width=8)  
g <- ggplot(meta, aes(x=RNA_UMAP1, y=RNA_UMAP2, color=RNA_cell_type)) +  
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
```

```

    scale_color_manual(values=covid_colors) +
    ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
    labs(color=CT_str,x='RNA UMAP1',y='RNA UMAP2') +
    guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_cellState',file_extension),
         plot=g,units='in',height=6,width=8,dpi=300)
}

```



In [33]: `state_order <- c("B", "PC", "pDC", "DC", "CD14 Monocytes", "CD16 Monocytes", "CD4", "CD8", "NK", "HSPC")`

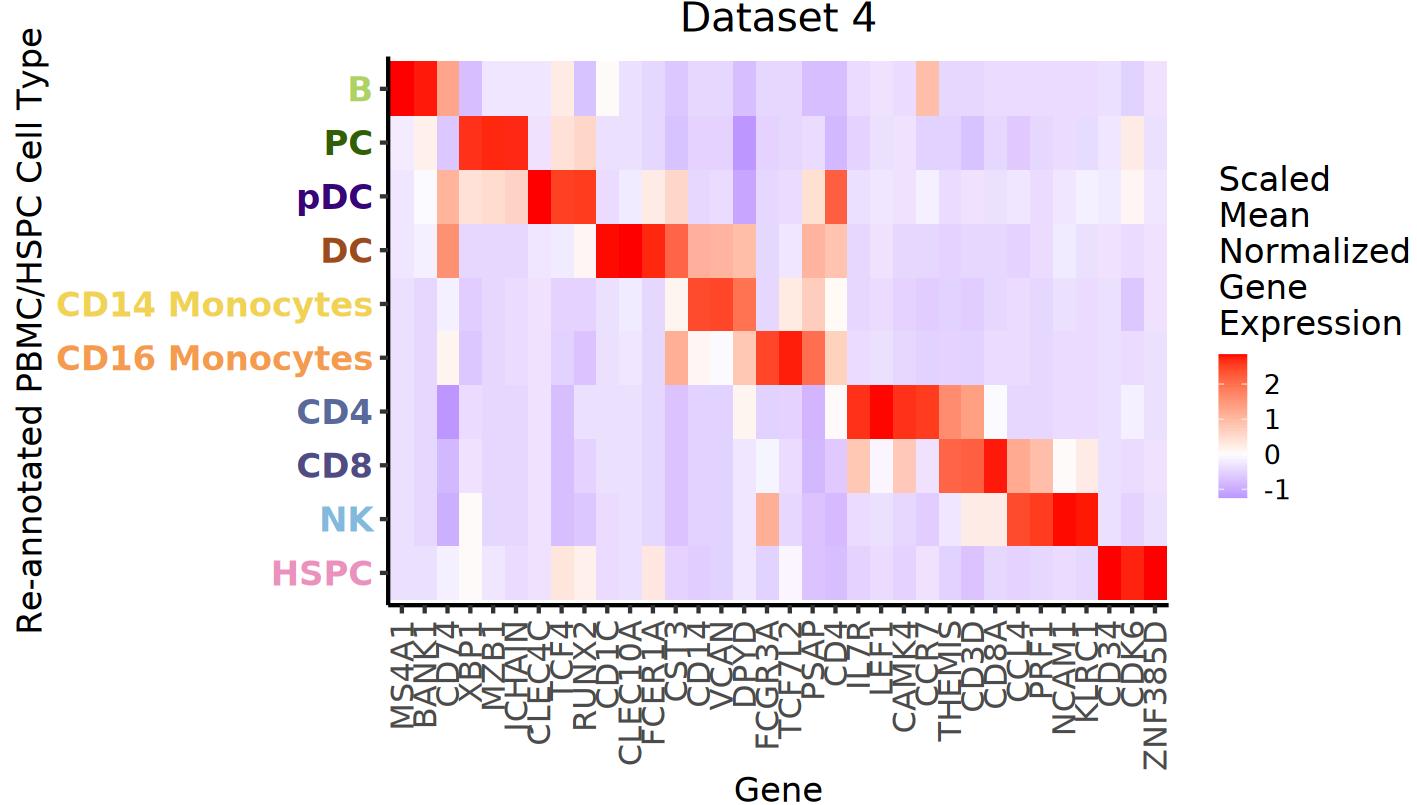
In [34]: `options(repr.plot.height=7,repr.plot.width=12)
g <- pseudobulk_scaled_heatmap(scaleGene_forHeatmap(chosenGenes,state_order,gxCT_norm),
 'Gene',gsub('\n',' ',CT_str),
 'Scaled\nMean\nNormalized\nGene\nExpression',
 plotTit=dataset_str_long,
 clustColors=covid_colors)
g <- g + theme(axis.text.x = element_text(size=19))`

```

print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_markerGeneExp', file_extension),
         plot=g, units='in', height=7, width=12, dpi=300)
}

```



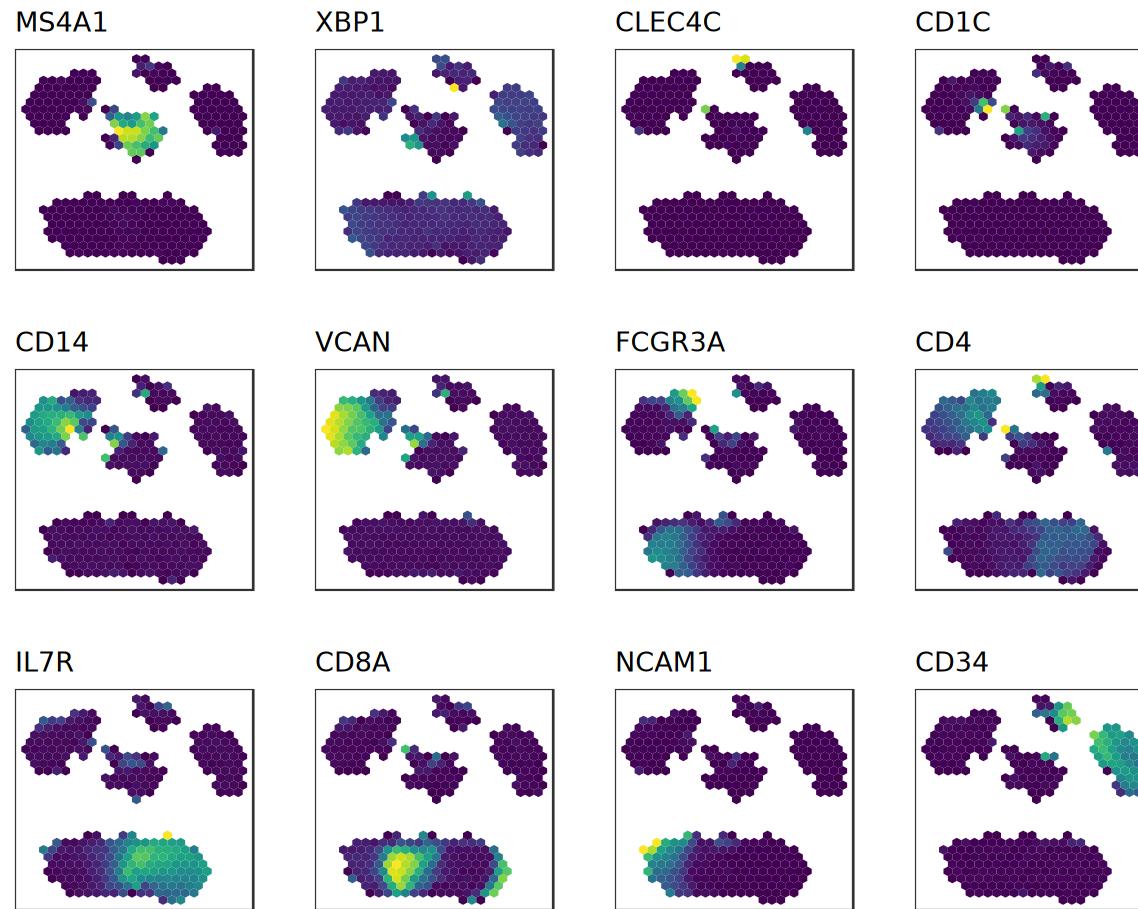
```

In [35]: genes_forUMAPs <- c('MS4A1', 'XBP1', 'CLEC4C', 'CD1C', 'CD14', 'VCAN', 'FCGR3A', 'CD4', 'IL7R', 'CD8A', 'NCAM1', 'CD3'
if(!all(genes_forUMAPs %in% chosenGenes)) stop('Genes for UMAP not in chosen genes')

options(repr.plot.height=8, repr.plot.width=10)
g <- plot_markerPeaks_norm_hex_v2(meta, gxc_norm[, rownames(meta)], 'RNA_UMAP1', 'RNA_UMAP2',
                                     plot_genes=genes_forUMAPs, plotCol=4,
                                     titleSize=16, hex_bins=24, cutCap=0)
grid.draw(g)

```

```
if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_markerGeneExp'), file_ex-  
plot=g, units='in', height=8, width=10, dpi=300)
```

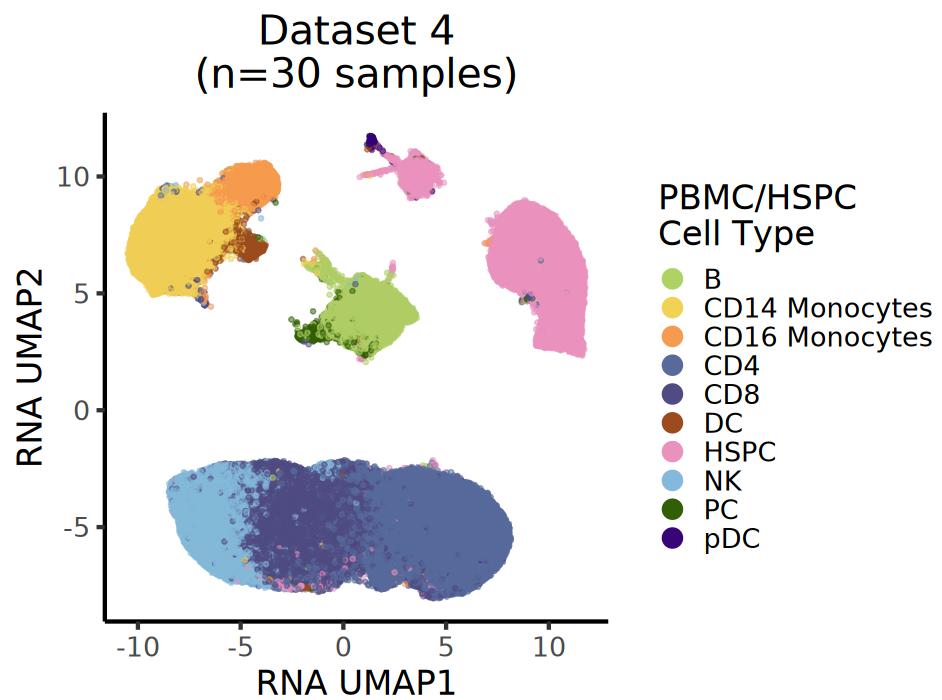


```
In [36]: options(repr.plot.height=6, repr.plot.width=8)  
g <- ggplot(meta, aes(x=RNA_UMAP1, y=RNA_UMAP2, color=RNA_ori_cell_type)) +  
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_manual(values=covid_colors) +  
  ggtitle(paste(sep='\n', dataset_str_long, sample_str)) +  
  labs(color=ori_CT_str, x='RNA UMAP1', y='RNA UMAP2') +  
  guides(colour = guide_legend(override.aes = list(size=5, alpha=1)))  
print(g)
```

```

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_oriCT', file_extension),
         plot=g, units='in', height=6, width=8, dpi=300)
}

```



```

In [37]: fisher_df <- calc_OR(meta, 'RNA_cell_type', 'RNA_ori_cell_type')

g <- plot_OR(fisher_df, 'RNA_cell_type', 'RNA_ori_cell_type',
              gsub('\n', ' ', CT_str), gsub('\n', ' ', ori_CT_str),
              state_order, state_order,
              clustColors=covid_colors)
g <- g + ggtitle(dataset_str_long) +
    theme(plot.title = element_text(hjust = 0.5),
          axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))

options(repr.plot.height=6, repr.plot.width=12)
print(g)

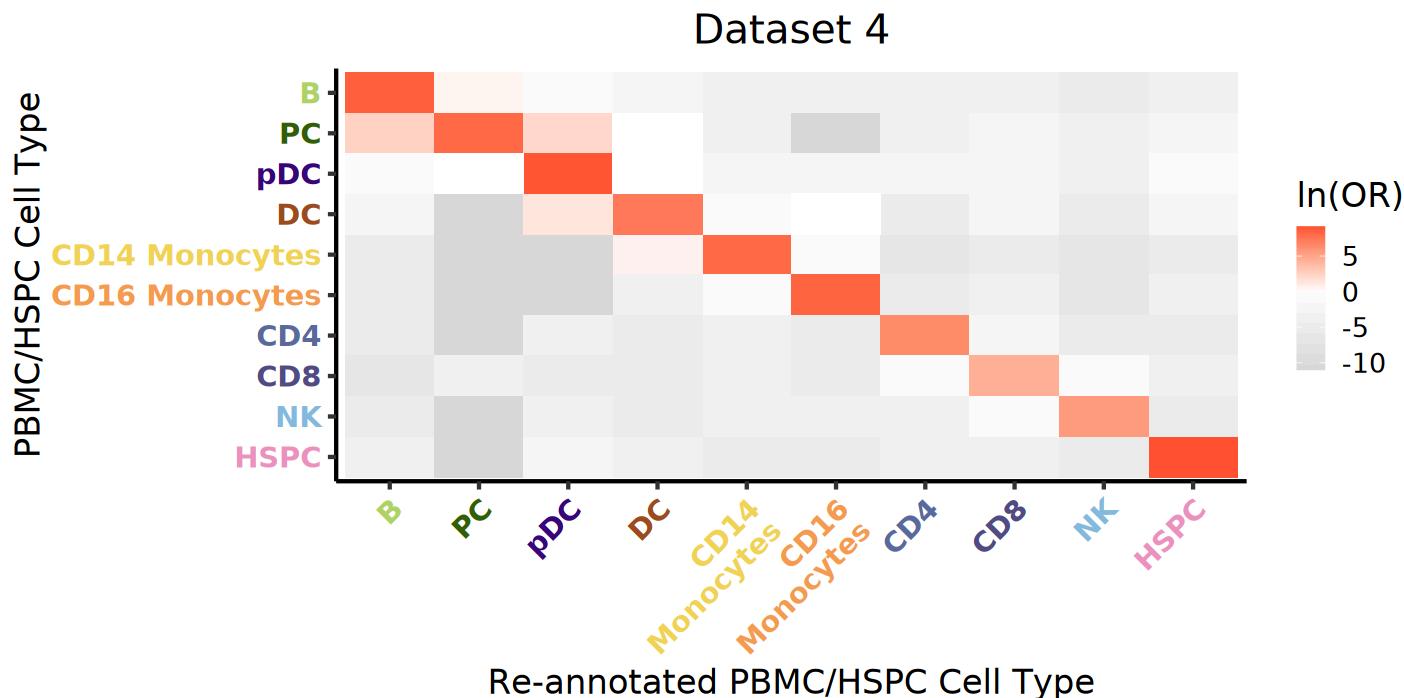
if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_oriCTlnOR', file_extension),

```

```

        plot=g,units='in',height=6,width=12,dpi=300)
}

```



```

In [38]: options(repr.plot.height=6,repr.plot.width=8.5)

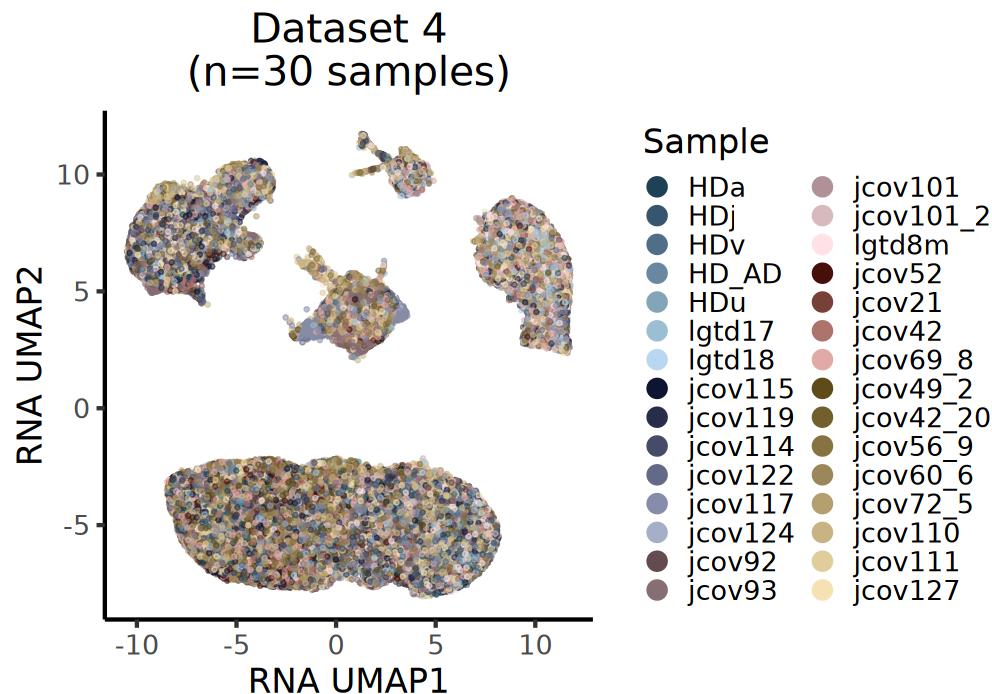
meta$sample_factor <- factor(meta$sample,levels=names(covid_colors))

set.seed(0)
g <- ggplot(meta[,sample(nrow(meta),nrow(meta)),],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=sample_factor)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_manual(values=covid_colors) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color='Sample',x='RNA UMAP1',y='RNA UMAP2') +
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

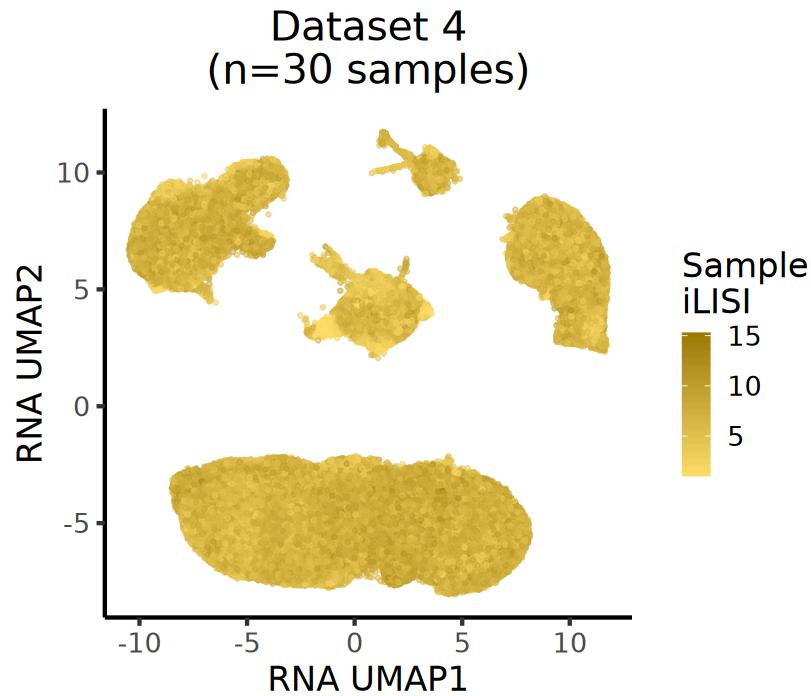
if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_sample',file_extension),

```

```
    plot=g,units='in',height=6,width=8.5,dpi=300)  
}
```



```
In [39]: options(repr.plot.height=6,repr.plot.width=7)  
  
set.seed(0)  
g <- ggplot(meta[,sample(nrow(meta),nrow(meta))],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_sample)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_gradient(low=iLISI_low_color,high=iLISI_high_color,limits=c(1,NA)) +  
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +  
  labs(color='Sample\niLISI',x='RNA UMAP1',y='RNA UMAP2')  
print(g)  
  
if(!is.na(save_dir)){  
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiSample',file_extension),  
         plot=g,units='in',height=6,width=7,dpi=300)  
}
```

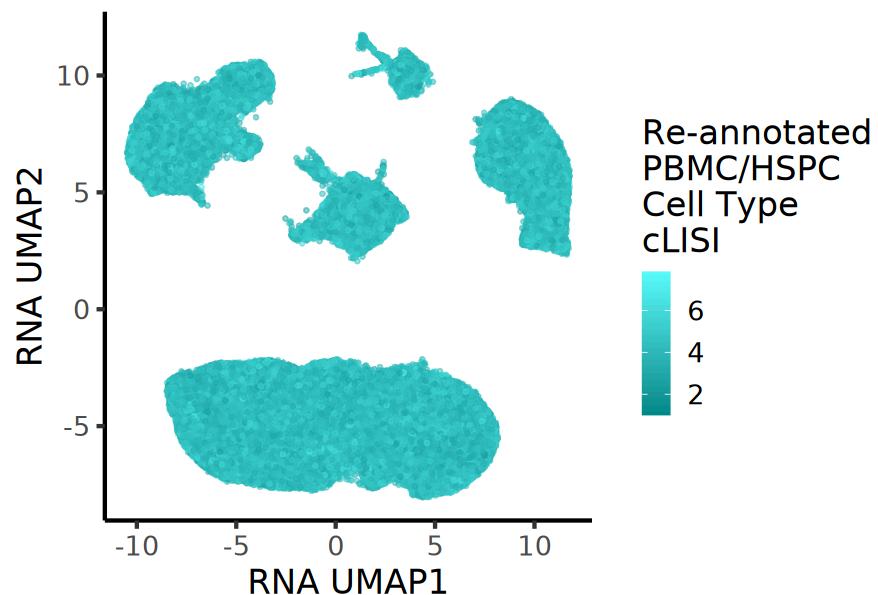


```
In [40]: options(repr.plot.height=6,repr.plot.width=7.5)

g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_cell_type)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=cLISI_low_color,high=cLISI_high_color,limits=c(1,NA)) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color=paste(sep='\n',CT_str,'cLISI'),x='RNA UMAP1',y='RNA UMAP2')
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiCellType',file_extension),
         plot=g,units='in',height=6,width=7.5,dpi=300)
}
```

Dataset 4
(n=30 samples)



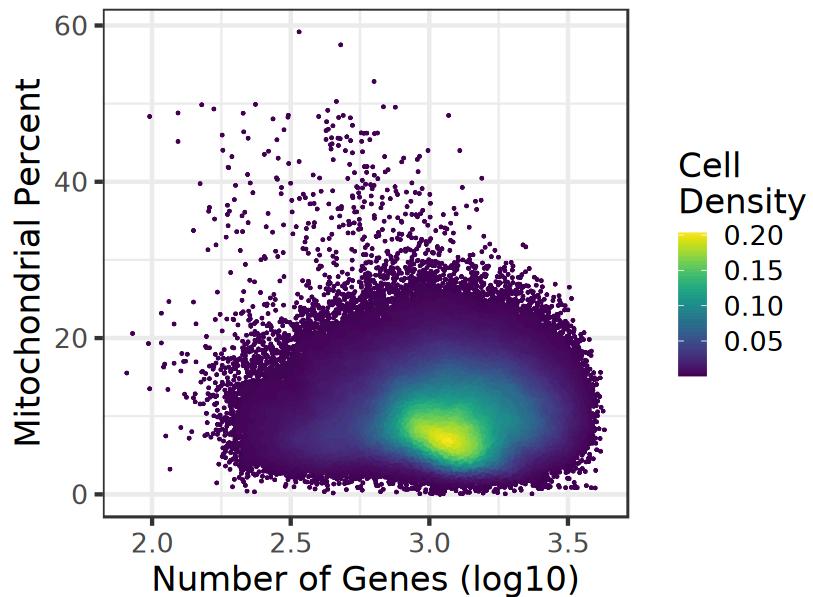
```
In [41]: options(repr.plot.height=6,repr.plot.width=7)

toPlot <- data.frame('log10_nGene'=log10(meta$nGene),'MTperc'=meta$MTperc)
toPlot$density <- get_2D_density(toPlot$log10_nGene,toPlot$MTperc,n=1000)

g <- ggplot(toPlot,aes(x=log10_nGene,y=MTperc,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Genes (log10)',y='Mitochondrial Percent',color='Cell\nDensity',
       title=paste(sep='\n',dataset_str_long,'snRNA-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_RNA_QC',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 4 snRNA-seq QC metrics



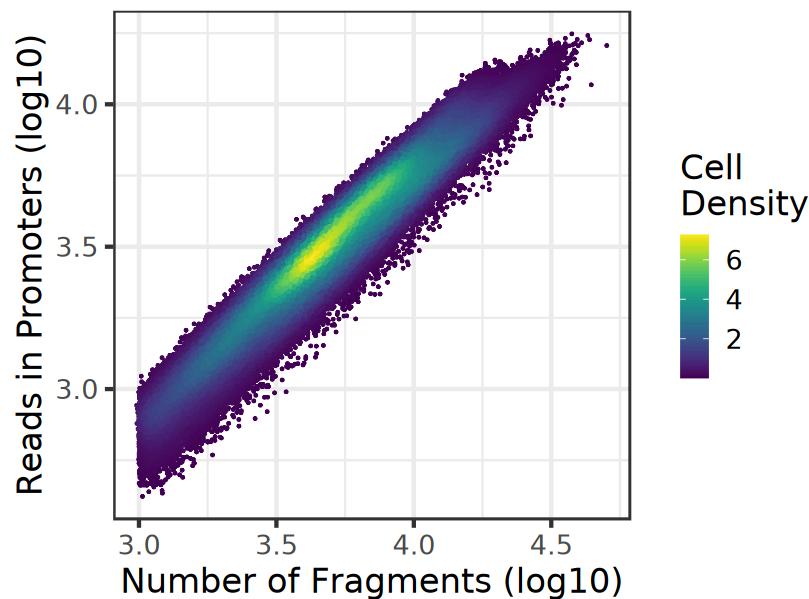
```
In [42]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nFrag'=log10(meta$nFrags), 'log10_Prom'=log10(meta$ReadsInPromoter))
toPlot$density <- get_2D_density(toPlot$log10_nFrag,toPlot$log10_Prom,n=1000)

g <- ggplot(toPlot,aes(x=log10_nFrag,y=log10_Prom,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Fragments (log10)',y='Reads in Promoters (log10)',
       color='Cell\nDensity',title= paste(sep='\n',dataset_str_long,'snATAC-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5)
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ', save_dir,dataset_str, '_ATAC_QC', file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 4 snATAC-seq QC metrics



Dataset 5

```
In [43]: data_dir <- '../data/dataset5/'  
dataset_str <- 'dataset5'  
dataset_str_long <- 'Dataset 5'  
CT_str <- 'Re-annotated\nHSPC Cell States'  
ori_CT_str <- 'HSPC Cell States'  
sample_str <- '(n=30 samples)'  
  
meta <- readRDS(paste(sep=' ', data_dir, dataset_str, '_metadata.rds'))  
gxc_norm <- readRDS(paste(sep=' ', data_dir, dataset_str, '_gxc_norm.rds'))  
gxCT_norm <- readRDS(paste(sep=' ', data_dir, dataset_str, '_gxCT_norm.rds'))  
chosenGenes <- readRDS(paste(sep=' ', data_dir, dataset_str, '_chosenGenes.rds'))
```

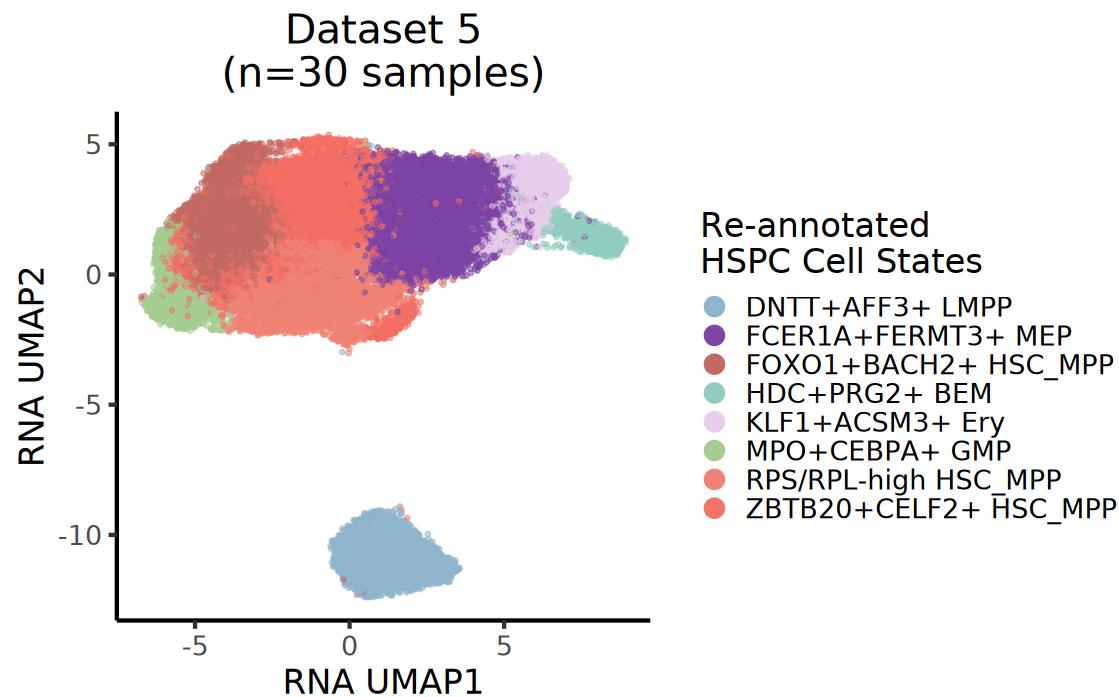
```
In [44]: options(repr.plot.height=6, repr.plot.width=9.5)  
g <- ggplot(meta, aes(x=RNA_UMAP1, y=RNA_UMAP2, color=RNA_cell_state)) +  
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
```

```

    scale_color_manual(values=covid_colors) +
    ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
    labs(color=CT_str,x='RNA UMAP1',y='RNA UMAP2') +
    guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_cellState',file_extension),
         plot=g,units='in',height=6,width=9.5,dpi=300)
}

```



In [45]: `state_order <- c('HSC_MPP-1', 'HSC_MPP-2', 'HSC_MPP-3', 'LMPP', 'MEP', 'Ery', 'BEM', 'GMP')`

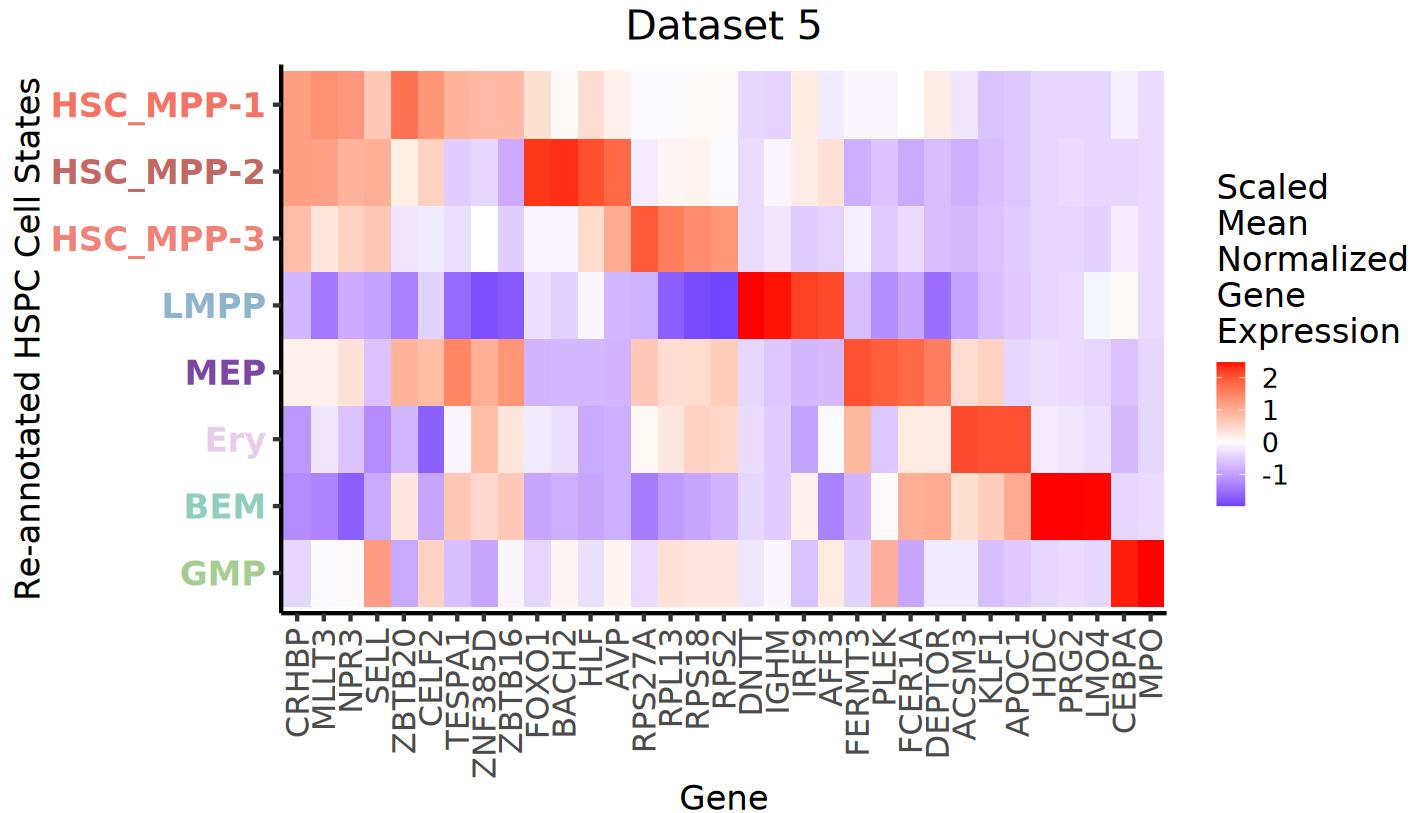
In [46]: `options(repr.plot.height=7,repr.plot.width=12)
g <- pseudobulk_scaled_heatmap(scaleGene_forHeatmap(chosenGenes,state_order,gxCT_norm),
 'Gene',gsub('\n',' ',CT_str),
 'Scaled\nMean\nNormalized\nGene\nExpression',
 plotTit=dataset_str_long,
 clustColors=covid_colors)
g <- g + theme(axis.text.x = element_text(size=19))`

```

print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_markerGeneExp', file_extension),
         plot=g, units='in', height=7, width=12, dpi=300)
}

```



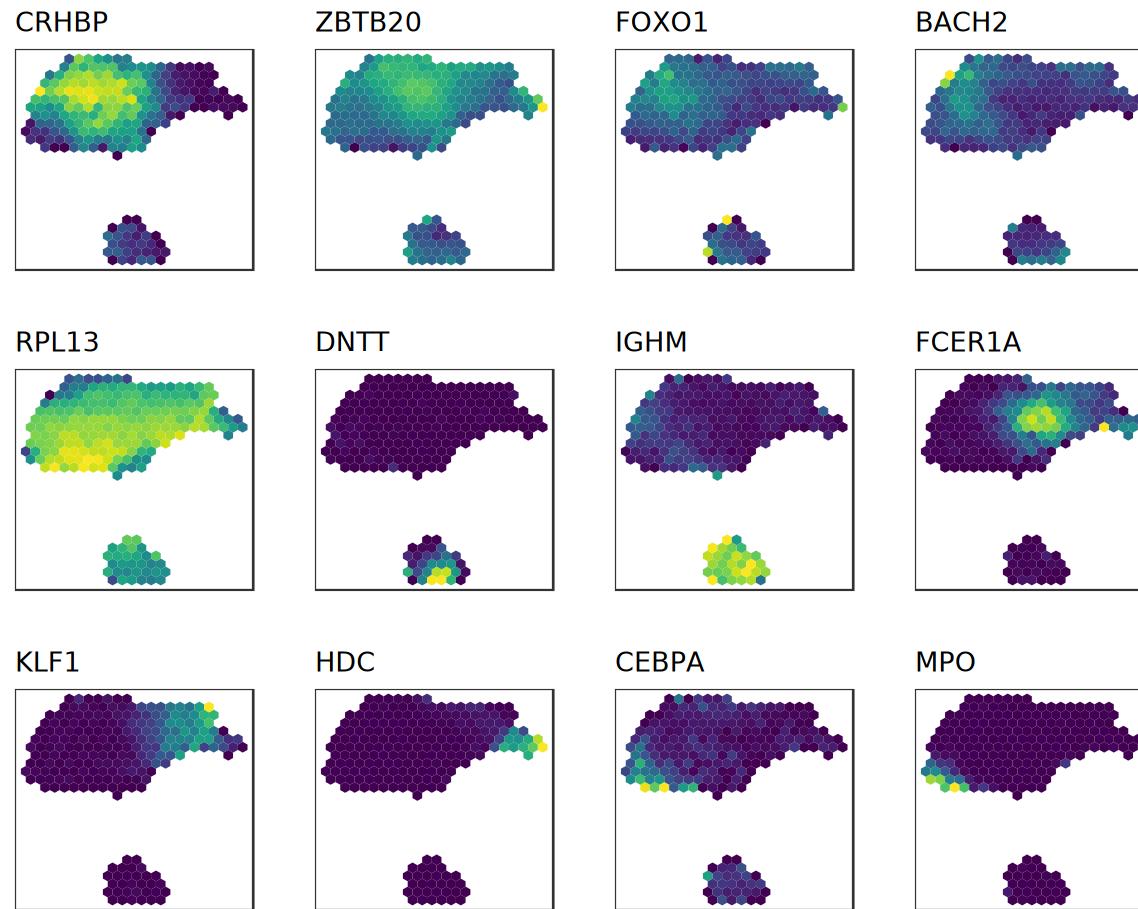
```

In [47]: genes_forUMAPs <- c('CRHBP', 'ZBTB20', 'FOXO1', 'BACH2', 'RPL13', 'DNTT', 'IGHM', 'FCER1A', 'KLF1', 'HDC',
if(!all(genes_forUMAPs %in% chosenGenes)) stop('Genes for UMAP not in chosen genes')

options(repr.plot.height=8, repr.plot.width=10)
g <- plot_markerPeaks_norm_hex_v2(meta, gxc_norm[, rownames(meta)], 'RNA_UMAP1', 'RNA_UMAP2',
                                     plot_genes=genes_forUMAPs, plotCol=4,
                                     titleSize=16, hex_bins=22, cutCap=0)
grid.draw(g)

```

```
if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_markerGeneExp'), file_ex-  
plot=g, units='in', height=8, width=10, dpi=300)
```

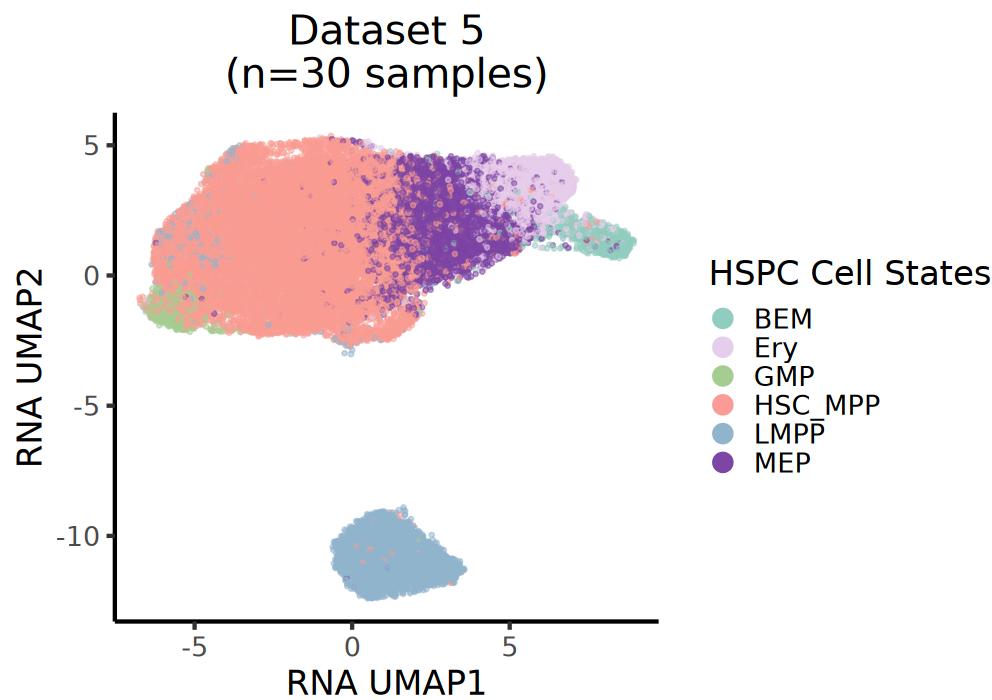


```
In [48]: options(repr.plot.height=6, repr.plot.width=8.5)  
g <- ggplot(meta, aes(x=RNA_UMAP1, y=RNA_UMAP2, color=RNA_ori_cell_state)) +  
  rasterise(geom_point(size=1, alpha=0.5), dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_manual(values=covid_colors) +  
  ggtitle(paste(sep='\n', dataset_str_long, sample_str)) +  
  labs(color=ori_CT_str, x='RNA UMAP1', y='RNA UMAP2') +  
  guides(colour = guide_legend(override.aes = list(size=5, alpha=1)))  
print(g)
```

```

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_UMAP_RNA_color_oriCT', file_extension),
         plot=g, units='in', height=6, width=8.5, dpi=300)
}

```



```

In [49]: fisher_df <- calc_OR(meta, 'RNA_state_abbr', 'RNA_ori_cell_state')

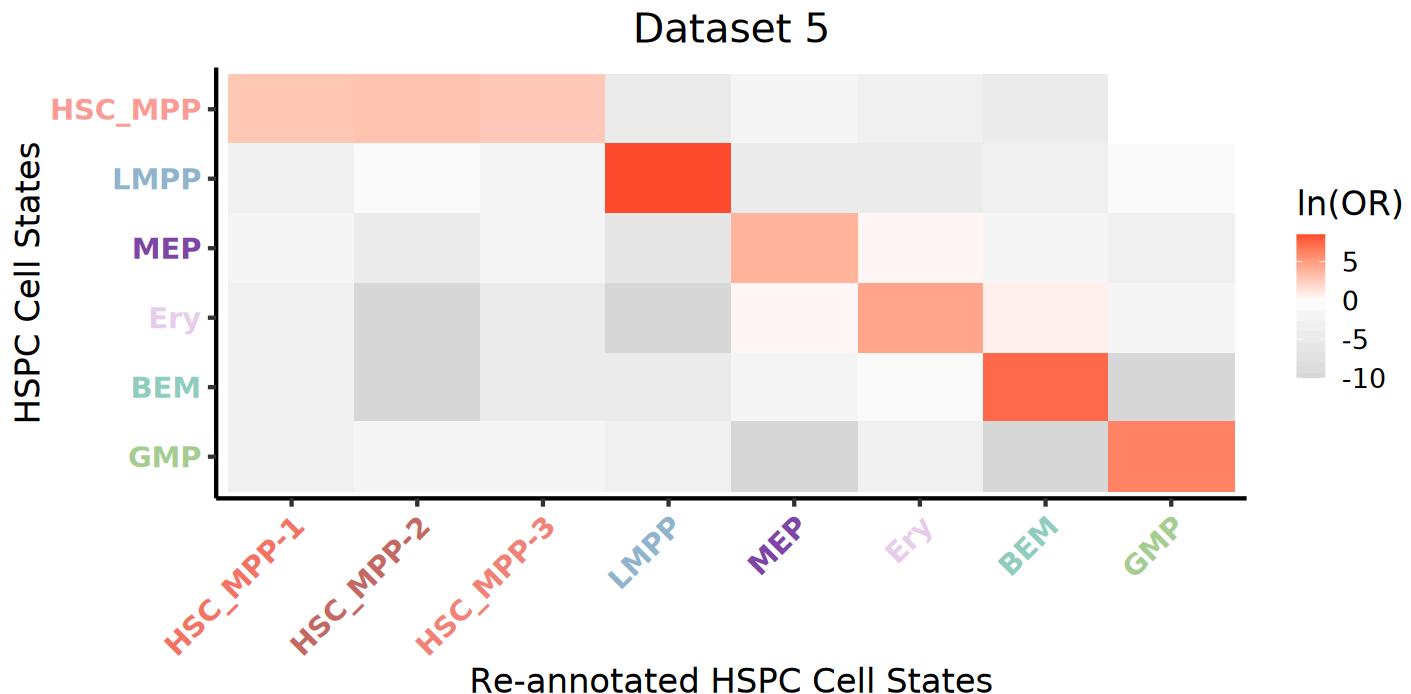
g <- plot_OR(fisher_df, 'RNA_state_abbr', 'RNA_ori_cell_state',
              gsub('\n', ' ', CT_str), gsub('\n', ' ', ori_CT_str),
              state_order, c('HSC_MPP', 'LMPP', 'MEP', 'Ery', 'BEM', 'GMP'),
              clustColors=covid_colors)
g <- g + ggtitle(dataset_str_long) +
      theme(plot.title = element_text(hjust = 0.5),
            axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))

options(repr.plot.height=6, repr.plot.width=12)
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ', save_dir, dataset_str, '_heatmap_oriCTlnOR', file_extension),
         plot=g, units='in', height=6, width=8.5, dpi=300)
}

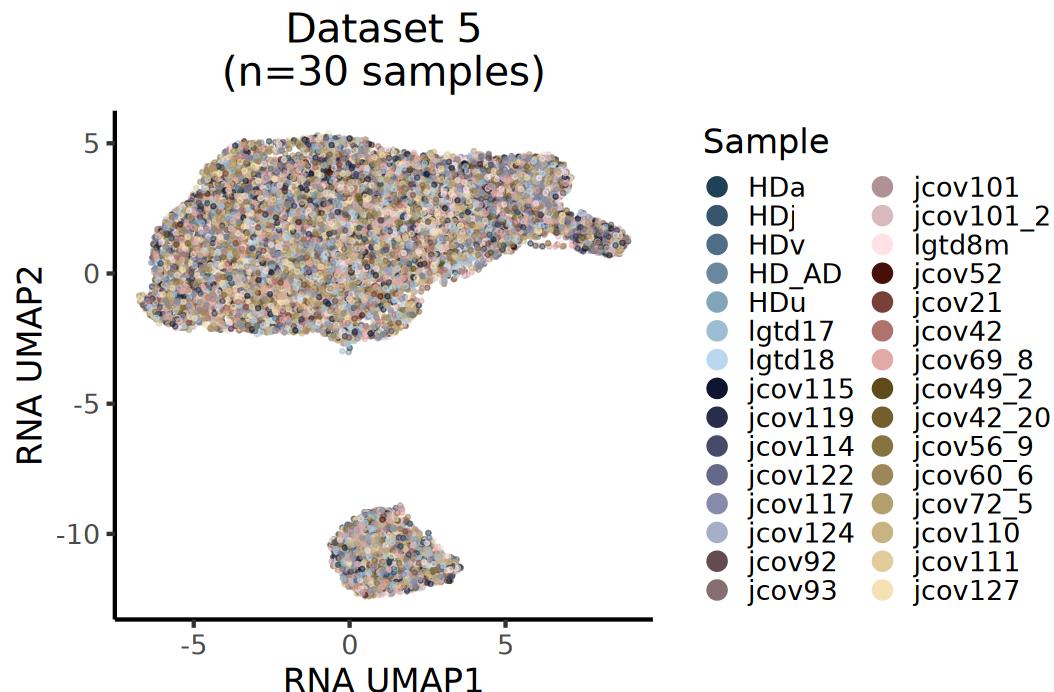
```

```
        plot=g,units='in',height=6,width=12,dpi=300)  
}
```



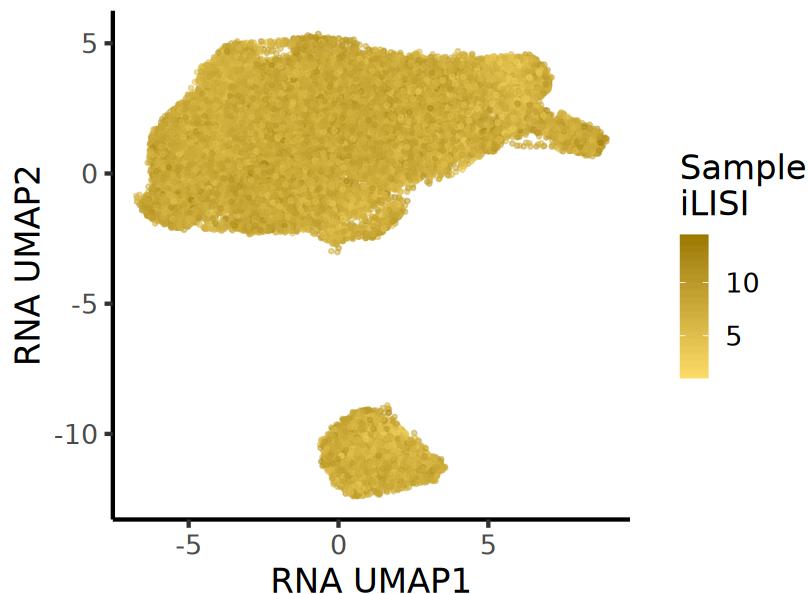
```
In [51]: options(repr.plot.height=6,repr.plot.width=9)  
  
meta$sample_factor <- factor(meta$sample,levels=names(covid_colors))  
  
set.seed(0)  
g <- ggplot(meta[,sample(nrow(meta),nrow(meta)),],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=sample_factor)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_manual(values=covid_colors) +  
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +  
  labs(color='Sample',x='RNA UMAP1',y='RNA UMAP2') +  
  guides(colour = guide_legend(override.aes = list(size=5,alpha=1)))  
print(g)  
  
if(!is.na(save_dir)){  
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_sample',file_extension),
```

```
    plot=g,units='in',height=6,width=9,dpi=300)  
}
```



```
In [52]: options(repr.plot.height=6,repr.plot.width=7)  
  
set.seed(0)  
g <- ggplot(meta[,sample(nrow(meta),nrow(meta))],aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_sample)) +  
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +  
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +  
  scale_color_gradient(low=iLISI_low_color,high=iLISI_high_color,limits=c(1,NA)) +  
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +  
  labs(color='Sample\niLISI',x='RNA UMAP1',y='RNA UMAP2')  
print(g)  
  
if(!is.na(save_dir)){  
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiSample',file_extension),  
         plot=g,units='in',height=6,width=7,dpi=300)  
}
```

Dataset 5
(n=30 samples)

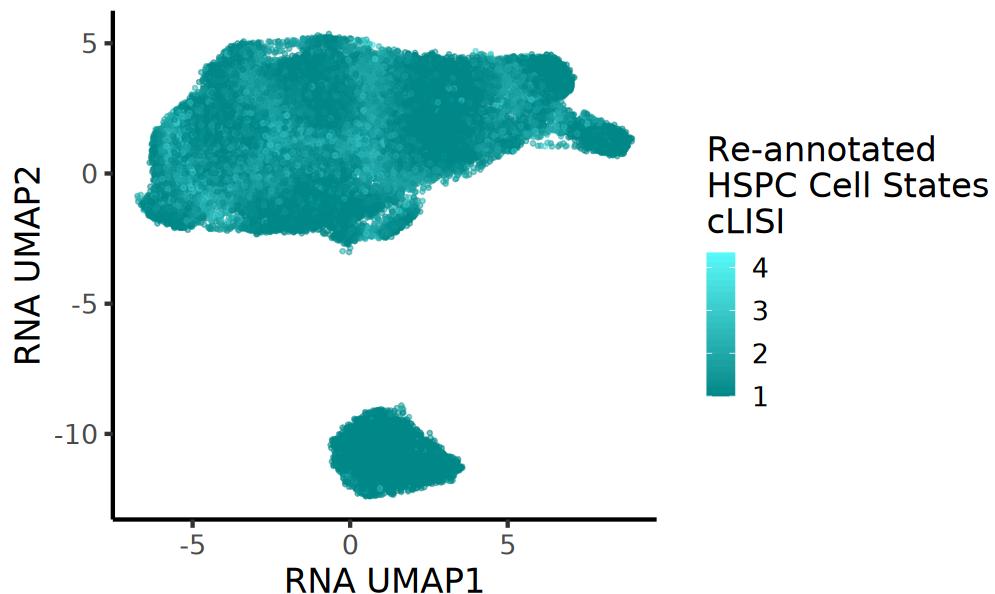


```
In [53]: options(repr.plot.height=6,repr.plot.width=8.5)

g <- ggplot(meta,aes(x=RNA_UMAP1,y=RNA_UMAP2,color=lisi_cell_state)) +
  rasterise(geom_point(size=1,alpha=0.5),dpi=300) +
  theme_classic(base_size=20) + theme(plot.title = element_text(hjust = 0.5)) +
  scale_color_gradient(low=cLISI_low_color,high=cLISI_high_color,limits=c(1,NA)) +
  ggtitle(paste(sep='\n',dataset_str_long,sample_str)) +
  labs(color=paste(sep='\n',CT_str,'cLISI'),x='RNA UMAP1',y='RNA UMAP2')
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_UMAP_RNA_color_lisiCellType',file_extension),
         plot=g,units='in',height=6,width=8.5,dpi=300)
}
```

Dataset 5
(n=30 samples)



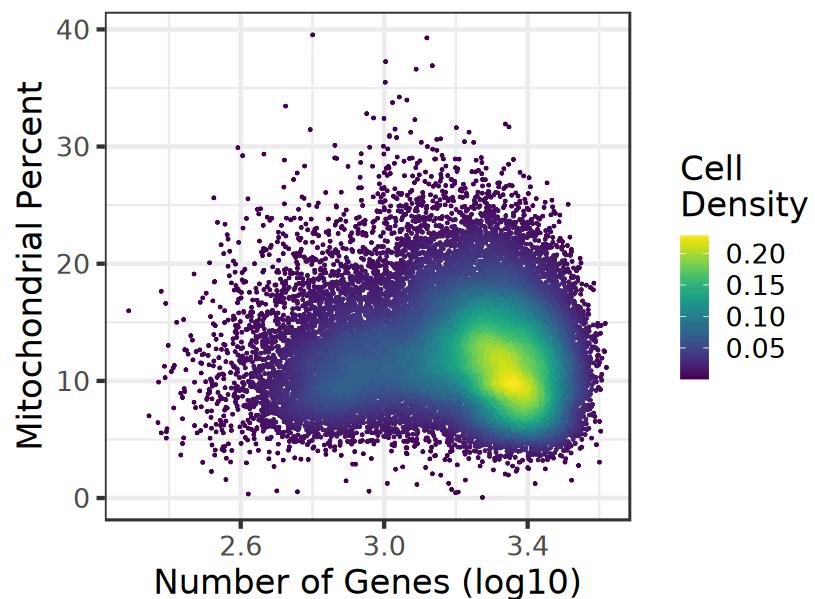
```
In [54]: options(repr.plot.height=6,repr.plot.width=7)

toPlot <- data.frame('log10_nGene'=log10(meta$nGene),'MTperc'=meta$MTperc)
toPlot$density <- get_2D_density(toPlot$log10_nGene,toPlot$MTperc,n=1000)

g <- ggplot(toPlot,aes(x=log10_nGene,y=MTperc,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Genes (log10)',y='Mitochondrial Percent',color='Cell\nDensity',
       title=paste(sep='\n',dataset_str_long,'snRNA-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5))
print(g)

if(!is.na(save_dir)){
  ggsave(file=paste(sep=' ',save_dir,dataset_str,'_RNA_QC',file_extension),
         plot=g,units='in',height=6,width=7,dpi=300)
}
```

Dataset 5 snRNA-seq QC metrics



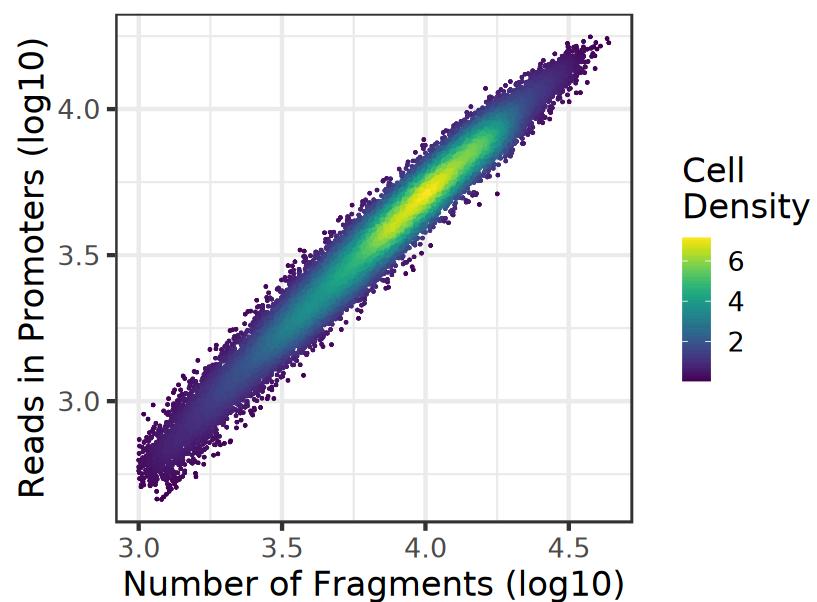
```
In [55]: options(repr.plot.height=6, repr.plot.width=7)

toPlot <- data.frame('log10_nFrag'=log10(meta$nFrags), 'log10_Prom'=log10(meta$ReadsInPromoter))
toPlot$density <- get_2D_density(toPlot$log10_nFrag,toPlot$log10_Prom,n=1000)

g <- ggplot(toPlot,aes(x=log10_nFrag,y=log10_Prom,color=density)) +
  rasterise(geom_point(size=0.5),dpi=300) +
  labs(x='Number of Fragments (log10)',y='Reads in Promoters (log10)',
       color='Cell\nDensity',title= paste(sep='\n',dataset_str_long,'snATAC-seq QC metrics')) +
  scale_color_viridis() + theme_bw(base_size = 20) + theme(plot.title = element_text(hjust = 0.5)
print(g)

if(!is.na(save_dir)){
  ggsave(file= paste(sep=' ', save_dir, dataset_str, '_ATAC_QC', file_extension),
         plot=g, units='in', height=6, width=7, dpi=300)
}
```

Dataset 5
snATAC-seq QC metrics



Session Info

```
In [57]: sessionInfo()
```

```
R version 4.3.3 (2024-02-29)
Platform: x86_64-conda-linux-gnu (64-bit)
Running under: CentOS Linux 7 (Core)

Matrix products: default
BLAS/LAPACK: /PHShome/kew47/miniconda3/envs/integrateATAC/lib/libopenblas-p0.3.27.so; LAPACK version 3.1
2.0

locale:
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8       LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

time zone: America/New_York
tzcode source: system (glibc)

attached base packages:
[1] grid      stats     graphics grDevices utils      datasets methods
[8] base

other attached packages:
[1] repr_1.1.7      gridExtra_2.3    RColorBrewer_1.1-3 scales_1.3.0
[5] viridis_0.6.5   viridisLite_0.4.2  ggrepel_0.9.5    ggrastr_1.0.2
[9] tidyverse_1.3.1  stringr_1.5.1    ggpubr_0.6.0    ggplot2_3.5.1
[13] presto_1.0.0    data.table_1.15.4  Rcpp_1.0.13     Rmisc_1.5.1
[17] plyr_1.8.9      lattice_0.22-6    gtools_3.9.5    Matrix_1.6-5

loaded via a namespace (and not attached):
[1] utf8_1.2.4        generics_0.1.3    rstatix_0.7.2   stringi_1.8.4
[5] digest_0.6.37     magrittr_2.0.3    evaluate_0.24.0  pbdZMQ_0.3-11
[9] fastmap_1.2.0     jsonlite_1.8.8    backports_1.5.0  purrr_1.0.2
[13] fansi_1.0.6      textshaping_0.4.0  abind_1.4-5    cli_3.6.3
[17] rlang_1.1.4      crayon_1.5.3    munsell_0.5.1   base64enc_0.1-3
[21] withr_3.0.1      ggbeeswarm_0.7.2  tools_4.3.3    uuid_1.2-1
[25] ggsignif_0.6.4    dplyr_1.1.4    colorspace_2.1-1 broom_1.0.6
[29] IRdisplay_1.1     vctrs_0.6.5    R6_2.5.1      lifecycle_1.0.4
[33] car_3.1-2        MASS_7.3-60.0.1  vipor_0.4.7    ragg_1.3.2
[37] pkgconfig_2.0.3   beeswarm_0.4.0   hexbin_1.28.3   pillar_1.9.0
[41] gtable_0.3.5     glue_1.7.0     systemfonts_1.1.0 tibble_3.2.1
```

```
[45] tidyselect_1.2.1    IRkernel_1.3.2      farver_2.1.2       htmltools_0.5.8.1
[49] labeling_0.4.3     carData_3.0-5      Cairo_1.6-2        compiler_4.3.3
```

In []: