

Myeloid figures

inputs

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

```
In [2]: CT <- 'myeloid'
CT_label <- 'myeloid'
data_prefix <- paste(sep='', '../data/', CT, '/', CT)
ATAC_meta <- readRDS(paste(sep='', data_prefix, '_ATAC_meta.rds'))
chosenPeaks <- readRDS(paste(sep='', data_prefix, '_chosenPeaks.rds'))
snATAC_pxc_norm <- readRDS(paste(sep='', data_prefix, '_snATAC_pxc_norm.rds'))
snRNA_gxc_norm <- readRDS(paste(sep='', data_prefix, '_snRNA_gxc_norm.rds'))
snATAC_pxCT_norm <- readRDS(paste(sep='', data_prefix, '_snATAC_pxCT_norm.rds'))
snRNA_gxCT_norm <- readRDS(paste(sep='', data_prefix, '_snRNA_gxCT_norm.rds'))
chromVARz_mat <- readRDS(paste(sep='', data_prefix, '_ArchR_chromVARz_JASP
AR2020.rds'))
ArchR_padj <- readRDS(paste(sep='', data_prefix, '_ArchR_padj_JASPAR2020.rds'))
CITE_meta <- readRDS(paste(sep='', data_prefix, '_CITE_meta.rds'))
class_state_df <- readRDS(paste(sep='', data_prefix, '_class_state_df.rds'))
LDA_res <- readRDS(paste(sep='', data_prefix, '_LDA_stats.rds'))
other_resol <- readRDS(paste(sep='', data_prefix, '_ATAC_otherRes.rds'))
CNA_LD <- readRDS(paste(sep='', data_prefix, '_CNA_lymphoidDensity.rds'))
```

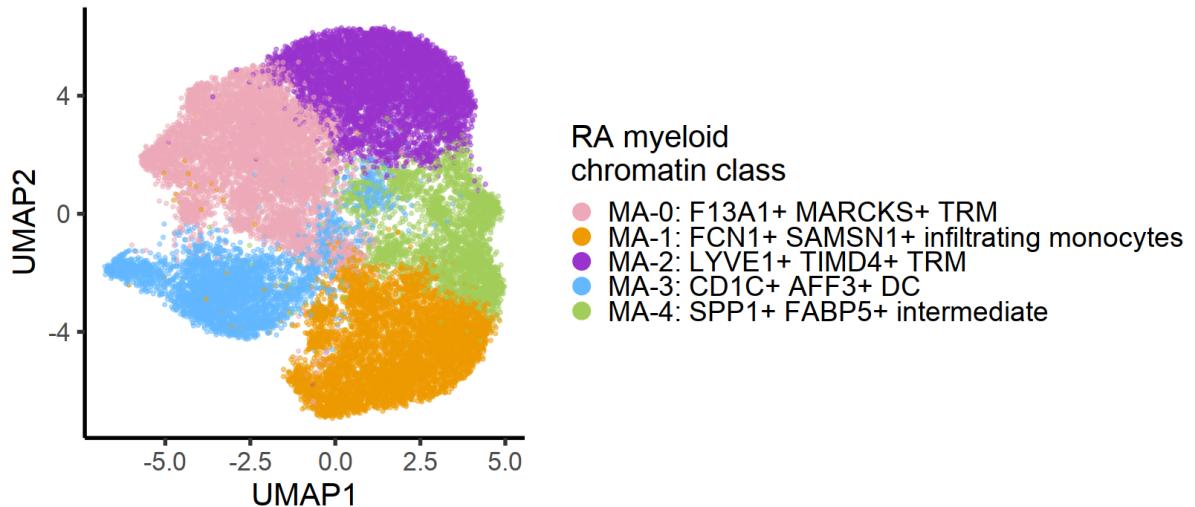
```
In [3]: ATAC_colors <- readRDS('../data/misc/ATAC_class_colors.rds')
CITE_colors <- readRDS('../data/misc/CITE_state_colors.rds')
ATAC_CITE_conv_df <- readRDS('../data/misc/ATAC_CITE_sample_conversion.rds')
```

```
In [26]: save_dir <- NA #'../output/' #or NA if don't want to save
```

ATAC classes

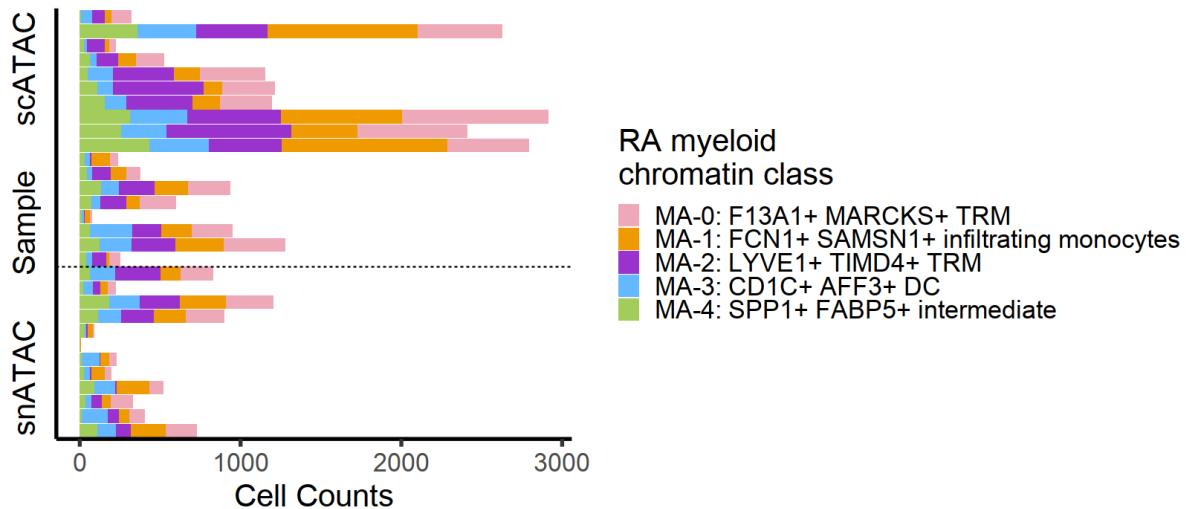
```
In [5]: #Fig 4a
options(repr.plot.height=6,repr.plot.width=13.5)
g <- ggplot(ATAC_meta,aes_string(x='UMAP1',y='UMAP2',color='cluster_name'))
  + geom_point(size=1,alpha=0.5) +
    theme_classic(base_size=25) + scale_color_manual(values=ATAC_colors) +
    labs(color= paste(sep=' ', 'RA ',CT_label,' \n chromatin class')) +
    theme(legend.text=element_text(size=22)) +
    guides(colour = guide_legend(override.aes = list(size=6,alpha=1)))
print(g)

if(!is.na(save_dir)) ggsave(file= paste(sep=' ', save_dir,CT, '_ATAC_class_UMAP.png'),
                           plot=g,units='in',height=6,width=13.5,dpi=600)
```



```
In [6]: #Fig S4a
options(repr.plot.height=6,repr.plot.width=13.5)
g <- cellCount_bySample_barPlot(ATAC_meta,'sample','cluster_name',
                                 paste(sep=' ', 'RA ',CT_label,'\\nchromatin
class'),ATAC_colors)
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir,CT,'_ATAC_class_c
ellCount.png'),
                           plot=g,units='in',height=6,width=13.5,dpi=60
0)
```



ATAC cluster markers

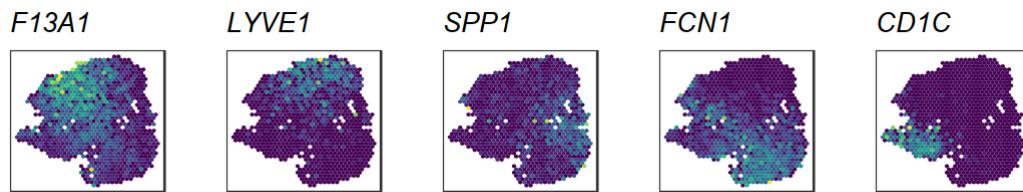
```
In [7]: chosenGenes <- names(chosenPeaks)
chosenPeaks <- chosenPeaks[!is.na(chosenPeaks)] #NA means no peak in gen
e's promoter
```

```
In [8]: #Fig 4b bottom
```

```
genes_forUMAPS <- c('F13A1', 'LYVE1', 'SPP1', 'FCN1', 'CD1C')
if(!all(genes_forUMAPS %in% names(chosenPeaks))) stop('Genes for UMAP not in chosen genes')

multiome_cells <- rownames(ATAC_meta[which(ATAC_meta$assay=='snATAC'),])

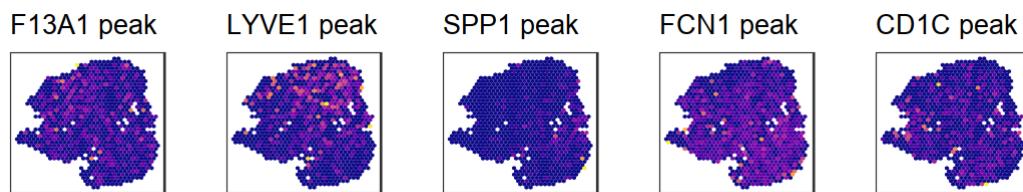
options(repr.plot.height=2,repr.plot.width=9)
g <- plot_markerPeaks_norm_hex_v2(ATAC_meta[multiome_cells],snRNA_gxc_norm[genes_forUMAPS,multiome_cells],'UMAP1','UMAP2',
                                     plot_genes=genes_forUMAPS,plotCol=length(genes_forUMAPS),
                                     titleSize=16,hex_bins=34,cutCap=0)
grid.draw(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_markerGene_U
MAP.png'),
                             plot=g,units='in',height=2,width=9,dpi=600)
```



```
In [9]: #Fig 4b top
```

```
toPlot <- snATAC_pxc_norm[unname(chosenPeaks[genes_forUMAPS]),multiome_c
ells]
rownames(toPlot) <- paste(sep=' ',names(chosenPeaks[genes_forUMAPS]),' pe
ak')

options(repr.plot.height=2,repr.plot.width=9)
g <- plot_markerPeaks_norm_hex_v2(ATAC_meta[multiome_cells],toPlot,'UMA
P1','UMAP2',
                                     plot_genes=rownames(toPlot),plotCol=nr
ow(toPlot),titleSize=16,hex_bins=34,cutCap=0,
                                     titleFace='plain',colorOpt='plasma')
grid.draw(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_markerPeak_U
MAP.png'),
                             plot=g,units='in',height=2,width=9,dpi=600)
```



```
In [10]: class_order <- c('MA-0', 'MA-2', 'MA-4', 'MA-1', 'MA-3')  
all(class_order %in% ATAC_meta$cluster_abbr)
```

TRUE

In [11]: #Fig S4b

```
res <- scaleFeat_forHeatmap(chosenGenes,class_order,chosenPeaks,snRNA_gx
CT_norm,snATAC_pxCT_norm)
snRNA_gxCT_norm_subset_scaled <- res$gxCT_norm_subset_scaled
snATAC_pxCT_norm_subset_scaled <- res$pxCT_norm_subset_scaled
fxCT_norm_subset_scaled <- res$fxCT_norm_subset_scaled

scale_lim <- max(abs(snRNA_gxCT_norm_subset_scaled),abs(snATAC_pxCT_norm
_subset_scaled),na.rm=TRUE)

options(repr.plot.height=7,repr.plot.width=9)
g <- pseudobulk_scaled_heatmap(snRNA_gxCT_norm_subset_scaled,'Gene',pas
t e('RA',CT_label,'chromatin class'),
                                'Scaled\nMean\nNormalized\nGene\nExpressi
on',
                                plotTit=paste('Scaled Mean Normalized Gen
e Expression\nof multiome cells by RA',
                                CT_label,'chromatin classe
s'),
                                scale_lim=scale_lim,clustColors=ATAC_col
rs)
print(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_markerGene_h
eatmap.png'),
                                plot=g,units='in',height=7,width=9,dpi=600)

g <- pseudobulk_scaled_heatmap(snATAC_pxCT_norm_subset_scaled,'Peak',pas
t e('RA',CT_label,'chromatin class'),
                                'Scaled\nMean\nNormalized\nPeak\nAccessib
ility',
                                plotTit=paste('Scaled Mean Normalized Pea
k Accessibility\nof multiome cells by RA',
                                CT_label,'chromatin classe
s'),
                                scale_lim=scale_lim,clustColors=ATAC_col
rs)
print(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_markerPeak_h
eatmap.png'),
                                plot=g,units='in',height=7,width=9,dpi=600)

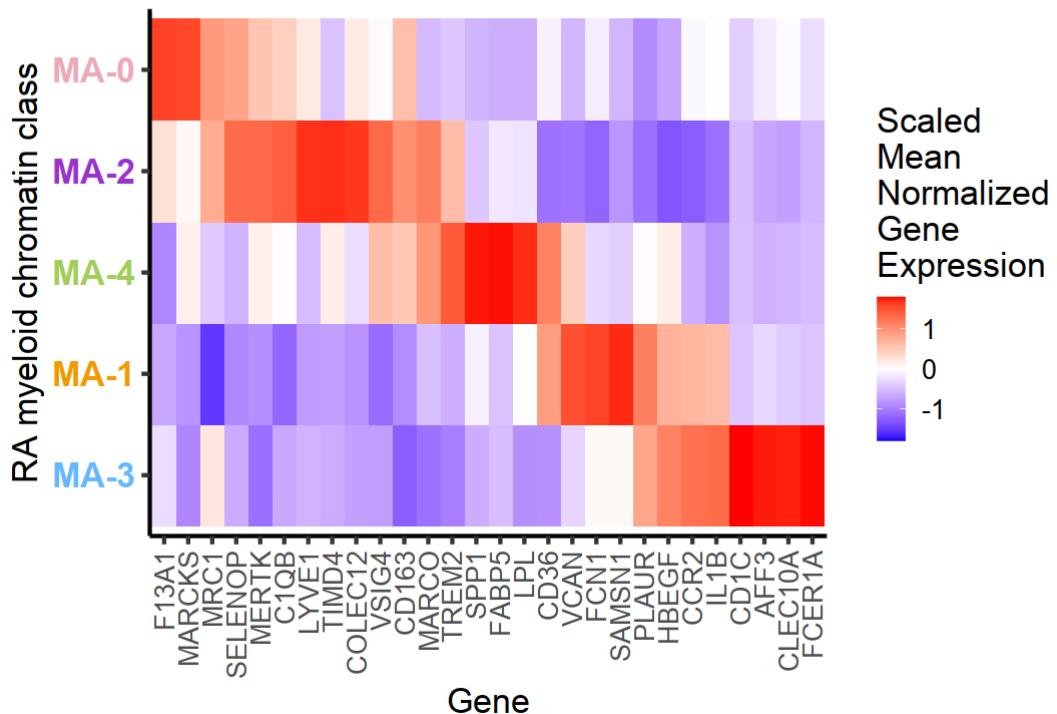
pearR <- cor.test(fxCT_norm_subset_scaled$gene_norm_scale,fxCT_norm_sub
set_scaled$peak_norm_scale,
                  method='pearson')

fxCT_norm_subset_scaled$label <- ''
fxCT_norm_subset_scaled[which(fxCT_norm_subset_scaled$gene=='CLEC10A' &
fxCT_norm_subset_scaled$cluster_abbr=='MA-3'),
                      'label'] <- 'CLEC10A'
fxCT_norm_subset_scaled[which(fxCT_norm_subset_scaled$gene=='HBEGF' & fx
CT_norm_subset_scaled$cluster_abbr=='MA-0'),
                      'label'] <- 'HBEGF'

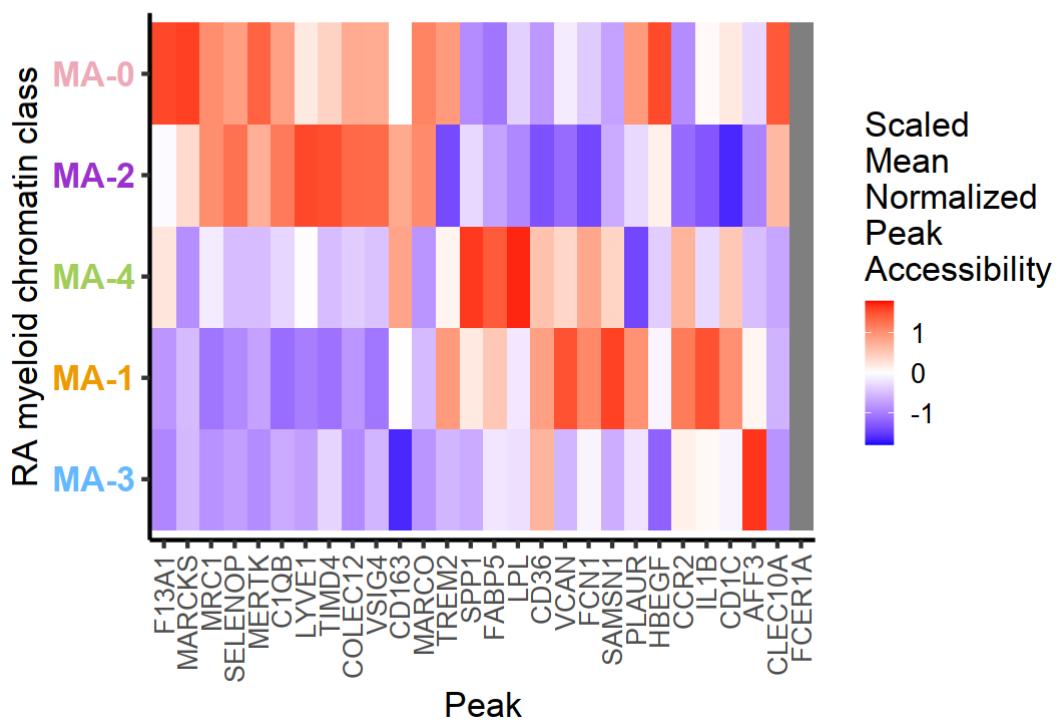
g <- ggplot(fxCT_norm_subset_scaled,
            aes_string(x='gene_norm_scale',y='peak_norm_scale',color='cl
```

```
uster_abbr',label='label')) +
    geom_point(size=2) + theme_classic(base_size=25) + scale_color_manual(values=ATAC_colors) +
    labs(x='Scaled Mean Normalized\nGene Expression',
         y='Scaled Mean Normalized\nPeak Accessibility',
         color=paste(sep=' ', 'RA ',CT_label,'\\nchromatin\\nclass')) +
    geom_abline(slope=1,intercept=0,linetype='dashed') +
    ggtitle(paste(sep=' ', 'R=',round(pearR$estimate,2),' p-value=',signif(pearR$p.value,3))) +
    theme(plot.title=element_text(hjust = 0.5)) + geom_text_repel(bo
x.padding = 0.5,size=6.5,fontface='bold',seed=0)
suppressWarnings(print(g)) #points excluded if peak does not exist
if(!is.na(save_dir)) suppressWarnings(ggsave(file=paste(sep=' ',save_dir,
CT,'_markerGenePeak_scatterplot.png'),
plot=g,units='in',height=7,
width=9,dpi=600))
```

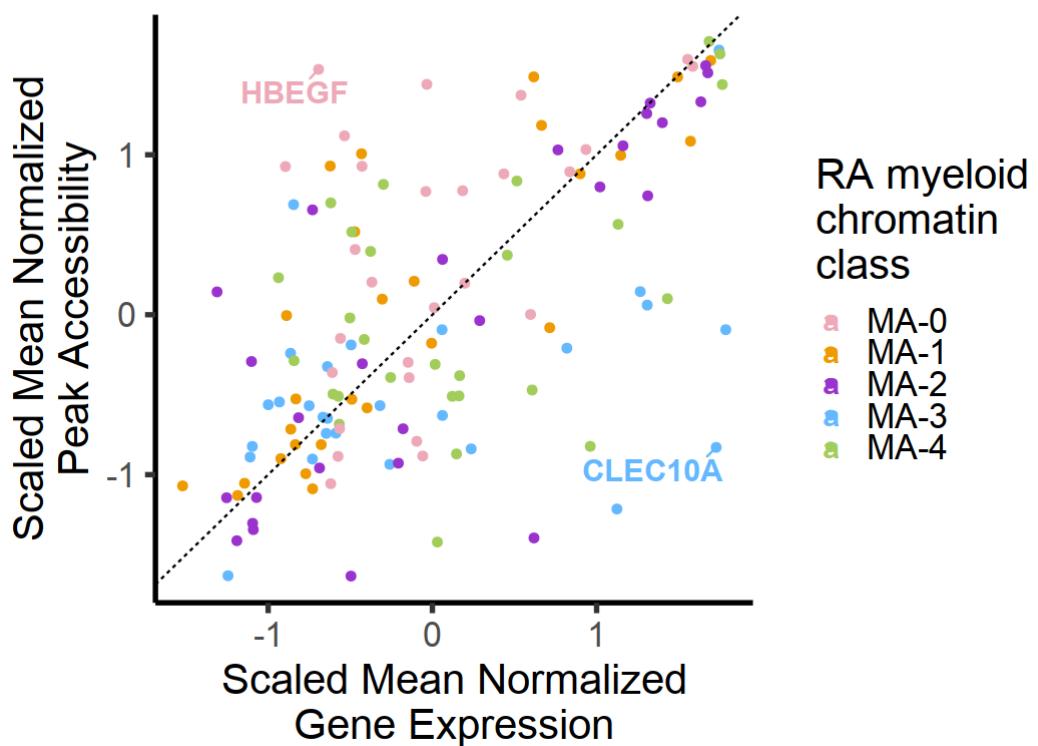
Scaled Mean Normalized Gene Expression of multiome cells by RA myeloid chromatin classes



Scaled Mean Normalized Peak Accessibility of multiome cells by RA myeloid chromatin classes



$R=0.61$ p-value=3.66e-15



TFs

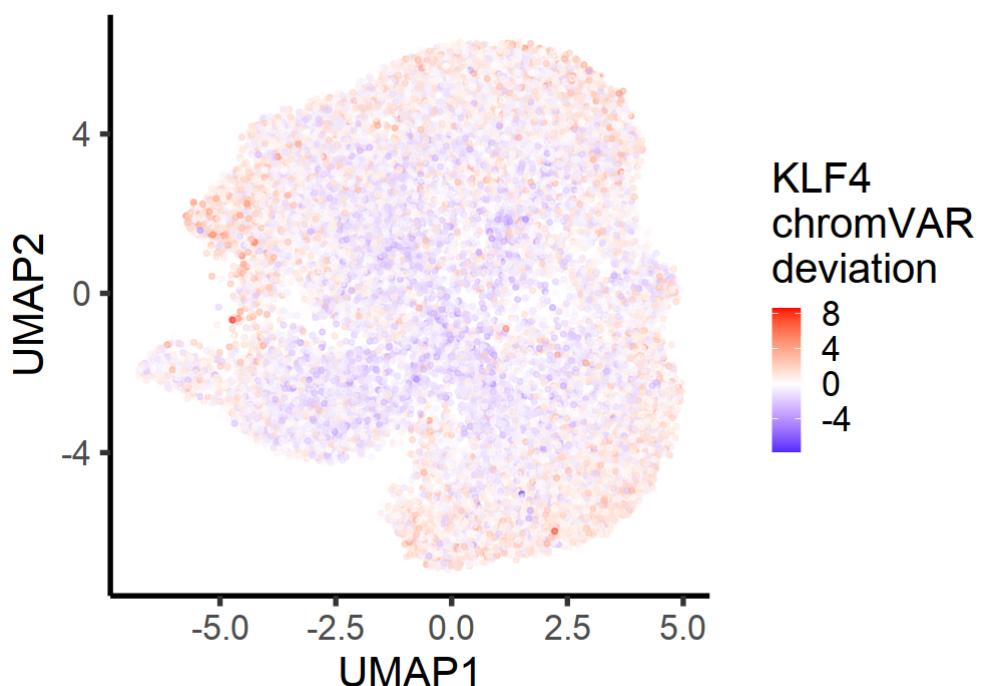
In [12]: #Fig 4c left

```
#fix cell names
split1 <- str_split_fixed(colnames(chromVARz_mat), '#', 2)
new_colnames <- paste(sep = ' ', split1[, 1], '_', str_split_fixed(split1[, 2], '-'), 2)[, 1])
if (!identical(sort(new_colnames), sort(rownames(ATAC_meta)))) stop('cell names not consistent b/t ATAC_meta and chromVAR')
colnames(chromVARz_mat) <- new_colnames

motif_toPlot <- 'KLF4_587'
toPlot <- cbind(ATAC_meta, 'motif'=chromVARz_mat[motif_toPlot, rownames(ATAC_meta)])

options(repr.plot.height=6,repr.plot.width=8.5)
g <- ggplot(toPlot,aes_string(x='UMAP1',y='UMAP2',color='motif')) + geom_point(size=1,alpha=0.5) +
  theme_classic(base_size=25) + scale_color_gradient2(low='blue', mid='white', high='red', midpoint=0) +
  labs(color= paste(sep = ' ', str_split_fixed(motif_toPlot, '_', 2)[, 1], '\nchromVAR\ndeviation'))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep = ' ', save_dir, CT, '_motif_', motif_toPlot, '_UMAP.png'),
                           plot=g, units='in', height=6, width=8.5, dpi=600)
```



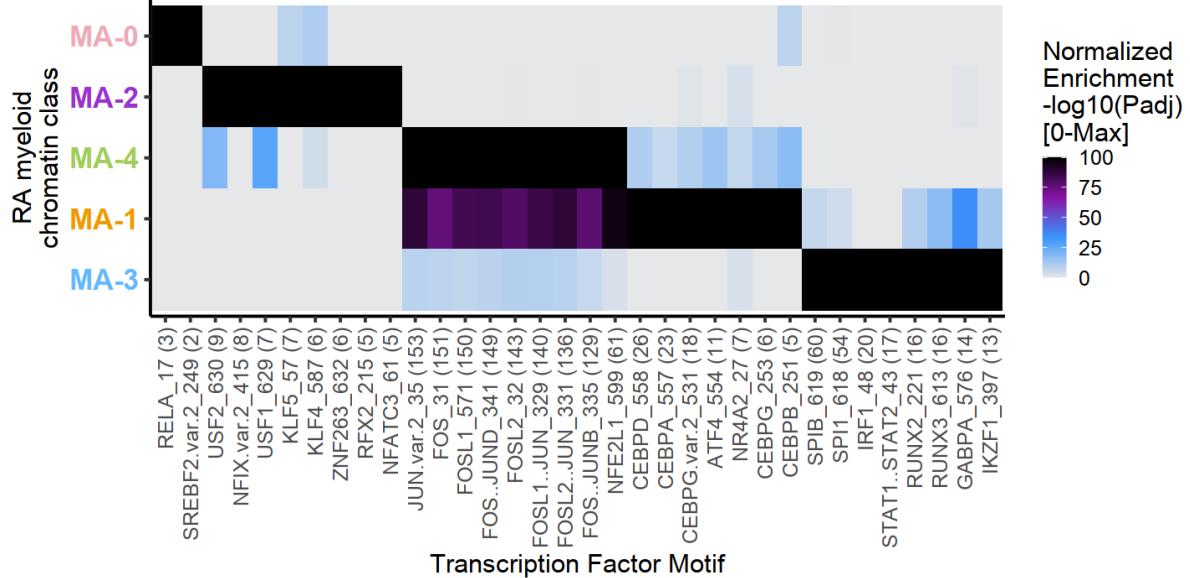
In [13]: #Fig 4c right

```
#add hyphen back
if(!identical(sort(colnames(ArchR_padj)),sort(colnames(snRNA_gxCT_norm))) &
  all(str_detect(colnames(ArchR_padj),'^[a-zA-Z]{2}[0-9]+$'))){
  colnames(ArchR_padj) <- lapply(colnames(ArchR_padj),FUN=function(s)
  {paste(sep=' ',substr(s,1,2),'-' ,
  substr(s,3,nchar(s)))})
}

if(!identical(sort(colnames(ArchR_padj)),
  sort(colnames(snRNA_gxCT_norm)))) stop('mxCT and gxCT matrices do not have same CT.')

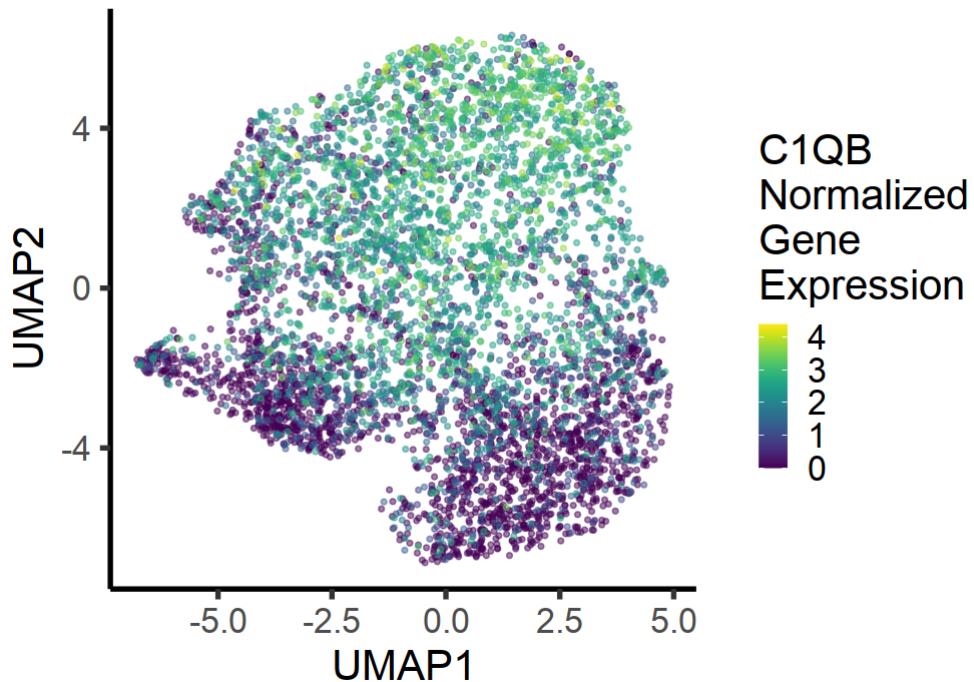
options(repr.plot.height=6,repr.plot.width=12)
g <- ArchR_topMotifs_KWspin(ArchR_padj,snRNA_gxCT_norm,cOrd=class_order,
cColors=ATAC_colors,
minE=2,num_mot=8,minGE=0.05,withinE=0.95,
mLab='Transcription Factor Motif',cLab=paste
(sep=' ', 'RA ',CT_label,' \nchromatin class'))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_motif_heatmap.png'),
plot=g,units='in',height=6,width=12,dpi=600)
```



```
In [14]: #Fig 4d left
```

```
gene_toPlot <- 'C1QB'  
toPlot <- cbind(ATAC_meta[multiome_cells,], 'gene'=snRNA_gxc_norm[gene_to  
Plot,multiome_cells])  
  
options(repr.plot.height=6,repr.plot.width=8.5)  
g <- ggplot(toPlot[order(toPlot$gene),],aes_string(x='UMAP1',y='UMAP2',c  
olor='gene')) +  
    geom_point(size=1,alpha=0.5) +  
    theme_classic(base_size=25) + scale_color_viridis(option  
= 'viridis') +  
    labs(color=paste(sep=' ',gene_toPlot,'\\nNormalized\\nGene  
\\nExpression'))  
print(g)  
  
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_gene_',gene_  
toPlot,'_UMAP.png'),  
                           plot=g,units='in',height=6,width=8.5,dpi=60  
0)
```

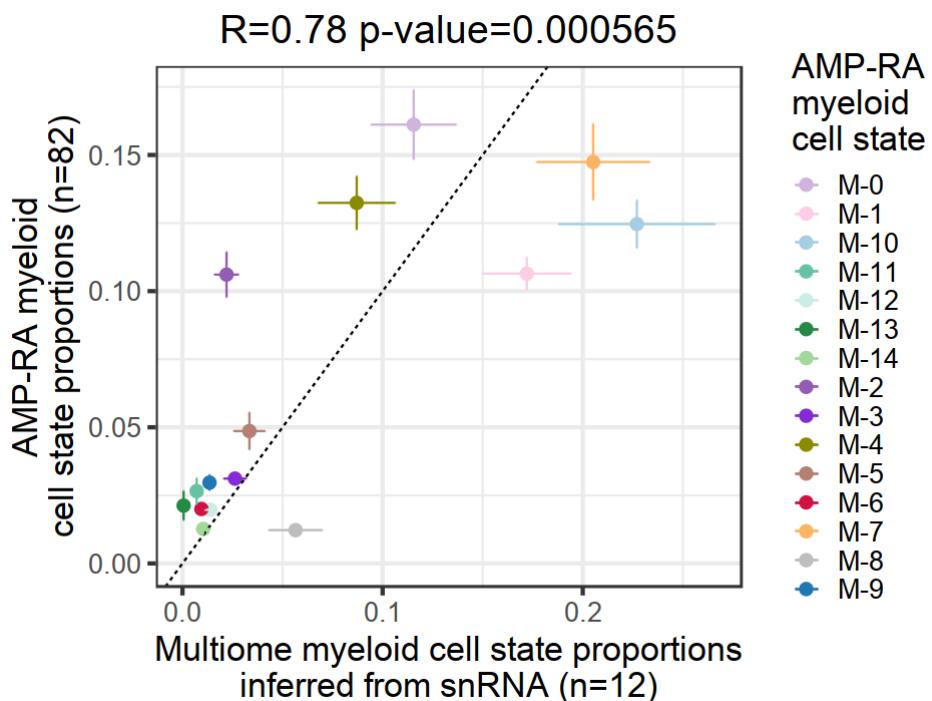


Transcriptional Cell States

In [15]: #Fig S8c

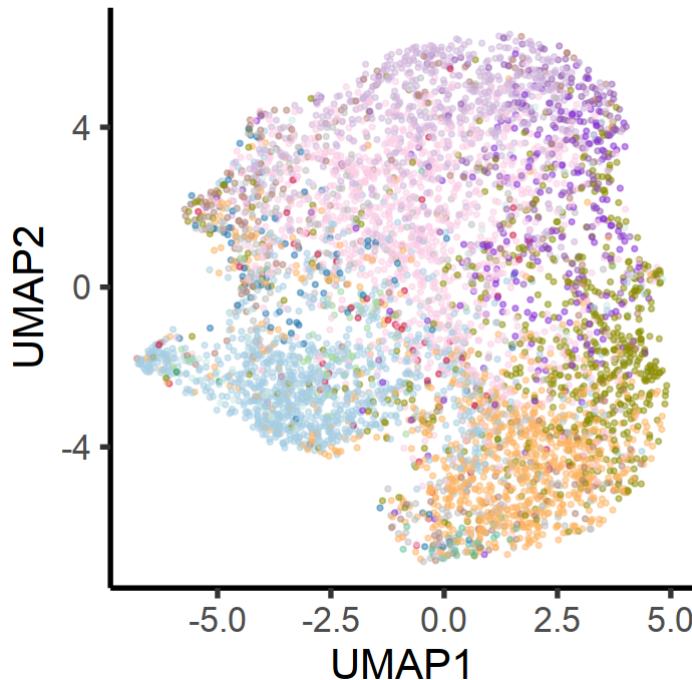
```
options(repr.plot.height=6,repr.plot.width=8)
g <- symp_prop_df(ATAC_meta[multiome_cells],CITE_meta,
                   paste(sep=' ', 'Multiome ',CT_label,' cell state proportions\ninferred from snRNA (n=',
                          length(unique(ATAC_meta[multiome_cells,'sample'])),')'),
                   paste(sep=' ', 'AMP-RA ',CT_label,'\ncell state proportions (n=',
                          length(unique(CITE_meta$sample))),')'),
                   paste(sep=' ', 'AMP-RA\n',CT_label,'\ncell state'),clust
Colors=CITE_colors)
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_ATAC_CITE_st
ate_prop.png'),
                             plot=g,units='in',height=6,width=8,dpi=600)
```



```
In [16]: #Fig 7c left
options(repr.plot.height=6,repr.plot.width=6)
g <- ggplot(ATAC_meta[multiome_cells,],aes_string(x='UMAP1',y='UMAP2',color='CITE')) +
    geom_point(size=1,alpha=0.5) +
    theme_classic(base_size=25) + scale_color_manual(values=CITE_colors) +
    theme(legend.position="none")
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,CT,'_snATAC_state_UMAP.png'),
                             plot=g,units='in',height=6,width=6,dpi=600)
```



```
In [17]: #setting order
class_conv_df <- unique(ATAC_meta[,c('cluster_name','cluster_abbr')])
rownames(class_conv_df) <- class_conv_df$cluster_abbr
full_class_order <- class_conv_df[class_order,'cluster_name']

class_state_df$class <- factor(class_state_df$class,levels=class_order)
state_order <- class_state_df[order(class_state_df$class,class_state_df$intOrd),'state']

state_conv_df <- unique(ATAC_meta[,c('CITE','CITE_abbr')])
rownames(state_conv_df) <- state_conv_df$CITE_abbr
full_state_order <- state_conv_df[state_order,'CITE']
```

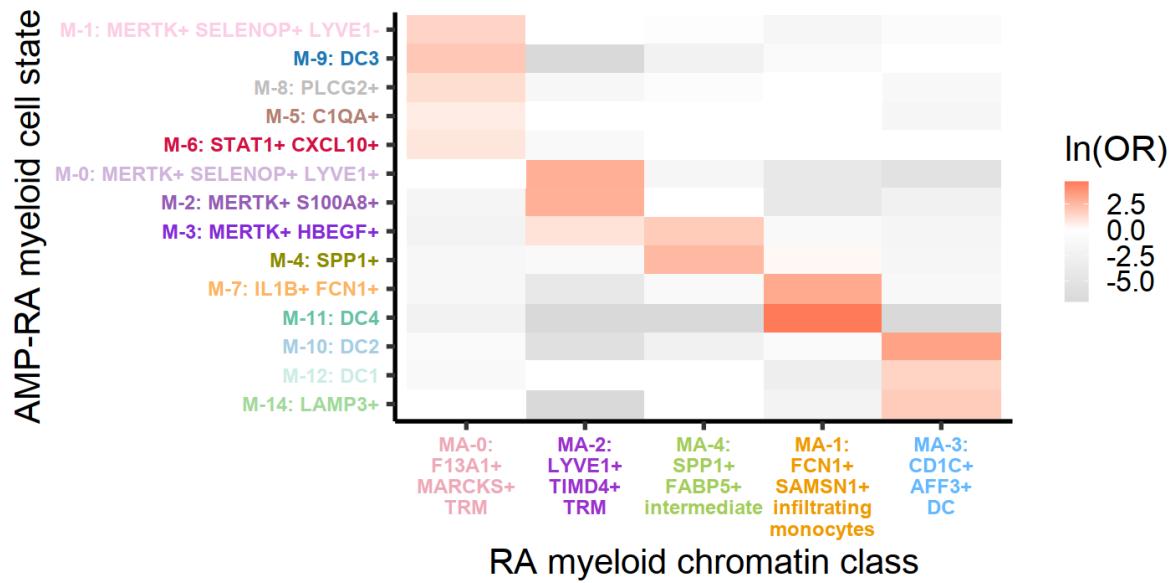
```
In [18]: #Fig 7c right
```

```
#only 2 M-13 cells, so excluding here
fisher_df <- calc_OR(ATAC_meta[which(ATAC_meta$assay=='snATAC' & ATAC_meta$CITE_abbr!='M-13'),], 'cluster_name', 'CITE')
write.table(fisher_df[,c('cluster_name', 'CITE', 'OR', 'pval', 'padj', 'CI_low', 'CI_high')],
            file=paste(sep=' ', save_dir, CT, '_class_state_OR_table.txt'), quote=FALSE, sep='\t', row.names=FALSE)

g <- plot_OR(fisher_df, 'cluster_name', 'CITE',
              paste('RA', CT_label, 'chromatin class'), paste('AMP-RA', CT_label, 'cell state'),
              full_class_order, full_state_order,
              clustColors=c(ATAC_colors, CITE_colors))

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

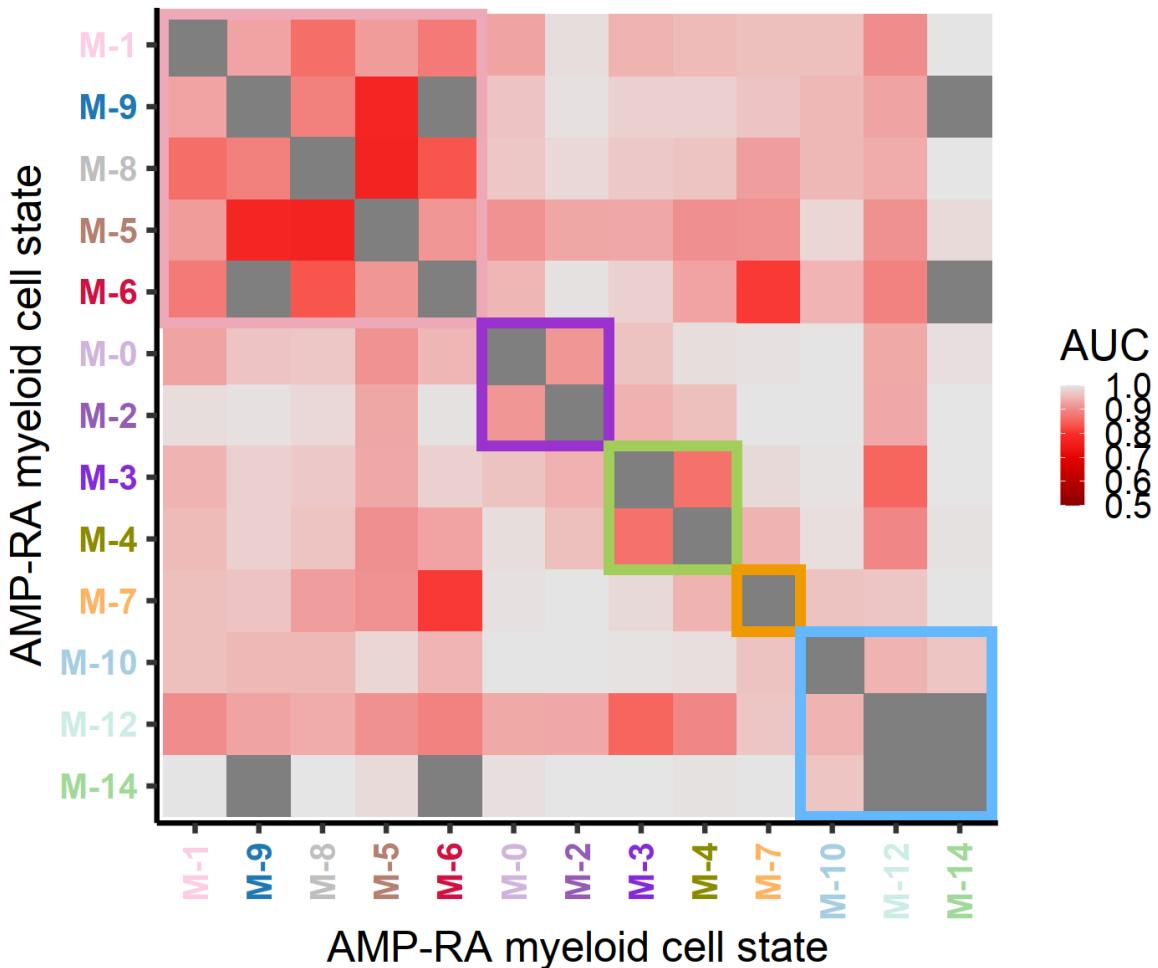
if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir, CT, '_class_state_OR_heatmap.png'),
                             plot=g, units='in', height=6, width=12, dpi=600)
```



In [19]: #Fig S11c

```
options(repr.plot.height=10,repr.plot.width=12)
g <- LDA_plots(LDA_res,CT,paste('AMP-RA',CT_label,'cell state'),
                 class_state_df=class_state_df,ctOrd_col='intOrd',ctOrd=cl
ass_order,
                 clustColors=c(CITE_colors,ATAC_colors))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_LDA_heatmap.
png'),
                           plot=g,units='in',height=10,width=12,dpi=60
0)
```

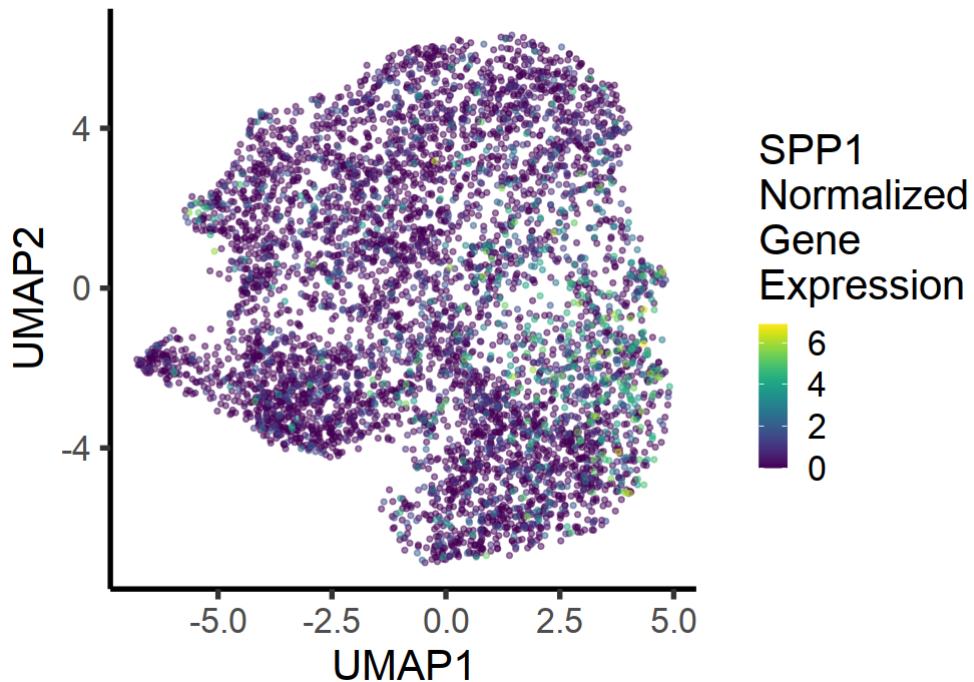


```
In [20]: #Fig S9c left
```

```
gene_toPlot <- 'SPP1'
toPlot <- cbind(ATAC_meta[multiome_cells,], 'gene'=snRNA_gxc_norm[gene_to
Plot,multiome_cells])

options(repr.plot.height=6,repr.plot.width=8.5)
g <- ggplot(toPlot[order(toPlot$gene),],aes_string(x='UMAP1',y='UMAP2',c
olor='gene')) +
    geom_point(size=1,alpha=0.5) +
    theme_classic(base_size=25) + scale_color_viridis(option
= 'viridis') +
    labs(color=paste(sep=' ',gene_toPlot,'\\nNormalized\\nGene
\\nExpression'))
print(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_gene_',gene_
toPlot,'_UMAP.png'),
                           plot=g,units='in',height=6,width=8.5,dpi=60
0)
```



additional resolutions

```
In [21]: #Fig S10c top
if(!identical(sort(rownames(other_resol)),sort(rownames(ATAC_meta)))) st
op('rownames need to be the same')
toPlot <- cbind(ATAC_meta,other_resol[rownames(ATAC_meta),])

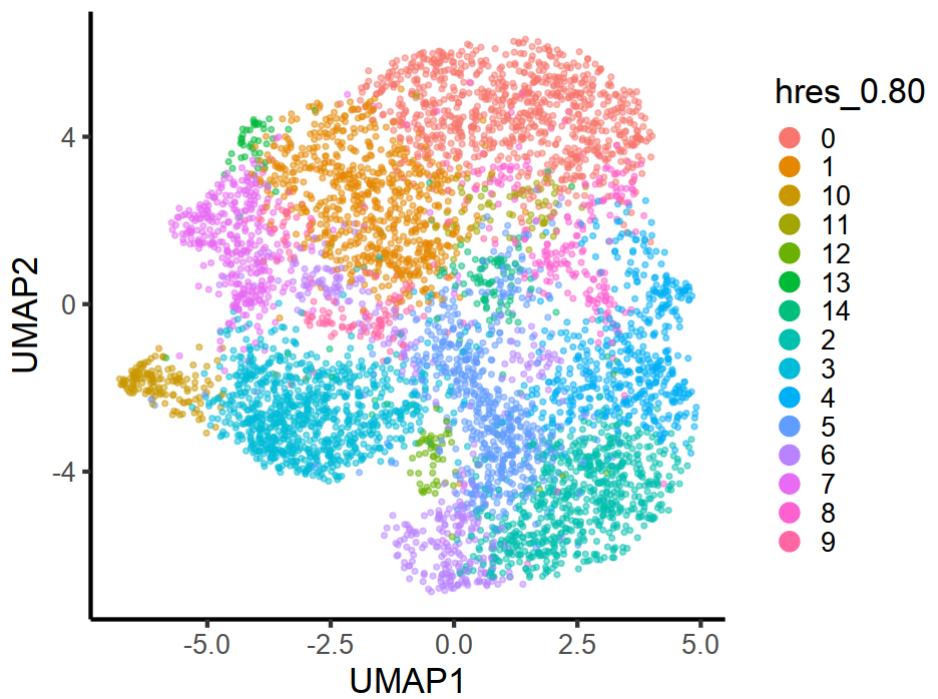
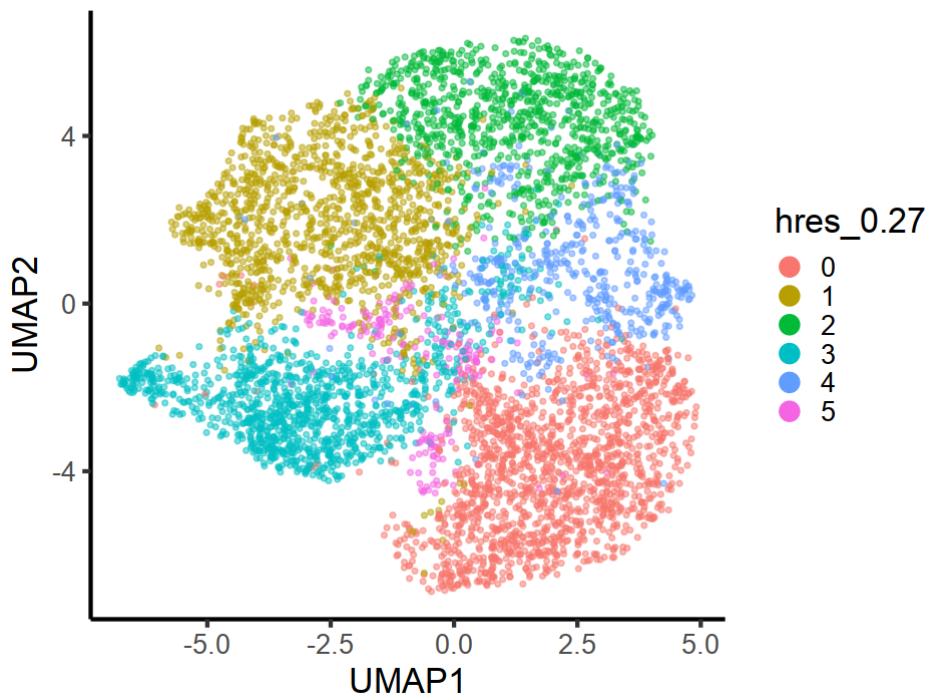
for(cc in colnames(other_resol)) {

    cluster_colors <- hue_pal()(length(unique(toPlot[,cc])))
    names(cluster_colors) <- sort(unique(toPlot[,cc]))

    options(repr.plot.height=6,repr.plot.width=8)
    g <- ggplot(toPlot[multiome_cells,],aes_string(x='UMAP1',y='UMAP2',c
olor=cc)) + geom_point(size=1,alpha=0.5) +
        theme_classic(base_size=20) + scale_color_manual(values=clus
ter_colors) +
        guides(colour = guide_legend(override.aes = list(size=5,alph
a=1)))
    print(g)

    if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_ATAC_',
c,'_UMAP.png'),
                                plot=g,units='in',height=6,width=8,dpi=6
00)
}

}
```



```
In [22]: #Fig S10c bottom
if(!identical(sort(rownames(other_resol)),sort(rownames(ATAC_meta)))) stop('rownames need to be the same')
toPlot <- cbind(ATAC_meta,other_resol[rownames(ATAC_meta),])

for(cc in colnames(other_resol)) {

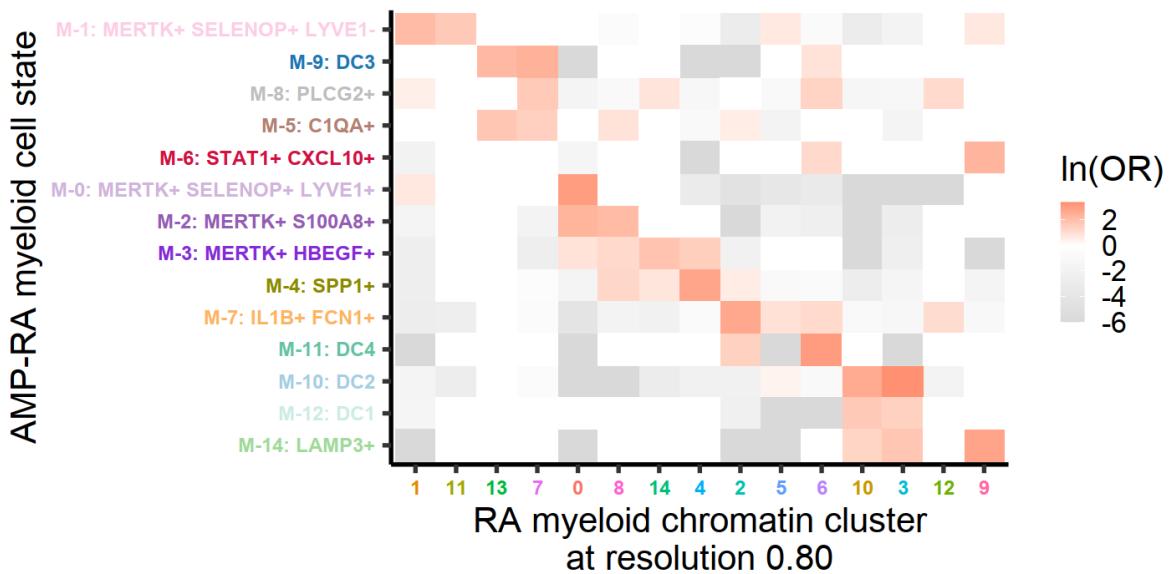
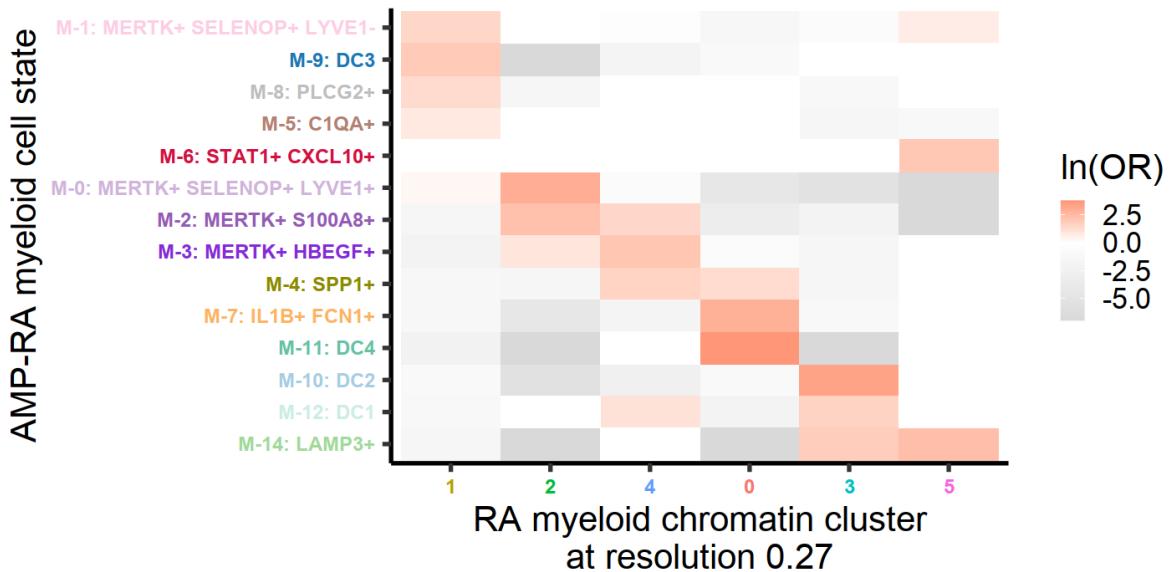
  cluster_colors <- hue_pal()(length(unique(toPlot[,cc])))
  names(cluster_colors) <- sort(unique(toPlot[,cc]))

  fisher_df <- calc_OR(toPlot[which(toPlot$assay=='snATAC' & toPlot$CI
TE_abbr!='M-13'),], cc, 'CITE')
  clustOrd <- reorder_col_diag_plotOR(fisher_df,cc,'CITE',yOrd=full_st
ate_order,mCol='lnOR',op='max')

  g <- plot_OR(fisher_df, cc, 'CITE',
                paste('RA',CT_label,'chromatin cluster\nat resolution',
str_split_fixed(cc,'_',2)[,2]),
                paste('AMP-RA',CT_label,'cell state'),
                clustOrd, full_state_order,
                clustColors=c(cluster_colors,CITE_colors))

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

  if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_',cc,'_s
tate_OR_heatmap.png'),
                                plot=g,units='in',height=6,width=12,dpi=
600)
}
```



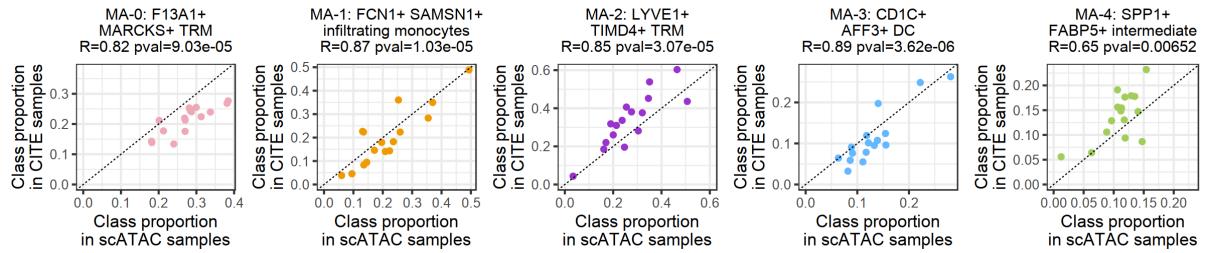
CITE donor proportions

In [23]: #Fig S12a

```
tVec <- lapply(sort(unique(ATAC_meta$cluster_name)), replace_space_newline_afterHalf, wiggle=4)
names(tVec) <- sort(unique(ATAC_meta$cluster_name))

options(repr.plot.height=4.25, repr.plot.width=4*length(unique(ATAC_meta$cluster_abbr)))
g <- donor_prop_comp_plot(ATAC_CITE_conv_df, ATAC_meta[which(ATAC_meta$as say=='scATAC'), ], CITE_meta,
                           clustColors=ATAC_colors, tSize=18, tVec=tVec)
grid.draw(g)

if(!is.na(save_dir)) ggsave(file=paste(sep=' ', save_dir, CT, '_ATAC_CITE_donor_prop.png'),
                             plot=g, units='in', height=4.25, width=4*length(unique(ATAC_meta$cluster_abbr)), dpi=600)
```



CNA associations

In [24]: #Fig 8b

```
CNA_LD_FDR <- 0.1
CNA_LD_globalp <- 0.005
CNA_title <- 'Lymphoid Density'
CNA_col <- 'cna_corr_dens'
class_col <- 'ATAC_cluster_name'

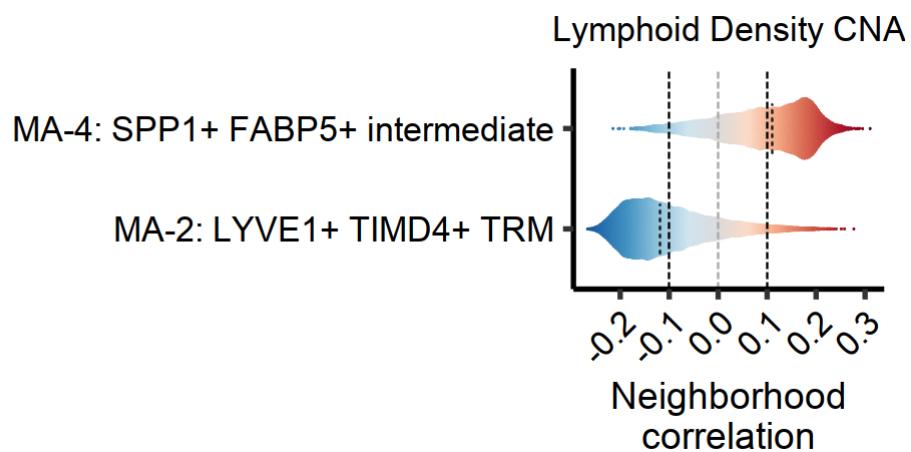
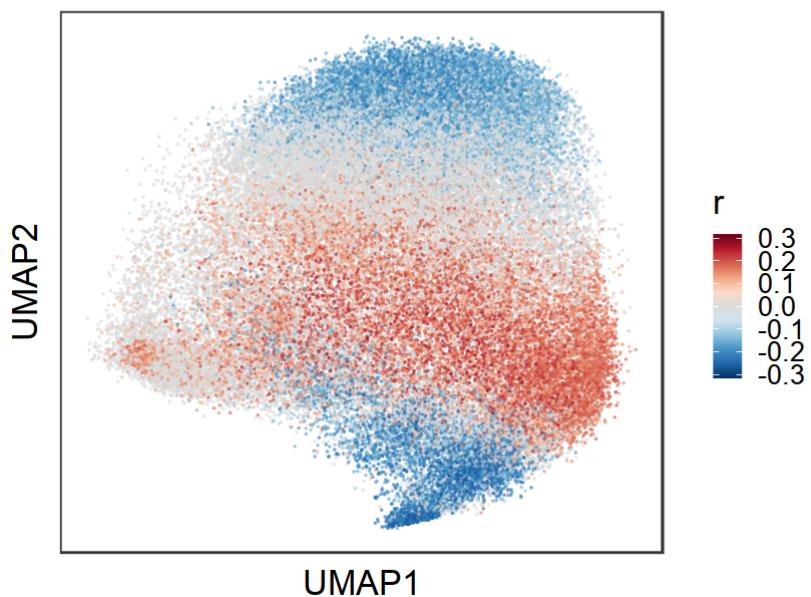
toPlot <- CNA_add_col(CITE_meta, CNA_LD, CNA_col)

options(repr.plot.height=6,repr.plot.width=7)
g <- CNA_umap_plots(toPlot,'ATAC_UMAP1','ATAC_UMAP2',CNA_col,
                      thisTitle=paste(CNA_title,'CNA correlations\n','p
                      =',CNA_LD_globalp),
                      smallPt=TRUE,fdr_thresh=CNA_LD_FDR)
print(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_',
                                         str_replace(CNA_title,' ','_'),'_CNA_UMAP.png'),
                                         plot=g,units='in',height=6,width=7,dpi=6
                                         00)

#only plot those classes whose median is above FDR thresholds
ll <- aggregate(toPlot[,CNA_col] ~ toPlot[,class_col], FUN=median)
colnames(ll) <- c(class_col,CNA_col)
CNA_classes <- ll[which(abs(ll[,CNA_col])>CNA_LD_FDR),class_col]

options(repr.plot.height=4,repr.plot.width=8)
g <- CNA_violin_plots(toPlot[which(toPlot[,class_col] %in% CNA_classes),],
                       class_col,CNA_col,CNA_LD_FDR,thisTitle=paste(CNA_t
                       itle,'CNA'))
print(g)
if(!is.na(save_dir)) ggsave(file=paste(sep=' ',save_dir,CT,'_',
                                         str_replace(CNA_title,' ','_'),'_CNA_violin.png'),
                                         plot=g,units='in',height=4,width=8,dpi=6
                                         00)
```

Lymphoid Density CNA correlations
 $p = 0.005$



Session Info

In [25]: `sessionInfo()`

```
R version 3.6.1 (2019-07-05)
Platform: x86_64-conda_cos6-linux-gnu (64-bit)
Running under: Red Hat Enterprise Linux Server release 6.5 (Santiago)

Matrix products: default
BLAS/LAPACK: /PHShome/kew47/miniconda3/lib/R/lib/libRblas.so

locale:
[1] en_US.UTF-8

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

other attached packages:
[1] repr_1.0.1      gridExtra_2.3    scales_1.1.1    viridis_0.5.1
[2] viridisLite_0.3.0 ggrepel_0.8.2   ggrastr_0.2.3   ggplot2_3.3.0
[3] tidyverse_1.0.3  stringr_1.4.0    ROCR_1.0-7     gplots_3.0.1
[4] Rmisc_1.5.1     plyr_1.8.6     lattice_0.20-41 gtools_3.8.2
[5] Matrix_1.2-18

loaded via a namespace (and not attached):
[1] pbdZMQ_0.3-3      beeswarm_0.2.3    tidyselect_1.1.0
[2] purrr_0.3.4       colorspace_1.4-1  vctrs_0.3.5
[3] generics_0.0.2    htmltools_0.4.0   base64enc_0.1-3
[4] rlang_0.4.8       hexbin_1.28.1    pillar_1.4.4
[5] glue_1.4.0        withr_2.2.0     RColorBrewer_1.1-2
[6] uuid_0.1-2        lifecycle_0.2.0   munsell_0.5.0
[7] gtable_0.3.0      caTools_1.18.0   evaluate_0.14
[8] labeling_0.3      Cairo_1.5-10    vigor_0.4.5
[9] IRdisplay_0.7.0   Rcpp_1.0.4.6    KernSmooth_2.23-15
[10] gdata_2.18.0     IRkernel_1.0.2.9000 jsonlite_1.7.1
[11] farver_2.0.3     digest_0.6.25   stringi_1.4.6
[12] dplyr_1.0.2       tools_3.6.1     bitops_1.0-6
[13] magrittr_1.5      tibble_3.0.1    crayon_1.3.4
[14] pkgconfig_2.0.3   ellipsis_0.3.1  ggbeeswarm_0.6.0
[15] R6_2.4.1          compiler_3.6.1
```

In []: