SNPs

inputs

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

In [2]:
```
CT <- 'SNPs'
data_prefix <- paste(sep='','../data/',CT,'/')
ATAC_pxCT_norm <- readRDS(paste(sep='',data_prefix,'ATAC_pxc_afc_SNPpeaks_pxCT_norm.rds')) #should get all peaks here!
chosenSNPs <- readRDS(paste(sep='',data_prefix,'ATAC_chosenSNPs.rds'))
```

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

In [15]:
```
save_dir <- NA #'../output/' #or NA if don't want to save
```

SNP matrix

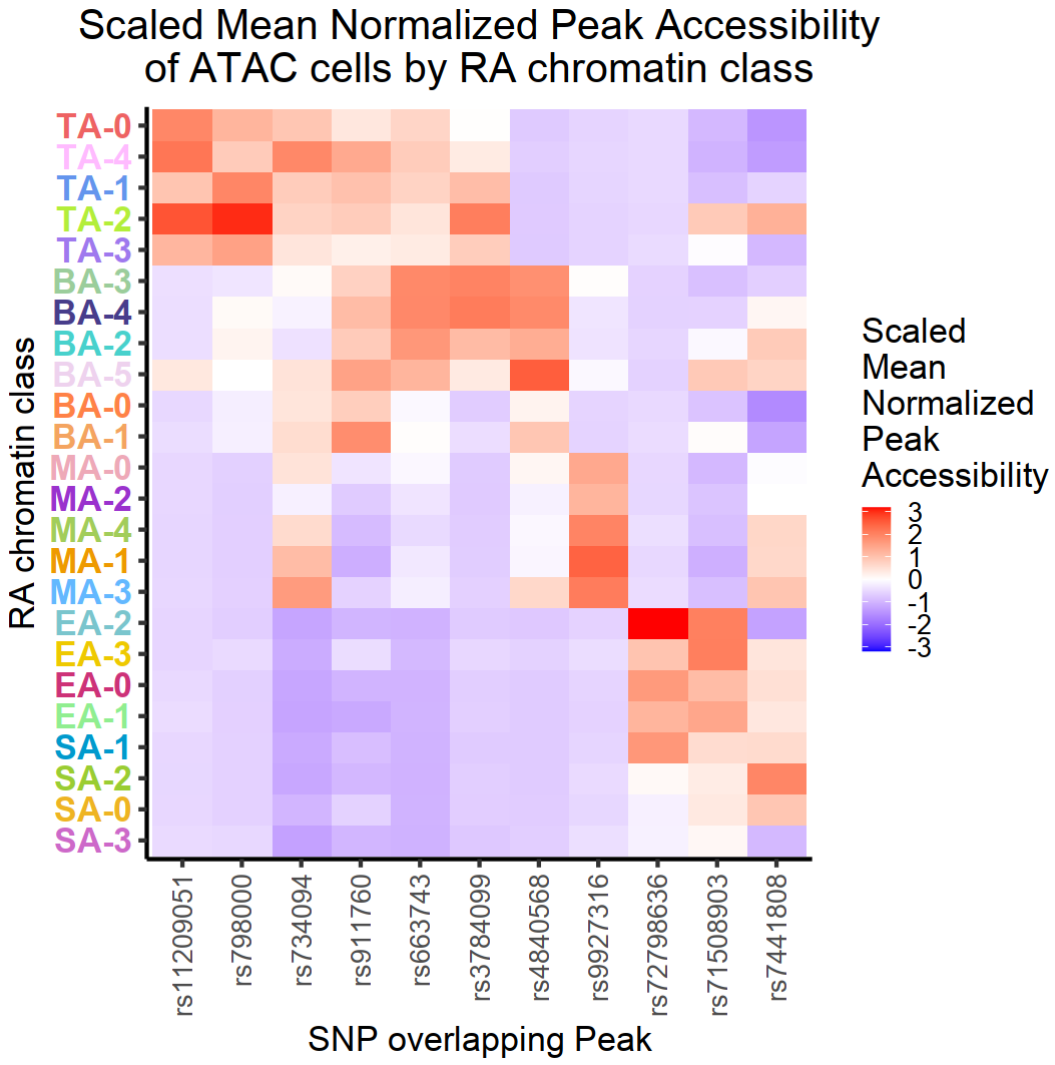
In [5]:
```
class_order <- c('TA-0','TA-4','TA-1','TA-2','TA-3',
                 'BA-3','BA-4','BA-2','BA-5','BA-0','BA-1',
                 'MA-0','MA-2','MA-4','MA-1','MA-3',
                 'EA-2','EA-3','EA-0','EA-1',
                 'SA-1','SA-2','SA-0','SA-3')
if(!all(class_order %in% colnames(ATAC_pxCT_norm))) stop('not all classes in pxCT')
if(!all(class_order %in% names(ATAC_colors))) stop('not all classes in colors')

if(!all(unname(chosenSNPs) %in% rownames(ATAC_pxCT_norm))) stop('not all chosen SNPs in pxCT')
```

In [6]:
```
#Fig 7d

ATAC_pxCT_norm_subset_scaled <- scalePeak_forHeatmap(names(chosenSNPs),c
lass_order,chosenSNPs,ATAC_pxCT_norm)

options(repr.plot.height=9,repr.plot.width=9)
g <- pseudobulk_scaled_heatmap(ATAC_pxCT_norm_subset_scaled,'SNP overlap
ping Peak','RA chromatin class',
                               'Scaled\nMean\nNormalized\nPeak\nAccessib
ility',
                               plotTit='Scaled Mean Normalized Peak Acce
ssibility\nof ATAC cells by RA chromatin class',
                               scale_lim=max(abs(ATAC_pxCT_norm_subset_s
caled)),clustColors=ATAC_colors)
print(g)
if(!is.na(save_dir)) ggsave(file=paste(sep='',save_dir,'ATAC_SNP_markerP
eak_heatmap.png'),
                            plot=g,units='in',height=9,width=9,dpi=600)
```



In [7]:
```
class_overlaps <- as.data.frame(rev(apply(ATAC_pxCT_norm_subset_scaled,
1,function(x){paste(names(x[x>1]),collapse=', ')})),
                                stringsAsFactors=FALSE)
colnames(class_overlaps) <- c('classOL')
class_overlaps
```

A data.frame: 11 × 1

	classOL
	<chr>
rs11209051	TA-3, TA-2, TA-4, TA-0
rs798000	TA-3, TA-2, TA-1, TA-0
rs734094	MA-3, MA-1, TA-4
rs911760	BA-1, BA-5, BA-4, TA-1, TA-4
rs663743	BA-5, BA-2, BA-4, BA-3
rs3784099	BA-2, BA-4, BA-3, TA-2, TA-1
rs4840568	BA-5, BA-2, BA-4, BA-3
rs9927316	MA-3, MA-1, MA-4, MA-2, MA-0
rs72798636	SA-1, EA-1, EA-0, EA-2
rs71508903	EA-1, EA-0, EA-3, EA-2
rs7441808	SA-2, TA-2

Wilcoxon tests

In [8]:
```
classCT_conv <- c('stromal','endothelial','myeloid','Bplasma','Tcell')
names(classCT_conv) <- c('S','E','M','B','T')

snps_gathered <- gather_SNPs(ATAC_pxCT_norm_subset_scaled,chosenSNPs,cla
ssCT_conv)
```

In [9]:
```
within <- snps_gathered[which(snps_gathered$rsID=='rs11209051' & snps_ga
thered$cellType=='Tcell'),'norm_pxCTmean_scale']
without <- snps_gathered[which(snps_gathered$rsID=='rs11209051' & snps_g
athered$cellType!='Tcell'),'norm_pxCTmean_scale']

wilcox.test(within,without,alternative = "greater")
```

```
Warning message in wilcox.test.default(within, without, alternative =
"greater"):
“cannot compute exact p-value with ties”

        Wilcoxon rank sum test with continuity correction

data:  within and without
W = 95, p-value = 0.0004165
alternative hypothesis: true location shift is greater than 0
```

In [10]:
```
within <- snps_gathered[which(snps_gathered$rsID=='rs4840568' & snps_gat
hered$cellType=='Bplasma'),'norm_pxCTmean_scale']
without <- snps_gathered[which(snps_gathered$rsID=='rs4840568' & snps_ga
thered$cellType!='Bplasma'),'norm_pxCTmean_scale']

wilcox.test(within,without,alternative = "greater")
```

```
        Wilcoxon rank sum test

data:  within and without
W = 107, p-value = 1.486e-05
alternative hypothesis: true location shift is greater than 0
```

In [11]:
```
within <- snps_gathered[which(snps_gathered$rsID=='rs798000' & snps_gath
ered$cellType=='Tcell'),'norm_pxCTmean_scale']
without <- snps_gathered[which(snps_gathered$rsID=='rs798000' & snps_gat
hered$cellType!='Tcell'),'norm_pxCTmean_scale']

wilcox.test(within,without,alternative = "greater")
```

```
        Wilcoxon rank sum test

data:  within and without
W = 95, p-value = 2.353e-05
alternative hypothesis: true location shift is greater than 0
```

In [12]:
```
within <- snps_gathered[which(snps_gathered$rsID=='rs9927316' & snps_gat
hered$cellType=='myeloid'),'norm_pxCTmean_scale']
without <- snps_gathered[which(snps_gathered$rsID=='rs9927316' & snps_ga
thered$cellType!='myeloid'),'norm_pxCTmean_scale']

wilcox.test(within,without,alternative = "greater")
```

```
Warning message in wilcox.test.default(within, without, alternative =
"greater"):
“cannot compute exact p-value with ties”

        Wilcoxon rank sum test with continuity correction

data:  within and without
W = 95, p-value = 0.0004165
alternative hypothesis: true location shift is greater than 0
```

In [13]:
```
within <- snps_gathered[which(snps_gathered$rsID=='rs734094' & (snps_gat
hered$cellType %in% c('myeloid','Tcell'))),
                        'norm_pxCTmean_scale']
without <- snps_gathered[which(snps_gathered$rsID=='rs734094' & !(snps_g
athered$cellType %in% c('myeloid','Tcell'))),
                         'norm_pxCTmean_scale']

wilcox.test(within,without,alternative = "greater")
```

```
        Wilcoxon rank sum test

data:  within and without
W = 131, p-value = 4.946e-05
alternative hypothesis: true location shift is greater than 0
```

Session Info

In [14]:
```
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
 [5] viridisLite_0.3.0 ggrepel_0.8.2     ggrastr_0.2.3     stringr_1.4.
0
 [9] ROCR_1.0-7        gplots_3.0.1.1    Rmisc_1.5.1       plyr_1.8.6
[13] lattice_0.20-41   gtools_3.8.2      tidyr_1.0.3       Matrix_1.2-1
8
[17] ggplot2_3.3.0

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.4.6         vipor_0.4.5          pillar_1.4.4
 [4] compiler_3.6.1       bitops_1.0-6         base64enc_0.1-3
 [7] tools_3.6.1          digest_0.6.25        uuid_0.1-2
[10] jsonlite_1.7.1       evaluate_0.14        lifecycle_0.2.0
[13] tibble_3.0.1         gtable_0.3.0         pkgconfig_2.0.3
[16] rlang_0.4.8          IRdisplay_0.7.0      IRkernel_1.0.2.9000
[19] beeswarm_0.2.3       withr_2.2.0          dplyr_1.0.2
[22] caTools_1.18.0       generics_0.0.2       vctrs_0.3.5
[25] tidyselect_1.1.0     glue_1.4.0           R6_2.4.1
[28] ggbeeswarm_0.6.0     gdata_2.18.0         pbdZMQ_0.3-3
[31] farver_2.0.3         purrr_0.3.4          magrittr_1.5
[34] ellipsis_0.3.1       htmltools_0.4.0      colorspace_1.4-1
[37] labeling_0.3         KernSmooth_2.23-15   stringi_1.4.6
[40] munsell_0.5.0        crayon_1.3.4         Cairo_1.5-10
```

In [ ]:
```

```