

Pig Cell Atlas - MafB

Domien

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Introduction

To investigate the conservedness of MafB to imprint Mac identity across species we quantified the correlation between Mafb expression and the expression of macrophage signature genes and MafB target genes in single cell atlases of mouse (Tabula Muris Senis), human (Tabula Sapiens), lemur (Tabula Microcebus), pig (Pig Cell Atlas), African clawed frog (Xenopus Cell Landscape) and zebrafish (Zebrafish Cell Landscape, ZCL).

Load packages

```
suppressMessages({  
  library(SeuratObject)  
  library(Seurat)  
  library(reticulate)  
  library(sceasy)  
  library(ggplot2)  
  library(ggrastr)  
  library(readxl)  
})
```

Download Pig Cell Atlas Seurat object from Pigatlas server

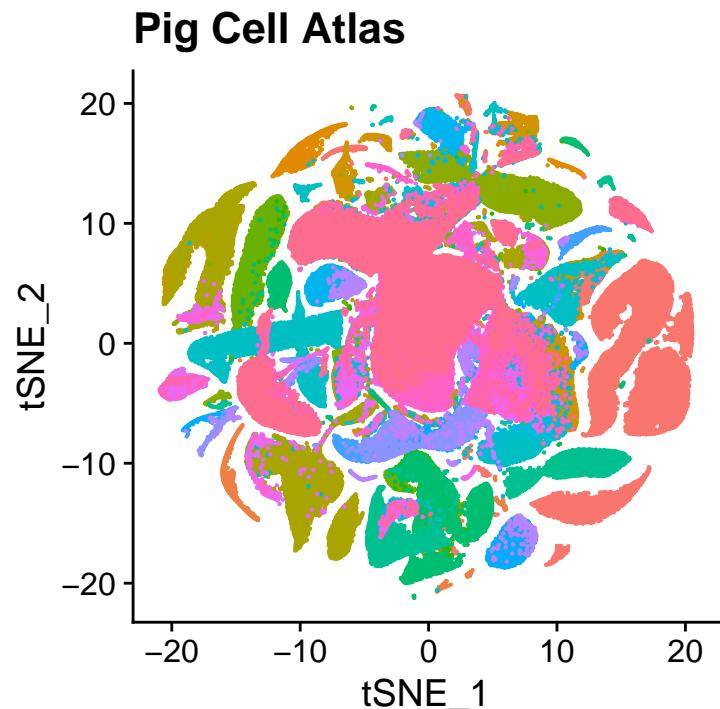
```
https://dreamapp.biomed.au.dk/pigatlas/
```

Load Pig Cell Atlas Seurat object

```
PCA <- readRDS("pig_atlas_20221014.rds")
```

Visualize clusters

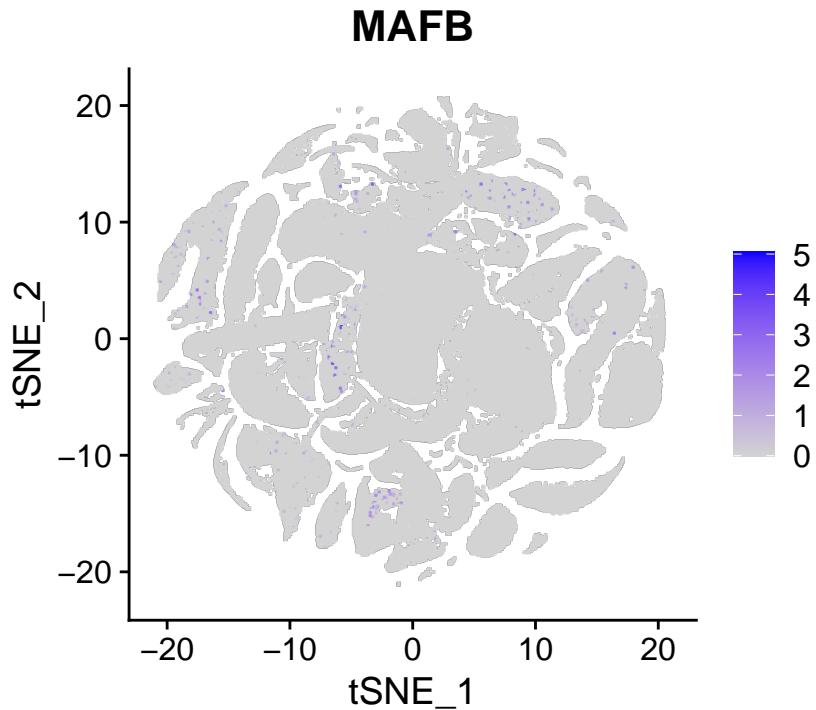
```
p1 <- DimPlot(PCA, reduction = "tsne", raster = F) + theme(legend.position = "none") +  
  ggtitle("Pig Cell Atlas")  
  
rasterize(p1, layers = "Point", dpi = 1200)
```



Calculate correlation between MAFB expression and Mac signature score

```
FeaturePlot(PCA, features = "MAFB", reduction = "tsne", raster = T)
```

```
## Rasterizing points since number of points exceeds 100,000.  
## To disable this behavior set 'raster=FALSE'
```

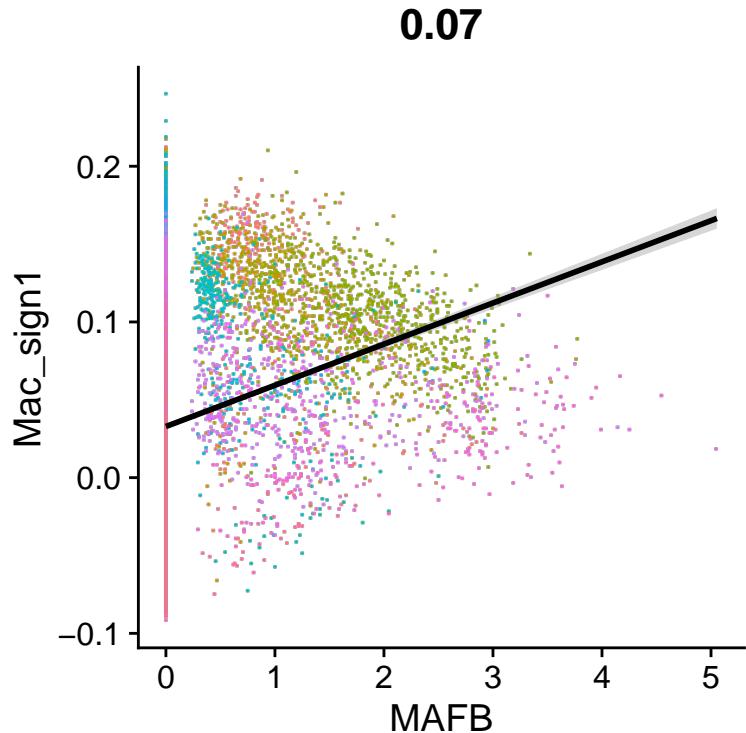


```
Mac_sign <- read_excel("Mac_sign_pig.xlsx")
Mac_sign <- Mac_sign$ortholog_name
Mac_sign <- intersect(Mac_sign, rownames(PCA))
PCA <- AddModuleScore(PCA, features = list(c(Mac_sign)), name = "Mac_sign")
```

```
FeatureScatter(PCA, feature1 = "MAFB", feature2 = "Mac_sign1",
  raster = T) + geom_smooth(method = "lm", colour = "black") +
  theme(legend.position = "none")
```

```
## Rasterizing points since number of points exceeds 100,000.
## To disable this behavior set 'raster=FALSE'
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



```

corr <- FetchData(PCA, vars = "MAFB")
corr <- cbind(corr, FetchData(PCA, vars = "Mac_sign1"))

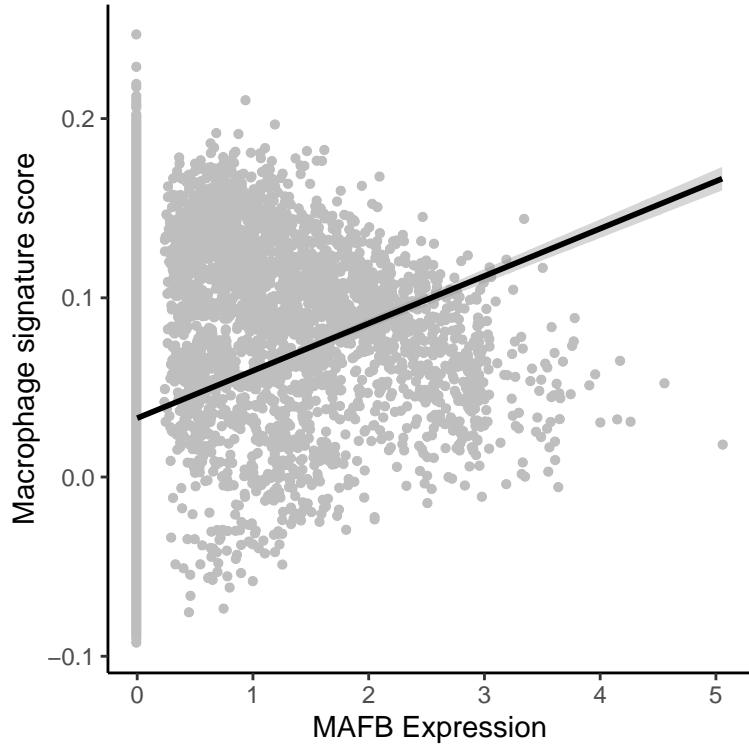
cor.test(corr$MAFB, corr$Mac_sign1, method = "pearson")

## 
## Pearson's product-moment correlation
##
## data: corr$MAFB and corr$Mac_sign1
## t = 39.91, df = 295415, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.06964334 0.07681674
## sample estimates:
##          cor
## 0.07323099

p2 <- ggplot(corr, aes(x = MAFB, y = Mac_sign1)) + geom_point(size = 1,
  colour = "grey") + geom_smooth(method = "lm", colour = "black") +
  xlab("MAFB Expression") + ylab("Macrophage signature score") +
  theme_classic()
rasterize(p2, layers = "Point", dpi = 600)

## `geom_smooth()` using formula = 'y ~ x'

```



Calculate correlation between MAFB expression and MafB target gene signature score

```
MafB_target_sign <- read_excel("MafB_target_pig.xlsx")

MafB_target_sign <- MafB_target_sign$ortholog_name

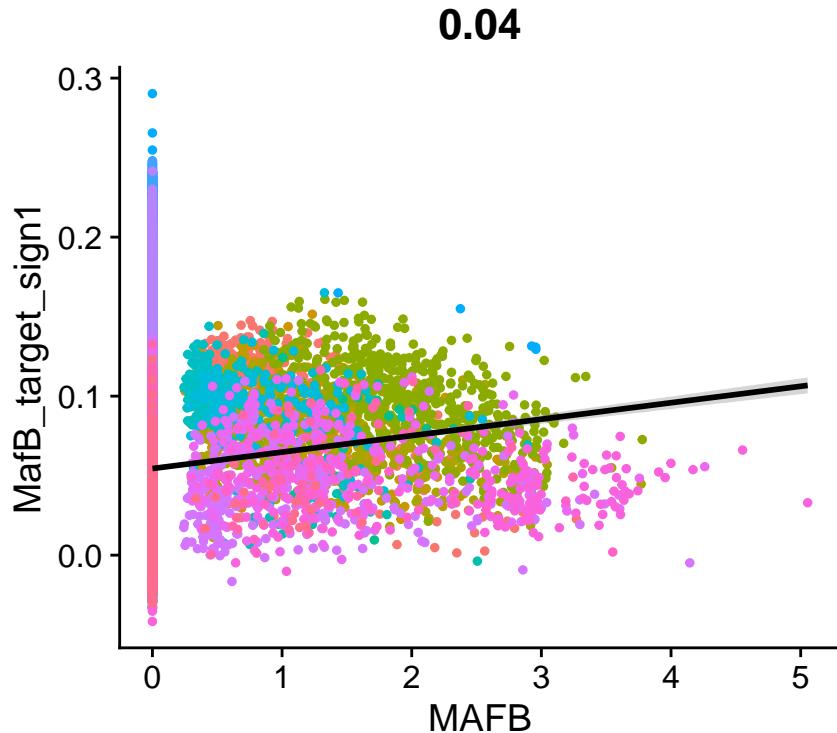
MafB_target_sign <- unique(MafB_target_sign)

MafB_target_sign <- intersect(MafB_target_sign, rownames(PCA))

PCA <- AddModuleScore(PCA, features = list(c(MafB_target_sign)),
  name = "MafB_target_sign")
```

```
FeatureScatter(PCA, feature1 = "MAFB", feature2 = "MafB_target_sign1",
  raster = F) + geom_smooth(method = "lm", colour = "black") +
  theme(legend.position = "none")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



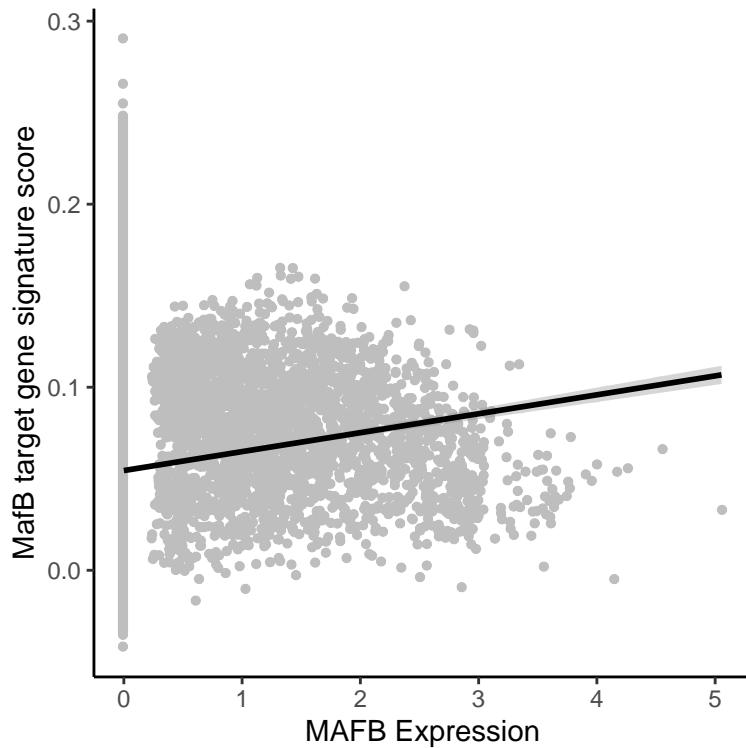
```
corr <- cbind(corr, FetchData(PCA, vars = "MafB_target_sign1"))

cor.test(corr$MAFB, corr$MafB_target_sign1, method = "pearson")
```

```
## 
## Pearson's product-moment correlation
##
## data: corr$MAFB and corr$MafB_target_sign1
## t = 20.581, df = 295415, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.03423802 0.04143978
## sample estimates:
##        cor
## 0.03783939
```

```
p3 <- ggplot(corr, aes(x = MAFB, y = MafB_target_sign1)) + geom_point(size = 1,
  colour = "grey") + geom_smooth(method = "lm", colour = "black") +
  xlab("MAFB Expression") + ylab("MafB target gene signature score") +
  theme_classic()
rasterize(p3, layers = "Point", dpi = 600)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



```

sessionInfo()

## R version 4.4.1 (2024-06-14)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 20.04.6 LTS
##
## Matrix products: default
## BLAS:    /usr/lib/x86_64-linux-gnublas/libblas.so.3.9.0
## LAPACK:  /usr/lib/x86_64-linux-gnulapack/liblapack.so.3.9.0
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8          LC_NUMERIC=C
## [3] LC_TIME=fr_BE.UTF-8          LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=fr_BE.UTF-8      LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=fr_BE.UTF-8         LC_NAME=C
## [9] LC_ADDRESS=C                 LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_BE.UTF-8   LC_IDENTIFICATION=C
##
## time zone: Europe/Brussels
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats      graphics   grDevices utils      datasets   methods    base
##
## other attached packages:
## [1] readxl_1.4.3      ggrastr_1.0.2      ggplot2_3.4.4      sceasy_0.0.7
## [5] reticulate_1.39.0 Seurat_4.3.0      SeuratObject_4.1.3 sp_2.1-4
##
## loaded via a namespace (and not attached):

```

```

## [1] deldir_2.0-4          pbapply_1.4-3           gridExtra_2.3
## [4] formatR_1.14           rlang_1.1.4            magrittr_2.0.3
## [7] RcppAnnoy_0.0.18       spatstat.geom_3.3-3   matrixStats_1.4.1
## [10] ggridges_0.5.3         compiler_4.4.1        mgcv_1.9-1
## [13] png_0.1-8              vctrs_0.6.5            reshape2_1.4.4
## [16] stringr_1.5.1          pkgconfig_2.0.3       fastmap_1.2.0
## [19] labeling_0.4.3         utf8_1.2.4             promises_1.2.0.1
## [22] rmarkdown_2.28          ggbeeswarm_0.7.2      purrr_1.0.2
## [25] xfun_0.47              jsonlite_1.8.9        goftest_1.2-2
## [28] highr_0.11             later_1.2.0           spatstat.utils_3.1-0
## [31] irlba_2.3.5.1          parallel_4.4.1       cluster_2.1.6
## [34] R6_2.5.1               ica_1.0-2             stringi_1.6.2
## [37] RColorBrewer_1.1-3     spatstat.data_3.1-2  parallelly_1.26.0
## [40] spatstat.univar_3.0-1  cellranger_1.1.0      lmtest_0.9-38
## [43] scattermore_0.7          Rcpp_1.0.13            knitr_1.48
## [46] tensor_1.5              future.apply_1.7.0    zoo_1.8-9
## [49] sctransform_0.4.1       httpuv_1.6.1          Matrix_1.6-1.1
## [52] splines_4.4.1           igraph_1.2.6          tidyselect_1.2.1
## [55] abind_1.4-5             rstudioapi_0.16.0     yaml_2.2.1
## [58] spatstat.random_3.3-2   codetools_0.2-19      miniUI_0.1.1.1
## [61] spatstat.explore_3.3-2 listenv_0.8.0          lattice_0.22-5
## [64] tibble_3.2.1            plyr_1.8.6            withr_3.0.1
## [67] shiny_1.9.1             ROCR_1.0-11           evaluate_1.0.0
## [70] Rtsne_0.15              future_1.21.0         survival_3.7-0
## [73] polyclip_1.10-0         fitdistrplus_1.1-5   pillar_1.9.0
## [76] KernSmooth_2.23-24      plotly_4.10.4         generics_0.1.0
## [79] munsell_0.5.1            scales_1.3.0          globals_0.14.0
## [82] xtable_1.8-4             glue_1.7.0            lazyeval_0.2.2
## [85] tools_4.4.1              data.table_1.14.0     RANN_2.6.1
## [88] leiden_0.3.8             Cairo_1.6-2           cowplot_1.1.1
## [91] grid_4.4.1               tidyverse_1.3.1        colorspace_2.1-1
## [94] nlme_3.1-165             patchwork_1.1.1       beeswarm_0.4.0
## [97] vipor_0.4.7              cli_3.6.3             spatstat.sparse_3.1-0
## [100] fansi_1.0.6             viridisLite_0.4.2      dplyr_1.1.4
## [103] uwot_0.2.2              gtable_0.3.5           digest_0.6.37
## [106] progressr_0.14.0         ggrepel_0.9.6          farver_2.1.2
## [109] htmlwidgets_1.5.3        htmtools_0.5.8.1      lifecycle_1.0.4
## [112] httr_1.4.7               mime_0.11             MASS_7.3-61

```