Tabula Muris Senis - MafB

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2025-09-11 15:03:37 +0200

Contents

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 sigature 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(ggplot2)
    library(dplyr)
    library(readxl)
    library(ggrastr)
})
```

Load Tabula Muris Senis Seurat object

```
tbms <- readRDS("/media/uliege/T7/SingleCellAtlas/tbms.rds")
```

Visualize clusters

```
p1 <- DimPlot(tbms, raster = F, group.by = "leiden") + theme(legend.position = "none") +
    ggtitle("Tabula Muris Senis")

rasterize(p1, layers = "Point", dpi = 1200)
```

Tabula Muris Senis
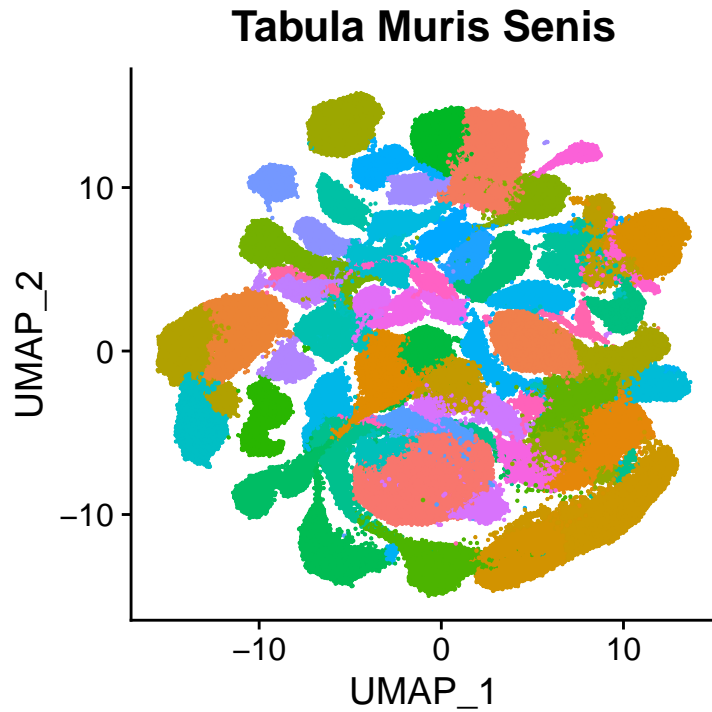
Calculate correlation between Mafb expression and Mac signature score

```
FeaturePlot(tbms, features = "Mafb", raster = T)
```

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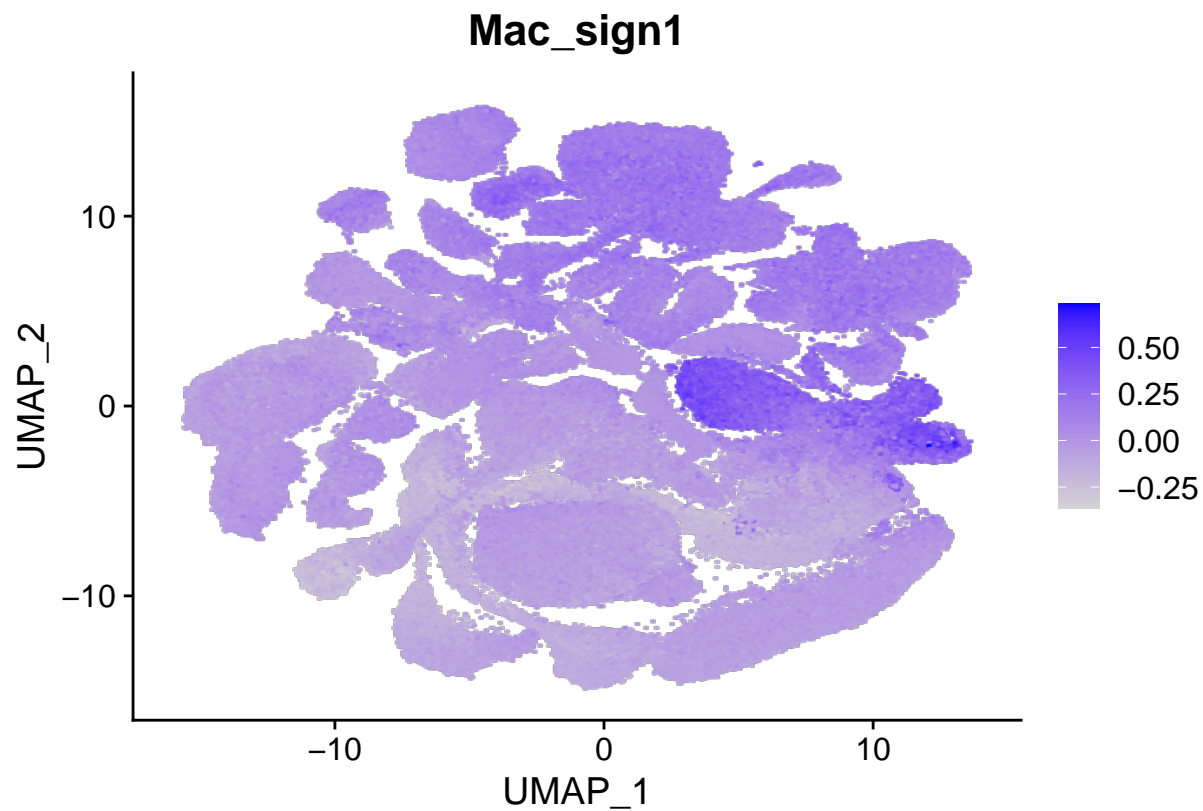
Mafb
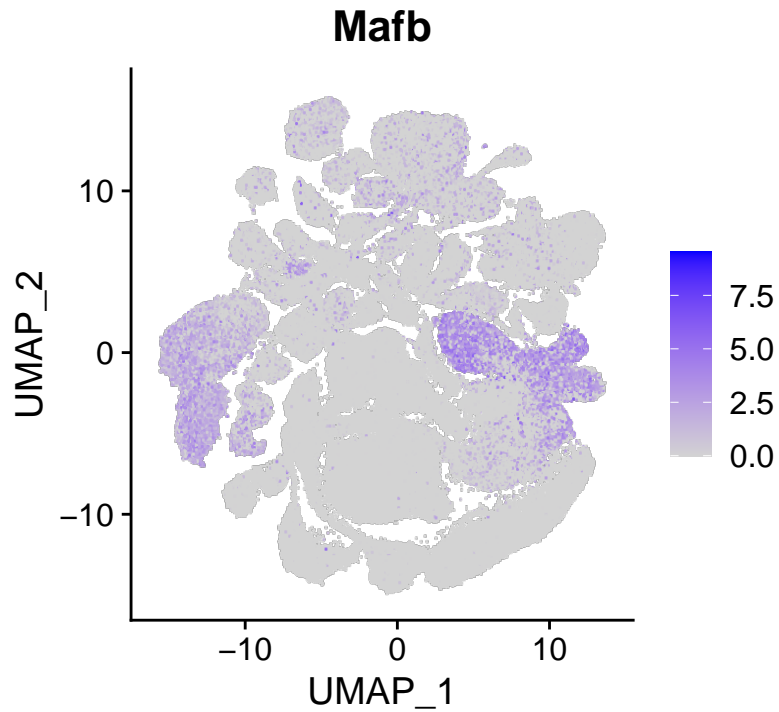

```r
Mac_sign <- read_excel("Mac_sign.xlsx")
Mac_sign <- Mac_sign$Gene_Symbol
Mac_sign <- intersect(Mac_sign, rownames(tbms))
tbms <- AddModuleScore(tbms, features = list(c(Mac_sign)), name = "Mac_sign")
```
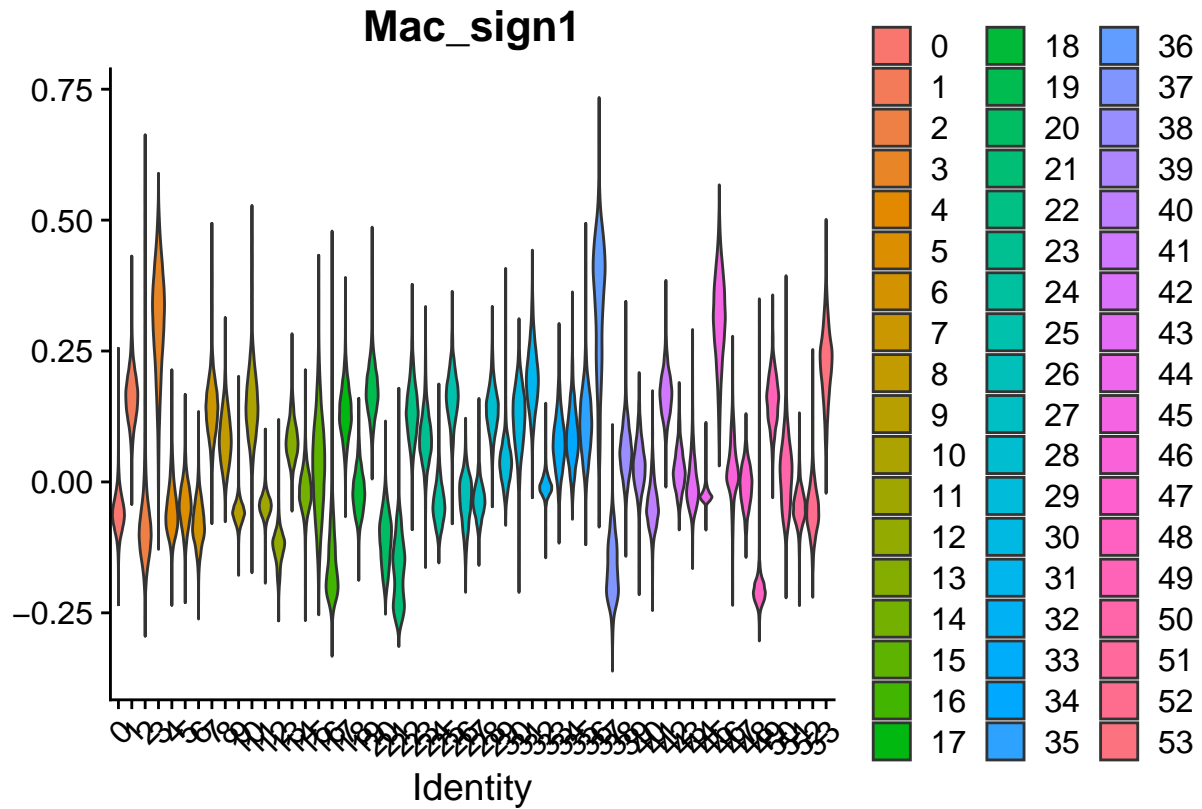
```r
FeaturePlot(tbms, features = "Mac_sign1", raster = T)
```

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

Mac_sign1

```
VlnPlot(tbms, features = "Mac_sign1", group.by = "louvain", pt.size = 0)
```

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

Mac_sign1


```
FeatureScatter(tbms, feature1 = "Mafb", feature2 = "Mac_sign1") +
    geom_smooth(method = "lm", colour = "black") + theme(legend.position = "none")
```
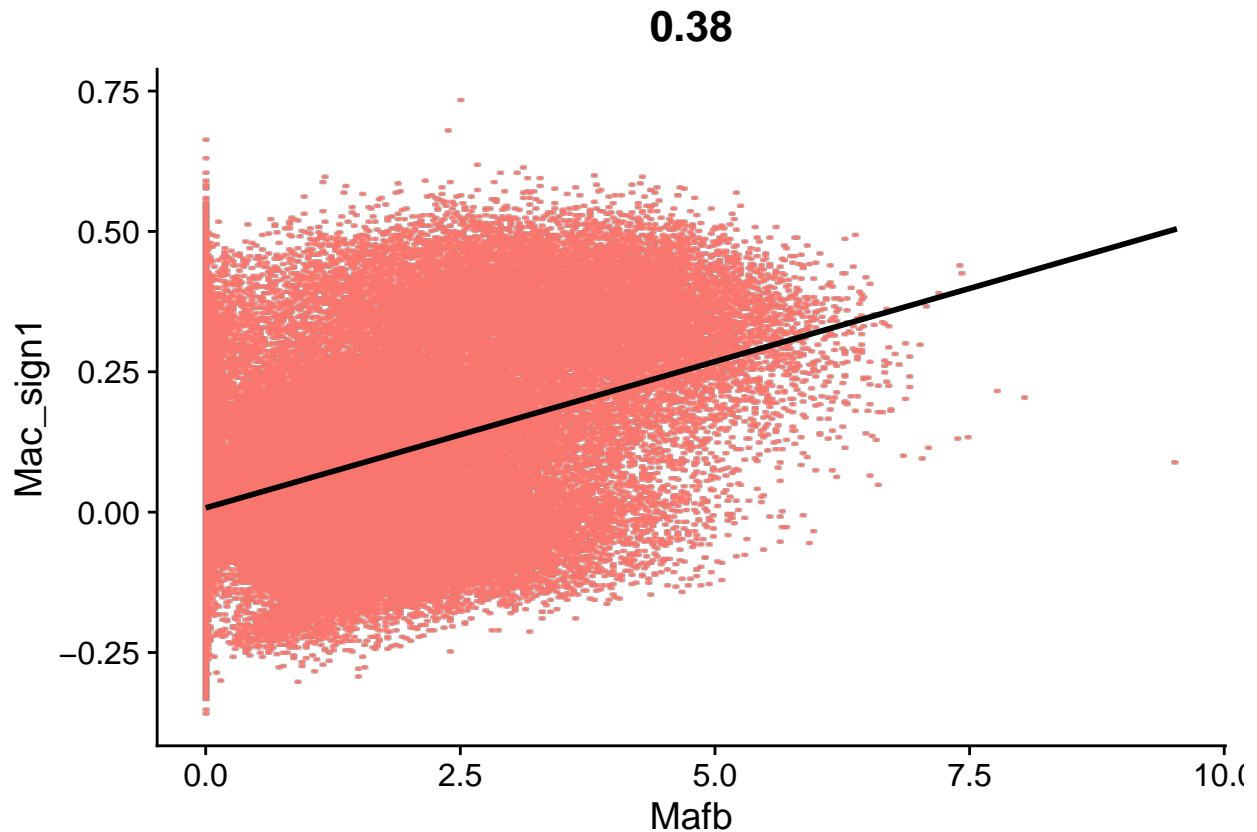
```
## Rasterizing points since number of points exceeds 100,000.
## To disable this behavior set 'raster=FALSE'
```

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

0.38


```
corr <- FetchData(tbms, vars = "Mafb")
corr <- cbind(corr, FetchData(tbms, 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 = 246.7, df = 356211, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3791959 0.3848053
## sample estimates:
##       cor
## 0.3820041
```

```
p2 <- ggplot(corr, aes(x = Mafb, y = Mac_sign1)) + geom_point(size = 0.1,
    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'
```
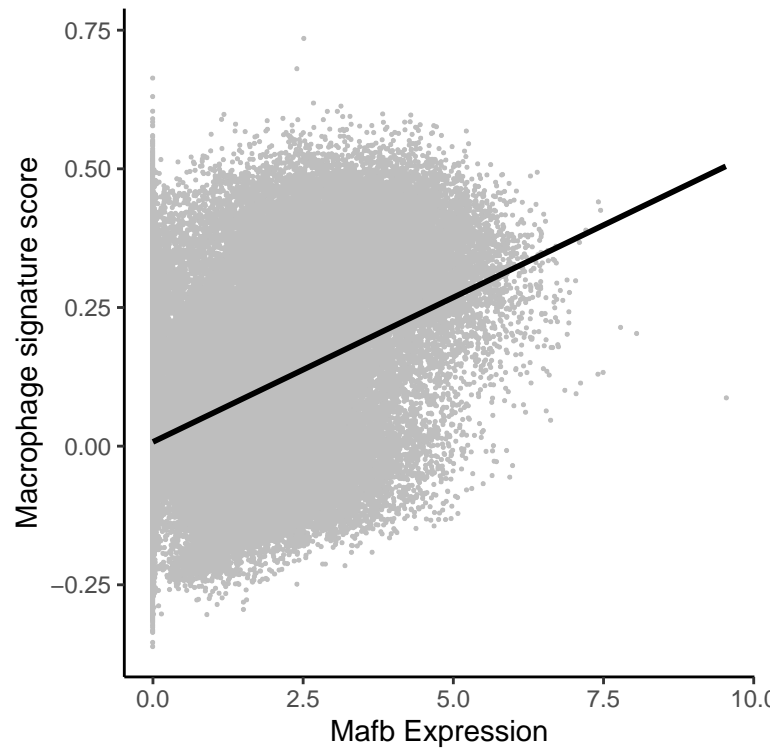
Calculate correlation between Mafb expression and MafB target gene signature score

```
MafB_target_genes <- read.csv("Conserved_MafB_target_genes_mouse.csv")

MafB_target_genes <- na.omit(unique(MafB_target_genes$ortholog_name))

MafB_target_genes <- intersect(MafB_target_genes, rownames(tbms))
tbms <- AddModuleScore(tbms, features = list(c(MafB_target_genes)),
    name = "MafB_target_sign")
```

```
FeaturePlot(tbms, features = "MafB_target_sign1", raster = T)
```

```
## Rasterizing points since number of points exceeds 100,000.
## To disable this behavior set 'raster=FALSE'
```
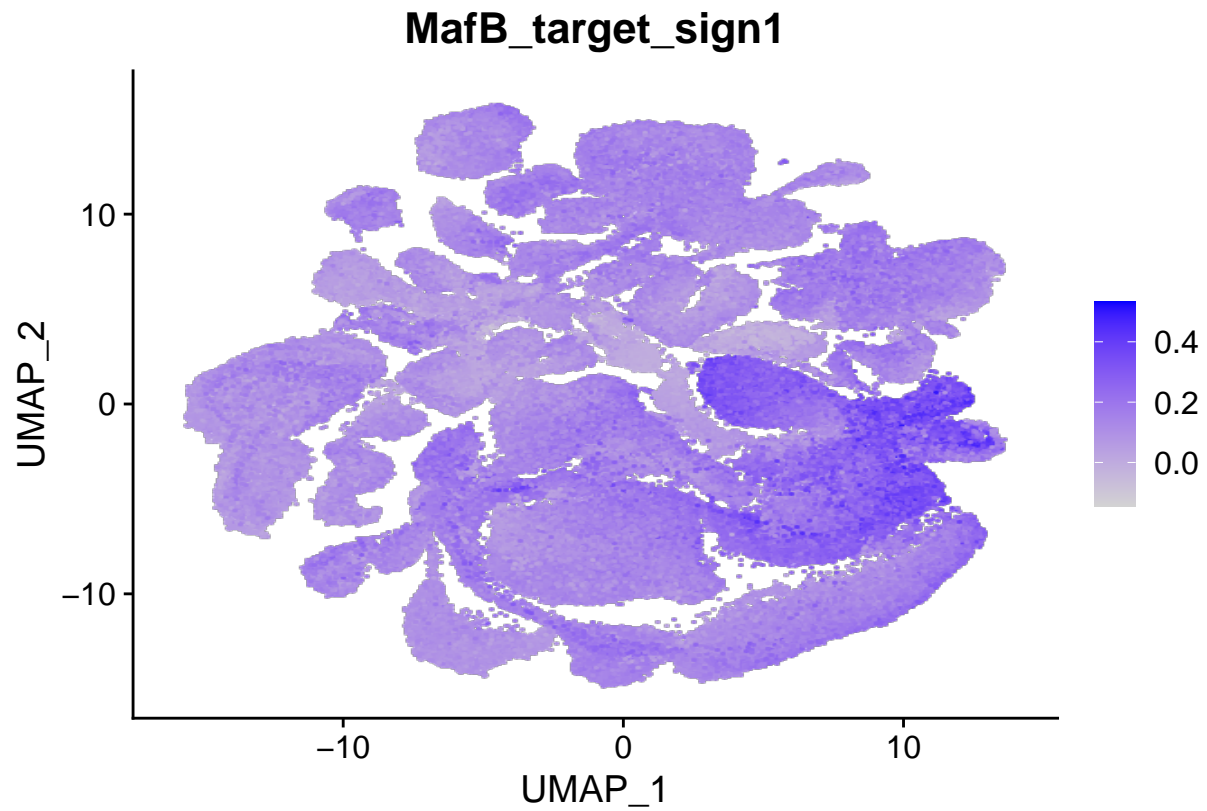
MafB_target_sign1


```
VlnPlot(tbms, features = "MafB_target_sign1", group.by = "louvain",
    pt.size = 0)
```

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

MafB_target_sign1

Identity
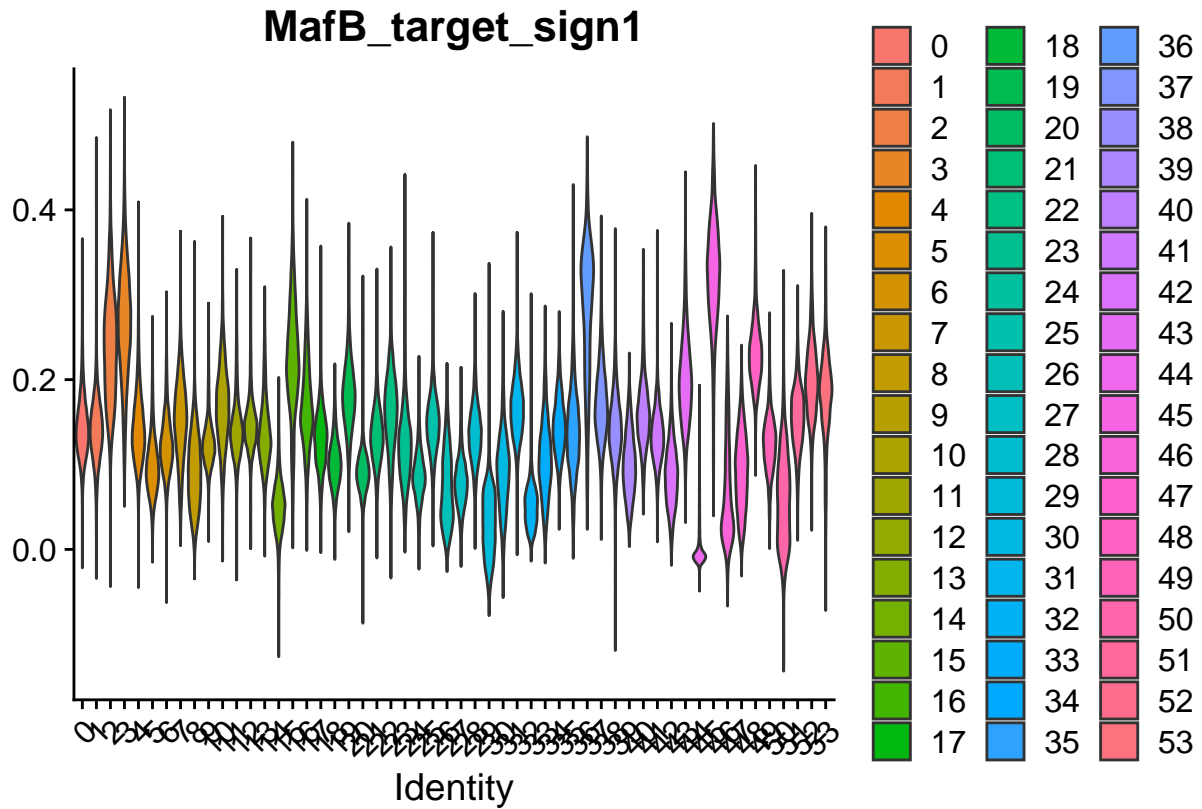
```
FeatureScatter(tbms, feature1 = "Mafb", feature2 = "MafB_target_sign1") +
    geom_smooth(method = "lm", colour = "black") + theme(legend.position = "none")
```
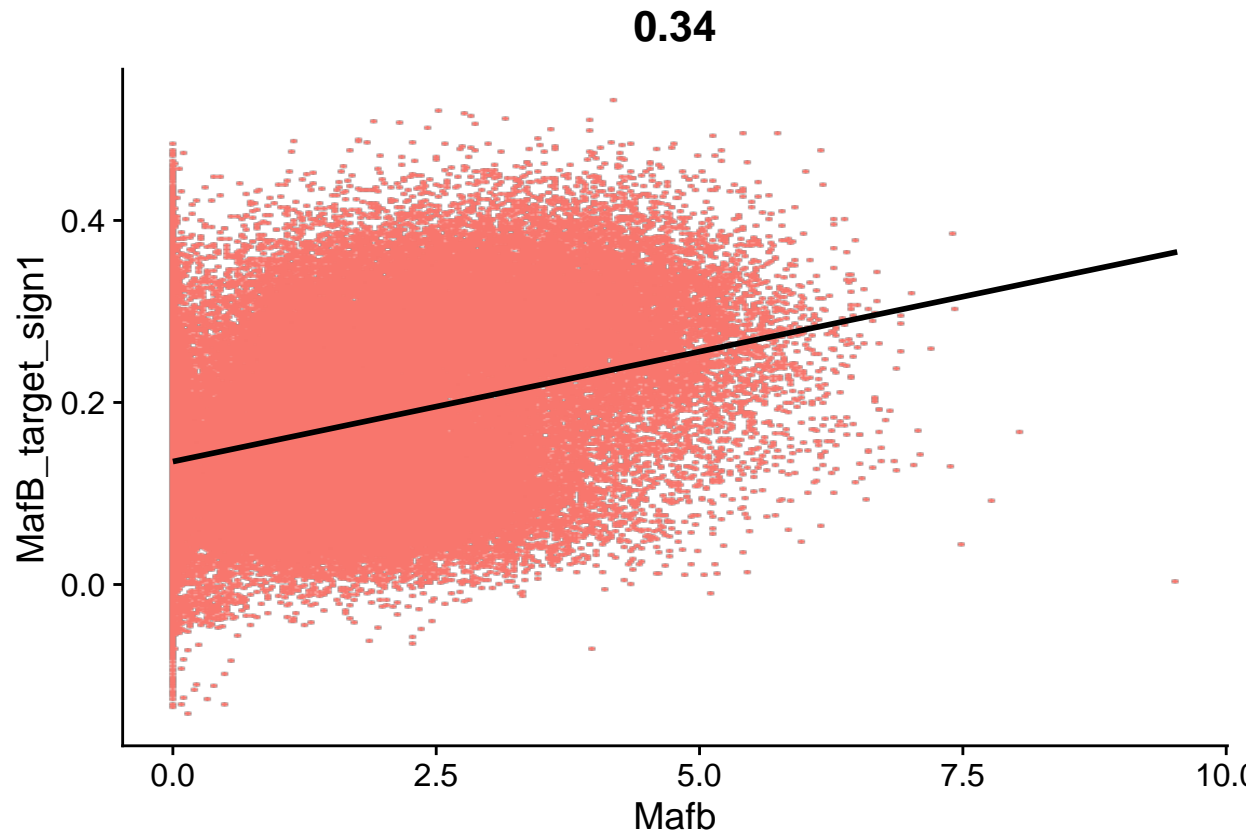
```
## Rasterizing points since number of points exceeds 100,000.
## To disable this behavior set `raster=FALSE`
```

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

0.34


```
corr <- cbind(corr, FetchData(tbms, 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 = 216.86, df = 356211, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3386011 0.3444030
## sample estimates:
##       cor
## 0.3415053
```

```
p3 <- ggplot(corr, aes(x = Mafb, y = MafB_target_sign1)) + geom_point(size = 0.1,
    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'
```
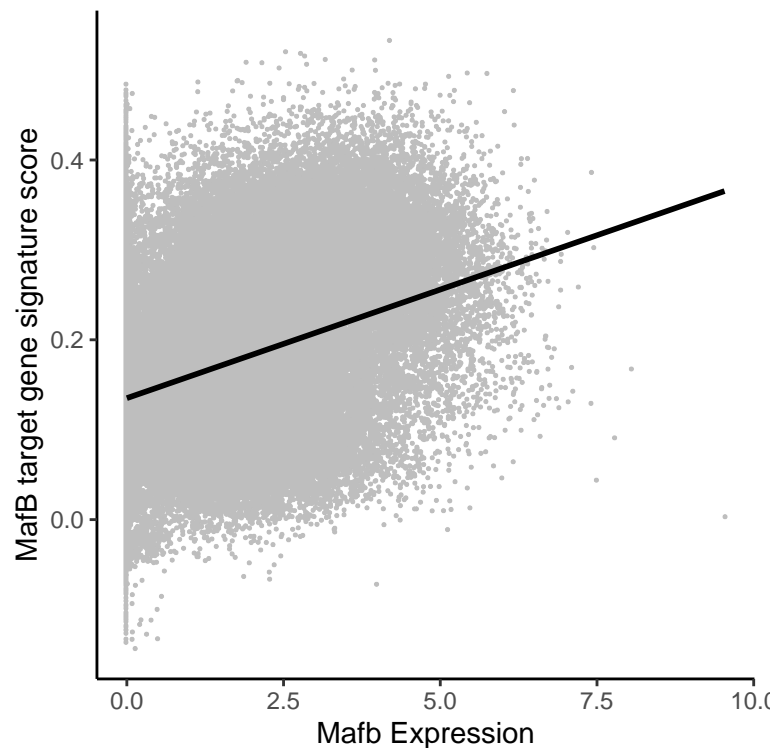
```
sessionInfo()
```

```
## 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-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/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] ggrastr_1.0.2      readxl_1.4.3      dplyr_1.1.4         ggplot2_3.4.4
## [5] 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    reticulate_1.39.0
##  [40] parallelly_1.26.0      spatstat.univar_3.0-1  cellranger_1.1.0
##  [43] lmtest_0.9-38          scattermore_0.7        Rcpp_1.0.13
##  [46] knitr_1.48             tensor_1.5             future.apply_1.7.0
##  [49] zoo_1.8-9              sctransform_0.4.1      httpuv_1.6.1
##  [52] Matrix_1.6-1.1         splines_4.4.1          igraph_1.2.6
##  [55] tidyselect_1.2.1       abind_1.4-5            rstudioapi_0.16.0
##  [58] yaml_2.2.1             spatstat.random_3.3-2  codetools_0.2-19
##  [61] miniUI_0.1.1.1         spatstat.explore_3.3-2 listenv_0.8.0
##  [64] lattice_0.22-5         tibble_3.2.1           plyr_1.8.6
##  [67] withr_3.0.1            shiny_1.9.1            ROCR_1.0-11
##  [70] evaluate_1.0.0         Rtsne_0.15             future_1.21.0
##  [73] survival_3.7-0         polyclip_1.10-0        fitdistrplus_1.1-5
##  [76] pillar_1.9.0           KernSmooth_2.23-24     plotly_4.10.4
##  [79] generics_0.1.0         munsell_0.5.1          scales_1.3.0
##  [82] globals_0.14.0         xtable_1.8-4           glue_1.7.0
##  [85] lazyeval_0.2.2         tools_4.4.1            data.table_1.14.0
##  [88] RANN_2.6.1             leiden_0.3.8           Cairo_1.6-2
##  [91] cowplot_1.1.1          grid_4.4.1             tidyr_1.3.1
##  [94] colorspace_2.1-1       nlme_3.1-165           patchwork_1.1.1
##  [97] beeswarm_0.4.0         vipor_0.4.7            cli_3.6.3
## [100] spatstat.sparse_3.1-0  fansi_1.0.6            viridisLite_0.4.2
## [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      htmltools_0.5.8.1      lifecycle_1.0.4
## [112] httr_1.4.7             mime_0.11              MASS_7.3-61
```