

scRNA-Seq RTM WT vs KO - Signature scoring

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2024-12-16 20:51:15 +0100

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Introduction

To objectively examine the effects of MafB deficiency on global and subset-specific mac identity, we used the global mac signature score generated above and created RTM subset-specific scores based on the DEGs of each RTM subset compared to other RTM in our scRNA-seq data. Interestingly, global mac signature scores were all significantly lower in Mafb-deficient RTMs as compared to their wild-type counterparts, except for MHC-II+ CM. Moreover, we found that each RTM subsets from Lyz2CreMafbfl/fl mice, except for SPM and IM, exhibited a significantly lower score for RTM-subset specific signatures as compared to their wild-type controls. Fourth, we mapped the monocyte signature and found that all Mafb-deficient RTM, except Ly6C+ CM, exhibited a significantly higher monocyte score as compared to wild-type RTM. These findings collectively support a profound disruption in global mac and RTM subset-specific identities in the absence of MafB in vivo, as well as a monocyte signature suggestive of immaturity and incomplete differentiation.

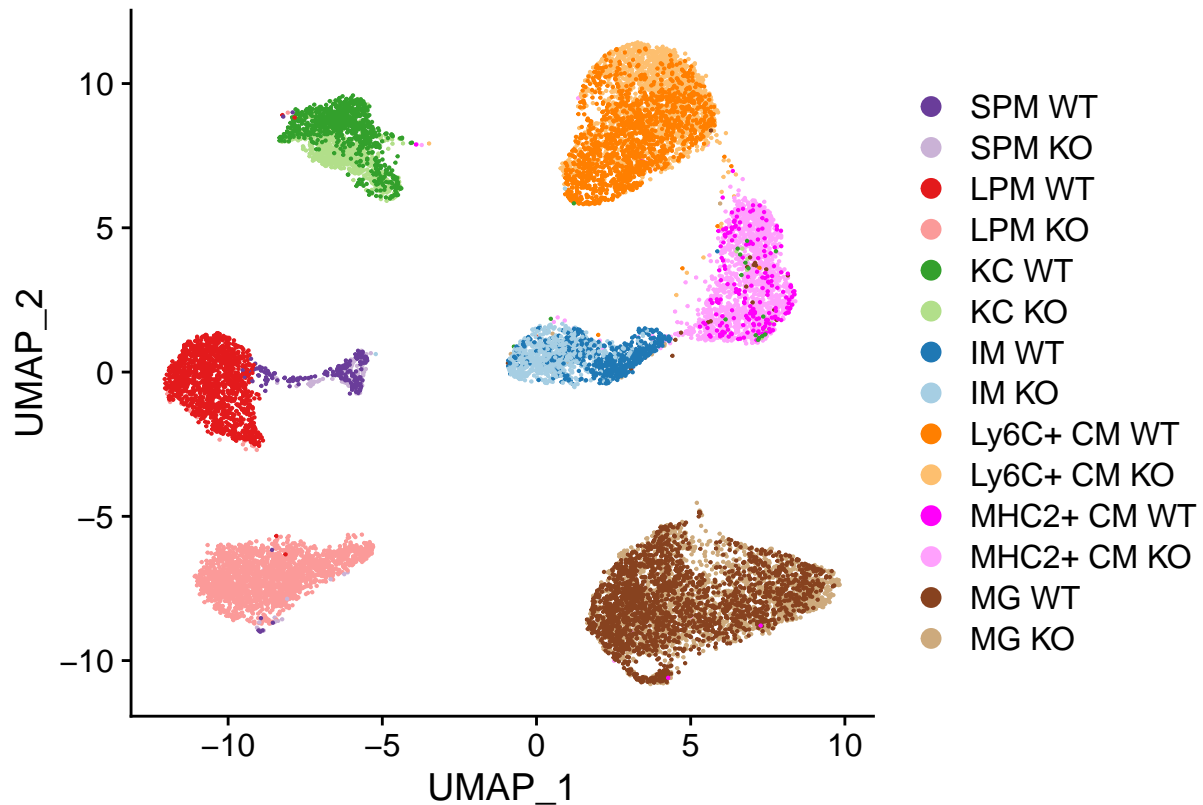
We identified MafB target genes by CUT&RUN on BMDM and found that the expression of MafB target genes was reduced in all RTM subsets from Lyz2CreMafbfl/fl mice. One binding site of MafB was situated in the Csf1r FIRE enhancer. Csf1r expression was reduced in SPM, KC and IM from Lyz2CreMafbfl/fl mice.

Load packages

```
suppressMessages({  
  library(Seurat)  
  library(SeuratObject)  
  library(limma)  
  library(ggplot2)  
  library(RColorBrewer)  
  library(dplyr)  
  library(readxl)  
})
```

Load Seurat object

```
sc <- readRDS("sc.rds")  
  
pal <- c("#6A3D9A", "#CAB2D6", "#E31A1C", "#FB9A99", "#33A02C",  
        "#B2DF8A", "#1F78B4", "#A6CEE3", "#FF7F00", "#FDBF6F", "#FF00FA",  
        "#FFA1FD", "#87421F", "#CDAA7D")  
  
DimPlot(sc, cols = pal)
```



Signature scoring

Macrophage signature score

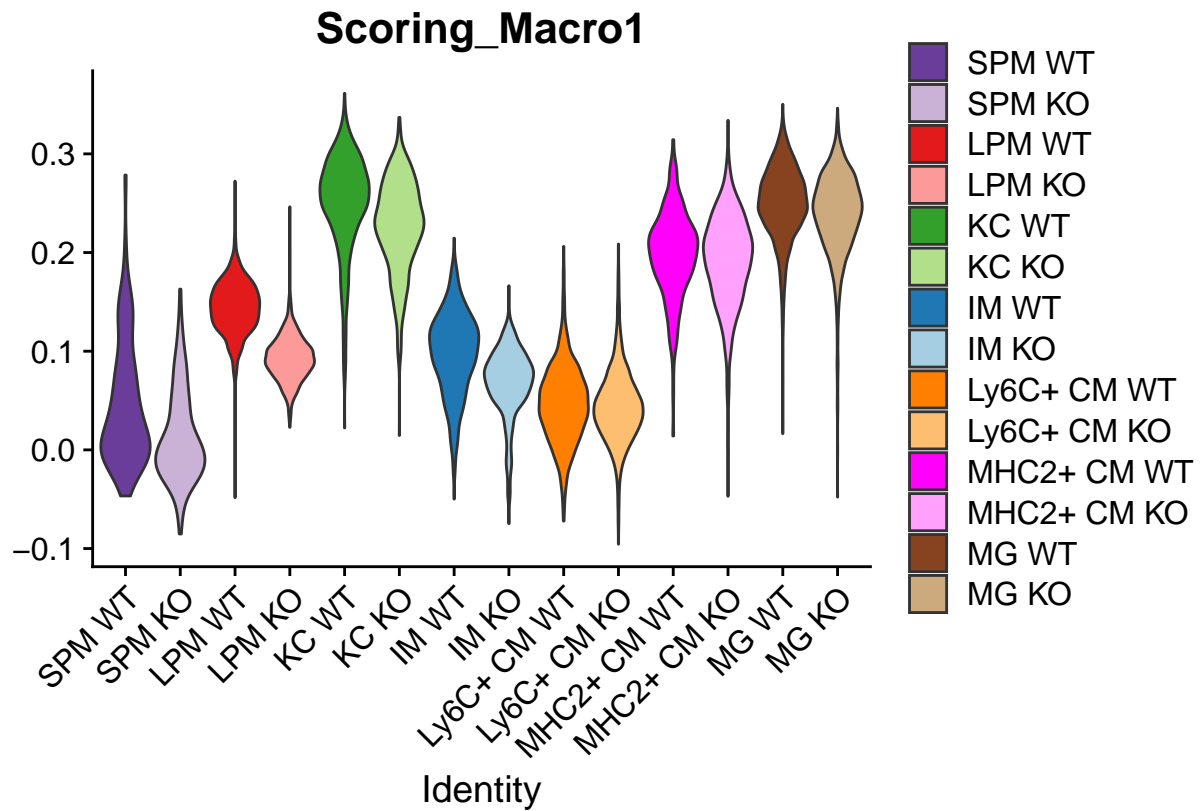
```
MacvscMo <- read.csv("Mac_sign.csv", header = T)

Mac.genes <- list(MacvscMo$Gene_Symbol)

sc <- AddModuleScore(sc, features = Mac.genes, name = "Scoring_Macro")

## Warning: The following features are not present in the object: Gm10134, Rny3,
## Snord49b, Pvt1, Rny1, Snord61, A930039A15Rik, Vaultrc5, Rnu3b1, Snord22,
## 9830001H06Rik, Rnu12, Snord47, F630111L10Rik, Epb4111, Snora16a, Snord15b,
## Snord16a, AW112010, B930036N10Rik, LOC100504914, Entpd4, Lphn2, Firre,
## Snord32a, G530011006Rik, Mir29c, Snord118, Snord35b, Snord35a, Gm6762, Snord3a,
## 39692, Snord116, Snord55, Snord73b, 3222401L13Rik, Vstm2a, Snord104, Gas5,
## Lipo1, Atosa, Stxbp3a, Gm10790, Malat1, Gm12191, C1rb, Snora7a, Ccr111, Phxr4,
## Snord49a, Lipf, Mir99ahg, Gm9909, Gm2897, Ppp4r3c1, C4a, not searching for
## symbol synonyms

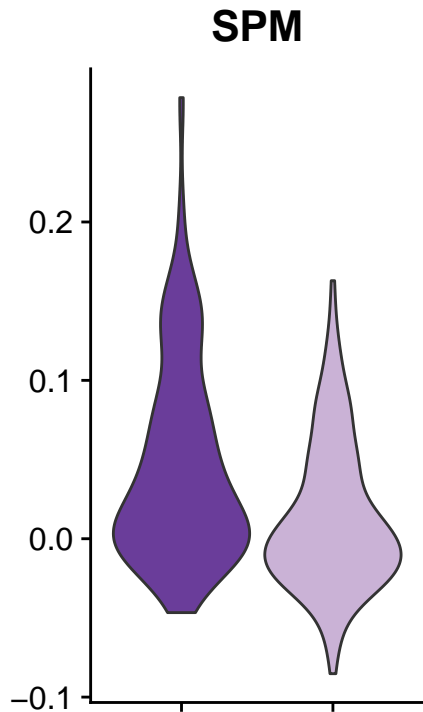
VlnPlot(sc, features = "Scoring_Macro1", cols = pal, pt.size = 0)
```



SPM

```
pal_SPM <- c("#6A3D9A", "#CAB2D6")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_SPM, pt.size = 0,
  idents = c("SPM WT", "SPM KO")) + ggtitle("SPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
metadata <- sc@meta.data
SPM_WT <- metadata[metadata$Condition == "SPM WT", ]
SPM_KO <- metadata[metadata$Condition == "SPM KO", ]

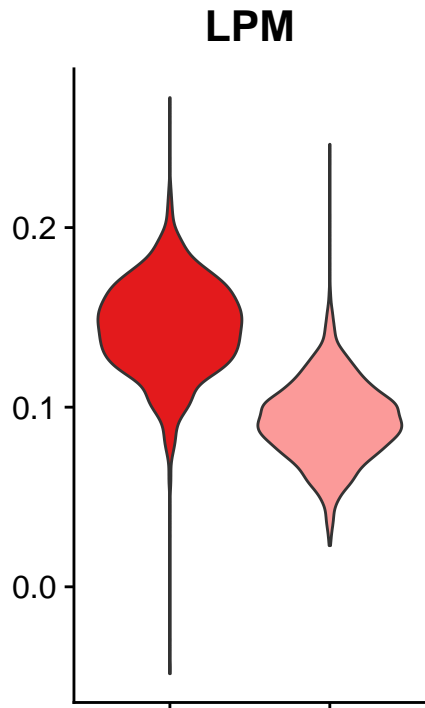
wilcox.test(SPM_WT$Scoring_Macro1, SPM_KO$Scoring_Macro1) #2.154e-07
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: SPM_WT$Scoring_Macro1 and SPM_KO$Scoring_Macro1
## W = 18790, p-value = 2.154e-07
## alternative hypothesis: true location shift is not equal to 0
```

LPM

```
pal_LPM <- c("#e31a1c", "#fb9a99")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_LPM, pt.size = 0,
  ids = c("LPM WT", "LPM KO")) + ggtitle("LPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
LPM_WT <- metadata[metadata$Condition == "LPM WT", ]
LPM_KO <- metadata[metadata$Condition == "LPM KO", ]

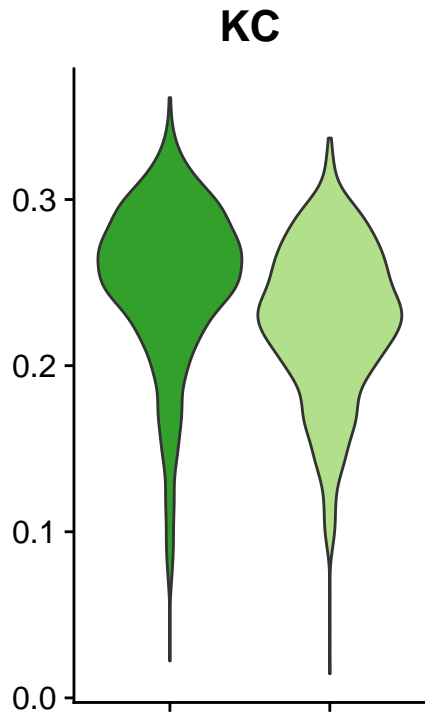
wilcox.test(LPM_WT$Scoring_Macro1, LPM_KO$Scoring_Macro1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: LPM_WT$Scoring_Macro1 and LPM_KO$Scoring_Macro1
## W = 2813333, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

KC

```
pal_KC <- c("#33a02c", "#b2df8a")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_KC, pt.size = 0,
  ident = c("KC WT", "KC KO")) + ggtitle("KC") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
KC_WT <- metadata[metadata$Condition == "KC WT", ]
KC_KO <- metadata[metadata$Condition == "KC KO", ]

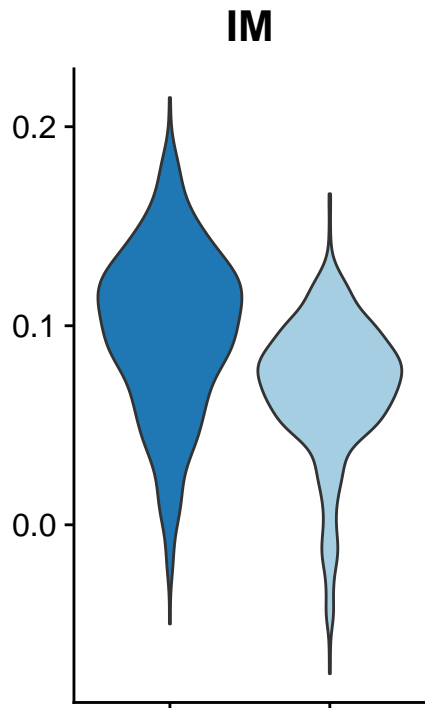
wilcox.test(KC_WT$Scoring_Macro1, KC_KO$Scoring_Macro1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$Scoring_Macro1 and KC_KO$Scoring_Macro1
## W = 422529, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

IM

```
pal_IM <- c("#1f78b4", "#a6cee3")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_IM, pt.size = 0,
  ids = c("IM WT", "IM KO")) + ggtitle("IM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
IM_WT <- metadata[metadata$Condition == "IM WT", ]
IM_KO <- metadata[metadata$Condition == "IM KO", ]

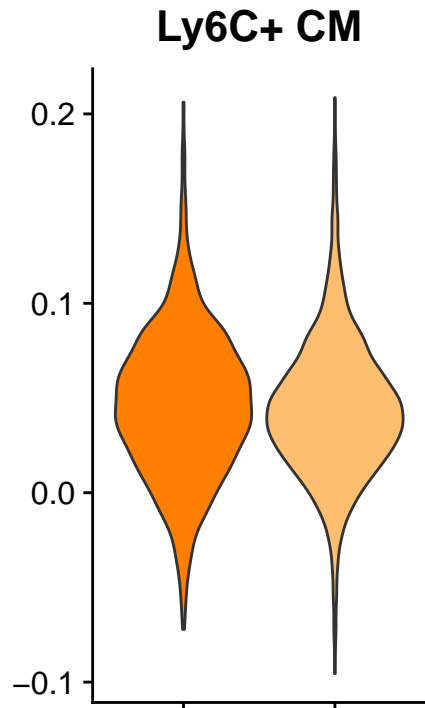
wilcox.test(IM_WT$Scoring_Macro1, IM_KO$Scoring_Macro1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$Scoring_Macro1 and IM_KO$Scoring_Macro1
## W = 314330, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

Ly6C+ CM

```
pal_Ly6C <- c("#FF7F00", "#FDBF6F")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_Ly6C, pt.size = 0,
  ids = c("Ly6C+ CM WT", "Ly6C+ CM KO")) + ggtitle("Ly6C+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```

```
Ly6C_WT <- metadata[metadata$Condition == "Ly6C+ CM WT", ]
Ly6C_KO <- metadata[metadata$Condition == "Ly6C+ CM KO", ]

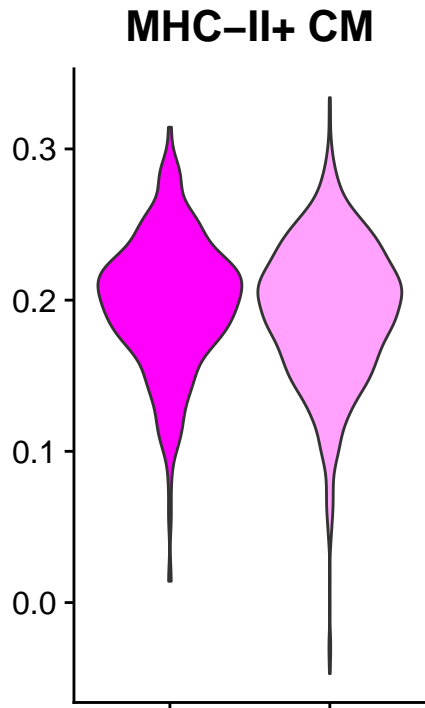
wilcox.test(Ly6C_WT$Scoring_Macro1, Ly6C_KO$Scoring_Macro1) #0.02762
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: Ly6C_WT$Scoring_Macro1 and Ly6C_KO$Scoring_Macro1
## W = 1321543, p-value = 0.02762
## alternative hypothesis: true location shift is not equal to 0
```

MHC-II+ CM

```
pal_MHC2 <- c("#FF00FA", "#FFA1FD")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_MHC2, pt.size = 0,
  ids = c("MHC2+ CM WT", "MHC2+ CM KO")) + ggtitle("MHC-II+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



```
MHC2_WT <- metadata[metadata$Condition == "MHC2+ CM WT", ]
MHC2_KO <- metadata[metadata$Condition == "MHC2+ CM KO", ]

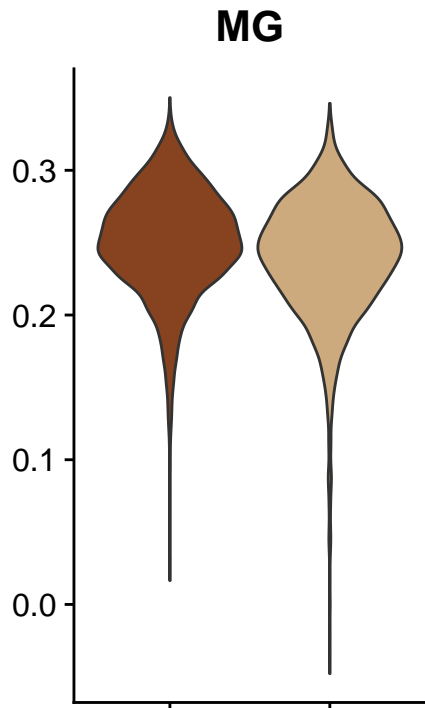
wilcox.test(MHC2_WT$Scoring_Macro1, MHC2_KO$Scoring_Macro1) #0.1286
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MHC2_WT$Scoring_Macro1 and MHC2_KO$Scoring_Macro1
## W = 155320, p-value = 0.1286
## alternative hypothesis: true location shift is not equal to 0
```

MG

```
pal_MG <- c("#87421F", "#CDAA7D")

VlnPlot(sc, features = "Scoring_Macro1", cols = pal_MG, pt.size = 0,
  ids = c("MG WT", "MG KO")) + ggtitle("MG") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

wilcox.test(MG_WT$Scoring_Macro1, MG_KO$Scoring_Macro1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$Scoring_Macro1 and MG_KO$Scoring_Macro1
## W = 2359869, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

RTM subset specific signature score

```
wt <- subset(sc, idents = c("SPM WT", "LPM WT", "KC WT", "IM WT",
  "Ly6C+ CM WT", "MHC2+ CM WT", "MG WT"))

markers <- FindAllMarkers(wt, only.pos = TRUE)
```

```
## Calculating cluster SPM WT
```

```
## Calculating cluster LPM WT
```

```
## Calculating cluster KC WT
```

```
## Calculating cluster IM WT
```

```
## Calculating cluster Ly6C+ CM WT
```

```
## Calculating cluster MHC2+ CM WT
```

```
## Calculating cluster MG WT
```

```
write.csv(markers, file = "markers.csv")
```

```
markers <- read.csv("markers.csv", header = T, row.names = 1)
```

SPM

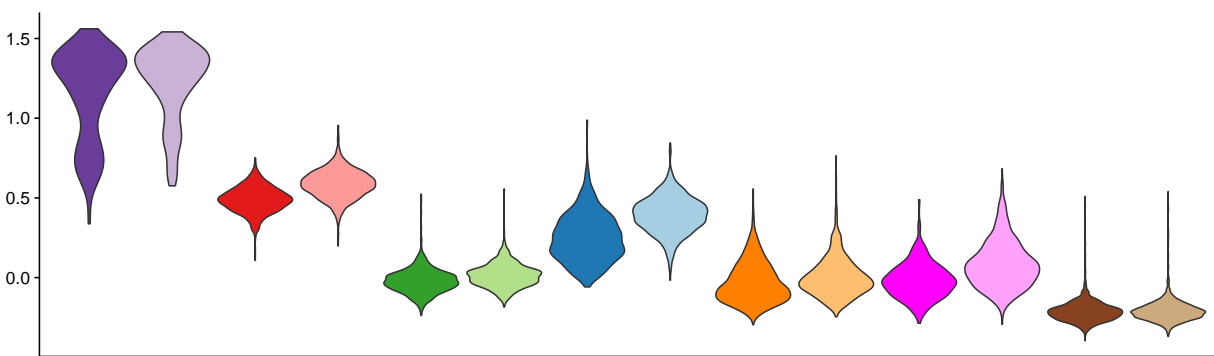
```
SPM.markers <- filter(markers, cluster == "SPM WT")
SPM.markers <- SPM.markers[SPM.markers$p_val_adj < 0.05 & abs(SPM.markers$avg_log2FC) >
  0.25, ]
SPM.markers <- SPM.markers[order(SPM.markers$avg_log2FC, decreasing = TRUE),
  ]
SPM.markers.top100 <- head(SPM.markers$gene, 100)

write.table(SPM.markers.top100, file = "SPM_sign.txt")

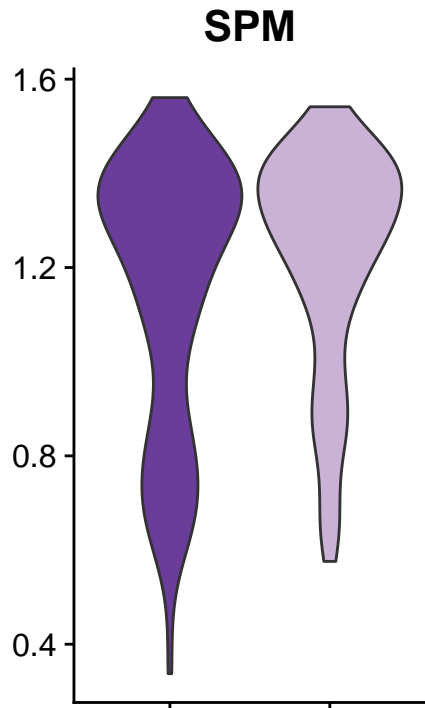
SPM.markers.top100 <- list(SPM.markers.top100)

sc <- AddModuleScore(sc, features = SPM.markers.top100, name = "SPM_sign")
```

```
VlnPlot(sc, features = "SPM_sign1", cols = pal, pt.size = 0) +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "SPM_sign1", cols = pal_SPM, pt.size = 0,
  ids = c("SPM WT", "SPM KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("SPM")
```



```
metadata <- sc@meta.data
SPM_WT <- metadata[metadata$Condition == "SPM WT", ]
SPM_KO <- metadata[metadata$Condition == "SPM KO", ]

wilcox.test(SPM_WT$SPM_sign1, SPM_KO$SPM_sign1) #0.03641
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: SPM_WT$SPM_sign1 and SPM_KO$SPM_sign1
## W = 12281, p-value = 0.03641
## alternative hypothesis: true location shift is not equal to 0
```

LPM

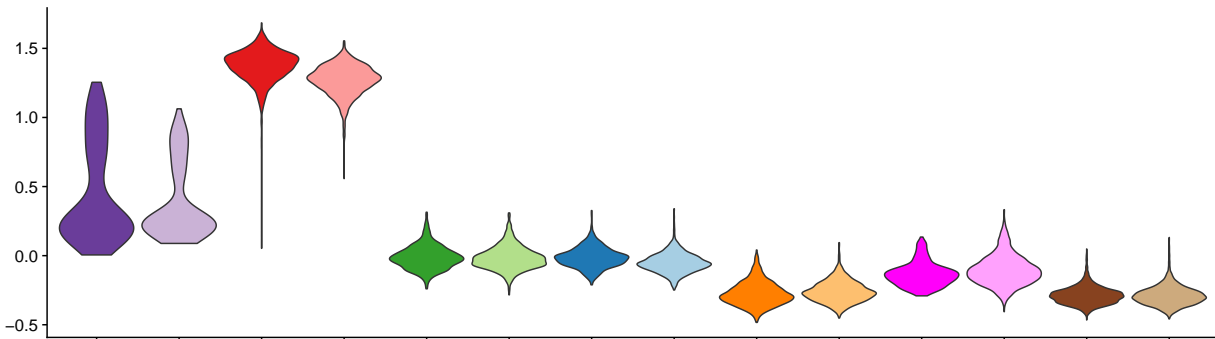
```
LPM.markers <- filter(markers, cluster == "LPM WT")
LPM.markers <- LPM.markers[LPM.markers$p_val_adj < 0.05 & abs(LPM.markers$avg_log2FC) >
0.25, ]
LPM.markers <- LPM.markers[order(LPM.markers$avg_log2FC, decreasing = TRUE),
]
LPM.markers.top100 <- head(LPM.markers$gene, 100)

write.table(LPM.markers.top100, file = "LPM_sign.txt")

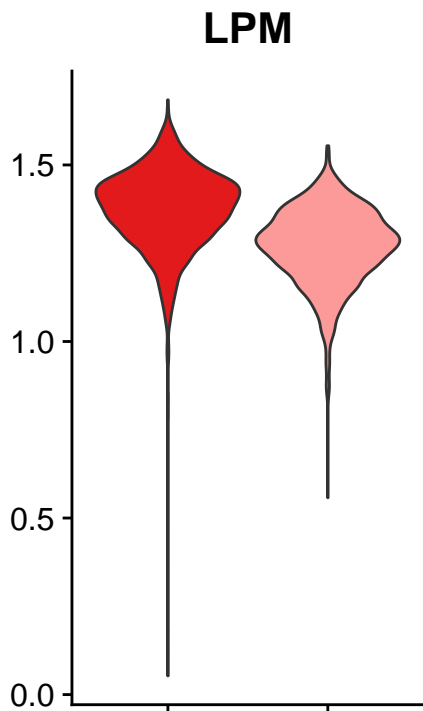
LPM.markers.top100 <- list(LPM.markers.top100)
```

```
sc <- AddModuleScore(sc, features = LPM.markers.top100, name = "LPM_sign")
```

```
VlnPlot(sc, features = "LPM_sign1", cols = pal, pt.size = 0) +  
  theme(legend.position = "none", axis.title.x = element_blank(),  
        axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "LPM_sign1", cols = pal_LPM, pt.size = 0,  
  ids = c("LPM WT", "LPM KO")) + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank()) +  
  ggtitle("LPM")
```



```
metadata <- sc@meta.data  
LPM_WT <- metadata[metadata$Condition == "LPM WT", ]
```

```
LPM_KO <- metadata[metadata$Condition == "LPM KO", ]

wilcox.test(LPM_WT$LPM_sign1, LPM_KO$LPM_sign1) #< 2.2e-16

##
## Wilcoxon rank sum test with continuity correction
##
## data: LPM_WT$LPM_sign1 and LPM_KO$LPM_sign1
## W = 2301210, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

KC

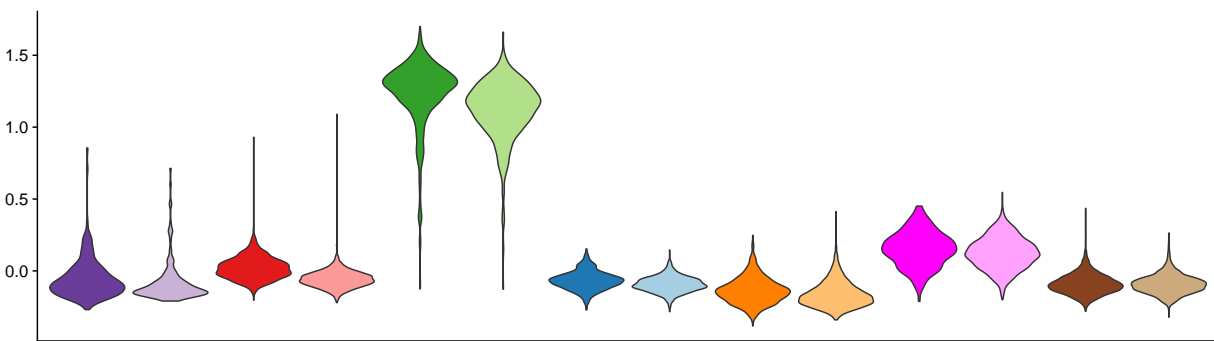
```
KC.markers <- filter(markers, cluster == "KC WT")
KC.markers <- KC.markers[KC.markers$p_val_adj < 0.05 & abs(KC.markers$avg_log2FC) >
  0.25, ]
KC.markers <- KC.markers[order(KC.markers$avg_log2FC, decreasing = TRUE),
  ]
KC.markers.top100 <- head(KC.markers$gene, 100)

write.table(KC.markers.top100, file = "KC_sign.txt")

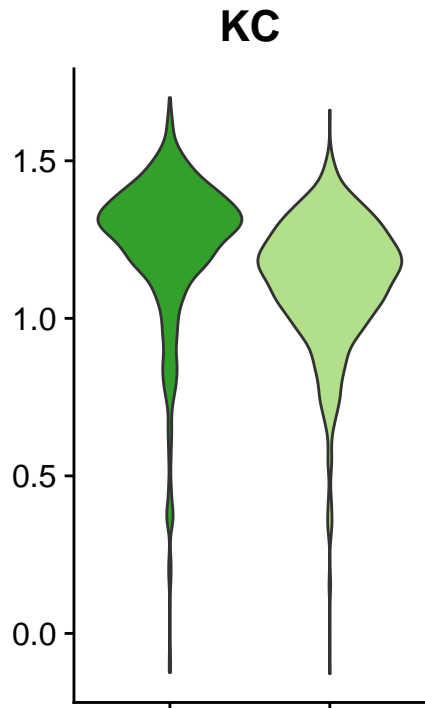
KC.markers.top100 <- list(KC.markers.top100)

sc <- AddModuleScore(sc, features = KC.markers.top100, name = "KC_sign")
```

```
VlnPlot(sc, features = "KC_sign1", cols = pal, pt.size = 0) +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "KC_sign1", cols = pal_KC, pt.size = 0,
  ids = c("KC WT", "KC KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("KC")
```



```
metadata <- sc@meta.data
KC_WT <- metadata[metadata$Condition == "KC WT", ]
KC_KO <- metadata[metadata$Condition == "KC KO", ]

wilcox.test(KC_WT$KC_sign1, KC_KO$KC_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$KC_sign1 and KC_KO$KC_sign1
## W = 451181, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

IM

```
IM.markers <- filter(markers, cluster == "IM WT")
IM.markers <- IM.markers[IM.markers$p_val_adj < 0.05 & abs(IM.markers$avg_log2FC) >
  0.25, ]
IM.markers <- IM.markers[order(IM.markers$avg_log2FC, decreasing = TRUE),
  ]
IM.markers.top100 <- head(IM.markers$gene, 100)

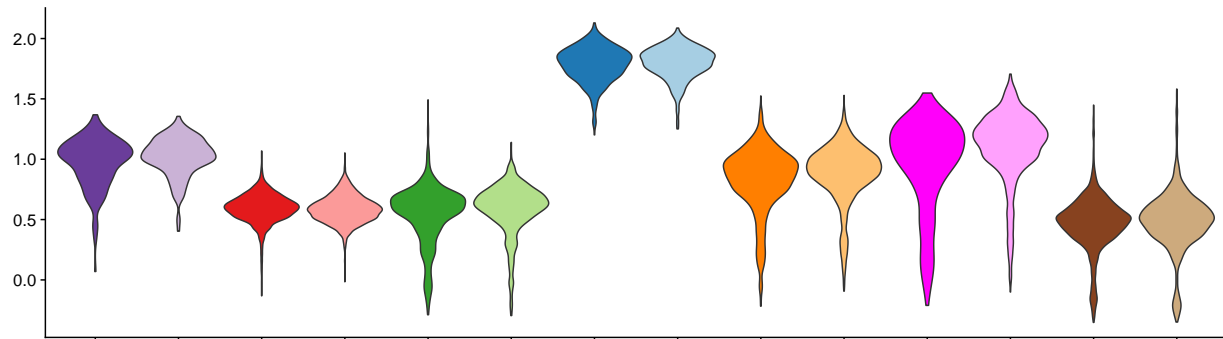
write.table(IM.markers.top100, file = "IM_sign.txt")

IM.markers.top100 <- list(IM.markers.top100)
```

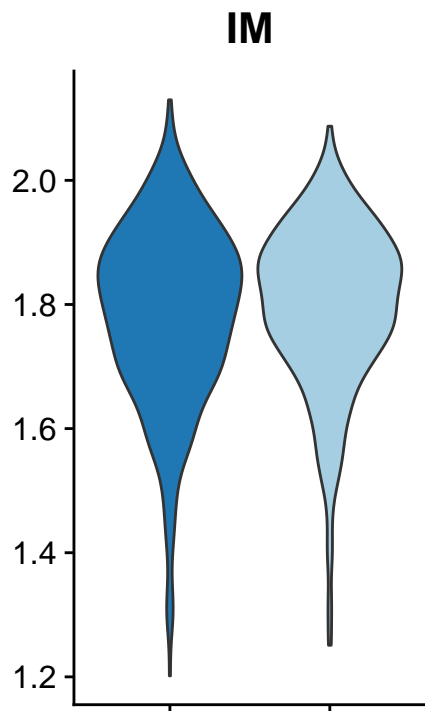


```
sc <- AddModuleScore(sc, features = IM.markers.top100, name = "IM_sign")
```

```
VlnPlot(sc, features = "IM_sign1", cols = pal, pt.size = 0) +  
  theme(legend.position = "none", axis.title.x = element_blank(),  
        axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "IM_sign1", cols = pal_IM, pt.size = 0,  
  ids = c("IM WT", "IM KO")) + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank()) +  
  ggtitle("IM")
```



```
metadata <- sc@meta.data  
IM_WT <- metadata[metadata$Condition == "IM WT", ]
```

```
IM_KO <- metadata[metadata$Condition == "IM KO", ]

wilcox.test(IM_WT$IM_sign1, IM_KO$IM_sign1) #0.1182

##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$IM_sign1 and IM_KO$IM_sign1
## W = 208587, p-value = 0.1182
## alternative hypothesis: true location shift is not equal to 0
```

Ly6C+ CM

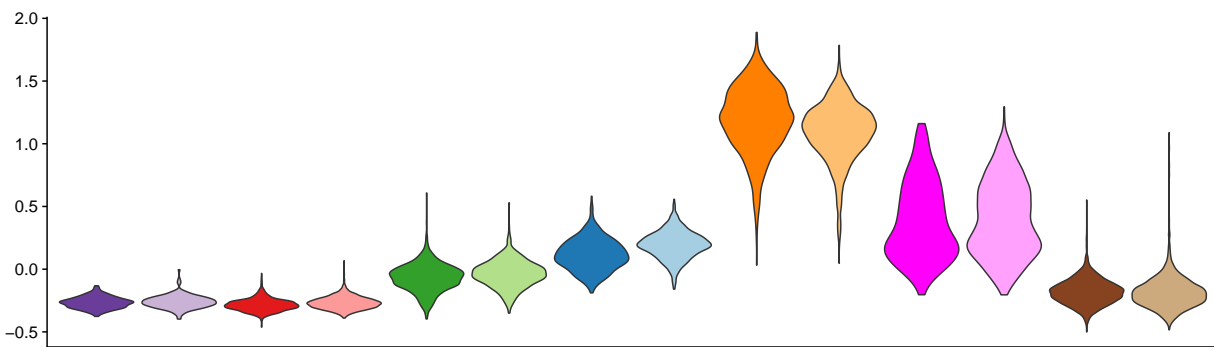
```
Ly6C.markers <- filter(markers, cluster == "Ly6C+ CM WT")
Ly6C.markers <- Ly6C.markers[Ly6C.markers$p_val_adj < 0.05 &
  abs(Ly6C.markers$avg_log2FC) > 0.25, ]
Ly6C.markers <- Ly6C.markers[order(Ly6C.markers$avg_log2FC, decreasing = TRUE),
  ]
Ly6C.markers.top100 <- head(Ly6C.markers$gene, 100)

write.table(Ly6C.markers.top100, file = "Ly6C_sign.txt")

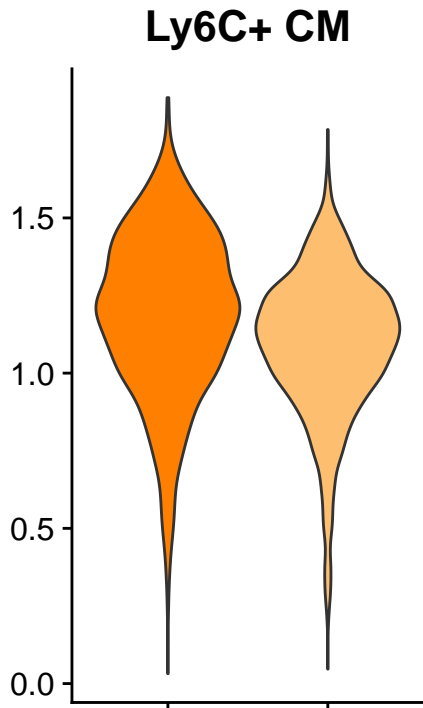
Ly6C.markers.top100 <- list(Ly6C.markers.top100)

sc <- AddModuleScore(sc, features = Ly6C.markers.top100, name = "Ly6C_sign")
```

```
VlnPlot(sc, features = "Ly6C_sign1", cols = pal, pt.size = 0) +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "Ly6C_sign1", cols = pal_Ly6C, pt.size = 0,
  idsents = c("Ly6C+ CM WT", "Ly6C+ CM KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("Ly6C+ CM")
```



```
metadata <- sc@meta.data
Ly6C_CM_WT <- metadata[metadata$Condition == "Ly6C+ CM WT", ]
Ly6C_CM_KO <- metadata[metadata$Condition == "Ly6C+ CM KO", ]

wilcox.test(Ly6C_CM_WT$Ly6C_sign1, Ly6C_CM_KO$Ly6C_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: Ly6C_CM_WT$Ly6C_sign1 and Ly6C_CM_KO$Ly6C_sign1
## W = 1556987, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

MHC-II+ CM

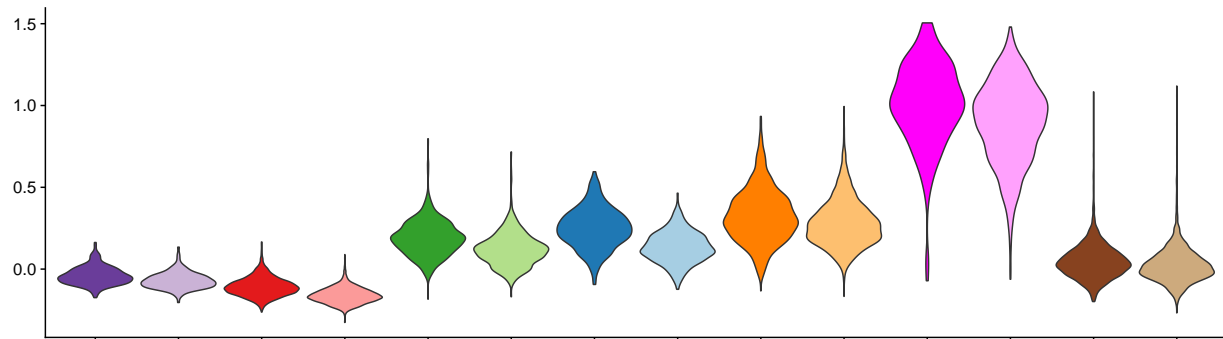
```
MHC2.markers <- filter(markers, cluster == "MHC2+ CM WT")
MHC2.markers <- MHC2.markers[MHC2.markers$p_val_adj < 0.05 &
  abs(MHC2.markers$avg_log2FC) > 0.25, ]
MHC2.markers <- MHC2.markers[order(MHC2.markers$avg_log2FC, decreasing = TRUE),
  ]
MHC2.markers.top100 <- head(MHC2.markers$gene, 100)

write.table(MHC2.markers.top100, file = "MHC2_sign.txt")

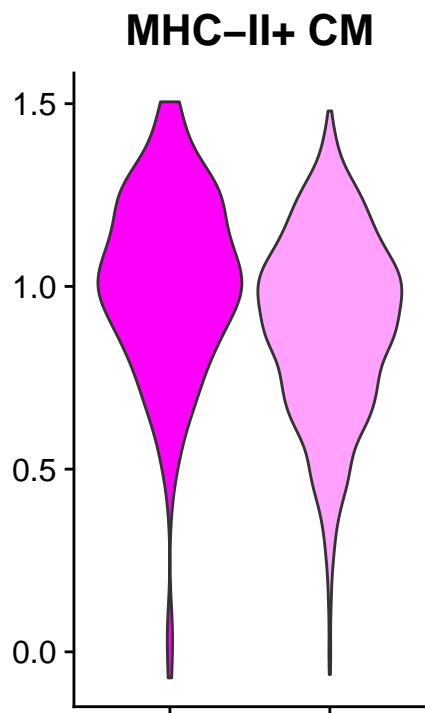
MHC2.markers.top100 <- list(MHC2.markers.top100)
```

```
sc <- AddModuleScore(sc, features = MHC2.markers.top100, name = "MHC2_sign")
```

```
VlnPlot(sc, features = "MHC2_sign1", cols = pal, pt.size = 0) +  
  theme(legend.position = "none", axis.title.x = element_blank(),  
        axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "MHC2_sign1", cols = pal_MHC2, pt.size = 0,  
  ids = c("MHC2+ CM WT", "MHC2+ CM KO")) + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank()) +  
  ggtitle("MHC-II+ CM")
```



```
metadata <- sc@meta.data  
MHC2_CM_WT <- metadata[metadata$Condition == "MHC2+ CM WT", ]
```

```
MHC2_CM_KO <- metadata[metadata$Condition == "MHC2+ CM KO", ]

wilcox.test(MHC2_CM_WT$MHC2_sign1, MHC2_CM_KO$MHC2_sign1) #2.388e-09
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MHC2_CM_WT$MHC2_sign1 and MHC2_CM_KO$MHC2_sign1
## W = 183967, p-value = 2.388e-09
## alternative hypothesis: true location shift is not equal to 0
```

MG

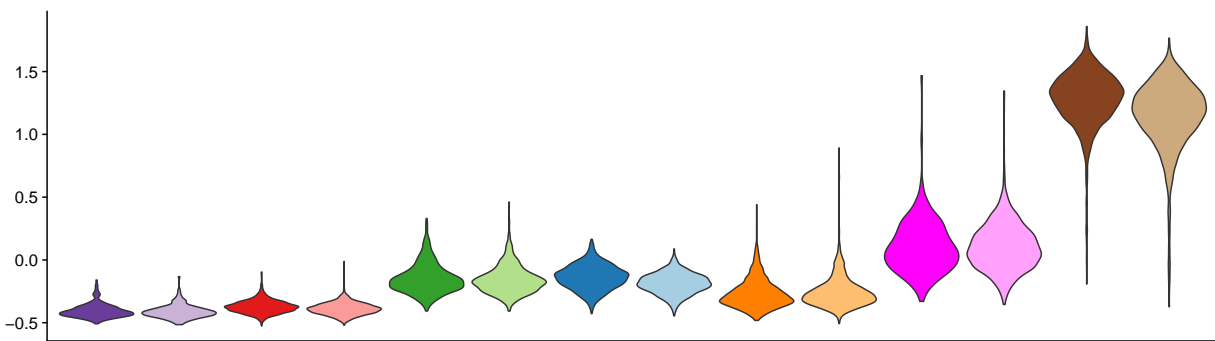
```
MG.markers <- filter(markers, cluster == "MG WT")
MG.markers <- MG.markers[MG.markers$p_val_adj < 0.05 & abs(MG.markers$avg_log2FC) >
  0.25, ]
MG.markers <- MG.markers[order(MG.markers$avg_log2FC, decreasing = TRUE),
  ]
MG.markers.top100 <- head(MG.markers$gene, 100)

write.table(MG.markers.top100, file = "MG_sign.txt")

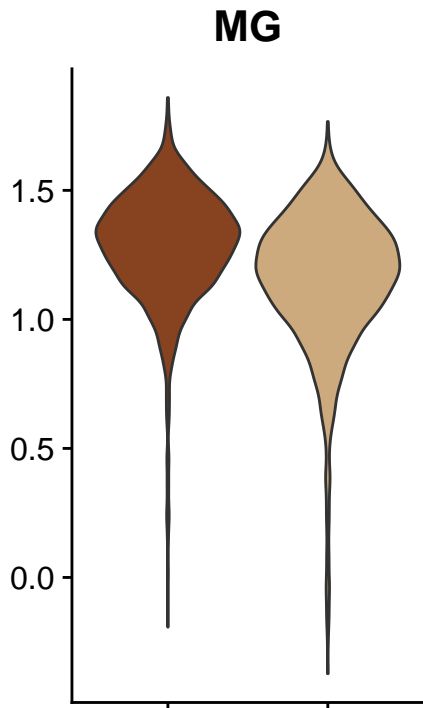
MG.markers.top100 <- list(MG.markers.top100)

sc <- AddModuleScore(sc, features = MG.markers.top100, name = "MG_sign")
```

```
VlnPlot(sc, features = "MG_sign1", cols = pal, pt.size = 0) +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank()) + ggtitle("")
```



```
VlnPlot(sc, features = "MG_sign1", cols = pal_MG, pt.size = 0,
  ids = c("MG WT", "MG KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("MG")
```



```
metadata <- sc@meta.data
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

wilcox.test(MG_WT$MG_sign1, MG_KO$MG_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$MG_sign1 and MG_KO$MG_sign1
## W = 2688279, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

Monocyte signature score

```
cMovsMac <- read.csv("Mo_sign.csv", header = T)

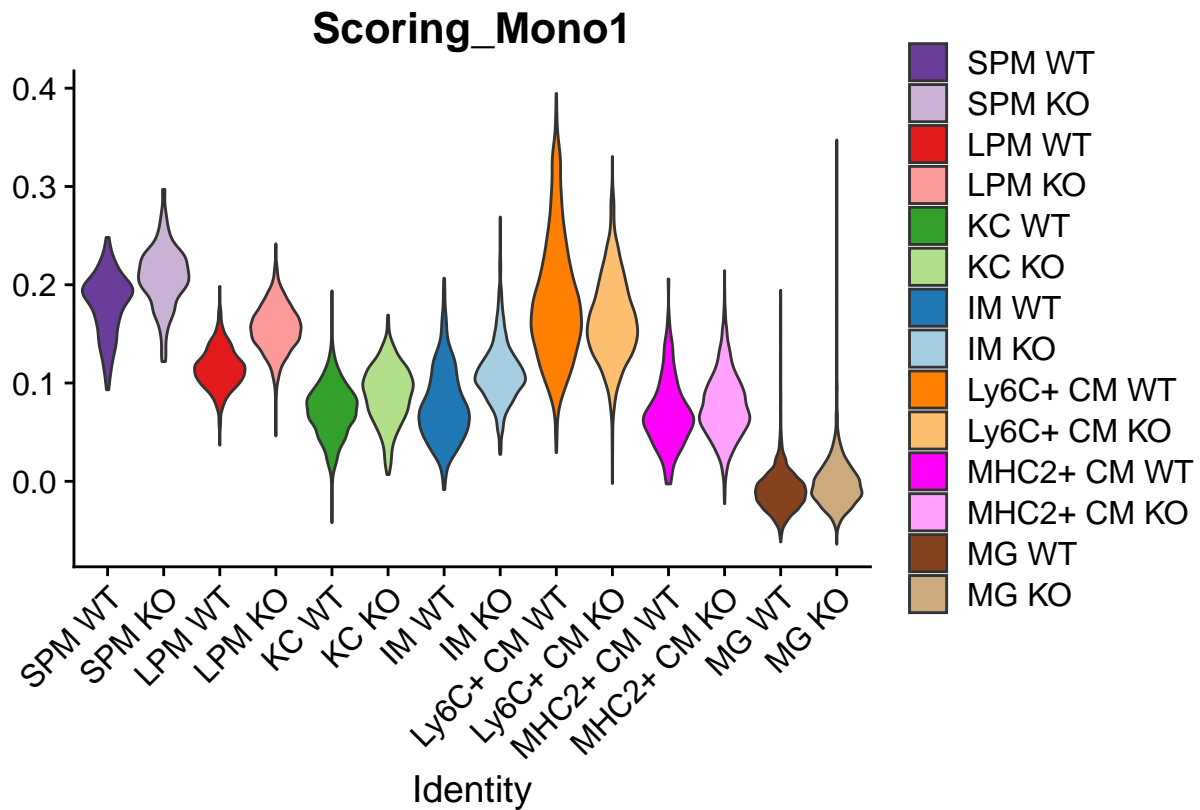
cMo.genes <- list(cMovsMac$Gene_Symbol)

sc <- AddModuleScore(sc, features = cMo.genes, name = "Scoring_Mono")
```

```
## Warning: The following features are not present in the object: Ly6a2,
## Serpinb10, E430024C06Rik, LOC625360, Hbb-b2, Hbb-b1, Mx1, Pira1, Morrbid, Mx2,
## Dleu2, Pira11, Mirt1, Mir223hg, Gm12250, 9330175E14Rik, Aim1, Oas1b, G6pd2,
## AI607873, 38961, Ugt1a9, 4930562F07Rik, Trex1, Prss34, Phospho1, Gm10759,
## 9430025C20Rik, Gvin3, 4930518I15Rik, Gm10099, Gas5, Mir15a, H2-T10,
```

```
## 2610524H06Rik, 4930426L09Rik, Mir17hg, Pgam2, Phf11, Gm10551, not searching for
## symbol synonyms
```

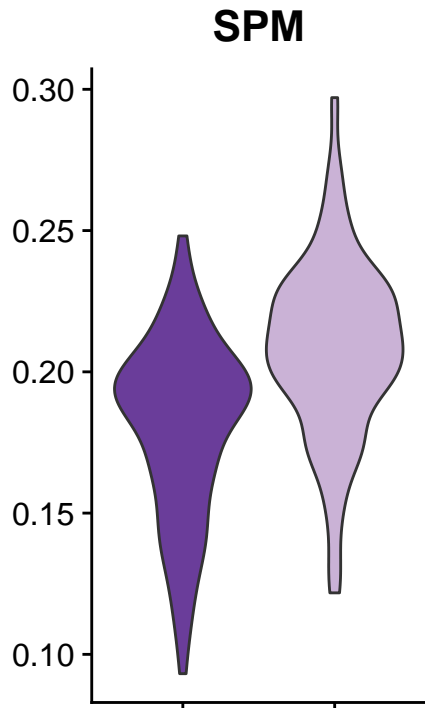
```
VlnPlot(sc, features = "Scoring_Mono1", cols = pal, pt.size = 0)
```



SPM

```
pal_SPM <- c("#6A3D9A", "#CAB2D6")
```

```
VlnPlot(sc, features = "Scoring_Mono1", cols = pal_SPM, pt.size = 0,
  ids = c("SPM WT", "SPM KO")) + ggtitle("SPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
metadata <- sc@meta.data
SPM_WT <- metadata[metadata$Condition == "SPM WT", ]
SPM_KO <- metadata[metadata$Condition == "SPM KO", ]

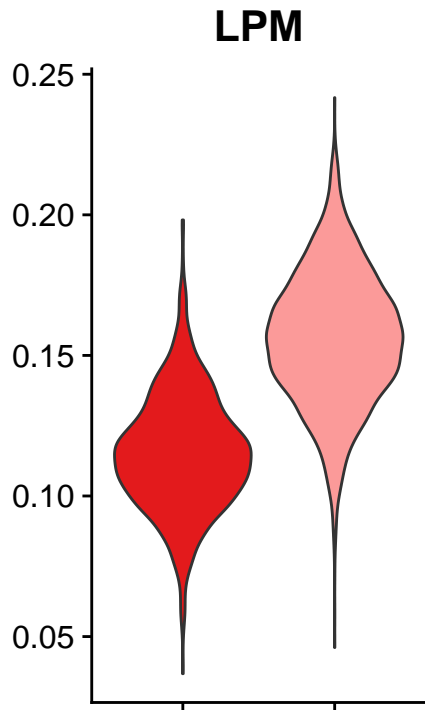
wilcox.test(SPM_WT$Scoring_Mono1, SPM_KO$Scoring_Mono1) #1.307e-14
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: SPM_WT$Scoring_Mono1 and SPM_KO$Scoring_Mono1
## W = 7262, p-value = 1.307e-14
## alternative hypothesis: true location shift is not equal to 0
```

LPM

```
pal_LPM <- c("#e31a1c", "#fb9a99")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_LPM, pt.size = 0,
  ids = c("LPM WT", "LPM KO")) + ggtitle("LPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```

```
LPM_WT <- metadata[metadata$Condition == "LPM WT", ]
LPM_KO <- metadata[metadata$Condition == "LPM KO", ]

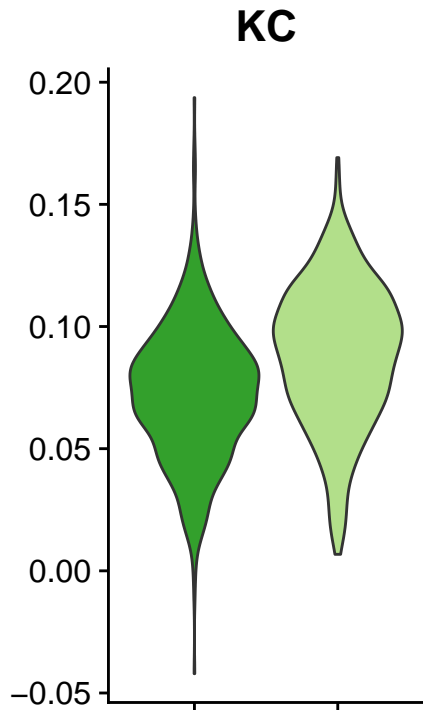
wilcox.test(LPM_WT$Scoring_Mono1, LPM_KO$Scoring_Mono1)  #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: LPM_WT$Scoring_Mono1 and LPM_KO$Scoring_Mono1
## W = 292555, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

KC

```
pal_KC <- c("#33a02c", "#b2df8a")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_KC, pt.size = 0,
  ids = c("KC WT", "KC KO")) + ggtitle("KC") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
KC_WT <- metadata[metadata$Condition == "KC WT", ]
KC_KO <- metadata[metadata$Condition == "KC KO", ]

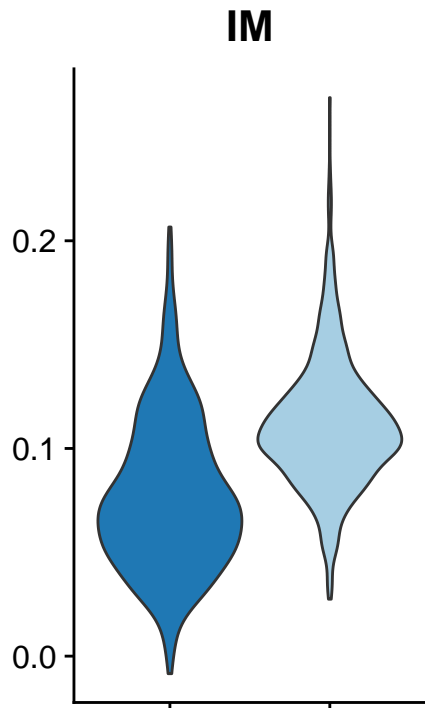
wilcox.test(KC_WT$Scoring_Mono1, KC_KO$Scoring_Mono1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$Scoring_Mono1 and KC_KO$Scoring_Mono1
## W = 213858, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

IM

```
pal_IM <- c("#1f78b4", "#a6cee3")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_IM, pt.size = 0,
  ids = c("IM WT", "IM KO")) + ggtitle("IM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
IM_WT <- metadata[metadata$Condition == "IM WT", ]
IM_KO <- metadata[metadata$Condition == "IM KO", ]

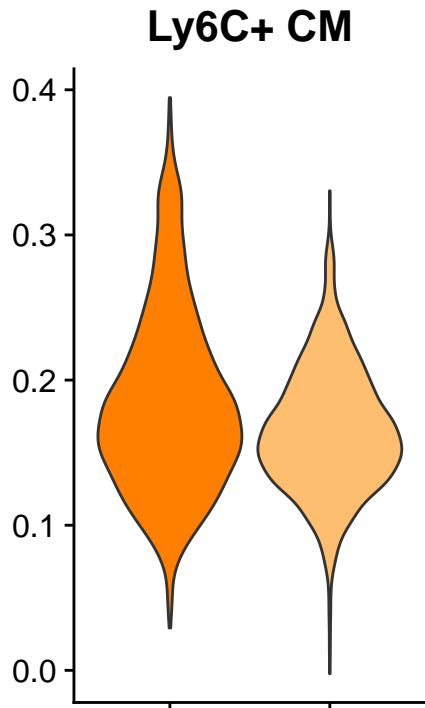
wilcox.test(IM_WT$Scoring_Mono1, IM_KO$Scoring_Mono1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$Scoring_Mono1 and IM_KO$Scoring_Mono1
## W = 98864, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

Ly6C+ CM

```
pal_Ly6C <- c("#FF7F00", "#FDBF6F")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_Ly6C, pt.size = 0,
  ids = c("Ly6C+ CM WT", "Ly6C+ CM KO")) + ggtitle("Ly6C+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



```
Ly6C_WT <- metadata[metadata$Condition == "Ly6C+ CM WT", ]
Ly6C_KO <- metadata[metadata$Condition == "Ly6C+ CM KO", ]

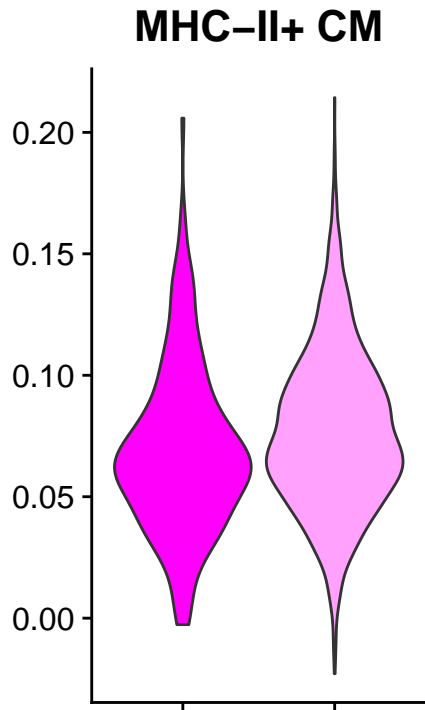
wilcox.test(Ly6C_WT$Scoring_Mono1, Ly6C_KO$Scoring_Mono1) #1.205e-14
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: Ly6C_WT$Scoring_Mono1 and Ly6C_KO$Scoring_Mono1
## W = 1464721, p-value = 1.205e-14
## alternative hypothesis: true location shift is not equal to 0
```

MHC-II+ CM

```
pal_MHC2 <- c("#FF00FA", "#FFA1FD")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_MHC2, pt.size = 0,
  ident = c("MHC2+ CM WT", "MHC2+ CM KO")) + ggtitle("MHC-II+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



```
MHC2_WT <- metadata[metadata$Condition == "MHC2+ CM WT", ]
MHC2_KO <- metadata[metadata$Condition == "MHC2+ CM KO", ]

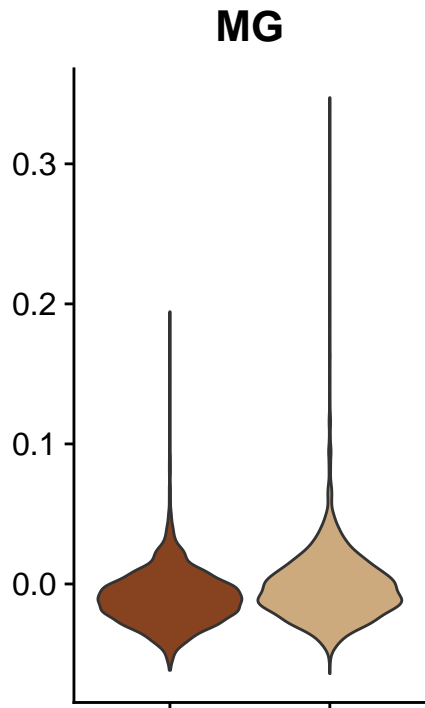
wilcox.test(MHC2_WT$Scoring_Mono1, MHC2_KO$Scoring_Mono1) #0.0005466
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MHC2_WT$Scoring_Mono1 and MHC2_KO$Scoring_Mono1
## W = 123279, p-value = 0.0005466
## alternative hypothesis: true location shift is not equal to 0
```

MG

```
pal_MG <- c("#87421F", "#CDAA7D")

VlnPlot(sc, features = "Scoring_Mono1", cols = pal_MG, pt.size = 0,
  ids = c("MG WT", "MG KO")) + ggtitle("MG") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

wilcox.test(MG_WT$Scoring_Mono1, MG_KO$Scoring_Mono1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$Scoring_Mono1 and MG_KO$Scoring_Mono1
## W = 1634349, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

Embrionically derived mac and Monocyte derived mac signature score

KC

```
Microarray_KC_EMvsMo <- read_excel("Microarray_KC_EMvsMo.xlsx")
Microarray_KC_EMvsMo <- na.omit(Microarray_KC_EMvsMo)
Microarray_KC_EMvsMo <- Microarray_KC_EMvsMo[Microarray_KC_EMvsMo$adj.P.Val <
  0.05 & abs(Microarray_KC_EMvsMo$logFC) > 1, ]

write.csv(Microarray_KC_EMvsMo, file = "Microarray_KC_EMvsMo.csv")

EM_KC_sign <- Microarray_KC_EMvsMo[Microarray_KC_EMvsMo$logFC >
  1, ]$Gene.symbol
```

```
EM_KC_sign <- list(EM_KC_sign)

sc <- AddModuleScore(sc, features = EM_KC_sign, name = "EM_KC_sign")

## Warning: The following features are not present in the object: Snurf///Snrpn,
## not searching for symbol synonyms

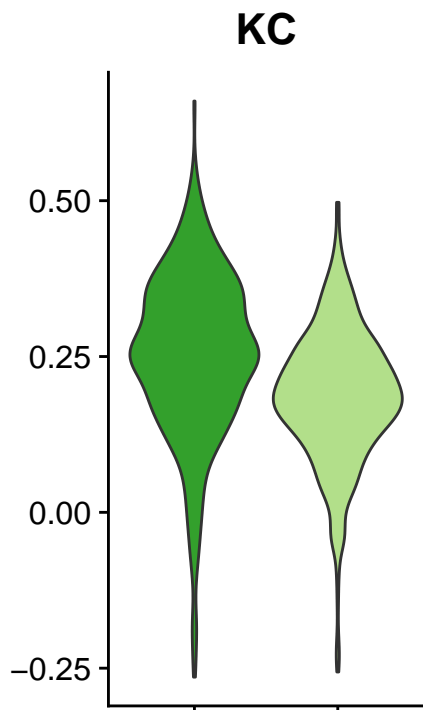
Mo_KC_sign <- Microarray_KC_EMvsMo[Microarray_KC_EMvsMo$logFC <
  -1, ]$Gene.symbol

Mo_KC_sign <- list(Mo_KC_sign)

sc <- AddModuleScore(sc, features = Mo_KC_sign, name = "Mo_KC_sign")

## Warning: The following features are not present in the object:
## LOC100038947///Sirpb1b///Sirpb1a, Ccdc109b, not searching for symbol synonyms

VlnPlot(sc, features = "EM_KC_sign1", cols = pal_KC, pt.size = 0,
  ids = c("KC WT", "KC KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("KC")
```

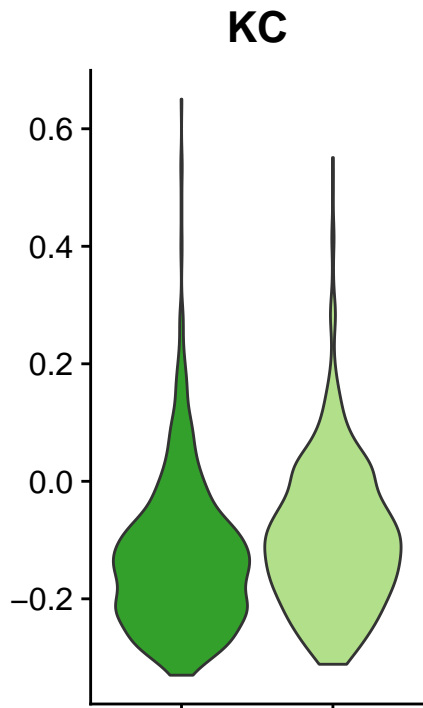


```
metadata <- sc@meta.data
KC_WT <- metadata[metadata$Condition == "KC WT", ]
KC_KO <- metadata[metadata$Condition == "KC KO", ]

wilcox.test(KC_WT$EM_KC_sign1, KC_KO$EM_KC_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$EM_KC_sign1 and KC_K0$EM_KC_sign1
## W = 427683, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

```
VlnPlot(sc, features = "Mo_KC_sign1", cols = pal_KC, pt.size = 0,
  ident = c("KC WT", "KC K0")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("KC")
```



```
wilcox.test(KC_WT$Mo_KC_sign1, KC_K0$Mo_KC_sign1) #P= 1.116e-10
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$Mo_KC_sign1 and KC_K0$Mo_KC_sign1
## W = 259572, p-value = 1.116e-10
## alternative hypothesis: true location shift is not equal to 0
```

IM

```
Bulk_RNAseq_IM_EMvsMo <- read_excel("Bulk_RNAseq_IM_EMvsMo.xlsx")

Bulk_RNAseq_IM_EMvsMo <- Bulk_RNAseq_IM_EMvsMo[Bulk_RNAseq_IM_EMvsMo$padj.y <
```



```

0.05 & abs(Bulk_RNAseq_IM_EMvsMo$log2FoldChange.y) > 1, ]

write.csv(Bulk_RNAseq_IM_EMvsMo, file = "Bulk_RNAseq_IM_EMvsMo.csv")

EM_IM_sign <- Bulk_RNAseq_IM_EMvsMo[Bulk_RNAseq_IM_EMvsMo$log2FoldChange.y <
-1, ]$Gene

EM_IM_sign <- list(EM_IM_sign)

sc <- AddModuleScore(sc, features = EM_IM_sign, name = "EM_IM_sign")

## Warning: The following features are not present in the object: H2.M2, not
## searching for symbol synonyms

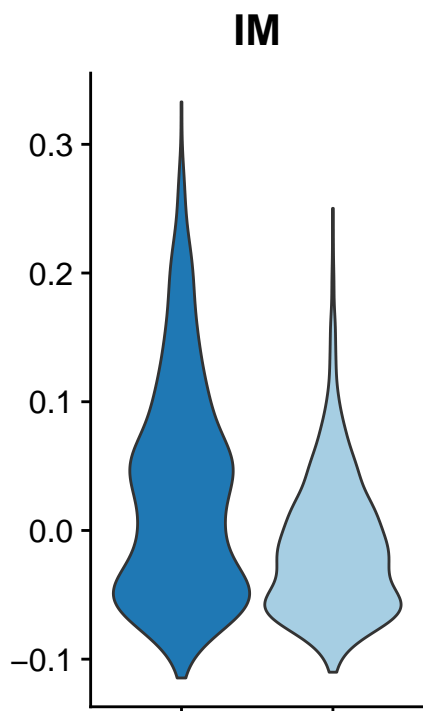
Mo_IM_sign <- Bulk_RNAseq_IM_EMvsMo[Bulk_RNAseq_IM_EMvsMo$log2FoldChange.y >
1, ]$Gene

Mo_IM_sign <- list(Mo_IM_sign)

sc <- AddModuleScore(sc, features = Mo_IM_sign, name = "Mo_IM_sign")

VlnPlot(sc, features = "EM_IM_sign1", cols = pal_IM, pt.size = 0,
  ids = c("IM WT", "IM KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("IM")

```



```

metadata <- sc@meta.data
IM_WT <- metadata[metadata$Condition == "IM WT", ]
IM_KO <- metadata[metadata$Condition == "IM KO", ]

wilcox.test(IM_WT$EM_IM_sign1, IM_KO$EM_IM_sign1) #< 2.2e-16

```

```

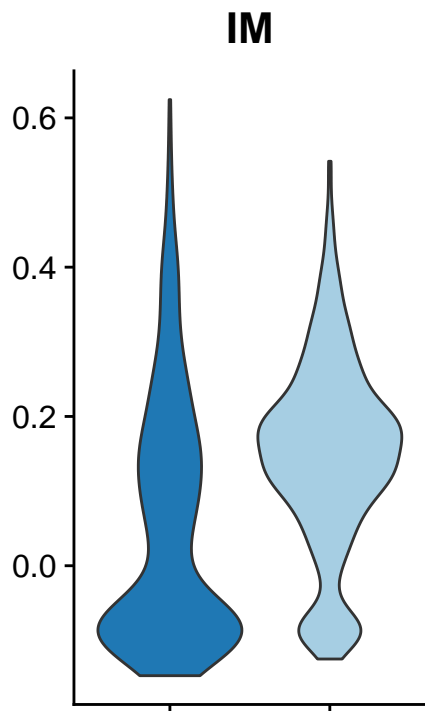
##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$EM_IM_sign1 and IM_KO$EM_IM_sign1
## W = 284975, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0

```

```

VlnPlot(sc, features = "Mo_IM_sign1", cols = pal_IM, pt.size = 0,
  ident = c("IM WT", "IM KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("IM")

```



```

wilcox.test(IM_WT$Mo_IM_sign1, IM_KO$Mo_IM_sign1) #< 2.2e-16

```

```

##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$Mo_IM_sign1 and IM_KO$Mo_IM_sign1
## W = 138648, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0

```

MG

```
Bulk_RNAseq_MG_EMvsMo <- read_excel("Bulk_RNAseq_MG_EMvsMo.xlsx",
  na = "NA")

Bulk_RNAseq_MG_EMvsMo <- Bulk_RNAseq_MG_EMvsMo[Bulk_RNAseq_MG_EMvsMo$p.value.45.1.45.2.nt <
  0.05 & abs(Bulk_RNAseq_MG_EMvsMo$FC.45.1.45.2.nt) > 1, ]

Bulk_RNAseq_MG_EMvsMo$diff <- Bulk_RNAseq_MG_EMvsMo$average.45.1.nt -
  Bulk_RNAseq_MG_EMvsMo$average.45.2.nt

EM_MG_sign <- Bulk_RNAseq_MG_EMvsMo[Bulk_RNAseq_MG_EMvsMo$diff <
  0, ]$Gene.Name

EM_MG_sign <- intersect(rownames(sc), EM_MG_sign)

EM_MG_sign <- head(EM_MG_sign, 100)

write.table(EM_MG_sign, file = "EM_MG_sign.txt")

EM_MG_sign <- list(EM_MG_sign)

sc <- AddModuleScore(sc, features = EM_MG_sign, name = "EM_MG_sign")

Mo_MG_sign <- Bulk_RNAseq_MG_EMvsMo[Bulk_RNAseq_MG_EMvsMo$diff >
  0, ]$Gene.Name

Mo_MG_sign <- intersect(rownames(sc), Mo_MG_sign)

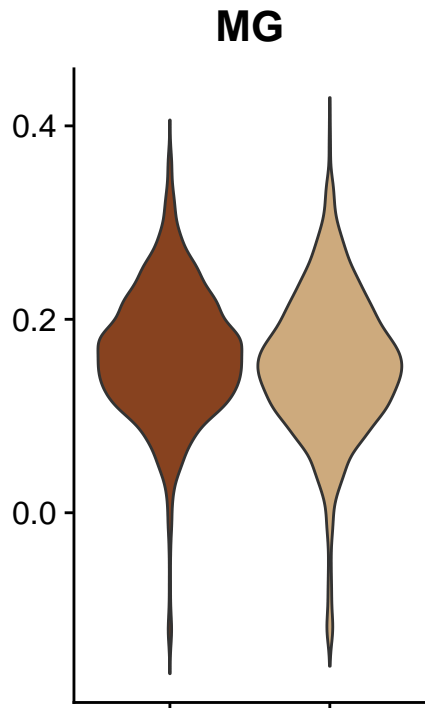
Mo_MG_sign <- head(Mo_MG_sign, 100)

write.table(Mo_MG_sign, file = "Mo_MG_sign.txt")

Mo_MG_sign <- list(Mo_MG_sign)

sc <- AddModuleScore(sc, features = Mo_MG_sign, name = "Mo_MG_sign")

VlnPlot(sc, features = "EM_MG_sign1", cols = pal_MG, pt.size = 0,
  ident = c("MG WT", "MG KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("MG")
```



```

metadata <- sc@meta.data
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

mean(MG_WT$EM_MG_sign1)

## [1] 0.1635021

mean(MG_KO$EM_MG_sign1)

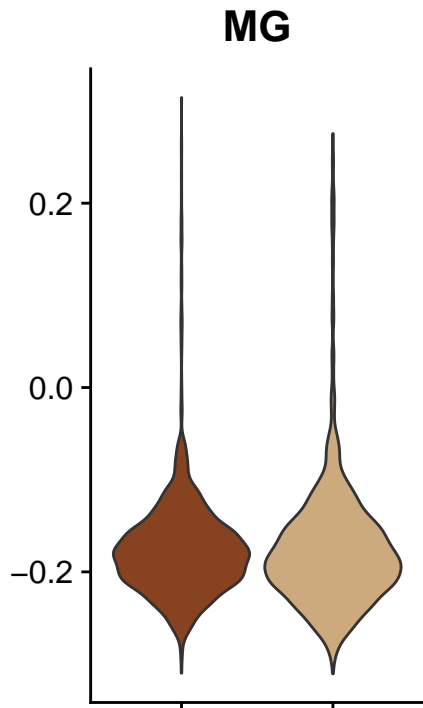
## [1] 0.1522682

wilcox.test(MG_WT$EM_MG_sign1, MG_KO$EM_MG_sign1) #p-value = 4.694e-07

##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$EM_MG_sign1 and MG_KO$EM_MG_sign1
## W = 2230982, p-value = 4.694e-07
## alternative hypothesis: true location shift is not equal to 0

VlnPlot(sc, features = "Mo_MG_sign1", cols = pal_MG, pt.size = 0,
  ids = c("MG WT", "MG KO")) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("MG")

```



```
metadata <- sc@meta.data
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

mean(MG_WT$Mo_MG_sign1)
```

```
## [1] -0.1756634
```

```
mean(MG_KO$Mo_MG_sign1)
```

```
## [1] -0.1750868
```

```
wilcox.test(MG_WT$Mo_MG_sign1, MG_KO$Mo_MG_sign1) #p-value = 0.02041
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$Mo_MG_sign1 and MG_KO$Mo_MG_sign1
## W = 2129965, p-value = 0.02041
## alternative hypothesis: true location shift is not equal to 0
```

MafB target gene signature score

MafB peaks were identified by CUT&RUN on BMDM

```

MafB_Peaks <- read_excel("MafB_Peaks.xlsx")

MafB_target_genes <- MafB_Peaks$`Gene Name`

MafB_target_genes <- unique(MafB_target_genes)

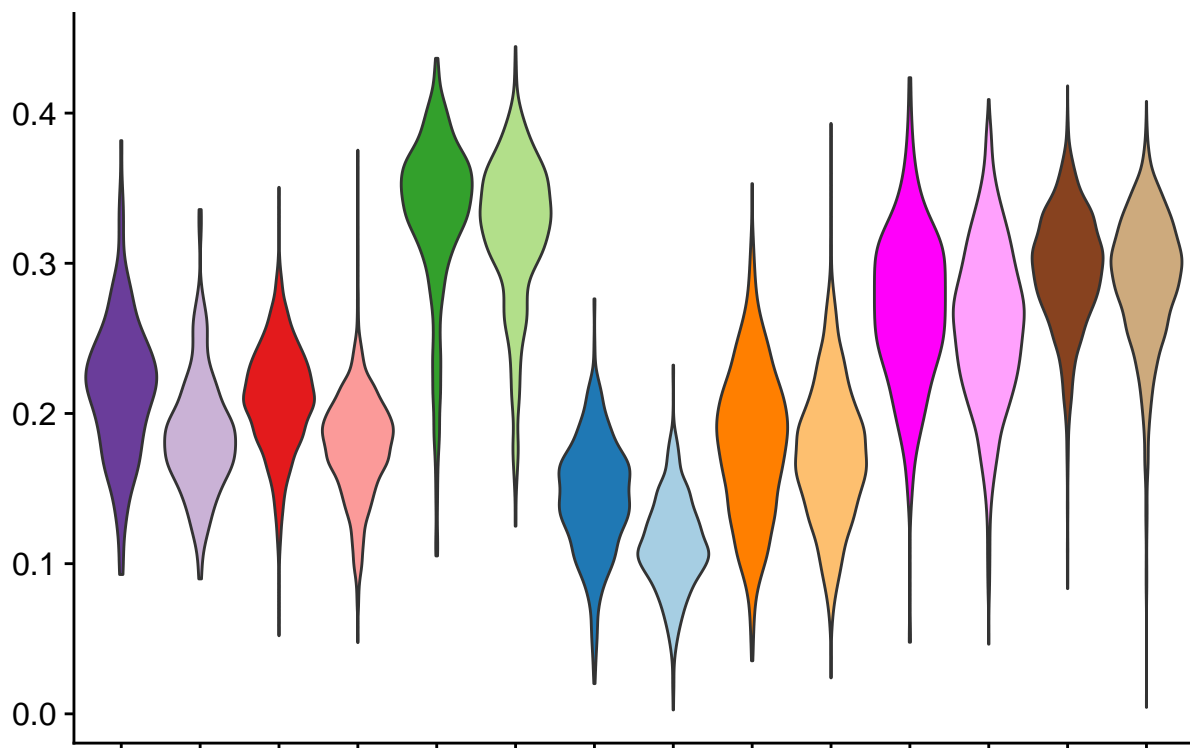
MafB_target_genes <- intersect(MafB_target_genes, rownames(sc))

MafB_target_genes_top500 <- head(MafB_target_genes, n = 500)
write.table(append(MafB_target_genes_top500, "#MafB_target_genes_top500",
0), file = "MafB_target_genes_top500.grp", row.names = FALSE,
col.names = FALSE, quote = FALSE)

sc <- AddModuleScore(sc, features = list(MafB_target_genes_top500),
name = "Mafb_sign")

VlnPlot(sc, features = "Mafb_sign1", cols = pal, pt.size = 0) +
theme(legend.position = "none", axis.title.x = element_blank(),
axis.text.x = element_blank()) + ggtitle("")

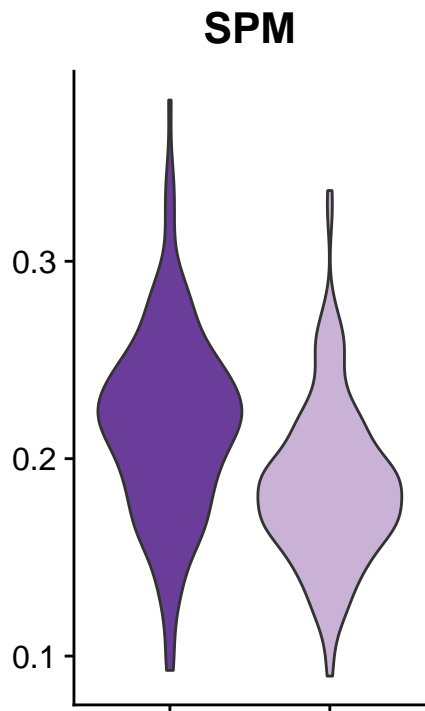
```



SPM

```
pal_SPM <- c("#6A3D9A", "#CAB2D6")
```

```
VlnPlot(sc, features = "Mafb_sign1", cols = pal_SPM, pt.size = 0,  
  ids = c("SPM WT", "SPM KO")) + ggtitle("SPM") + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



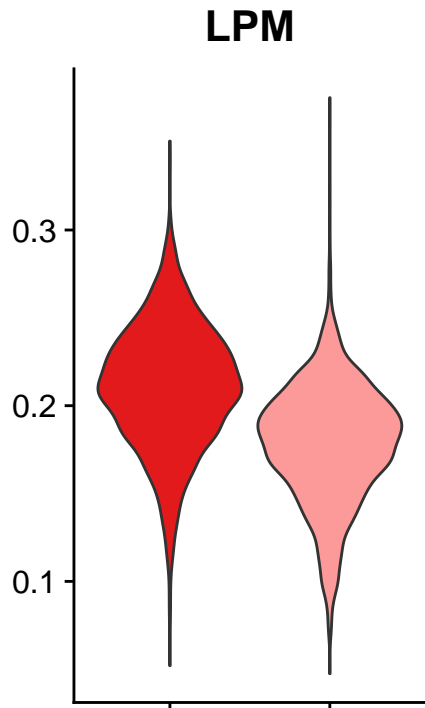
```
metadata <- sc@meta.data  
SPM_WT <- metadata[metadata$Condition == "SPM WT", ]  
SPM_KO <- metadata[metadata$Condition == "SPM KO", ]  
  
wilcox.test(SPM_WT$Mafb_sign1, SPM_KO$Mafb_sign1) #3.08e-11
```

```
##  
## Wilcoxon rank sum test with continuity correction  
##  
## data: SPM_WT$Mafb_sign1 and SPM_KO$Mafb_sign1  
## W = 20093, p-value = 3.08e-11  
## alternative hypothesis: true location shift is not equal to 0
```

LPM

```
pal_LPM <- c("#e31a1c", "#fb9a99")
```

```
VlnPlot(sc, features = "Mafb_sign1", cols = pal_LPM, pt.size = 0,  
  ids = c("LPM WT", "LPM KO")) + ggtitle("LPM") + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
LPM_WT <- metadata[metadata$Condition == "LPM WT", ]
LPM_KO <- metadata[metadata$Condition == "LPM KO", ]

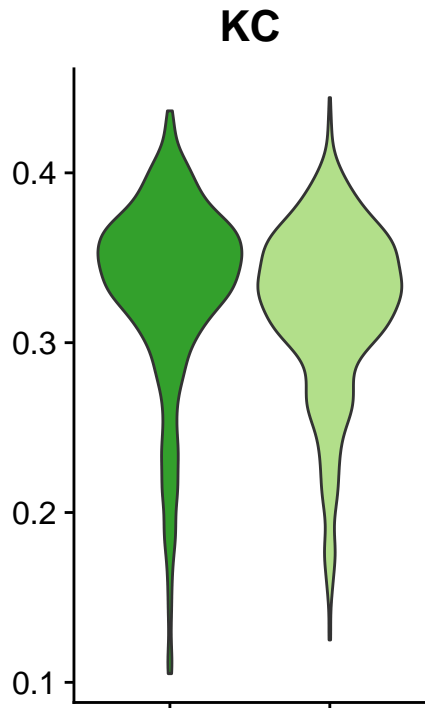
wilcox.test(LPM_WT$Mafb_sign1, LPM_KO$Mafb_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: LPM_WT$Mafb_sign1 and LPM_KO$Mafb_sign1
## W = 2266533, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

KC

```
pal_KC <- c("#33a02c", "#b2df8a")

VlnPlot(sc, features = "Mafb_sign1", cols = pal_KC, pt.size = 0,
  ids = c("KC WT", "KC KO")) + ggtitle("KC") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```

```
KC_WT <- metadata[metadata$Condition == "KC WT", ]
KC_KO <- metadata[metadata$Condition == "KC KO", ]

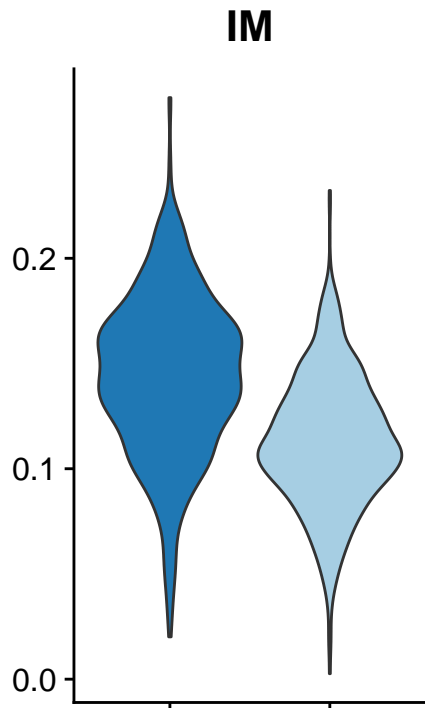
wilcox.test(KC_WT$Mafb_sign1, KC_KO$Mafb_sign1) #3.096e-09
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: KC_WT$Mafb_sign1 and KC_KO$Mafb_sign1
## W = 373739, p-value = 3.096e-09
## alternative hypothesis: true location shift is not equal to 0
```

IM

```
pal_IM <- c("#1f78b4", "#a6cee3")

VlnPlot(sc, features = "Mafb_sign1", cols = pal_IM, pt.size = 0,
  ids = c("IM WT", "IM KO")) + ggtitle("IM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
IM_WT <- metadata[metadata$Condition == "IM WT", ]
IM_KO <- metadata[metadata$Condition == "IM KO", ]

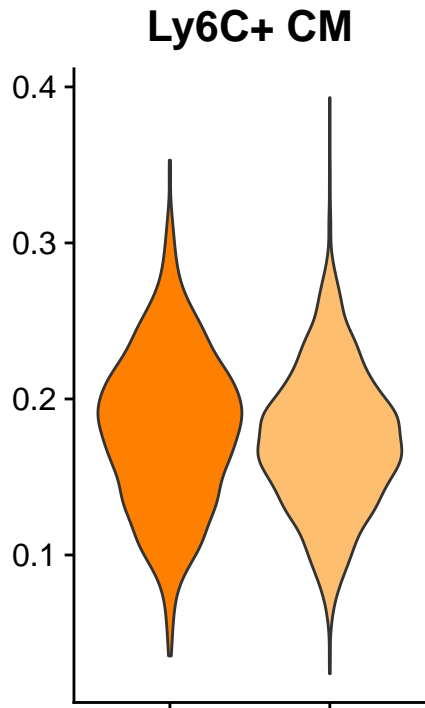
wilcox.test(IM_WT$Mafb_sign1, IM_KO$Mafb_sign1) #< 2.2e-16
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: IM_WT$Mafb_sign1 and IM_KO$Mafb_sign1
## W = 328255, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0
```

Ly6C+ CM

```
pal_Ly6C <- c("#FF7F00", "#FDBF6F")

VlnPlot(sc, features = "Mafb_sign1", cols = pal_Ly6C, pt.size = 0,
  ids = c("Ly6C+ CM WT", "Ly6C+ CM KO")) + ggtitle("Ly6C+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



```
Ly6C_WT <- metadata[metadata$Condition == "Ly6C+ CM WT", ]
Ly6C_KO <- metadata[metadata$Condition == "Ly6C+ CM KO", ]

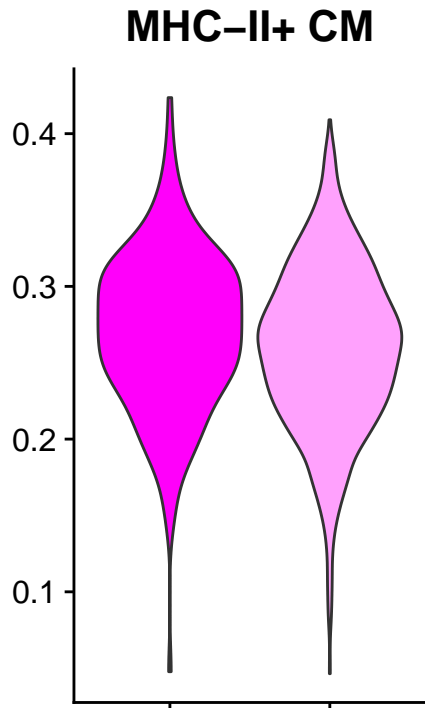
wilcox.test(Ly6C_WT$Mafb_sign1, Ly6C_KO$Mafb_sign1) #2.816e-06
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: Ly6C_WT$Mafb_sign1 and Ly6C_KO$Mafb_sign1
## W = 1385982, p-value = 2.816e-06
## alternative hypothesis: true location shift is not equal to 0
```

MHC-II+ CM

```
pal_MHC2 <- c("#FF00FA", "#FFA1FD")

VlnPlot(sc, features = "Mafb_sign1", cols = pal_MHC2, pt.size = 0,
  ident = c("MHC2+ CM WT", "MHC2+ CM KO")) + ggtitle("MHC-II+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



```
MHC2_WT <- metadata[metadata$Condition == "MHC2+ CM WT", ]
MHC2_KO <- metadata[metadata$Condition == "MHC2+ CM KO", ]

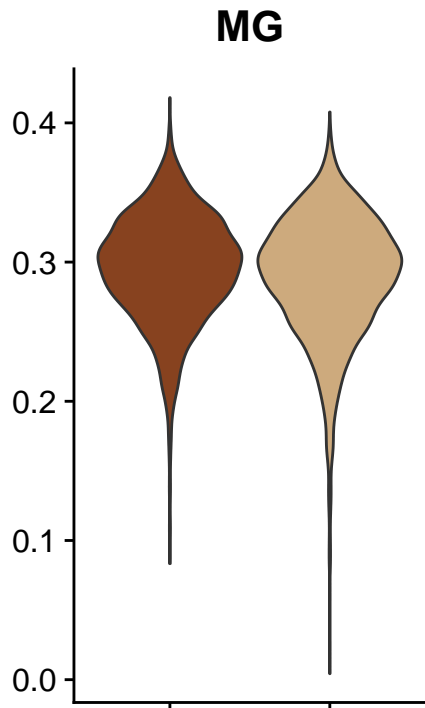
wilcox.test(MHC2_WT$Mafb_sign1, MHC2_KO$Mafb_sign1) #0.006117
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MHC2_WT$Mafb_sign1 and MHC2_KO$Mafb_sign1
## W = 163187, p-value = 0.006117
## alternative hypothesis: true location shift is not equal to 0
```

MG

```
pal_MG <- c("#87421F", "#CDAA7D")

VlnPlot(sc, features = "Mafb_sign1", cols = pal_MG, pt.size = 0,
  ids = c("MG WT", "MG KO")) + ggtitle("MG") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



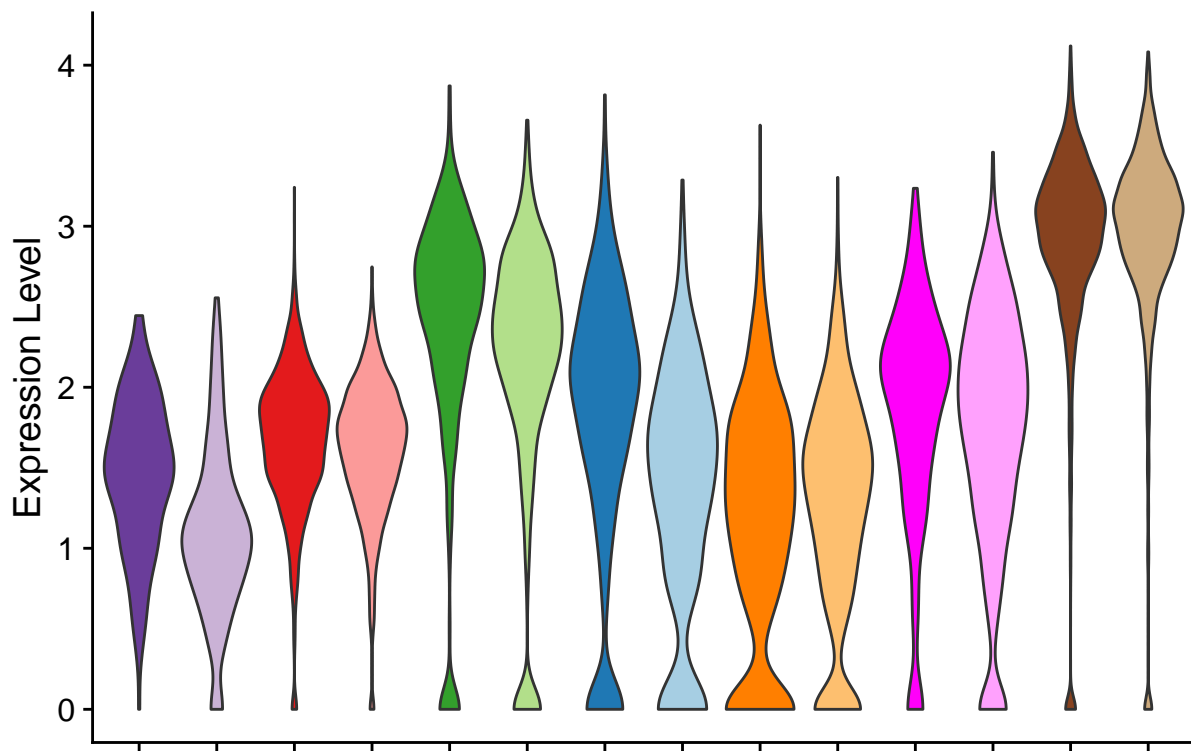
```
MG_WT <- metadata[metadata$Condition == "MG WT", ]
MG_KO <- metadata[metadata$Condition == "MG KO", ]

wilcox.test(MG_WT$Mafb_sign1, MG_KO$Mafb_sign1) #0.0001445
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: MG_WT$Mafb_sign1 and MG_KO$Mafb_sign1
## W = 2184993, p-value = 0.0001445
## alternative hypothesis: true location shift is not equal to 0
```

Csflr expression

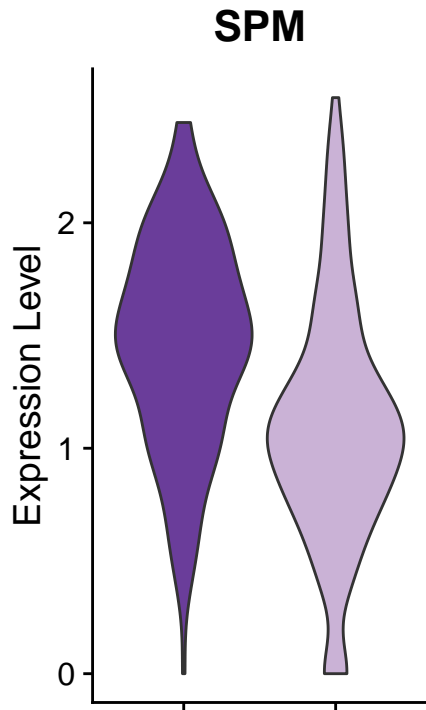
```
VlnPlot(sc, features = "Csflr", cols = pal, pt.size = 0) + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank()) +
  ggtitle("")
```



SPM

```
pal_SPM <- c("#6A3D9A", "#CAB2D6")

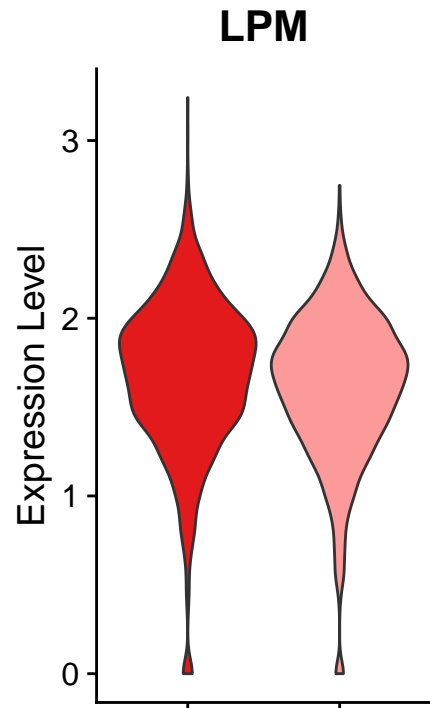
VlnPlot(sc, features = "Csfr", cols = pal_SPM, pt.size = 0,
  ids = c("SPM WT", "SPM KO")) + ggtitle("SPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



LPM

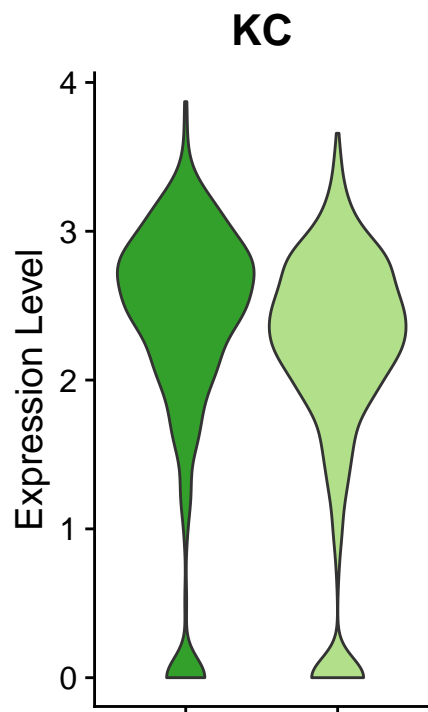
```
pal_LPM <- c("#e31a1c", "#fb9a99")

VlnPlot(sc, features = "Csfr1", cols = pal_LPM, pt.size = 0,
  ids = c("LPM WT", "LPM KO")) + ggtitle("LPM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



KC

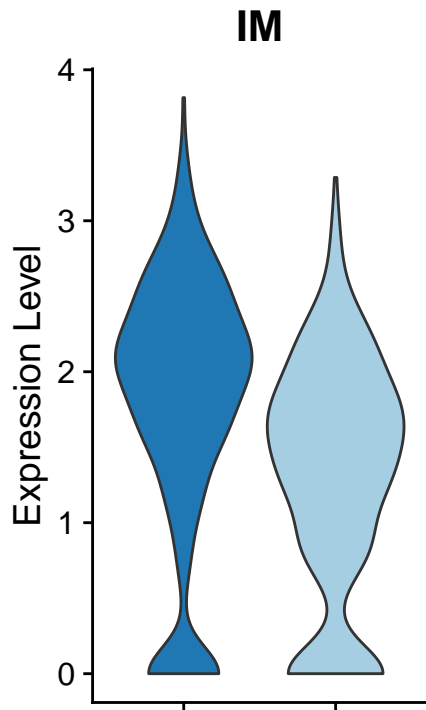
```
pal_KC <- c("#33a02c", "#b2df8a")  
  
VlnPlot(sc, features = "Csflr", cols = pal_KC, pt.size = 0, ids = c("KC WT",  
  "KC KO")) + ggtitle("KC") + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank())
```

IM

```
pal_IM <- c("#1f78b4", "#a6cee3")

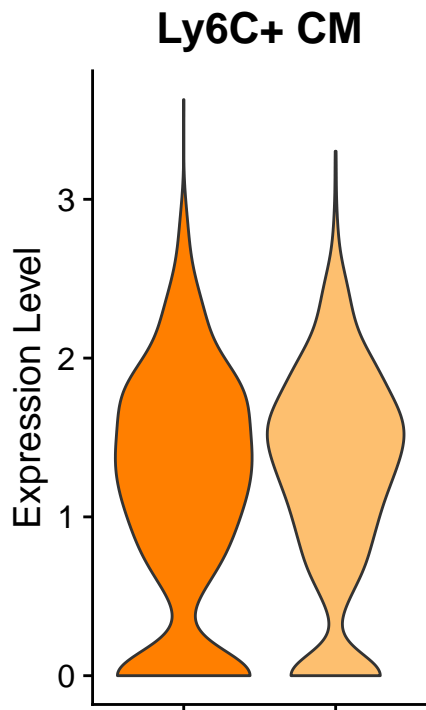
VlnPlot(sc, features = "Csflr", cols = pal_IM, pt.size = 0, ids = c("IM WT",
  "IM KO")) + ggtitle("IM") + theme(legend.position = "none",
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



Ly6C+ CM

```
pal_Ly6C <- c("#FF7F00", "#FDBF6F")

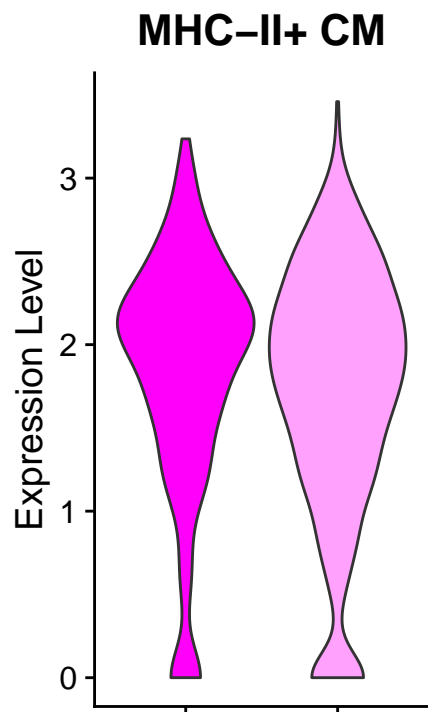
VlnPlot(sc, features = "Csfr1", cols = pal_Ly6C, pt.size = 0,
  ids = c("Ly6C+ CM WT", "Ly6C+ CM KO")) + ggtitle("Ly6C+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



MHC-II+ CM

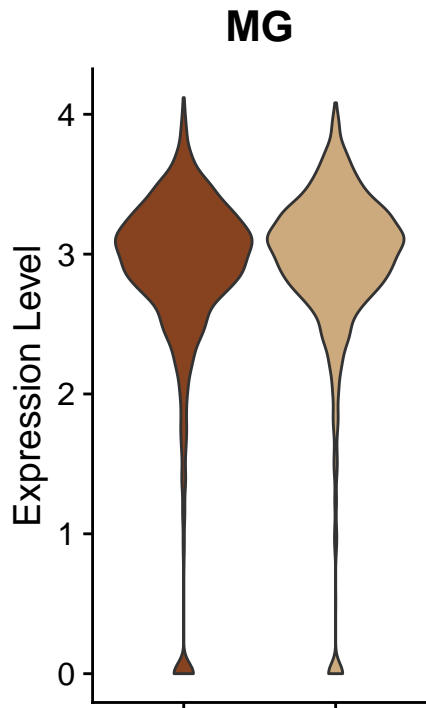
```
pal_MHC2 <- c("#FF00FA", "#FFA1FD")

VlnPlot(sc, features = "Csfr1", cols = pal_MHC2, pt.size = 0,
  idents = c("MHC2+ CM WT", "MHC2+ CM KO")) + ggtitle("MHC-II+ CM") +
  theme(legend.position = "none", axis.title.x = element_blank(),
    axis.text.x = element_blank())
```



MG

```
pal_MG <- c("#87421F", "#CDAA7D")  
  
VlnPlot(sc, features = "Csfr1", cols = pal_MG, pt.size = 0, ids = c("MG WT",  
  "MG KO")) + ggtitle("MG") + theme(legend.position = "none",  
  axis.title.x = element_blank(), axis.text.x = element_blank())
```



```
sessionInfo()
```

```
## R version 4.2.3 (2023-03-15 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19045)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=Dutch_Netherlands.utf8  LC_CTYPE=Dutch_Netherlands.utf8
## [3] LC_MONETARY=Dutch_Netherlands.utf8 LC_NUMERIC=C
## [5] LC_TIME=Dutch_Netherlands.utf8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] readxl_1.4.3      dplyr_1.1.4      RColorBrewer_1.1-3 ggplot2_3.4.4
## [5] limma_3.54.2      SeuratObject_4.1.3 Seurat_4.3.0
##
## loaded via a namespace (and not attached):
## [1] Rtsne_0.17          colorspace_2.1-0    deldir_2.0-2
## [4] ellipsis_0.3.2      ggridges_0.5.5      rstudioapi_0.15.0
## [7] spatstat.data_3.0-3 farver_2.1.1        leiden_0.4.3.1
## [10] listenv_0.9.0       ggrepel_0.9.4       fansi_1.0.6
## [13] codetools_0.2-19    splines_4.2.3       knitr_1.45
## [16] polyclip_1.10-6     spam_2.10-0         jsonlite_1.8.8
## [19] ica_1.0-3           cluster_2.1.4       png_0.1-8
## [22] uwot_0.1.16         shiny_1.8.0         sctransform_0.4.1
```

## [25]	spatstat.sparse_3.0-3	compiler_4.2.3	httr_1.4.7
## [28]	Matrix_1.6-4	fastmap_1.1.1	lazyeval_0.2.2
## [31]	cli_3.6.2	later_1.3.2	formatR_1.14
## [34]	htmltools_0.5.7	tools_4.2.3	dotCall64_1.1-1
## [37]	igraph_1.6.0	gtable_0.3.5	glue_1.6.2
## [40]	RANN_2.6.1	reshape2_1.4.4	Rcpp_1.0.11
## [43]	scattermore_1.2	cellranger_1.1.0	vctrs_0.6.5
## [46]	spatstat.explore_3.2-5	nlme_3.1-162	progressr_0.14.0
## [49]	lmtest_0.9-40	spatstat.random_3.2-2	xfun_0.39
## [52]	stringr_1.5.1	globals_0.16.2	mime_0.12
## [55]	miniUI_0.1.1.1	lifecycle_1.0.4	irlba_2.3.5.1
## [58]	goftest_1.2-3	future_1.33.1	MASS_7.3-58.2
## [61]	zoo_1.8-12	scales_1.3.0	promises_1.2.1
## [64]	spatstat.utils_3.0-4	parallel_4.2.3	yaml_2.3.7
## [67]	reticulate_1.34.0	pbapply_1.7-2	gridExtra_2.3
## [70]	stringi_1.8.3	highr_0.10	rlang_1.1.2
## [73]	pkgconfig_2.0.3	matrixStats_1.2.0	evaluate_0.23
## [76]	lattice_0.20-45	ROCR_1.0-11	purrr_1.0.2
## [79]	tensor_1.5	labeling_0.4.3	patchwork_1.1.3
## [82]	htmlwidgets_1.6.4	cowplot_1.1.2	tidyselect_1.2.1
## [85]	parallelly_1.36.0	RcppAnnoy_0.0.21	plyr_1.8.9
## [88]	magrittr_2.0.3	R6_2.5.1	generics_0.1.3
## [91]	withr_3.0.1	pillar_1.9.0	fitdistrplus_1.1-11
## [94]	survival_3.5-3	abind_1.4-5	sp_2.1-2
## [97]	tibble_3.2.1	future.apply_1.11.1	KernSmooth_2.23-20
## [100]	utf8_1.2.4	spatstat.geom_3.2-7	plotly_4.10.3
## [103]	rmarkdown_2.25	grid_4.2.3	data.table_1.14.10
## [106]	digest_0.6.31	xtable_1.8-4	tidyr_1.3.0
## [109]	httpuv_1.6.13	munSELL_0.5.1	viridisLite_0.4.2