Supplemental Information

1 Installation

To install tigeR package, please enter the following command in R:

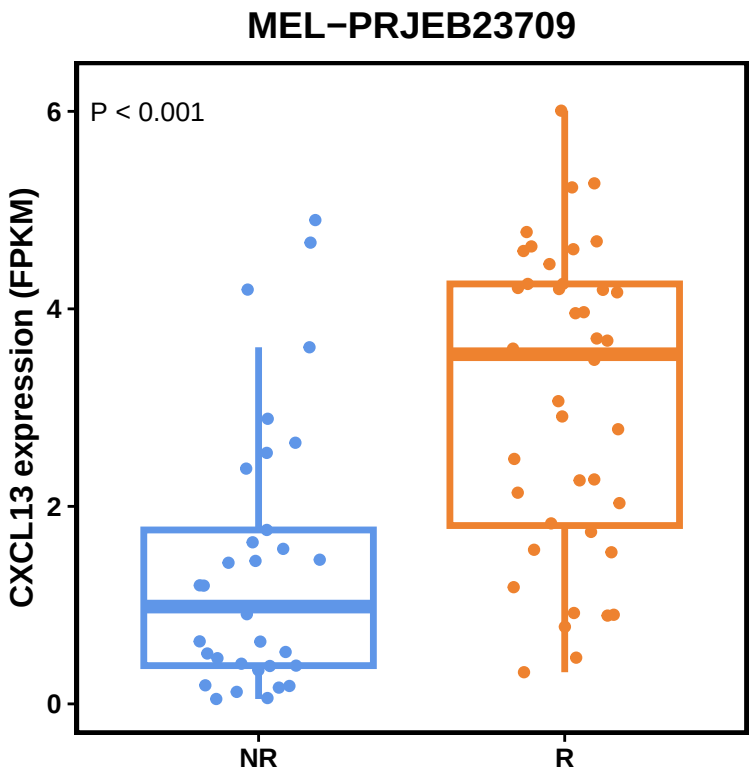
```
if (!requireNamespace("devtools", quietly = TRUE))
  install.packages("BiocManager")
devtools::install_github("YuLab-SMU/tigeR")
devtools::install_github("YuLab-SMU/tigeR.data")
```

2 Evaluating biomarkers associated with immunotherapy response (Figure 3)

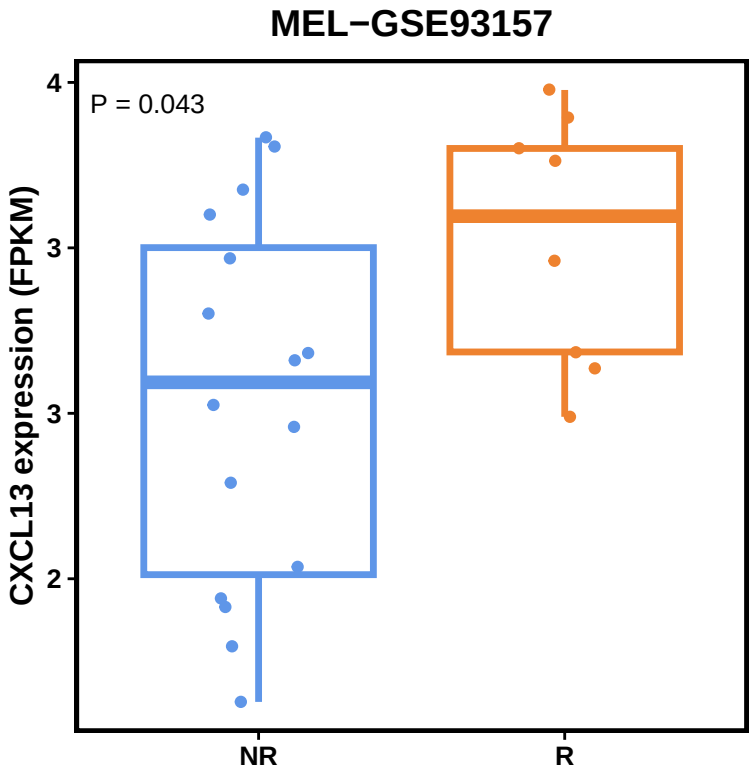
To reproduce the analysis in this document, several extra packages are `required`.

```
library(tigeR)
library(tigeR.data)
library(ggplot2)
library(SummarizedExperiment)
library(patchwork)
```

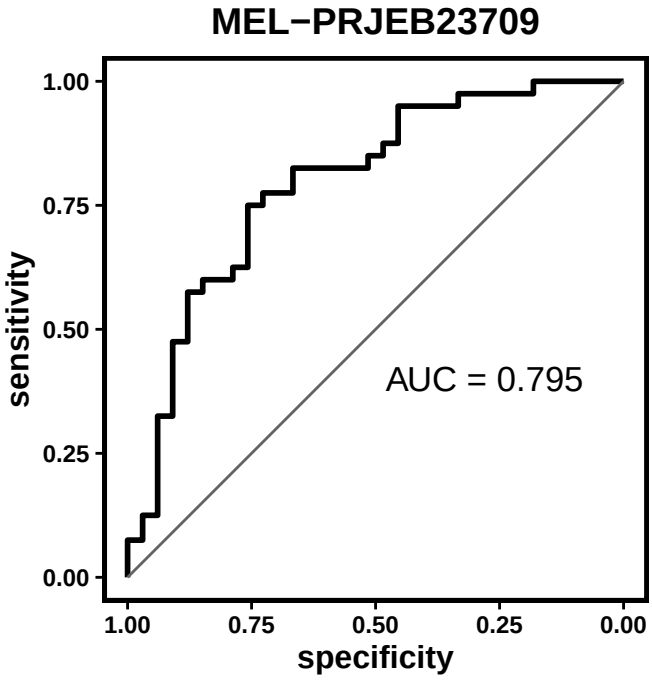
```
fig.3A <-
  diff_biomk(MEL_PRJEB23709,gene = "CXCL13",type = "Response",
             p.round=3,p.pos = c(0.05,0.60),textcol="black") +
  ylim(0,6.2) +
  ggtitle("MEL-PRJEB23709") +
  ylab("CXCL13 expression (FPKM)") +
  theme(legend.position = "none")
fig.3A
```



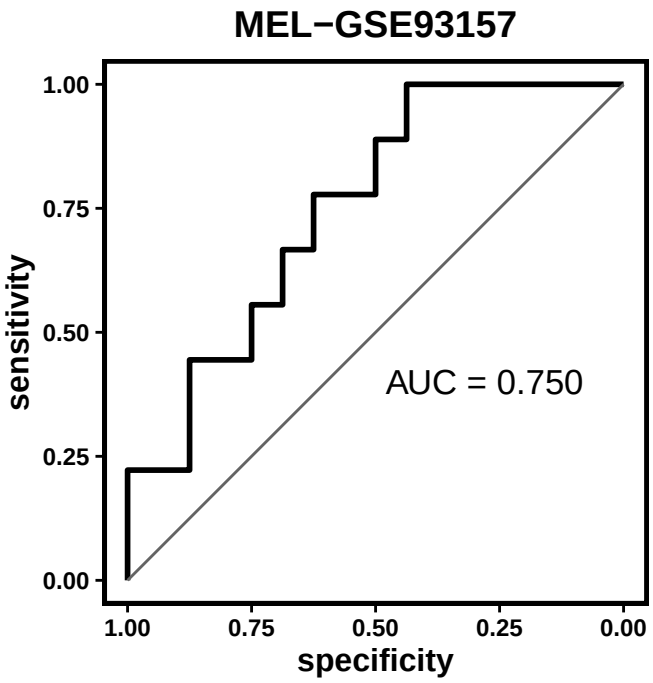

```
fig.3B <-
  diff_biomk(MEL_GSE93157,gene = "CXCL13",type = "Response",
             p.round=3,p.pos = c(0.05,0.355),textcol="black") +
  ylim(2.1,3.6) +
  scale_y_continuous(labels = scales::number_format(accuracy = 1)) +
  ggtitle("MEL-GSE93157") +
  ylab("CXCL13 expression (FPKM)") +
  theme(legend.position = "none")
fig.3B
```



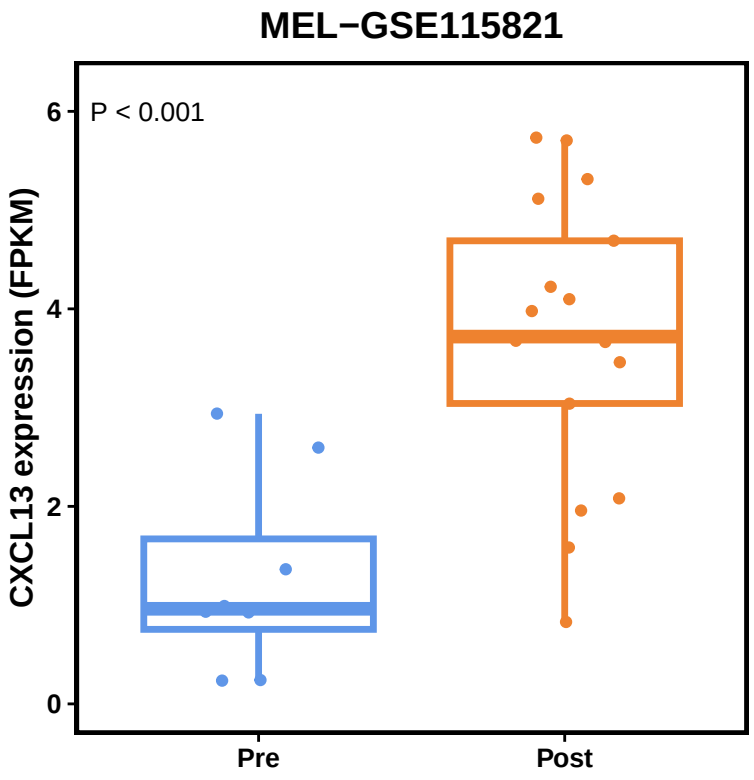

```
fig.3C <-
  roc_biomk(MEL_PRJEB23709,Signature = "CXCL13",textcol = "black",
            auc.pos = c(0.28,0.4))[[2]] +
  ggtitle("MEL-PRJEB23709")
fig.3C
```



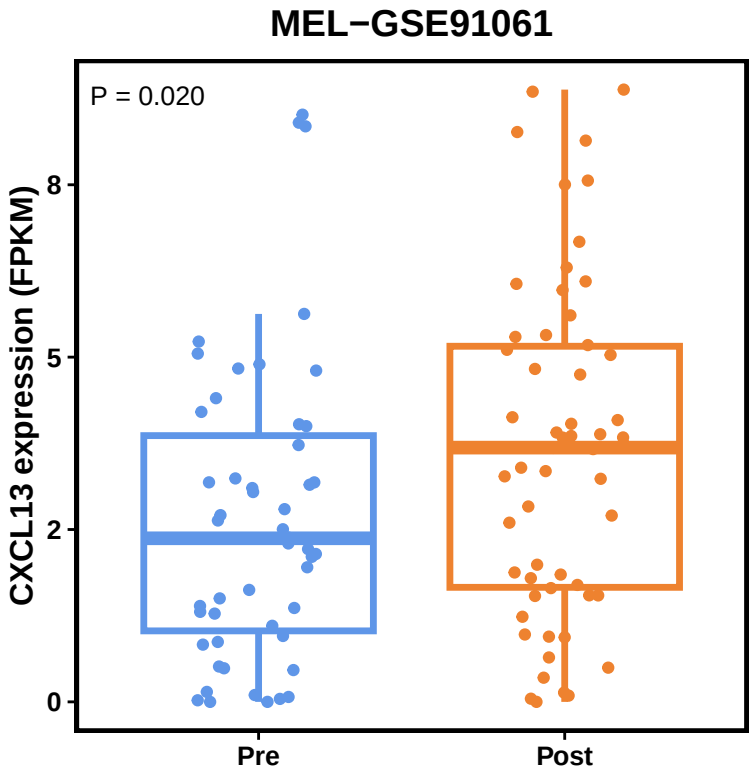

```
fig.3D <-
  roc_biomk(MEL_GSE93157,Signature = "CXCL13",textcol = "black",
            auc.pos=c(0.28,0.4))[[2]] +
  ggtitle("MEL-GSE93157")
fig.3D
```



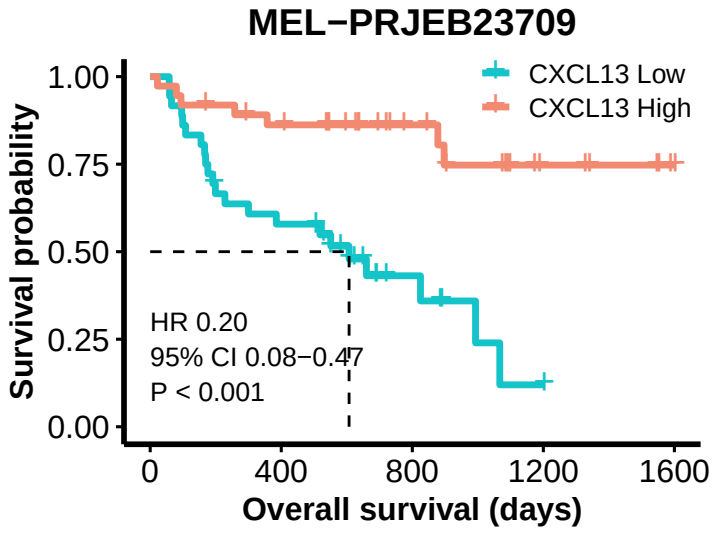

```
idx_CTLA <- MEL_GSE115821$Therapy=="anti-PD-1"
fig.3E <-
  diff_biomk(MEL_GSE115821[,MEL_GSE115821$Therapy=="anti-PD-1"],
             gene = "CXCL13",type = "Treatment",p.round=3,
             log_sc = TRUE,p.pos = c(0.05,0.60),textcol="black") +
  ylim(0,6.2) +
  ggtitle("MEL-GSE115821") +
  ylab("CXCL13 expression (FPKM)") +
  theme(legend.position = "none")
fig.3E
```



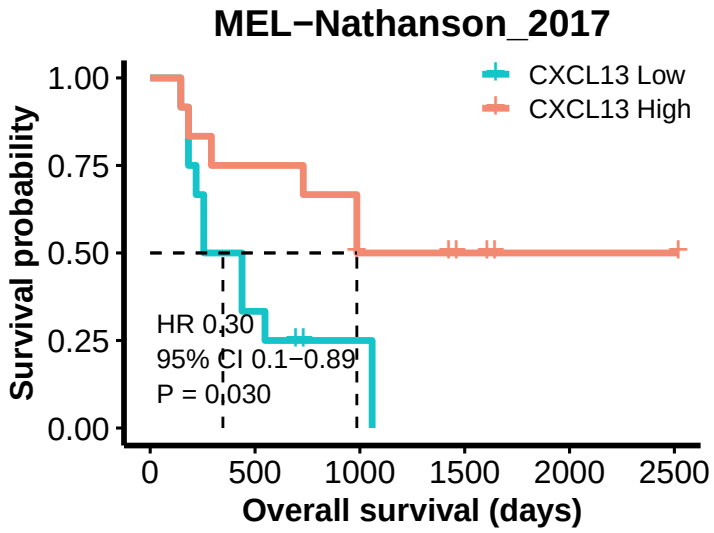

```
fig.3F <-
  diff_biomk(MEL_GSE91061,gene = "CXCL13",type = "Treatment",
             p.round=3,log_sc = TRUE,p.pos = c(0.05,0.88),textcol="black") +
  ylim(0,9) +
  scale_y_continuous(labels = scales::number_format(accuracy = 1)) +
  ggtitle("MEL-GSE91061") +
  ylab("CXCL13 expression (FPKM)") +
  theme(legend.position = "none")
fig.3F
```



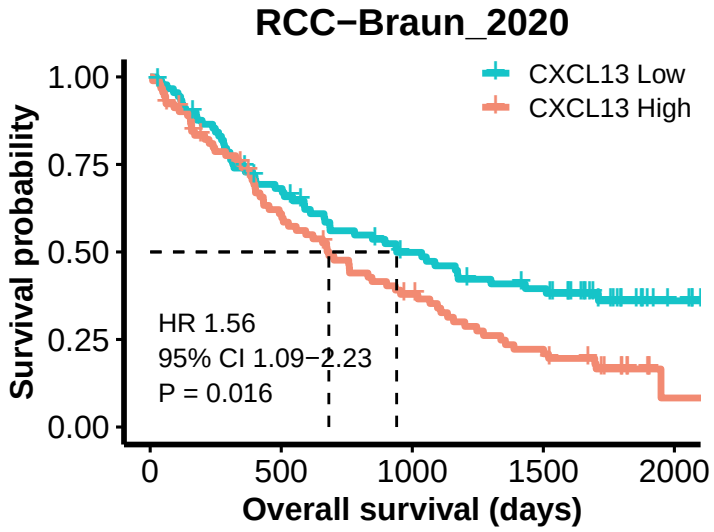

```
fig.3G <-
  surv_biomk(MEL_PRJEB23709,gene = "CXCL13",lg.pos=c(0.8,0.92),
             val.pos = c(0,0.2),lg.text = "specific")$plot +
  theme(plot.margin = unit(c(3, 1, 1, 1), "lines"),
        legend.key.height = unit(0,"cm"),
        legend.key.spacing.y = unit(0,"cm"),
        legend.key.size = unit(0,"cm")) +
  ggtitle("MEL-PRJEB23709")
fig.3G
```



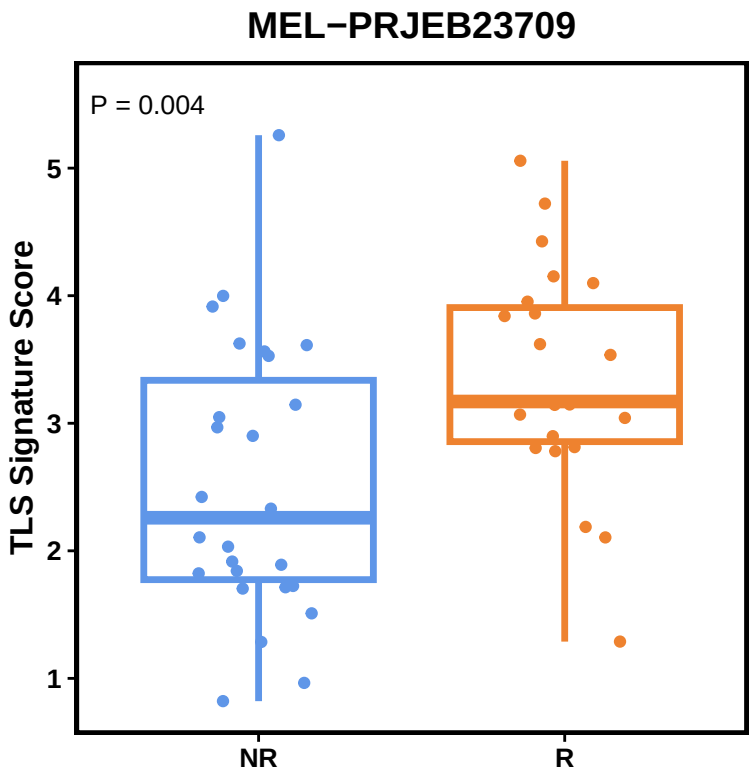

```
fig.3H <-
  surv_biomk(MEL_Nathanson_2017,gene = "CXCL13",lg.pos=c(0.8,0.92),p.round = 3,
             lg.text = "specific",PT_drop = FALSE)$plot +
  theme(plot.margin = unit(c(3, 1, 1, 1), "lines"),
        legend.key.height = unit(0,"cm"),
        legend.key.spacing.y = unit(0,"cm"),
        legend.key.size = unit(0,"cm")) +
  ggtitle("MEL-Nathanson_2017")
fig.3H
```



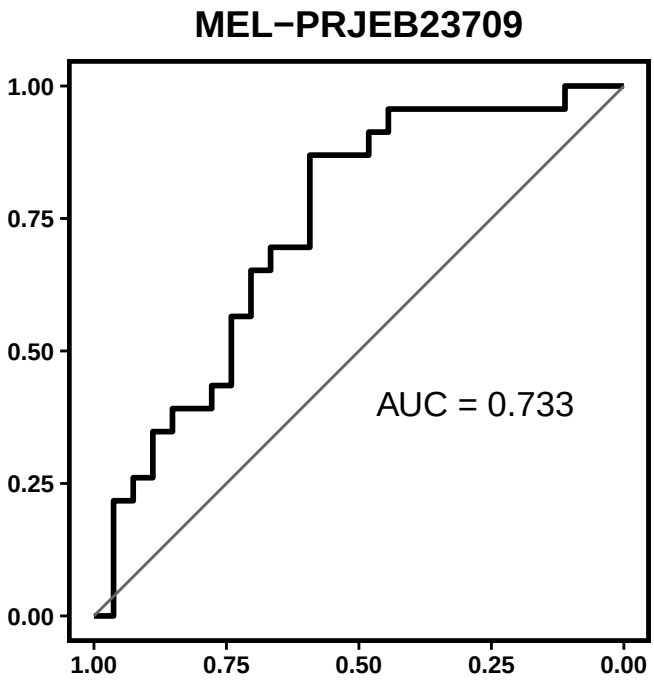
```
fig.3I <-
  surv_biomk(RCC_Braun_2020[,RCC_Braun_2020$Therapy == "anti-PD-1"],
                gene = "CXCL13",lg.pos=c(0.8,0.92),p.round = 3,
                lg.text = "specific")$plot +
  theme(plot.margin = unit(c(3, 1, 1, 1), "lines"),
        legend.key.height = unit(0,"cm"),
        legend.key.spacing.y = unit(0,"cm"),
        legend.key.size = unit(0,"cm")) +
  ggtitle("RCC-Braun_2020")
fig.3I
```



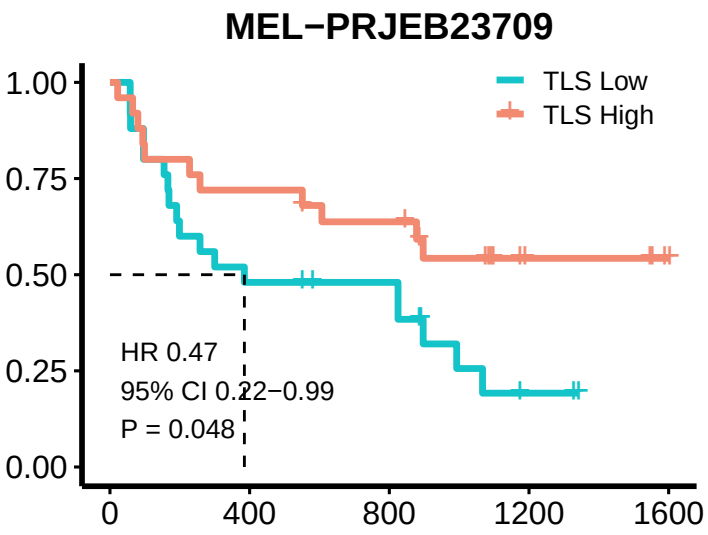

```
fig.3J <-
  diff_biomk(MEL_PRJEB23709[,MEL_PRJEB23709$Therapy=="anti-PD-1"],
            gene=Average_mean_Sigs$TLS,type = "Response",
            p.round=3,PT_drop = FALSE,p.pos = c(0.05,0.55),
            textcol = "black") +
  ylim(0.8,5.6) +
  ggtitle("MEL-PRJEB23709") +
  ylab("TLS Signature Score") +
  theme(legend.position = "none")
fig.3J
```



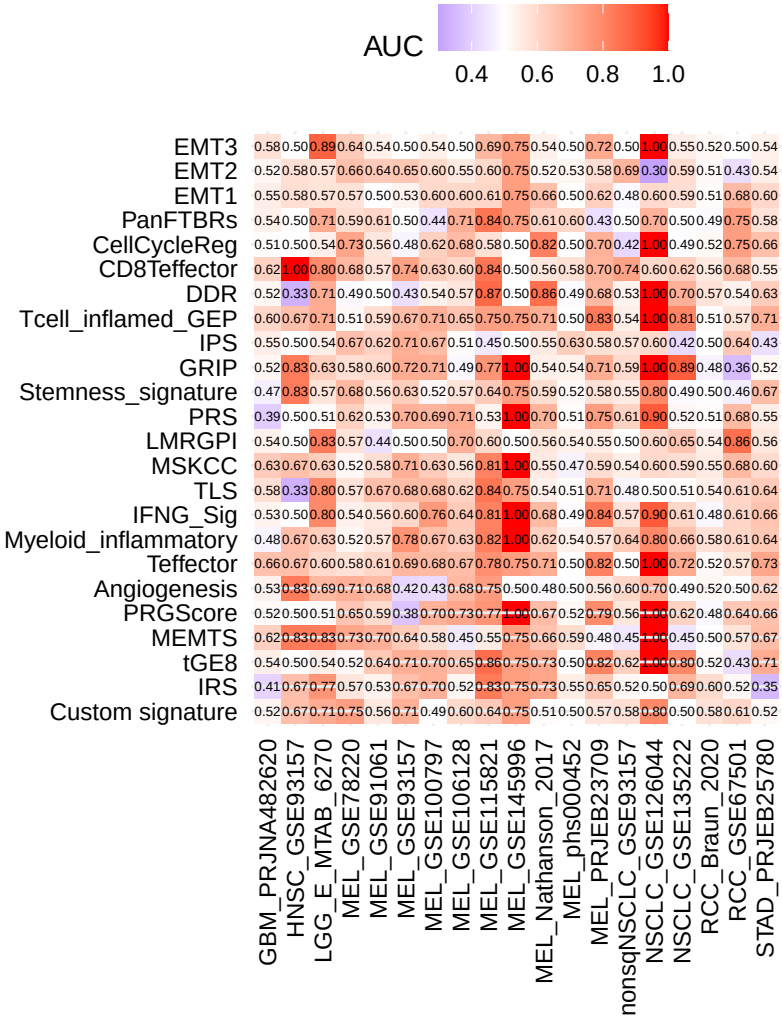

```
fig.3K <-
  roc_biomk(MEL_PRJEB23709[,MEL_PRJEB23709$Therapy=="anti-PD-1"],
            Signature=Average_mean_Sigs$TLS,PT_drop=FALSE,
            textcol = "black",auc.pos = c(0.28,0.4))[[2]] +
  theme(axis.title.y = element_blank(),
        axis.title.x = element_blank()) +
  ggtitle("MEL-PRJEB23709")
fig.3K
```




```
fig.3L <-
  surv_biomk(MEL_PRJEB23709[,MEL_PRJEB23709$Therapy=="anti-PD-1"],
             gene=Average_mean_Sigs$TLS,PT_drop=FALSE,
             lg.pos=c(0.8,0.92),p.round = 3,
             lg.text="specific",lg="TLS")$plot +
  theme(axis.title.y = element_blank(),
        axis.title.x = element_blank(),
        plot.margin = unit(c(3, 1, 1, 1), "lines"),
        legend.key.height = unit(0,"cm"),
        legend.key.spacing.y = unit(0,"cm"),
        legend.key.size = unit(0,"cm")) +
  ggtitle("MEL-PRJEB23709")
fig.3L
```




```
SE_list <- list(GBM_PRJNA482620,HNSC_GSE93157,LGG_E_MTAB_6270,MEL_GSE78220,
                MEL_GSE91061,MEL_GSE93157,MEL_GSE100797,MEL_GSE106128,
                MEL_GSE115821,MEL_GSE145996,MEL_Nathanson_2017,MEL_phs000452,
                MEL_PRJEB23709,nonsqNSCLC_GSE93157,NSCLC_GSE126044,NSCLC_GSE135222,
                RCC_Braun_2020,RCC_GSE67501,STAD_PRJEB25780)
names(SE_list) <- Dataloader()[,1][-7]
fig.3M <-
  compare_biomk(SE=SE_list,Signature = ipt[1:72],method = "Weighted_mean",PT_drop = FALSE,
                val.size=1.8) +
  theme(axis.title.x = element_blank(),
        axis.title.y = element_blank(),
        legend.position = "top",
        legend.direction = "horizontal")
fig.3M
```



3 Identifying tumor microenvironment compositions associated with immunotherapy response (Figure 4)

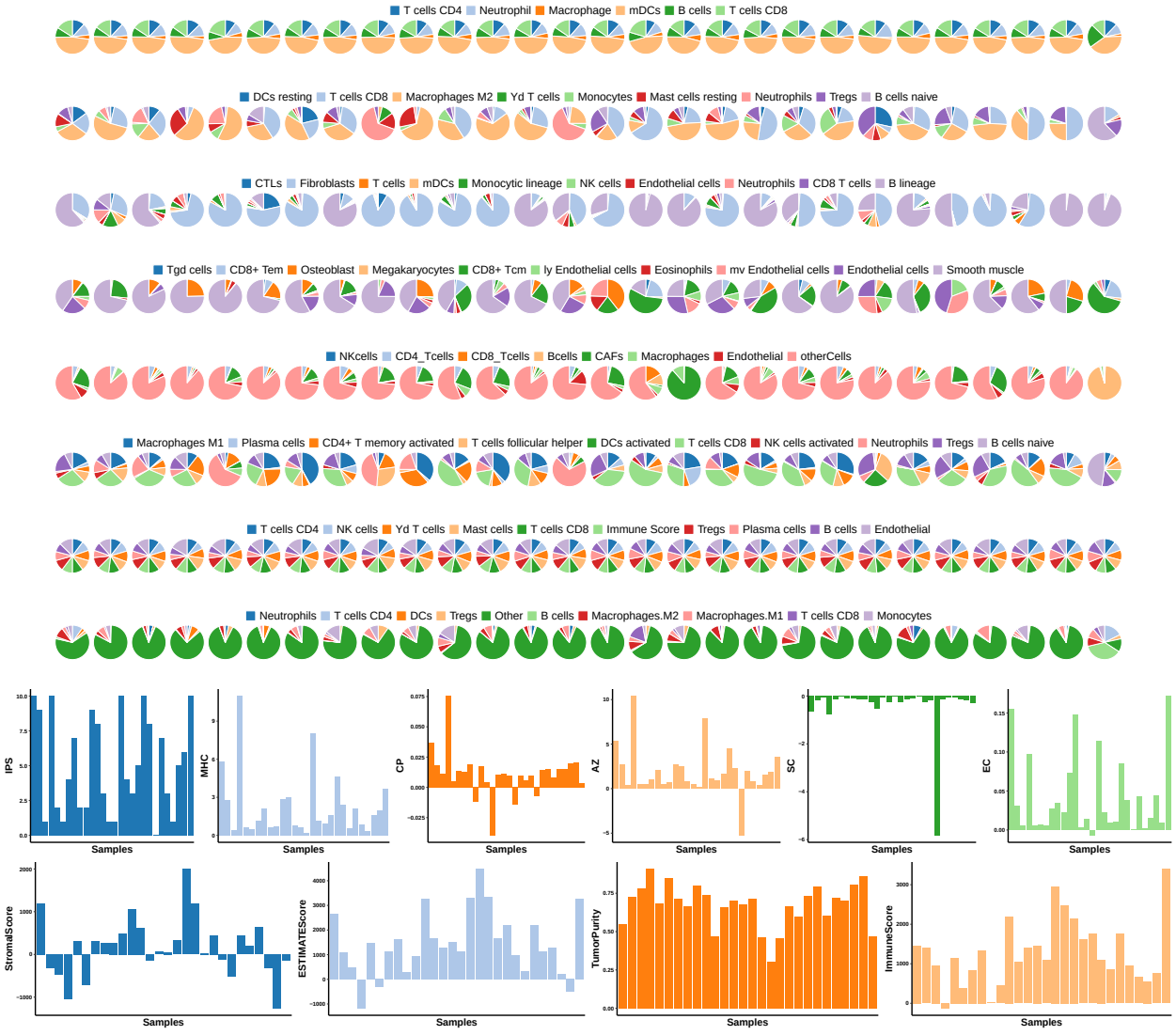
Tumor microenvironment analysis is crucial for understanding tumor immune evasion mechanisms and predicting the efficacy of immunotherapy. It provides insights into the interactions between tumor cells, immune cells, and stromal components that influence the anti-tumor immune response and treatment outcomes. Here we analyze the relation between tumor microenvironment and immunotherapy outcome.

```
## TIMER
frac1 <- deconv_TME(MEL_GSE78220,method="TIMER")
cell1 <- c("T cells CD4","Neutrophil", "Macrophage","mDCs",
           "B cells", "T cells CD8")
cell_name_filter(frac1)
pie1 <- fraction_pie(cell_name_filter(frac1),
                     feature=factor(cell1, levels = cell1))

## CIBERSORT
frac2 <- deconv_TME(MEL_GSE78220,method="CIBERSORT")
  cell2 <- c("DCs resting", "T cells CD8", "T cells CD4 naive",
           "Macrophages M2", "Yd T cells", "Monocytes",
           "Mast cells resting", "Neutrophils", "Tregs",
           "B cells naive")
pie2 <- fraction_pie(cell_name_filter(frac2[[1]][1:22,]),
                     feature=factor(cell2, levels = cell2))
```

```
## MCPCounter
frac3 <- deconv_TME(MEL_GSE78220,method="MCPCounter")
cell3 <- c("CTLs", "Fibroblasts", "T cells", "mDCs", "Monocytic lineage",
           "NK cells", "Endothelial cells", "Neutrophils", "CD8 T cells", "B lineage")
pie3 <- fraction_pie(cell_name_filter(frac3),
                     feature=factor(cell3, levels = cell3))
## xCell
frac4 <- deconv_TME(MEL_GSE78220,method="xCell")
cell4 <- c("Tgd cells", "CD8+ Tem", "Osteoblast", "Megakaryocytes", "CD8+ Tcm",
           "ly Endothelial cells", "Eosinophils", "mv Endothelial cells",
           "Endothelial cells", "Smooth muscle")
pie4 <- fraction_pie(cell_name_filter(frac4),
                     feature=factor(cell4, levels = cell4))
## IPS
frac5 <- deconv_TME(MEL_GSE78220,method="IPS")
cell5 <- c("IPS", "MHC", "CP", "AZ", "SC", "EC")
bar5 <-
draw_bar(cell_name_filter(frac5),
         feature=factor(cell5, levels = cell5))
## EPIC
frac6 <- deconv_TME(MEL_GSE78220,method="epic")
cell6 <- c("NKcells", "CD4_Tcells", "CD8_Tcells", "Bcells", "CAFs",
           "Macrophages", "Endothelial", "otherCells")
pie6 <- fraction_pie(cell_name_filter(frac6),
                     feature=factor(cell6, levels = cell6))
## ESTIMATE
frac7 <- deconv_TME(MEL_GSE78220,method="ESTIMATE")
cell7 <- c("StromalScore", "ESTIMATEScore", "TumorPurity", "ImmuneScore")
bar7 <- draw_bar(cell_name_filter(frac7),
                 feature=factor(cell7, levels = cell7))
## ABIS
frac8 <- deconv_TME(MEL_GSE78220,method="ABIS")
cell8 <-  c("Macrophages M1", "Plasma cells", "CD4+ T memory activated",
            "T cells follicular helper", "DCs activated", "T cells CD8",
            "NK cells activated", "Neutrophils", "Tregs", "B cells naive")
pie8 <- fraction_pie(cell_name_filter(frac8),
                     feature=factor(cell8, levels = cell8))
## ConsensusTME
frac9 <- deconv_TME(MEL_GSE78220,method="ConsensusTME")
cell9 <- c("T cells CD4", "NK cells", "Yd T cells", "Mast cells",
           "T cells CD8", "Immune Score", "Tregs", "Plasma cells",
           "B cells", "Endothelial")
pie9 <- fraction_pie(cell_name_filter(frac9),
                     feature=factor(cell9, levels = cell9))
## quanTIseq
frac10 <- deconv_TME(MEL_GSE78220,method="quanTIseq")
cell10 <- c("Neutrophils", "T cells CD4", "DCs", "Tregs", "Other", "B cells",
            "Macrophages.M2", "Macrophages.M1", "T cells CD8", "Monocytes")
pie10 <- fraction_pie(cell_name_filter(frac10),
                      feature=factor(cell10,levels = cell10))
bar_IPS <-
  gridExtra::grid.arrange(bar5[[1]],bar5[[2]],bar5[[3]],
                          bar5[[4]],bar5[[5]],bar5[[6]],nrow=1)
```

```
bar_ESTIMATE <-
  gridExtra::grid.arrange(bar7[[1]],bar7[[2]],
                          bar7[[3]],bar7[[4]],nrow=1)
grob_list <-
  list(pie1, pie2, pie3, pie4, pie6, pie8, pie9, pie10,
       bar_IPS, bar_ESTIMATE)
```

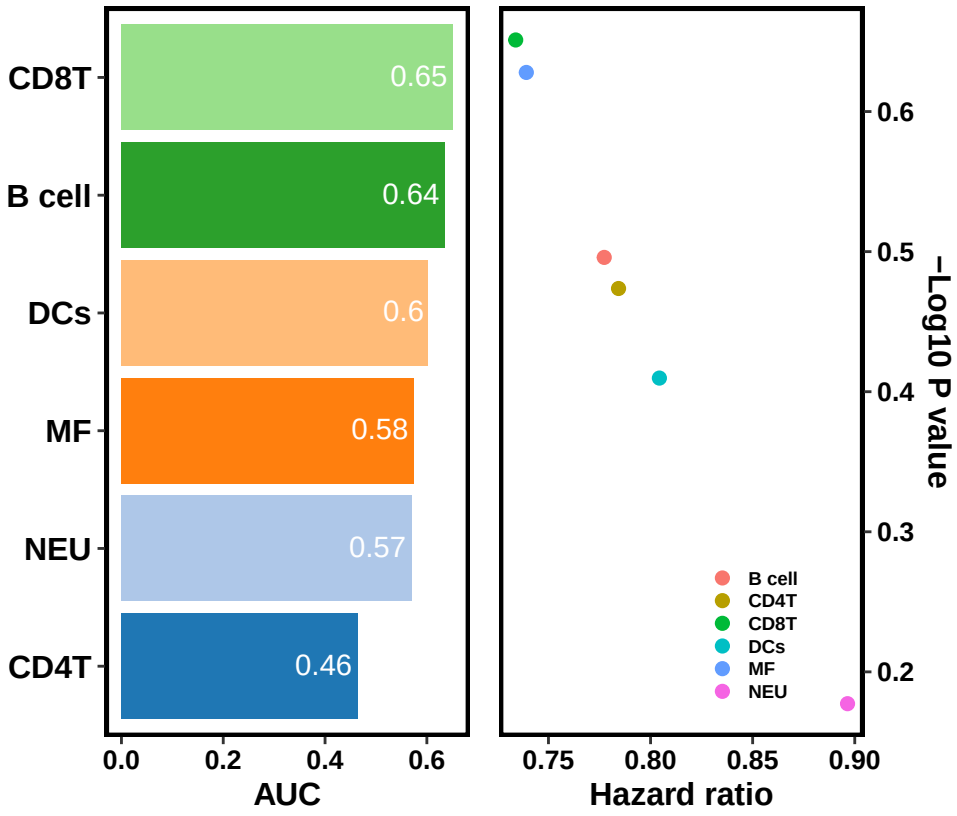
```
gridExtra::grid.arrange(grobs = grob_list, ncol = 1,
                        heights = c(1, 1, 1, 1, 1, 1, 1, 1, 2, 2))
```



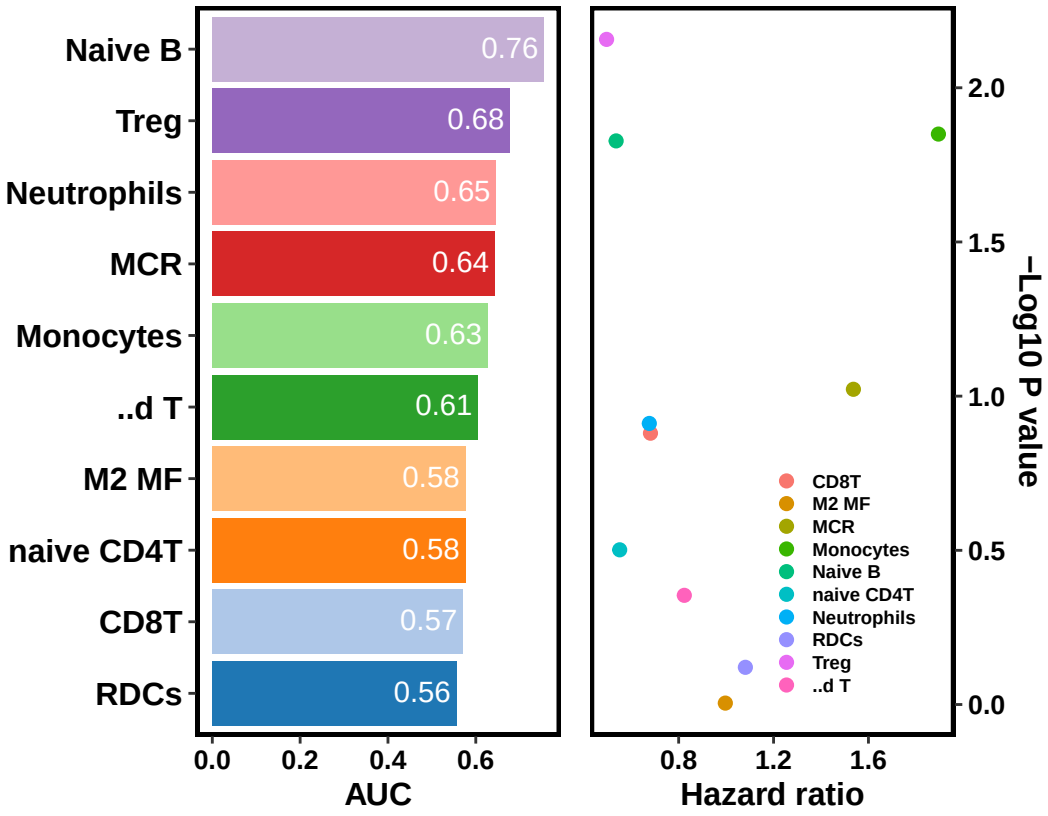

```
## TIMER
TM <- deconv_TME(MEL_GSE91061,method = "TIMER")
```

```
## Found 125 genes with uniform expression within a single batch (all zeros);
these will not be adjusted for batch.
```

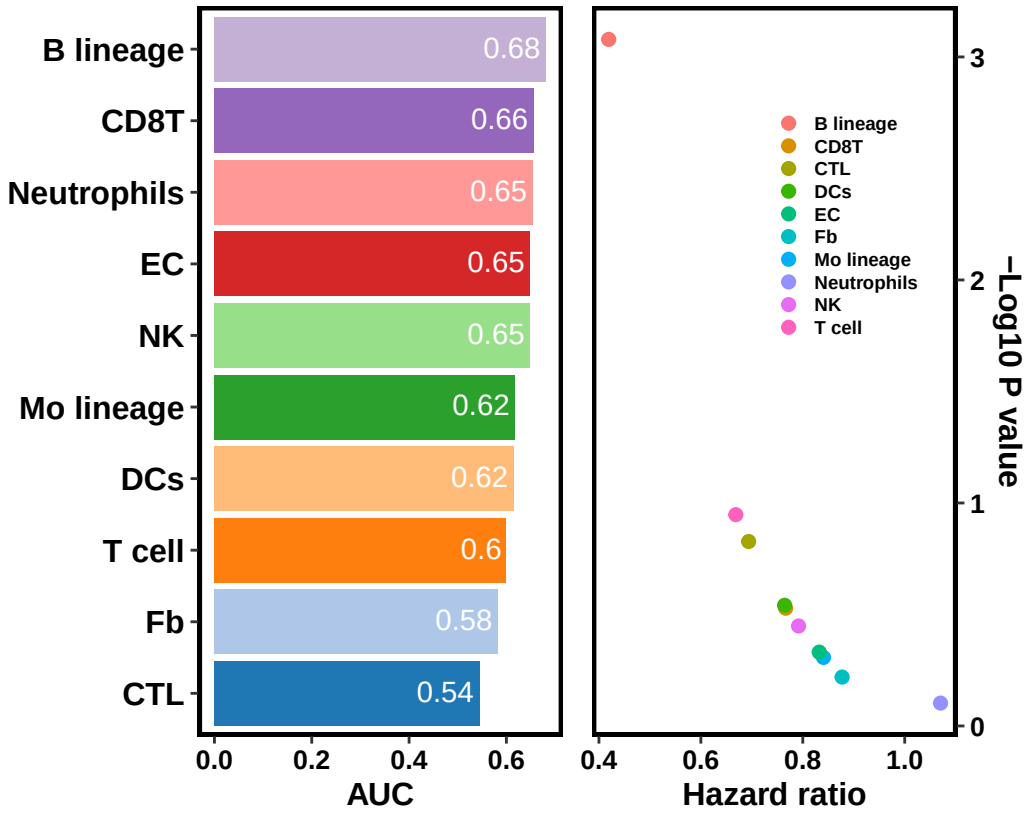
```
TM_SE <- SummarizedExperiment(assays=SimpleList(TM),
                              colData=colData(MEL_GSE91061))
fig.4B <- browse_biomk(SE=cell_name_standardization(TM_SE))
fig.4B
```




```
## CIBERSORT
CISORT <- deconv_TME(MEL_GSE91061,
                     method="CIBERSORT")
CIBER_SE <- SummarizedExperiment(assays=SimpleList(CISORT[[1]][1:22,]),
                                 colData=colData(MEL_GSE91061))
fig.4C <- browse_biomk(SE=cell_name_standardization(CIBER_SE),lg.pos = c(0.7,0.21))
fig.4C
```



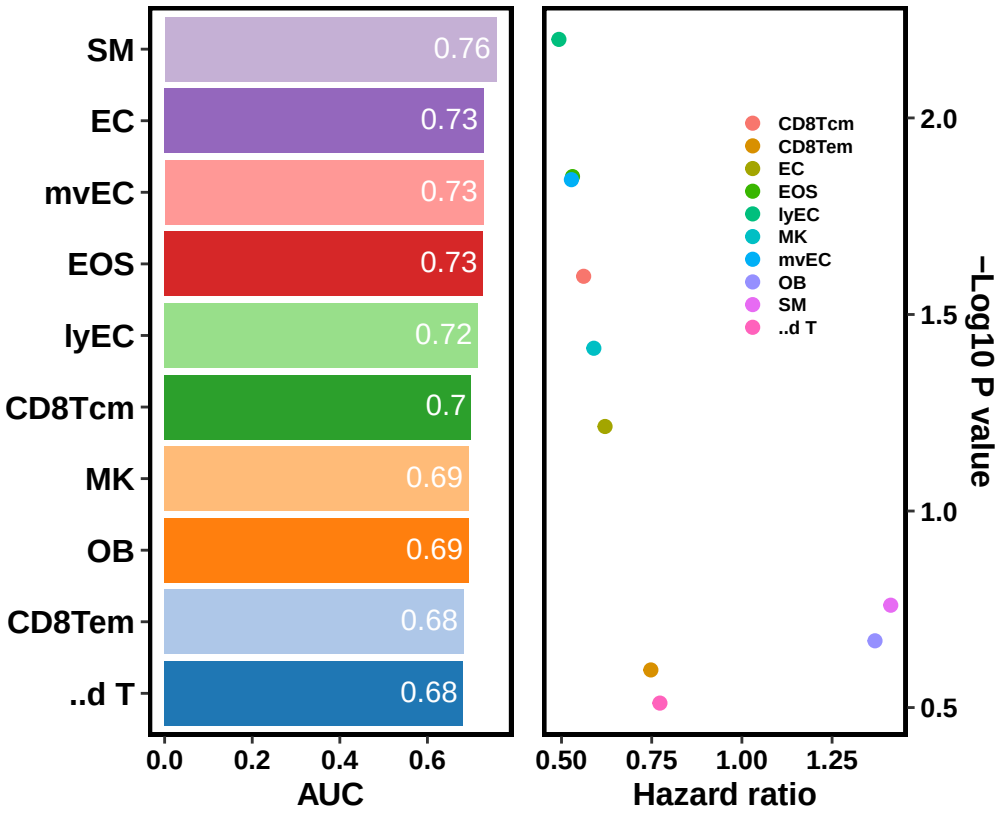

```
## MCPCounter
MCP <- deconv_TME(MEL_GSE91061,
                  method="MCPCounter")
MCP_SE <- SummarizedExperiment(assays=SimpleList(MCP),
                               colData=colData(MEL_GSE91061))
fig.4D <- browse_biomk(cell_name_standardization(MCP_SE),lg.pos = c(0.7,0.7))
fig.4D
```



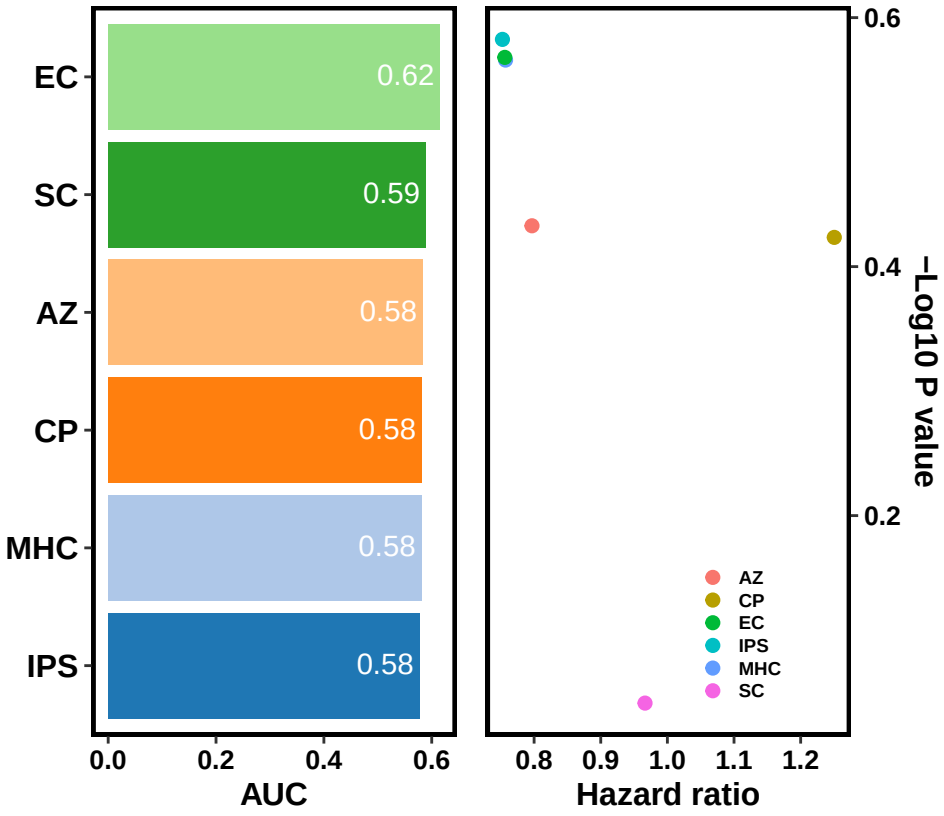

```
## xCell
xCl <- deconv_TME(MEL_GSE91061,
                  method="xCell")
```

```
## [1] "Num. of genes: 10808"
## Setting parallel calculations through a MulticoreParam back-end
## with workers=4 and tasks=100.
## Estimating ssGSEA scores for 489 gene sets.
## [1] "Calculating ranks..."
## [1] "Calculating absolute values from ranks..."
##   |                                                                      |
```

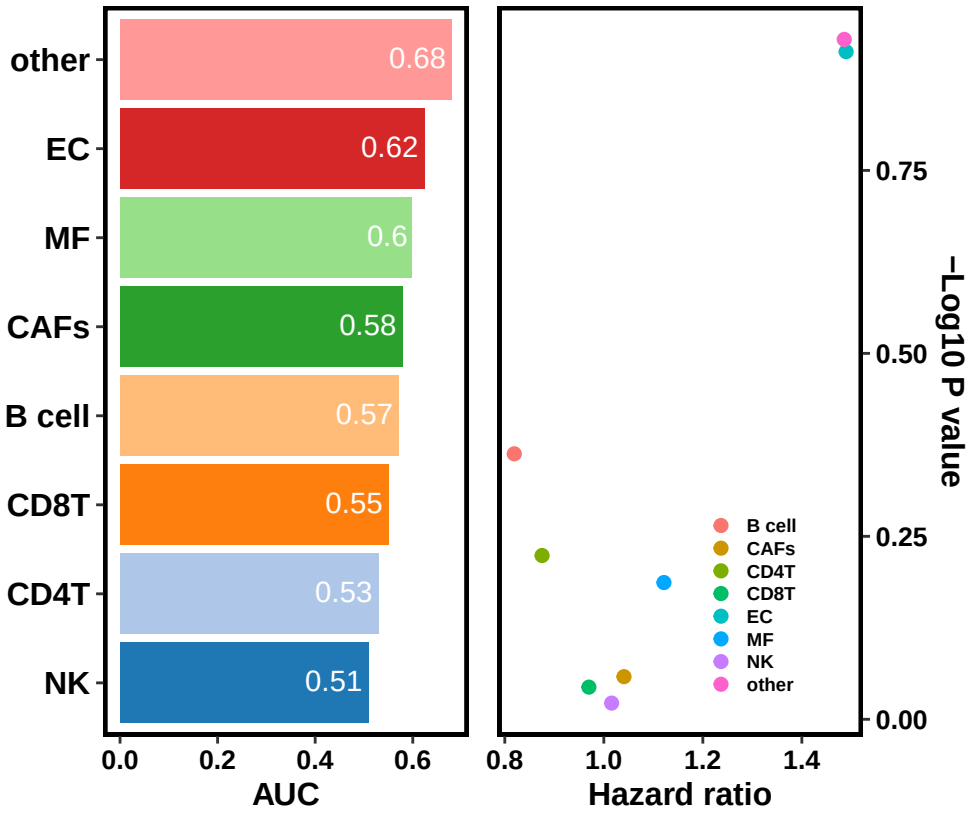
```
xCl_SE <- SummarizedExperiment(assays=SimpleList(xCl),
                               colData=colData(MEL_GSE91061))
fig.4E <- browse_biomk(cell_name_standardization(xCl_SE),lg.pos = c(0.7,0.7))
fig.4E
```




```
## IPS
Ips <- deconv_TME(MEL_GSE91061,
                  method="IPS")
Ips_SE <- SummarizedExperiment(assays=SimpleList(Ips),
                               colData=colData(MEL_GSE91061))
fig.4F <- browse_biomk(Ips_SE)
fig.4F
```



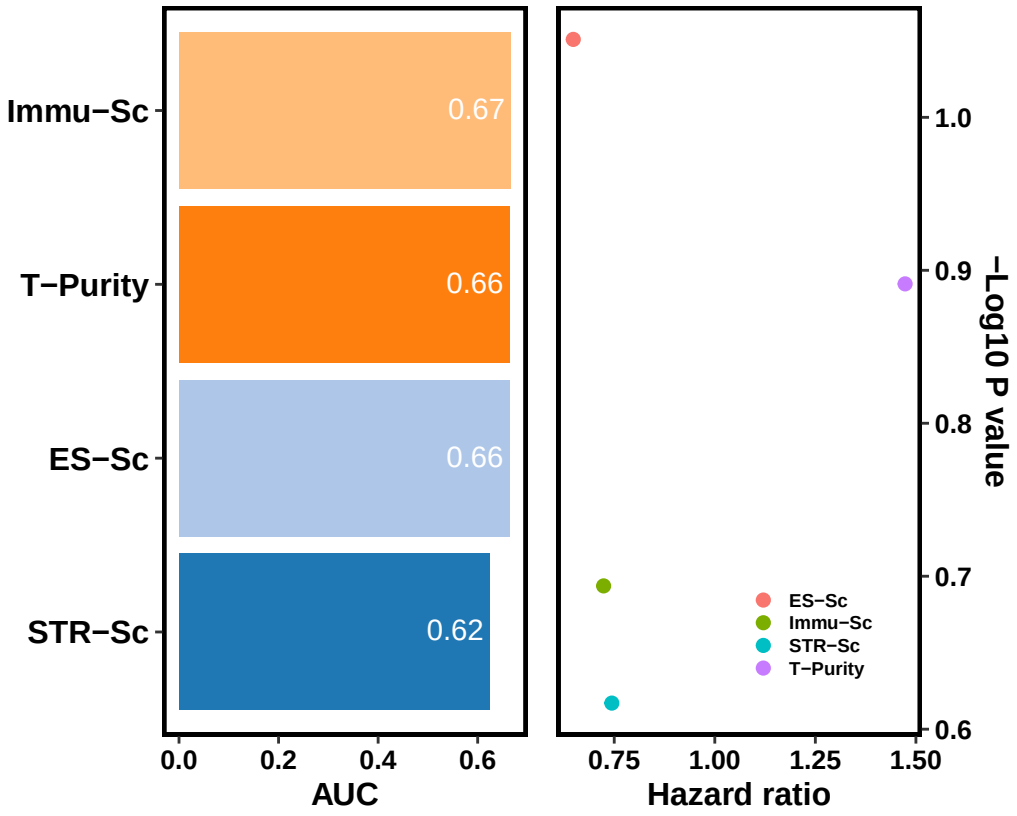

```
## EPIC
Epc <- deconv_TME(MEL_GSE91061,
                  method="epic")
Epc_SE <- SummarizedExperiment(assays=SimpleList(Epc),
                               colData=colData(MEL_GSE91061))
fig.4G <- browse_biomk(cell_name_standardization(Epc_SE),lg.pos=c(0.7,0.18))
fig.4G
```



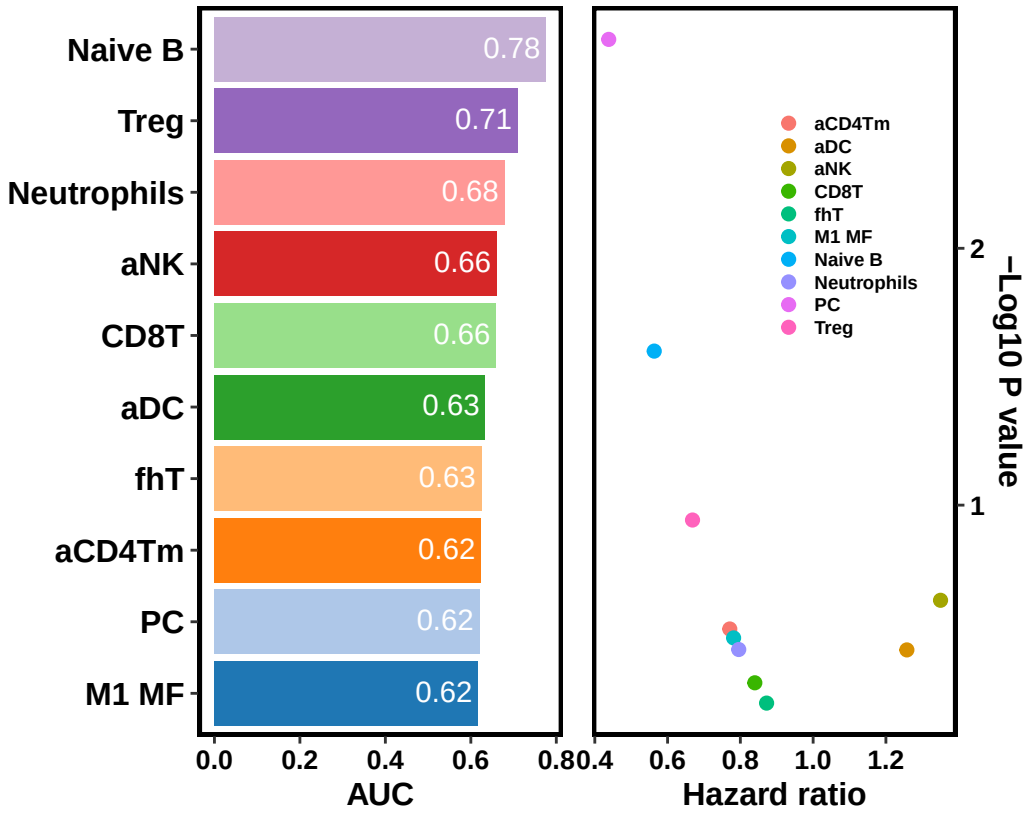

```
## ESTIMATE
Est <- deconv_TME(MEL_GSE91061,
                  method="ESTIMATE")
```

```
## [1] "Merged dataset includes 10130 genes (282 mismatched)."
## [1] "1 gene set: StromalSignature  overlap= 137"
## [1] "2 gene set: ImmuneSignature  overlap= 141"
```

```
Est_SE <- SummarizedExperiment(assays=SimpleList(Est),
                               colData=colData(MEL_GSE91061))
fig.4H <- browse_biomk(cell_name_standardization(Est_SE))
fig.4H
```



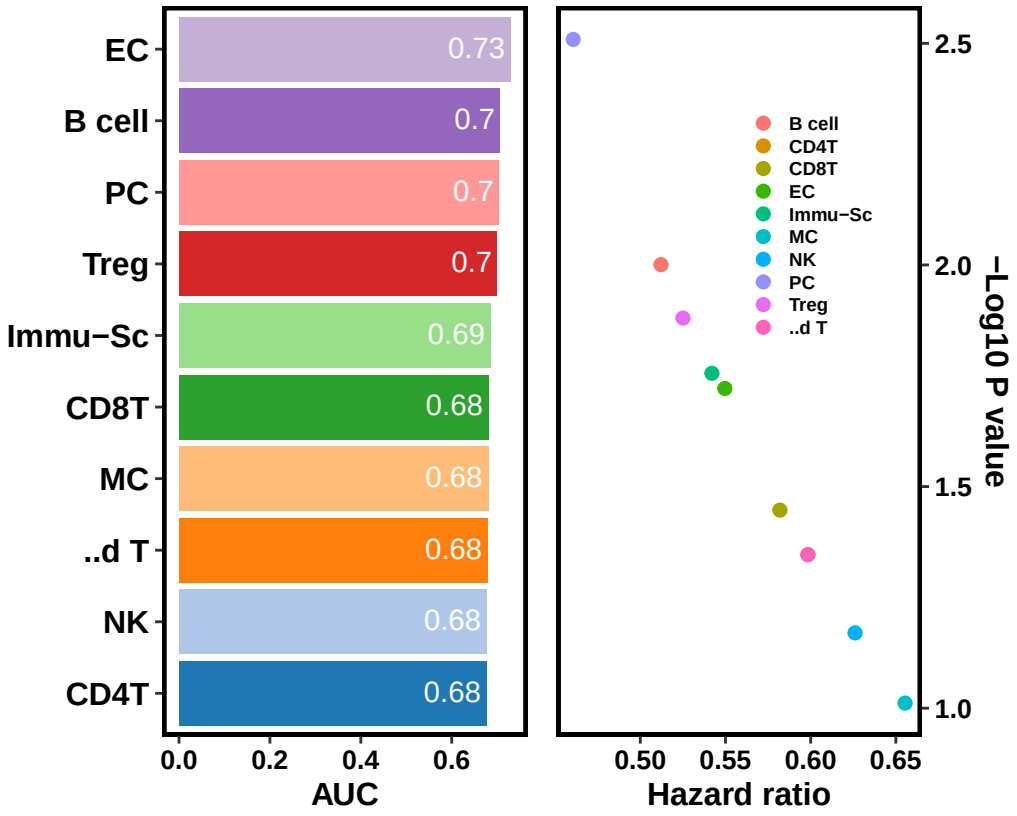

```
## ABIS
Abs <- deconv_TME(MEL_GSE91061,
                  method="ABIS")
Abs_SE <- SummarizedExperiment(assays=SimpleList(Abs),
                               colData=colData(MEL_GSE91061))
fig.4I <- browse_biomk(cell_name_standardization(Abs_SE),lg.pos=c(0.7,0.7))
fig.4I
```



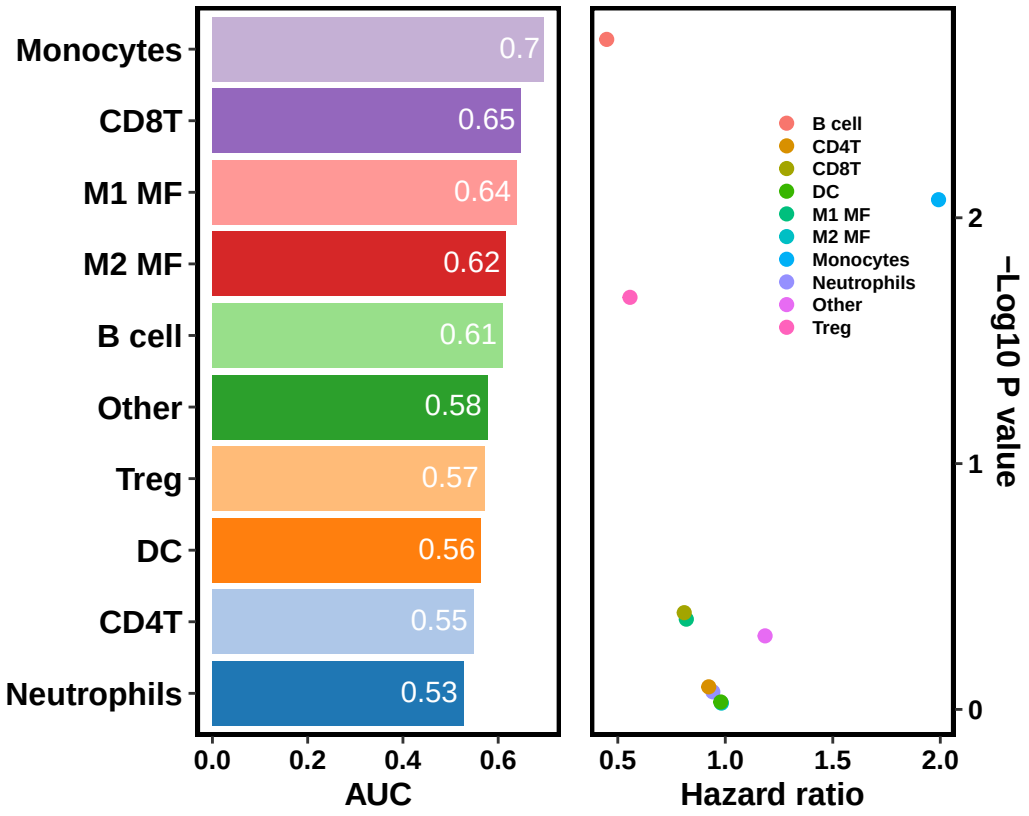

```
## ConsensusTME
CTM <- deconv_TME(MEL_GSE91061,
                  method="ConsensusTME")
```

```
## Producing ConsensusTME Estimates Using The Following Parameters:
##  Statistical Framework: "ssgsea"
##  Gene Sets For Cancer Type: "SKCM"
##  Sample Size: 109
## Estimating ssGSEA scores for 19 gene sets.
## [1] "Calculating ranks..."
## [1] "Calculating absolute values from ranks..."
##   |                                                                      |
##
## [1] "Normalizing..."
```

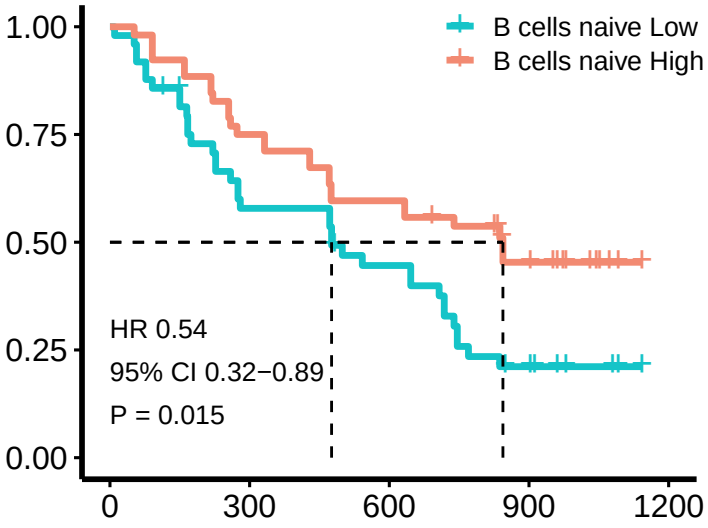
```
CTM_SE <- SummarizedExperiment(assays=SimpleList(CTM),
                               colData=colData(MEL_GSE91061))
fig.4J <- browse_biomk(cell_name_standardization(CTM_SE),lg.pos=c(0.7,0.7))
fig.4J
```



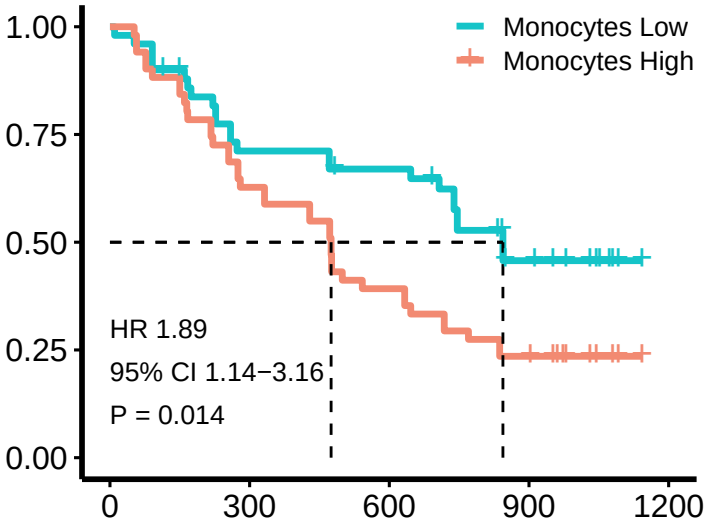

```
## quanTIseq
qTI <- deconv_TME(MEL_GSE91061,
                  method="quanTIseq")
qTI_SE <- SummarizedExperiment(assays=SimpleList(qTI),
                               colData=colData(MEL_GSE91061))
fig.4K <- browse_biomk(cell_name_standardization(qTI_SE),lg.pos=c(0.7,0.7))
fig.4K
```




```
## L
t1 <- surv_biomk(CIBER_SE,gene = "B cells naive",lg.pos=c(0.8,0.92),
                 val.pos = c(0,0.2),lg.text = "specific",PT_drop = FALSE,
                 p.round = 3)
fig.4L <- t1$plot + theme(axis.title.y = element_blank(),
                          axis.title.x = element_blank(),
                          plot.margin = unit(c(3, 1, 1, 1), "lines"),
                          legend.key.height = unit(0,"cm"),
                          legend.key.spacing.y = unit(0,"cm"),
                          legend.key.size = unit(0,"cm"))
fig.4L
```




```
## M
t2 <- surv_biomk(CIBER_SE,gene = "Monocytes",lg.pos=c(0.8,0.92),
                 val.pos = c(0,0.2),lg.text = "specific",PT_drop = FALSE,
                 p.round = 3)
fig.4M <- t2$plot + theme(axis.title.y = element_blank(),
                      axis.title.x = element_blank(),
                      plot.margin = unit(c(3, 1, 1, 1), "lines"),
                      legend.key.height = unit(0,"cm"),
                      legend.key.spacing.y = unit(0,"cm"),
                      legend.key.size = unit(0,"cm"))
fig.4M
```



4 Constructing immunotherapy response prediction model (Figure 5)

We then construct a prediction Model module for robust immunotherapy response prediction.

```
library(tigeR)
library(SummarizedExperiment)
library(magrittr)
# Data preparation
SE_origin <- cbind(MEL_GSE91061,
                   MEL_phs000452,
                   MEL_Nathanson_2017)

exp <-
  dataProcess_SE(data_standardization(SE_origin, type = c(1,2,3,4)),
                 Signature = NULL,rmBE = TRUE,response_NR=TRUE,
                 turn2HL=FALSE)
```

```
## Found 24344 genes with uniform expression within a single batch (all zeros);
these will not be adjusted for batch.
```

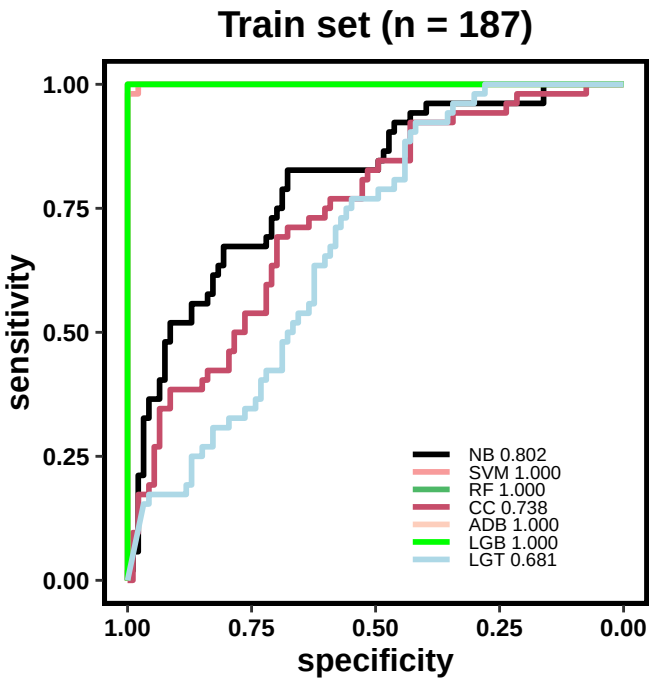
```
cf <-
  dataProcess_SE(data_standardization(SE_origin,type=c(1,2)),
                         Signature = NULL,rmBE = FALSE,response_NR=TRUE,
                         turn2HL=FALSE) %>%
  TIMER_SE(type="SKCM") %>%
  to1()
```

```
## Found 7 genes with uniform expression within a single batch (all zeros);
these will not be adjusted for batch.
```

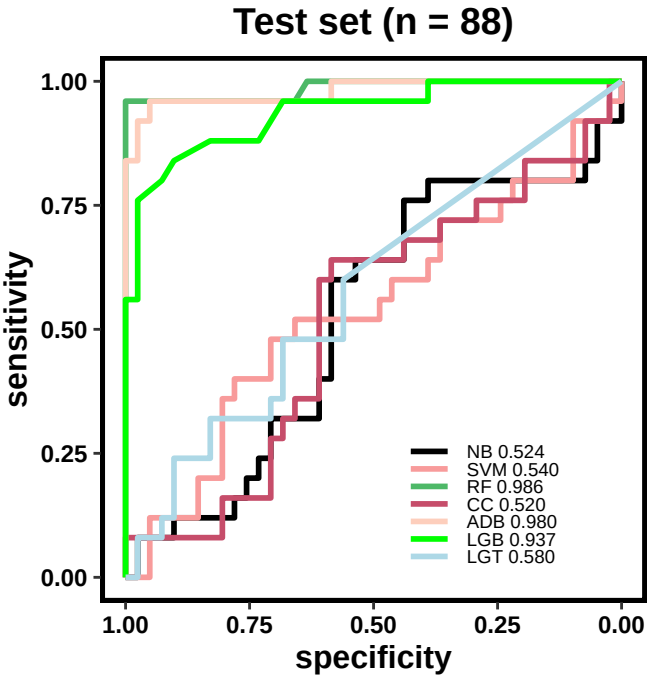
```
sg <-
  dataProcess_SE(data_standardization(SE_origin,type=c()),
                 Signature = NULL,rmBE = FALSE,response_NR=TRUE,
                 turn2HL=FALSE) %>%
  score_biomk_SE(sg_SE,PT_drop = FALSE) %>%
  to1()


final_SE <- rbind(exp,cf,sg)

set.seed(6)
idx <- sample(1:275,size=187)
SE_obj_train <- final_SE[,idx]
SE_obj_test <- final_SE[,-idx]


m <- t(
  apply(assay(exp)[,idx], 1, function(x){
    if(length(which(x==0))*5>length(x))
      return(rep(NA,length(x)))
    else
      return(x)
  }))
colnames(m) <- colnames(assay(exp)[,idx])
vars <- na.omit(
  apply(m,1,var,na.rm=TRUE))
selected_genes <- names(vars[vars>0.1])

NB_model <- build_Model(SE_obj_train,
                        Model = "NB",
                        feature_genes = c(selected_genes,
                                          rownames(cf),
                                          rownames(sg)),
                        rmBE = FALSE,
                        response_NR = TRUE,
                        laplace=0)

RF_model <- build_Model(SE_obj_train,
                        Model = "RF",
                        feature_genes = c(selected_genes,
                                          rownames(cf),
                                          rownames(sg)),
                        rmBE = FALSE,
                        response_NR = TRUE)

SVM_model <- build_Model(SE_obj_train,
                         Model = "SVM",
                         feature_genes = c(selected_genes,
                                           rownames(cf),
                                           rownames(sg)),
                         rmBE = FALSE,
                         response_NR = TRUE)
```

```
CC_model <- build_Model(SE_obj_train,
                        Model = "CC",
                        feature_genes = c(selected_genes,
                                          rownames(cf),
                                          rownames(sg)),
                        rmBE = FALSE,
                        response_NR = TRUE)
ADB_model <- build_Model(SE_obj_train,
                         Model = "ADB",
                         feature_genes = c(selected_genes,
                                           rownames(cf),
                                           rownames(sg)),
                         rmBE = FALSE,
                         response_NR = TRUE)
LGB_model <- build_Model(SE_obj_train,
                         Model = "LGB",
                         feature_genes = c(selected_genes,
                                           rownames(cf),
                                           rownames(sg)),
                         rmBE = FALSE,
                         response_NR = TRUE)
LGT_model <- build_Model(SE_obj_train,
                         Model = "LGT",
                         feature_genes = c(selected_genes,
                                           rownames(cf),
                                           rownames(sg)),
                         rmBE = FALSE,
                         response_NR = TRUE)
```

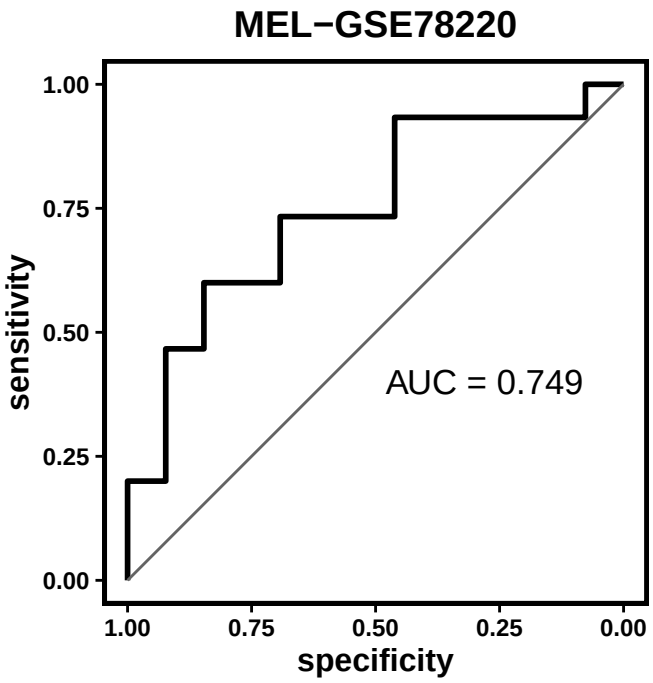
```
## B
pp1=test_Model(NB_model,SE=SE_obj_train)
pp2=test_Model(SVM_model,SE=SE_obj_train)
pp3=test_Model(RF_model,SE=SE_obj_train)
pp4=test_Model(CC_model,SE=SE_obj_train)
pp5=test_Model(ADB_model,SE=SE_obj_train)
pp6=test_Model(LGB_model,SE=SE_obj_train)
pp7=test_Model(LGT_model,SE=SE_obj_train)

fig.5B <-
  compare_roc(list(pp1[[1]],pp2[[1]],pp3[[1]],
                   pp4[[1]],pp5[[1]],pp6[[1]],pp7[[1]])) +
  ggtitle("Train set (n = 187)") +
  theme(plot.title = element_text(hjust = 0.5, size = 14, face="bold"))
fig.5B
```



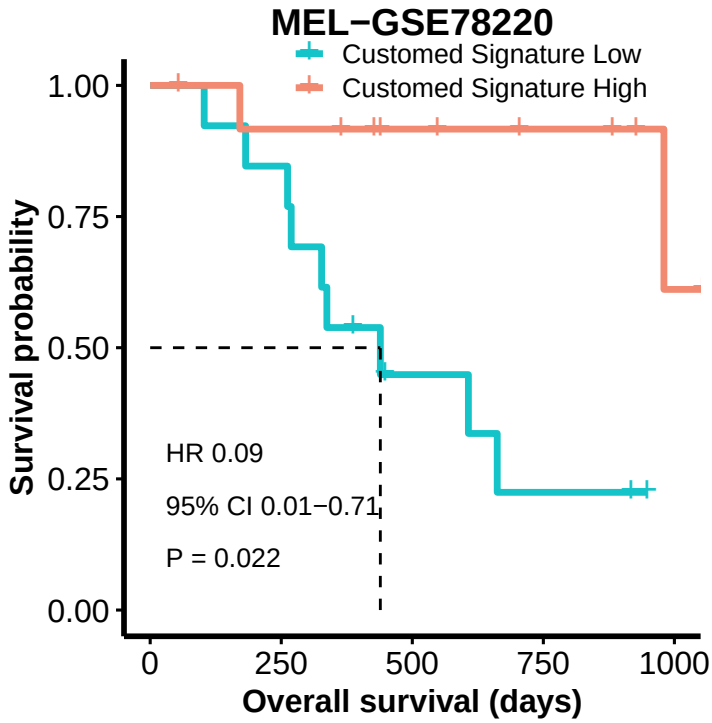

```
## C
p1=test_Model(NB_model,SE=SE_obj_test)
p2=test_Model(SVM_model,SE=SE_obj_test)
p3=test_Model(RF_model,SE=SE_obj_test)
p4=test_Model(CC_model,SE=SE_obj_test)
p5=test_Model(ADB_model,SE=SE_obj_test)
p6=test_Model(LGB_model,SE=SE_obj_test)
p7=test_Model(LGT_model,SE=SE_obj_test)

fig.5C <-
  compare_roc(list(p1[[1]],p2[[1]],p3[[1]],
                   p4[[1]],p5[[1]],p6[[1]],p7[[1]])) +
  ggtitle("Test set (n = 88)") +
  theme(plot.title = element_text(hjust = 0.5, size = 14, face="bold"))
fig.5C
```



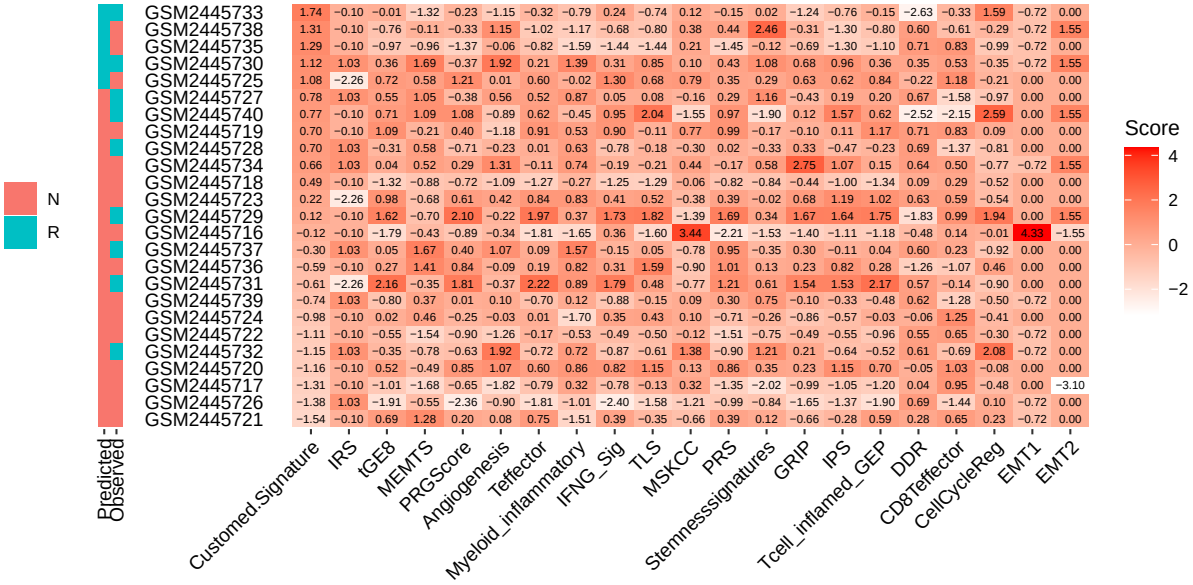

```
## D
ipt <- RF_model$importance[,1]
fig.5D <-
  roc_biomk(SE=MEL_GSE78220,Signature = ipt,
            method = "Weighted_mean",PT_drop = FALSE,
            textcol = "black",auc.pos = c(0.28,0.4))[[2]] +
  ggtitle("MEL-GSE78220")
fig.5D
```




```
## E
fig.5E <-
  surv_biomk(MEL_GSE78220,gene = ipt, method="Weighted_mean",PT_drop=TRUE,
             lg.pos=c(0.6,0.98), p.round = 3,lg.text = "specific",
             lg="Customed Signature")$plot +
  ggtitle("MEL-GSE78220") +
  theme(plot.margin = unit(c(3, 1, 1, 1), "lines"),
        legend.key.height = unit(0,"cm"),
        legend.key.spacing.y = unit(0,"cm"),
        legend.key.size = unit(0,"cm"))
fig.5E
```




```
## F
F <-
  pred_response(SE=MEL_GSE93157,Signature = ipt,
                method = "Weighted_mean",threshold = 0.8,
                PT_drop = FALSE,sort_by = "Customed.Signature",
                group_by = "Customed.Signature",show.Observed = TRUE,
                rankscore = FALSE)
F
```


N
R
Predicted
Observed
Score
4
2
0
−2
GSM2445733 1.74 −0.10 −0.01 −1.32 −0.23 −1.15 −0.32 −0.79 0.24 −0.74 0.12 −0.15 0.02 −1.24 −0.76 −0.15 −2.63 −0.33 1.59 −0.72 0.00
GSM2445738 1.31 −0.10 −0.76 −0.11 −0.33 1.15 −1.02 −1.17 −0.68 −0.80 0.38 0.44 2.46 −0.31 −1.30 −0.80 0.60 −0.61 −0.29 −0.72 1.55
GSM2445735 1.29 −0.10 −0.97 −0.96 −1.37 −0.06 −0.82 −1.59 −1.44 −1.44 0.21 −1.45 −0.12 −0.69 −1.30 −1.10 0.71 0.83 −0.99 −0.72 0.00
GSM2445730 1.12 1.03 0.36 1.69 −0.37 1.92 0.21 1.39 0.31 0.85 0.10 0.43 1.08 0.68 0.96 0.36 0.35 0.53 −0.35 −0.72 1.55
GSM2445725 1.08 −2.26 0.72 0.58 1.21 0.01 0.60 −0.02 1.30 0.68 0.79 0.35 0.29 0.63 0.62 0.84 −0.22 1.18 −0.21 0.00 0.00
GSM2445727 0.78 1.03 0.55 1.05 −0.38 0.56 0.52 0.87 0.05 0.08 −0.16 0.29 1.16 −0.43 0.19 0.20 0.67 −1.58 −0.97 0.00 0.00
GSM2445740 0.77 −0.10 0.71 1.09 1.08 −0.89 0.62 −0.45 0.95 2.04 −1.55 0.97 −1.90 0.12 1.57 0.62 −2.52 −2.15 2.59 0.00 1.55
GSM2445719 0.70 −0.10 1.09 −0.21 0.40 −1.18 0.91 0.53 0.90 −0.11 0.77 0.99 −0.17 −0.10 0.11 1.17 0.71 0.83 0.09 0.00 0.00
GSM2445728 0.70 1.03 −0.31 0.58 −0.71 −0.23 0.01 0.63 −0.78 −0.18 −0.30 0.02 −0.33 0.33 −0.47 −0.23 0.69 −1.37 −0.81 0.00 0.00
GSM2445734 0.66 1.03 0.04 0.52 0.29 1.31 −0.11 0.74 −0.19 −0.21 0.44 −0.17 0.58 2.75 1.07 0.15 0.64 0.50 −0.77 −0.72 1.55
GSM2445718 0.49 −0.10 −1.32 −0.88 −0.72 −1.09 −1.27 −0.27 −1.25 −1.29 −0.06 −0.82 −0.84 −0.44 −1.00 −1.34 0.09 0.29 −0.52 0.00 0.00
GSM2445723 0.22 −2.26 0.98 −0.68 0.61 0.42 0.84 0.83 0.41 0.52 −0.38 0.39 −0.02 0.68 1.19 1.02 0.63 0.59 −0.54 0.00 0.00
GSM2445729 0.12 −0.10 1.62 −0.70 2.10 −0.22 1.97 0.37 1.73 1.82 −1.39 1.69 0.34 1.67 1.64 1.75 −1.83 0.99 1.94 0.00 1.55
GSM2445716 −0.12 −0.10 −1.79 −0.43 −0.89 −0.34 −1.81 −1.65 0.36 −1.60 3.44 −2.21 −1.53 −1.40 −1.11 −1.18 −0.48 0.14 −0.01 4.33 −1.55
GSM2445737 −0.30 1.03 0.05 1.67 0.40 1.07 0.09 1.57 −0.15 0.05 −0.78 0.95 −0.35 0.30 −0.11 0.04 0.60 0.23 −0.92 0.00 0.00
GSM2445736 −0.59 −0.10 0.27 1.41 0.84 −0.09 0.19 0.82 0.31 1.59 −0.90 1.01 0.13 0.23 0.82 0.28 −1.26 −1.07 0.46 0.00 0.00
GSM2445731 −0.61 −2.26 2.16 −0.35 1.81 −0.37 2.22 0.89 1.79 0.48 −0.77 1.21 0.61 1.54 1.53 2.17 0.57 −0.14 −0.90 0.00 0.00
GSM2445739 −0.74 1.03 −0.80 0.37 0.01 0.10 −0.70 0.12 −0.88 −0.15 0.09 0.30 0.75 −0.10 −0.33 −0.48 0.62 −1.28 −0.50 −0.72 0.00
GSM2445724 −0.98 −0.10 0.02 0.46 −0.25 −0.03 0.01 −1.70 0.35 0.43 0.10 −0.71 −0.26 −0.86 −0.57 −0.03 −0.06 1.25 −0.41 0.00 0.00
GSM2445722 −1.11 −0.10 −0.55 −1.54 −0.90 −1.26 −0.17 −0.53 −0.49 −0.50 −0.12 −1.51 −0.75 −0.49 −0.55 −0.96 0.55 0.65 −0.30 −0.72 0.00
GSM2445732 −1.15 1.03 −0.35 −0.78 −0.63 1.92 −0.72 0.72 −0.87 −0.61 1.38 −0.90 1.21 0.21 −0.64 −0.52 0.61 −0.69 2.08 −0.72 0.00
GSM2445720 −1.16 −0.10 0.52 −0.49 0.85 1.07 0.60 0.86 0.82 1.15 0.13 0.86 0.35 0.23 1.15 0.70 −0.05 1.03 −0.08 0.00 0.00
GSM2445717 −1.31 −0.10 −1.01 −1.68 −0.65 −1.82 −0.79 0.32 −0.78 −0.13 0.32 −1.35 −2.02 −0.99 −1.05 −1.20 0.04 0.95 −0.48 0.00 −3.10
GSM2445726 −1.38 1.03 −1.91 −0.55 −2.36 −0.90 −1.81 −1.01 −2.40 −1.58 −1.21 −0.99 −0.84 −1.65 −1.37 −1.90 0.69 −1.44 0.10 −0.72 0.00
GSM2445721 −1.54 −0.10 0.69 1.28 0.20 0.08 0.75 −1.51 0.39 −0.35 −0.66 0.39 0.12 −0.66 −0.28 0.59 0.28 0.65 0.23 −0.72 0.00
Customed.Signature
IRS
tGE8
MEMTS
PRGScore
Angiogenesis
Teffector
Myeloid_inflammatory
IFNG_Sig
TLS
MSKCC
PRS
Stemnesssignatures
GRIP
IPS
Tcell_inflamed_GEP
DDR
CD8Teffector
CellCycleReg
EMT1
EMT2