

Cancer programs - Kinker et al

```
library(Seurat)
library(plyr)
library(pheatmap)
library(RColorBrewer)

rhps <- read.delim('../GSKinker_RHPs.txt', check.names = F)
head(rhps)
```

```
## Cell Cycle - G1/S Cell Cycle - G2/M Skin Pigmentation EMT I EMT II
## 1 HIST1H4C AURKA PHACTR1 DKK1 MYL9
## 2 CLSPN CENPF DCT PMEPA1 SERPINE1
## 3 ATAD2 PLK1 MITF C12orf75 THBS1
## 4 E2F1 TOP2A CHCHD6 CYR61 FN1
## 5 HELLS UBE2C MBP IL8 IL32
## 6 RRM2 ASPM GDF15 SORBS2 LAMC2
## IFN Response EMT III p53-Dependent Senescence Epithelial Senescence
## 1 ISG20 LAMA3 CDKN1A SLPI
## 2 IFIT3 LAMB3 NEAT1 LCN2
## 3 ISG15 LAMC2 POLD4 ELF3
## 4 OASL CDKN1A MXD4 S100A9
## 5 IFIT1 FAM83A MMP24-AS1 S100P
## 6 IFIT2 ITGA2 PNRC1 SAA1
## Stress Response Protein Maturation Proteasomal Degradation
## 1 DDIT3 HSPA5 PSMA3
## 2 SNHG12 RPN2 PSMC4
## 3 SLC3A2 SLC3A2 PRDX1
## 4 PPP1R15A PDIA3 PSMC2
## 5 GADD45B LGALS3BP EIF4A3
## 6 GADD45A MCM7 MDH1
```

```
subdataset <- readRDS('../tmp/crc_smc.malignantcells.Rds')
head(subdataset@meta.data); nrow(subdataset@meta.data) # 17334
```

```
## nCount_RNA nFeature_RNA Library
## AAACCTGCATACGCCG-1-PM-PS-0001-T-A1 35998 4823 PM-PS-0001-T-A1
## AAACCTGGTCGCATAT-1-PM-PS-0001-T-A1 31383 5252 PM-PS-0001-T-A1
## AAACCTGTCCCTTGCA-1-PM-PS-0001-T-A1 7302 1713 PM-PS-0001-T-A1
## AAACGGGAGGGAAACA-1-PM-PS-0001-T-A1 3759 1233 PM-PS-0001-T-A1
## AAACGGGTATAGGTA-1-PM-PS-0001-T-A1 23097 3874 PM-PS-0001-T-A1
## AAAGATGAGCCGAAT-1-PM-PS-0001-T-A1 14860 3282 PM-PS-0001-T-A1
## Patient Sample Cell_subtype RNA_snn_res.0.3
## AAACCTGCATACGCCG-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 2
## AAACCTGGTCGCATAT-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 0
## AAACCTGTCCCTTGCA-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 2
## AAACGGGAGGGAAACA-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 1
```

```
## AAACGGGGTATAGGTA-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 1
## AAAGATGAGGCCGAAT-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 2
```

```
## [1] 17334
```

```
label <- subdataset@meta.data[, c(3,4,7)]
colnames(label)[3] <- "res_0.3"
label <- subset(label, !res_0.3 %in% c('7'))
label <- droplevels(label)
head(label, n=3); nrow(label) # 17276
```

```
##                                     Library Patient res_0.3
## AAACCTGCATACGCCG-1-PM-PS-0001-T-A1 PM-PS-0001-T-A1 SMC01      2
## AAACCTGGTCGCATAT-1-PM-PS-0001-T-A1 PM-PS-0001-T-A1 SMC01      0
## AAACCTGTCCCTTGCA-1-PM-PS-0001-T-A1 PM-PS-0001-T-A1 SMC01      2
```

```
## [1] 17276
```

```
rhps_scores <- data.frame(matrix(ncol = length(levels(label$res_0.3)), nrow = ncol(rhps)))
colnames(rhps_scores) <- levels(label$res_0.3)
rownames(rhps_scores) <- colnames(rhps)
rhps_scores
```

```
##           0  1  2  3  4  5  6
## Cell Cycle - G1/S NA NA NA NA NA NA
## Cell Cycle - G2/M NA NA NA NA NA NA
## Skin Pigmentation NA NA NA NA NA NA
## EMT I NA NA NA NA NA NA NA
## EMT II NA NA NA NA NA NA NA
## IFN Response NA NA NA NA NA NA NA
## EMT III NA NA NA NA NA NA NA
## p53-Dependent Senescence NA NA NA NA NA NA NA
## Epithelial Senescence NA NA NA NA NA NA NA
## Stress Response NA NA NA NA NA NA NA
## Protein Maturation NA NA NA NA NA NA NA
## Proteasomal Degradation NA NA NA NA NA NA NA
```

```
for (clst in colnames(rhps_scores)) {
  tmpObj <- subset(subdataset, idents = clst)
  tmpExpr <- as.matrix(GetAssayData(tmpObj, slot = 'data'))

  tmpExprMean <- data.frame(row.names = rownames(tmpExpr),
                            Symbol = unlist(lapply(rownames(tmpExpr), function (x) unlist(strsplit(as.character(x), '_')))),
                            cluster = rowMeans(tmpExpr))

  head(tmpExprMean)

  for (rhp in colnames(rhps)) {
    rhp_genes <- as.character(rhps[, rhp][rhps[, rhp] != ""])
    tmpExprMean_rhp_genes <- subset(tmpExprMean, Symbol %in% rhp_genes)
    head(tmpExprMean_rhp_genes)
    rhps_scores[rhp, clst] <- mean(tmpExprMean_rhp_genes$cluster)
  }
}
```

```
}
}
```

```
head(rhp_scores, n=3)
```

```
##              0              1              2              3              4
## Cell Cycle - G1/S 0.08063864 0.05219887 0.2878732 0.05997496 0.06871475
## Cell Cycle - G2/M 0.07644820 0.06443931 0.3475173 0.06596869 0.08088368
## Skin Pigmentation 0.22521813 0.26241780 0.2219094 0.12645031 0.25496137
##              5              6
## Cell Cycle - G1/S 0.05527019 0.1178972
## Cell Cycle - G2/M 0.06457555 0.1415242
## Skin Pigmentation 0.10796311 0.2306110
```

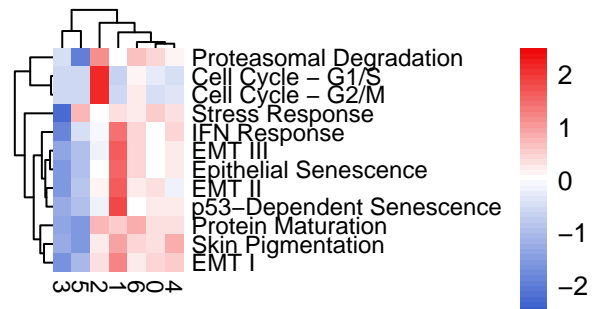
```
min(rhp_scores)
```

```
## [1] 0.05219887
```

```
max(rhp_scores)
```

```
## [1] 1.036172
```

```
pheatmap(rhp_scores, scale = 'row', #filename = '../res_various/res_0.3/gskinker_rhps.pdf',
          treeheight_row = 10, treeheight_col = 10,
          cellwidth = 7, cellheight = 7, fontsize_row = 9, fontsize_col = 9, border_color = NA,
          clustering_distance_rows = 'euclidean', clustering_distance_cols = 'euclidean', clustering_method = 'ward.D2',
          breaks = c(-25:25)/10,
          color = colorRampPalette(c("#3a5fcd", 'white', "#ee0000"))(n = 51))
```



```
#dev.off()
```